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Livre des Résumés
Alternative quantifications of landscape complementarity to model gene flow in banded longhorn beetles

Typocerus v. velutinus (Olivier)

Rapid progression of anthropogenic activities has altered the structure and function of natural landscapes. Species that rely on multiple habitats (i.e. complementary habitats) to complete their life may be especially at risk. A previous study integrated habitat complementarity into a habitat suitability “surface” for flower longhorn beetles (Cerambycidae: Lepturinae), and quantified landscape connectivity using a novel approach of surface metrology metrics. This surface model has been validated with pairwise genetic distances for the banded longhorn beetle (Typocerus v. velutinus) in Indiana, USA. However, this approach has not been compared to other commonly used connectivity models in a landscape genetics context. Here, we compare the gradient surface model to three alternatives, including patch mosaic model, least cost path model, and circuit theory model. Results from Maximum Likelihood Population Effects modelling suggested that the gradient surface model may better capture the landscape heterogeneity and therefore better explain gene flow in species that naturally persist along environmental gradients. Our findings may inform future studies that seek to model connectivity in complex landscapes.

Investigating the impacts of chronic exposure to environmental stressors on wild bee populations in Pennsylvania over 120 years

Despite the economic and ecological importance of wild bees for agricultural processes and wild plant communities around the world, the current state of these pollinator populations is poorly understood. Previous research suggests bee populations are declining as a result of the impacts of many environmental stressors, including the impacts of anthropogenic land-use change and climate change. Although researchers have extensively studied the acute effects of these stressors, very little evidence exists concerning their chronic effects on pollinator populations. Our research addresses these questions by analyzing historical datasets of bee population dynamics in relation to changes in key environmental stressors. We have compiled an extensive database of over 20,000 wild bee records from Pennsylvania collected over the last 120 years. This provides a unique opportunity to understand the large-scale changes in bee populations in this US state over a considerable time period. Historical datasets, tracking changes in climate, the patterns of pesticide use, and land use change, can then be compared spatio-temporally to this 120-year dataset. Results from our analyses will provide a greater understanding of the chronic impacts of these stressors and inform future conservation strategies to improve the health of wild bees.

The evolution of male harm and local adaptation of adult male vs. female fitness in different mating environments

Mating/fertilization success and fecundity are influenced by sexual interactions among individuals, the nature and frequency of which can vary among different environments. We allowed 63 populations of Drosophila melanogaster to independently evolve in one of three mating environments that alter sexual interactions: one involved enforced monogamy while the other two permitted polygamy in either structurally simple standard fly vials or in larger “cages” with added complexity. Adult male and female reproductive fitness were measured after 16 and 28 generations respectively via full
We observed relatively little evolutionary divergence among treatments with respect to female fitness. In contrast, there was strong divergence in male fitness. We observed strong reciprocal local adaptation between the two "classic" treatments (monogamy and "simple" polygamy). However, males from the "complex" polygamy performed well in all three mating environments. Follow-up studies show there is strong divergence in male harm among these treatments.

Ahsaei, Seyed Mohammad, University of Tehran; Soraya Rodriguez-Rojo, Department of Chemical Engineering and Environmental Technology, University of Valladolid; María José Cocero, Department of Chemical Engineering and Environmental Technology, University of Valladolid; Khalil Talebi, Department of Plant Protection, University College of Agriculture & Natural Resources, University of Tehran

Insecticidal activity of spray dried microencapsulated essential oil of *Rosmarinus officinalis* against *Tribolium confusum*

*Rosmarinus officinalis* (Lamiaceae) essential oil contain components with insecticidal properties that can be used as pesticide for stored product pests. In the present study, it was encapsulated in octenyl succinic anhydride (OSA) - starch in order to test its insecticidal activity against *Tribolium confusum*. First an oil-in-water emulsion was prepared and afterwards, it was dried by spray-drying technique. The emulsions were characterized regarding particle size (461-854 nm), stability and encapsulated oil efficiency (67.8-87.6%). Also, solid formulations were characterized by particle size (8.29-11.35 µm), encapsulation efficiency (5.5-52.6%). Fumigant toxicity results revealed that microencapsulated oil was more effective than non-formulated oil against beetles in long time. The LC50 values were 122.8 and 178.4 µl/L for pure and microcapsules of rosemary with adults, respectively. Similarly, it was demonstrated that microencapsulation of the essential oil increases its persistence: non-formulated oil has not insecticidal activity after 15 days of the storage period, whereas at the same period, the mortality rate against *T. confusum* of rosemary microencapsulated oil was 46.7%.

Aidemouni, Milia

Optimal alpha – Is the traditional statistical threshold (? = 0.05) for Null Hypothesis Significance Testing a problem?

Null Hypothesis Significance Testing (NHST) remains a statistical method of choice used to provide evidence for or against an effect. The common threshold used among researchers to identify significant results is ? = 0.05 following Neyman-Pearson’s and Fisher’s recommendations. Many of the drawbacks of null hypothesis significance testing revolve around the arbitrary choice of ? = 0.05, the sensitivity to sample size, and the poor understanding of statistical power (Stephens et al., 2007). A better alternative has been described in Mudge, et al., (2012), which is the use of optimal alpha – a threshold that is study-specific and that minimizes the probability/cost of making either a Type I or II error. Thresholds based on optimal alpha are theoretically superior to the 0.05 threshold because they minimize errors but if both thresholds would usually result in the same conclusion then the superiority of optimal alpha has little practical importance. 100 ecology research articles were sampled and conclusions that were originally published using the 0.05 threshold were compared to the conclusions that would have been reached using optimal ?. Results show that in 22% of the tests conclusions were inconsistent. This suggests that using the traditional threshold is often leading to wrong conclusions in ecology and ecologists using NHST should apply optimal ? rather than the 0.05 threshold.

Airst, Jason, Nova Scotia Lands and Forestry

Moose habitat use in Cape Breton

The moose population of the Greater Highland Ecosystem in Cape Breton has declined over the last 5 years. The goal of our study was to determine the habitat types moose use and see if the availability of these habitats has declined over time. Areas with more 20 to 60-year-old softwood forest had higher numbers of moose. This was true for areas that were traditionally softwood forest, but have experienced abnormal forest succession, due to high moose herbivory (moose meadows). The opposite was true for areas with more regenerative forest (< 20-years-old). Also, as road density increased, moose abundance decreased. Since 20 to 60-year-old softwood forest was widely available across the region, a
lack of optimal habitat was not the cause of the moose decline. Instead, human activity largely explains where moose were found on the landscape. So, to increase the moose population, land use practices must change.

Allen, Emily, Saint Mary's University; Laura Weir, Saint Mary's University

Operational sex ratio influences sexually-selected male behaviour and morphology

The operational sex ratio (OSR, defined as the number of males to females with the potential to mate at any given time) in a population is often used a metric to predict the intensity of competition for mates. In Japanese medaka (Oryzias latipes), males actively compete for females using displays of aggression and courtship. Previous research using choice experiments has indicated that females prefer males who court more, as well as males with larger body and anal fin size. However, mating advantage associated with specific traits may vary with OSR and potentially result in behavioural and morphological changes over generations. We examined the interactive effects of OSR and generation on mating-related behaviour and morphology by housing fish in four different OSR treatments ranging from female-biased to highly male-biased. Courtship behaviour decreased and aggression increased as OSR became more male-biased, and aggression was best explained by male body size. Second-generation males exhibited higher overall levels of aggression and courtship than first-generation males. Interestingly, patterns in courtship behaviour with respect to OSR were maintained by males introduced to novel OSR treatments. This suggests that OSR has an influence on mating-related traits both intra- and inter-generationally.

Allen, Samantha, University of Guelph – OVC; Claire Jardine; Nikki Colucci; Tara Furukawa-Stoffer; Aruna Ambagala; Kathleen Hooper-McGrevy; Mark Ruder; Nicole Nemeth

Risk assessment for the incursion and establishment of orbiviruses in Southern Ontario, Canada

Epizootic hemorrhagic disease viruses (EHDV) and bluetongue viruses (BTV) are midge-borne orbiviruses presenting an imminent threat to Ontario's wildlife and livestock populations. These viruses are spreading northward in North America, which may be facilitated by changing climatic conditions. Recent detection of BTV antibody-positive cattle and Culicoides sonorensis in the province suggest that Ontario is at risk for the establishment of EHDV and BTV. Ontario ruminants are immunologically naïve to these viruses; thus, their introduction may negatively impact wild cervid and livestock populations through morbidity and mortality. We sought to characterize Culicoides spp. biology and assess for recent or ongoing transmission of EHDV and BTV in wild cervids and livestock in Ontario for two spring-summer field seasons (2017-2018). During two field seasons (2017-18), CDC-type LED light traps were placed on farms and in natural areas across southwestern Ontario, and Culicoides spp. midges were taxonomically and molecularly identified. Blood from wild cervids and livestock were assessed for antibodies to EHDV and BTV by ELISA and subsequent virus neutralization assay for serotyping. During the 2017 field season, we collected 19,126 Culicoides spp., including individuals of at least eight species: C. sonorensis, C. variipennis, C. biguttatus, C. crepuscularis, C. stellifer, C. travisi, C. haematopotus and C. venustus, with the most commonly identified species being in the subgenus Avaritia. Thus far, in 2018, we have collected 7,604 Culicoides spp., with C. biguttatus being the most commonly identified. Regional, temporal, and climatic patterns in vector proportions and distribution and seroprevalence data will be statistically analyzed. These results will help improve current policies and practices for safeguarding Ontario wild cervid and livestock populations.

Almdal, Crystal, Department of Entomology, University of Manitoba; Alejandro C. Costamagna, Department of Entomology, University of Manitoba

Effect of Landscape Complexity on Aphis glycines Matsumura (Hemiptera: Aphididae) and Their Natural Enemies

The soybean aphid Aphis glycines Matsumura (Hemiptera: Aphididae) is an invasive species and a major crop pest of soybean in North America. Therefore, it is imperative we understand the factors that regulate Aphis glycines. Previous work has demonstrated Aphis glycines suppression is higher when there is a higher proportion of cereals and a lower proportion of canola in the landscape during low aphid years in Manitoba. The aim of our research is to determine how
landscape complexity affects soybean aphid control by its natural enemies. A predator exclusion experiment was set up in 23 soybean fields for a period of two weeks in July-August 2017(12) and 2018(11), to determine the level of Aphis glycines suppression at varying landscape complexities. Weekly aphid counts were conducted on experimental plants and field plants. Generalist predators were collected within soybean and the adjacent habitat by sweep net sampling. Bi-directional malaise traps were used to collect generalist predators immigrating to soybean. All habitats within a 2km radius from the study soybean field were mapped. We predict landscapes with higher diversity will promote greater pest suppression and higher natural enemy abundances. Results to be presented.

Anderson, Spencer, Trent University; Steeve D. Côté; Julien H. Richard; Aaron B. A. Shafer

Genetic Basis of Extreme Phenotypes in White-Tailed Deer

Antler size of white-tailed deer (*Odocoileus virginianus*) is a trait that is controlled by a variety of factors including nutrition, age, and host genetics. As white-tailed deer are an intensively managed and hunted species, understanding the underlying genetic factors associated with variation in phenotypes can provide information for managers to target in the optimization of traits such as antler size. We used genomic techniques that utilized pooled whole genome re-sequencing of individuals representing extreme antler phenotypes to identify quantitative trait loci of large effect across the entire genome. Samples were selected from a database containing phenotypic data for 3974 male white-tailed deer from Anticosti Island, Quebec, with DNA from the top individuals for large and small antlers being combined in equal quantities in two representative pools. Sequencing for each pool was performed on the Illumina HiSeq-X platform for overall coverage of 50x per pool. As expected the genome-wide analysis revealed a largely homogenous genome, but also detected significant and highly diverged regions between large and small antler pools; these regions represent putative antler genes. We have identified and will discuss the underlying genes of interest that are related to extreme antler phenotypes.

Anderson, Madelaine, University of Western Ontario; Brian Branfireun; Zoë Lindo

Mercury’s Journey from Litter to Soils in the Boreal Forest

Litterfall is a major input of carbon and mercury (Hg) into forest soils but the controls governing the release of Hg from litter to soil are poorly understood. Carbon inputs differ in amount and quality between coniferous and deciduous litter and may control the fate of Hg. We used a mesocosm experiment with coniferous or deciduous litter from the southern boreal forest to examine the transfer of Hg from litter to soil over three months. Soil porewater was sampled biweekly alternating for carbon quality analysis using excitation and emission matrices and dissolved organic carbon (DOC) content, and total Hg. Carbon to nitrogen ratios of both litters decreased over time, while the excitation and emission indices showed a shift in carbon quality in porewater corresponding with decomposition and leaching of carbon. Mercury in porewater from deciduous litter peaked after 6 weeks, coinciding with a peak in DOC and a peak in the excitation and emission Humification index. Taken together this suggests that Hg released is a function of decomposition. Understanding the controls of decomposition on Hg storage and release in forest soils will contribute to better predictions of recovery timing in contaminated watersheds and how climate change will impact mercury cycling.

Anderson, Jennifer, University of New Brunswick; Stephen B. Heard, University of New Brunswick; Deepa Pureswaran, Canadian Forest Service, Laurentian Forestry Centre

Promiscuity with a native congener may be hindering the North American spread of the European spruce borer, *Tetropium fuscum*

*Tetropium fuscum* is a European longhorn beetle, native to Western Europe and Northern Eurasia, that invaded Halifax, Nova Scotia, Canada circa 1990. In the 25-30 years since its introduction into North America, *T. fuscum* has spread less than 100 km from its point of introduction. Contrasted with the invasive Emerald Ash Borer, which also invaded North America from Asia around 1990, the North American range expansion of *T. fuscum* is less than 10% that of Emerald Ash Borer. We propose that the slow North American spread of *T. fuscum* is at least partially due to interactions with the native congener Tetropium cinnamopterum. *T. fuscum* and *T. cinnamopterum* are morphologically and ecologically very
similar, sharing closely timed emergence in the spring, as well as similar host plant choices and mating behaviours. One of the most intriguing similarities is that the male-produced mating and aggregation pheromone blends in both species share the molecule fuscumol as the attractive component. We ask whether mate choice errors and mating disruption could be mechanisms contributing to the slow North American spread of T. fuscum. No-choice mating data show T. fuscum males mate with T. cinnamopterum females as readily as with T. fuscum females. Choice mating experiments show that T. fuscum males attempt to mate with heterospecific females even in the presence of a conspecific female, suggesting that mating errors may take place in the field. The presence of a second female has no significant effect on duration of copulation in mating pairs, regardless of whether the female engaged in copula is heterospecific or conspecific to the male. Our results support mate choice error as a possible contributing factor to the slow North American spread of T. fuscum.

Anderson, Gail, Simon Fraser University

The Use of Forensic Entomology to Right a Miscarriage of Justice

The value of insects in homicide investigations is now well accepted and well known. Estimating the minimum age of the oldest insect stage on the remains provides the minimum tenure of insects on the body and hence infers the minimum elapsed time since death. It is difficult, however, to use forensic entomology in cold cases as insect evidence is usually no longer available or was never collected in the first place. The case presented here is extremely unusual as no insects were present and it was the lack of insects that allowed an estimation of elapsed time since death rather than their presence.

Angel, Phil, UBC; Brian Leander; María Herranz; Varsha Mathur

Haplozoan parasites the evolution of a compartmentalized syncytium

Haplozoans are intestinal parasites of a specific group of maldanid marine annelids. Haplozoans are dinoflagellates, yet distinctly abnormal. Traditional dinoflagellates are unicellular with two flagella arising from their ventral side. Instead, Haplozoans have a mysterious multicellular trophont stage. In addition, standard 18S molecular data has failed to resolve their placement among the dinoflagellate lineages. They are one of many parasitic dinoflagellate lineages that remains placed within the Blastodiniales, a polyphyletic order of "convenience" that does not suit modern dinoflagellate phylogenies. We used SEM, LM, and confocal microscopy to characterize haplozoon axiothellae morphology and clarify their enigmatic multi-cellular appearance. We also prepared a transcriptome from h. axiothellae to reveal it's true placement within the Dinoflagellata. Results are currently being interpreted.

Arce, Bernal, University of Guelph

Plant structures as a driver of arthropod communities

Plant structure can drive the space and shape of a habitat, which in turn can impact arthropod communities. Structure may be a strong driver for predators if it limits their ability to catch prey which would affect their assemblage and recruitment into new habitats. This study manipulated the plant identity (chosen as analogs of increasing heterogeneity) and density (directly correlated to space availability) in 48 plots to evaluate their effects on arthropods in a realistic setting. The experiment had a factorial design with plots composed of oats, soybeans, a mixture of these two, and a mixture of oats, soybeans, flax, and sunflowers planted at two levels of density. Ten baseline sites were sampled in the surrounding area: five in an open field and five in a neighbouring tree line. The arthropods were sampled and identified to family, and their richness, abundance, and beta diversity were evaluated. Plant samples were harvested at the experiments conclusion to test whether plant biomass and tissue quality were important co-variates with structure. Plots with spare soybeans had higher predator and non-predator abundance (p=0.003 and p=0.048 respectively), and predator and non-predator richness (p=0.003 and p=0.048 respectively), than dense soybeans. Predator richness was significantly higher in the tree line sites than in plots containing oats (p=0.006) or soybeans (p=0.046), while non-predator richness did not significantly change. Beta diversity, as measured by multiple site Bray-Curtis, was symmetrical among predators and non-predators across all
treatments. Plant biomass and tissue chemistry trends did not translate into responses in the arthropod community. These results suggest that predator and non-predator arthropods do not have differing sensitivities to plant structures.

Arjomandi, Elham, PhD student at Carleton; Jayne E. Yack

Acoustic Communication in Bark Beetles: What's left to learn?

Bark beetles (Coleoptera: Curculionidae: Scolytinae) are common pests of several tree species throughout the world. Management of these pests requires knowledge of their life cycle, communication systems and sensory ecology. While many species are reported to communicate acoustically, there are major gaps in our knowledge of this sensory modality. We highlight some of these major gaps using recent examples from our laboratory. I. Mechanisms. We review the gaps in our knowledge on how sounds are made, and report on one of the lesser-known mechanisms- Gula-Prosternal stridulation-using Scolytus multistriatus Marsham as an example. II. Who makes sounds? We review what we know to date on the taxonomic distribution of sound production, and possible misunderstandings about sexual dimorphism in sound communication. III. Function of signals. Bark beetles are reported to signal in a variety of contexts, including mating, stress, territorial and rivalry settings. However, there is little experimental evidence testing hypotheses on how and why signals vary between contexts and between individuals. We will use examples from North American genera including Ips, Dendroctonus and Scolytus to discuss signal variability and function. Sensory mechanisms for sound or vibration reception, and possible roles for acoustic communication in larvae are also discussed.

Aubin, Jaclyn, Memorial University of Newfoundland; Eric Vander Wal, Memorial University of Newfoundland; Robert Michaud, Groupe de Recherche et d'Éducation sur les Mammifères Marins

Why should I care? Patterns and prospective drivers of allocare in St. Lawrence Estuary belugas

Allocare, investment in offspring from non-parents, poses an evolutionary enigma. While the fitness trade-offs driving parental care are universal, the evolutionary mechanisms driving allocare are diverse. Across taxa, allocare may be driven by the need for subadults to gain parenting experience (learning-to-parent), by an indiscriminate attraction towards newborns (natal attraction), by kin selection, or by reciprocation. However, given the disconnect between allomaternal and recipient offspring fitness, offspring only consistently benefit from allocare driven by kin selection and reciprocation. Among belugas (Delphinapterus leucas), allocare has been reported in wild and captive populations, but its underlying mechanisms remain unexplored. We quantified allomaternal associations in St. Lawrence Estuary (SLE) belugas to determine which mechanisms are consistent with patterns of allocare in this population. We observed significantly more adult than subadult allomothers (p < 0.001) and found that allomaternal investment remained constant as offspring aged, inconsistent with learning-to-parent and natal attraction, but consistent with kin selection and reciprocation. To determine possible benefits to offspring, we tested the contexts in which allocare occurred. We found that water temperature predicted both calf allocare occurrence and juvenile allocare duration, suggesting that allocare in SLE belugas provides energetic benefits to both vulnerable calves and older, more independent juveniles.

Austen, Emily, Mount Allison University

Within-plant variation in nectar spur length in Halenia deflexa exceeds variation in other floral and vegetative characters

Variation among the repeated organs within a plant (e.g., flower-to-flower variation, or leaf-to-leaf variation) can be large, and can sometimes exceed among-plant variation in these same structures. I am initiating a research program to investigate the ecological significance and evolutionary potential of within-plant variation, using the spurred gentian Halenia deflexa as a model system. Analysis of herbarium specimens reveals that nectar spur length, flower size, and internode length (a vegetative character) all vary more within plants than they do among plants, but nectar spur length exhibits the most within-plant variation of all. Because spur size and shape generally affects the mechanical fit between plant and pollinator, the large within-plant variation in spur size in Halenia deflexa may be associated with within-plant variation in pollinator service. In field experiments this summer, we are testing associations between spur length, pollinator visitation, and mating system.
Bahar, MD, Agriculture & Agri-Food Canada; Olivia Doran

Lifetable of the Pollen Beetle (*Brassicogethes viridescens*) correlated with Degree Days and Canola

The rape pollen beetle, *Brassicogethes viridescens* Fabricius (Coleoptera: Nitidulidae) is an introduced pest of Brassicaceae plants in eastern North America. The predicted geographical expansion of this pest to major canola growing areas in Canada heightened the need for information on the life cycle of *B. viridescens*. A field study was carried out in 2014, 2015 and 2017 to determine the life cycle relative to the canola crop phenology and accumulated degree-days (DD) in Prince Edward Island, Canada. Sticky traps, manual collection of buds, pupation traps, and adult emergence traps were used to assess the timing of the different life stages. Results showed that *B. viridescens* were active between late May and early September and required 250-332 DD above a 10°C developmental threshold to complete their development (egg to newly emerged adult) with one generation per year. Photoperiod or food availability but not temperature, were the main driving factors in the life cycle of *B. viridescens*. Appearance of different life stages coincided with canola phenology, and the number of damaged buds was positively correlated to the number of buds containing *B. viridescens* larvae. This information can be used as a decision making tool for timing of insecticide application.

Bahia, Gursimran, York University; Nadejda Tsvetkov; Avideh Khalili; Amro Zayed

Can honey bees detoxify Neonicotinoids.

Canadian honeybees have experienced high colony mortality in recent years with neonicotinoid usage on crops being a major contributing factor. In 2018, the Canadian Association of Professional Apicurists reported that the national winter loss of bee colonies was 32.6%. Neonicotinoids are a class of agricultural pesticides that are chemically similar to nicotine. They are highly agonistic to insect nicotinic acetylcholine receptors (nAChRs), compared to the mammalian nAChRs. Honey bees tend to be more sensitive to N-nitro neonicotinoids (imidacloprid, clothianidin, thiamethoxam) compared to the N-cyano class (thiacloprid) due to the latter being more easily metabolized by the honeybee. Here we examine if honey bees that survive exposure to the N-nitro neonicotinoid clothianidin have different levels of expression of specific detoxification enzymes (e.g. CYP9Q1-3, a family of cytochrome p450 monooxygenases responsible for metabolizing neonicotinoids) relative to honey bees that die after exposure to clothianidin. We compared the expression of CYP9Q genes of bees of different genotypes after feeding them a field realistic dose (4.6 ppb), as well as a LD50 dose (29 ppb) of clothianidin.

Baici, Jennifer, Trent University; Dr. Jeff Bowman, Ontario Ministry of Natural Resources, Trent University

Modelling the size and distribution of Ontarios Wild Turkey Population

Wild turkeys were extirpated from Ontario, Canada in 1909 as a result of habitat loss and overhunting. Through wildlife exchange agreements with the United States, 4400 individuals were reintroduced in 1986. Although Ontario’s reintroduction has seemingly been very successful, little is known about the size and distribution of the population. Using helicopter surveys, road surveys, and citizen science data compiled from eBird and iNaturalist, we will estimate the current size and distribution of Ontario’s wild turkey population. We will develop a spatial distribution model to explore the relationship between wild turkey flock locations and landscape features, (e.g. forest type and livestock presence). Modelling the spatial distribution of wild turkey flocks will inform us about the current distribution of Ontario’s turkeys, and allow us to predict how populations might change over time in response to factors such as habitat loss and climate change. By comparing flock detections across survey methods, this research will also allow us to develop robust monitoring protocol for this species. Because wild turkeys are a harvested game species, understanding the current population extent and how to best monitor changes over time is essential in ensuring the continued, sustainable harvest of wild turkeys and their persistence in Ontario.
Impact of annual forage intercropping on weed control in a semiarid environment

Soil microbial communities play a critical role in the cycling of phosphorus (P) in soil, but are also sensitive to alterations in soil chemistry. A better understanding of how crop management practices impact the cycling of P and soil microbial communities that mediate these processes will enable the design of more P-efficient cropping systems. In this experiment, we used a long-term continuous wheat cropping system to determine the effects of nitrogen (N) and P fertilization on the soil microbiome and its P cycling capacity. Soil samples were collected at anthesis and post-harvest from four treatments (1. N and P fertilization; 2. N fertilization and no P fertilization; 3. P fertilization and no N fertilization; 4. no fertilization) in the cropping system to assess extracellular enzyme activity, various soil chemical properties, and the soil microbiome using shotgun metagenomic sequencing. Long-term N fertilization and P fertilization to a lesser extent caused a significant decrease in soil pH and caused a shift in phosphatase activity. The metagenomic profiles revealed that N fertilization, but not P fertilization significantly altered the composition of the microbial community involved in P cycling processes. Overall, N fertilization increased the relative abundance of most functional genes that code for P cycling processes, whereas the effect of P fertilization was primarily limited to select genes involved in phosphonate degradation. Redundancy analysis determined that the most important predictors of the P cycling gene composition were several P chemistry properties, soil pH, and N fertilization. These predictors explained a high proportion of the variation ($r^2 = 0.87$) and variance partitioning revealed that each of these predictors were tightly interconnected. This study highlights the impact that long-term crop management practices can have on P cycling processes. Future research is focused on understanding the mechanisms by which N fertilization alters soil P cycling in agroecosystems.

Bainard, Luke. Long-term nitrogen fertilization alters the composition and phosphorus cycling capacity of the soil microbiome in a semi-arid agroecosystem

The interactive effects of phenotype and environment on dispersal dynamics

Dispersal, the movement of organisms between populations, influences ecological and evolutionary dynamics including metapopulation persistence and local adaptation. Empirical research has shown that dispersal is influenced by several environmental and phenotypic variables; however, these studies have come to contradictory conclusions. For example, some studies find that dispersers are larger than non-dispersers, while others find the opposite pattern. My goal was to test the hypothesis that the effects of phenotype and environment on dispersal vary across ecological contexts, producing variability in dispersal patterns. I tested this with the use of theoretical modeling and empirical investigations. I developed an individual based model of the evolution of dispersal in response to the joint effects of body condition and population density. I found that dispersal evolved to be a positive threshold function of density, and the value of this threshold depended on condition. In a mark-release-recapture (MRR) study, I found that dispersal in the backswimmer, Notonecta undulata, depended on the three-way interaction between population density, body mass, and sex. Finally, in a series of experiments, I found that parasitism risk from ectoparasitic Hydrachnidia mites induced dispersal in healthy backswimmers, but infected backswimmers had low dispersal ability. MRR data demonstrated that mite infection eliminated positive density-dependent dispersal in backswimmers. My work convincingly demonstrates that the number and phenotypes of dispersers varies across ecological contexts. This suggests that the impact of dispersal on ecological and evolutionary dynamics including metapopulation persistence and local adaptation, will vary across space and time.

Balasingham, Katherine, University of Toronto; Nathan R. Lovejoy

Selection in Visual Opsins in Beloniformes Potentially Driven by Habitat and Behaviour
Beloniformes (i.e. needlefishes, halfbeaks, medakas, and flyingfishes) are surface-dwelling, schooling, epipelagic fishes that play an important role in oceanic food webs and fish farming. They are an extremely diverse family with intriguing morphological traits such as needle-like jaws or enlarged pectoral fins for flight. Belonids also contain marine-derived lineages; freshwater species that evolved from marine ancestors upon invasion of freshwaters. Shifting between freshwater and marine habitats fundamentally changes the requirements in visual perception in key vision genes (i.e. opsins). Marine waters are abundant in short, high-energy wavelengths due to low turbidity making these systems blue-shifted. Freshwater systems of the same depth are more turbid and attenuate blue light resulting in long, low-energy wavelengths of red light, thus freshwater habitats are red-shifted. However, constrained to the upper limits of the water column marine and freshwater belonids are exposed to the full light spectrum and rely on colour vision, whereas deep-dwelling fishes rely on dim-light vision due to reduced light availability. We use molecular approaches to analyze the rate of nucleotide substitutions in Beloniformes to assess the selective pressures on dim-light and colour vision genes by family and habitat. Our results indicate vast divergent selection among the colour opsins based on family and habitat, with greater positive selection in medium-wavelength (green-sensitive) opsins in freshwater belonids and in the needlefish family, and long-wavelength (red-sensitive) opsins in flyingfishes. Although belonging to the same order, these families differ in spatial distribution, diet, and physiology; factors that likely drive divergent selection in visual opsins.

Baldwin, Sarah, McGill University; Daniel J. Schoen

Inbreeding depression is difficult to purge in self-incompatible populations of *Leavenworthia alabamica*

Whether inbreeding depression can be purged is a primary factor in the evolution of mating systems as well as being important in other fields such as conservation and crop improvement. To test if inbreeding depression could be purged from the self-incompatible species *Leavenworthia alabamica*, an experimental (“Ancestral”) treatment was first created from self-incompatible populations. A Purged” treatment was then created by self-pollinating plants from the same populations for three generations. If inbreeding depression could be easily purged, this method would produce a purged population fewer recessive, deleterious mutations of large effect. Fitness components across the lifespan and malformed phenotype frequencies were evaluated in progeny derived from selfing and outcrossing plants from the Ancestral and Purged treatments. Fitness component means and inbreeding depression were largely unchanged by three generations of forced self-pollination, and there was no reduction in the frequency of plants exhibiting malformed phenotypes. Our results indicate that inbreeding depression in this species is largely due to recessive mutations of mild effect, consistent with the observation that self-incompatibility is maintained in most populations of *L. alabamica*, despite the presence of genetic variants with weaker self-incompatibility.

Balluffi-Fry, Juliana, Memorial University; Shawn J. Leroux; Yolanda F. Wiersma; Travis R. Heckford; Matteo Rizzuto; Isabella C. Richmond; Eric Vander Wal

A multiscale test of selection for plant elemental variation by moose reveals individual-based trade-offs of forage quantity and quality

Herbivores consider the variation of two major classifications of plant resources: quantities (biomass), and qualities (nutritional content and digestibility). To test for patterns between plant quantity and quality selection by a large herbivore requires landscape-wide quantitative estimates of both forage quantity and quality. Here, we use stoichiometric distribution models (StDMs) to predict elemental measures of understory white birch quality (% nitrogen) and quantity (g carbon/m^2) across two boreal landscapes. We analyzed GPS-collared moose (n=14) selection for forage quantity and quality at the landscape, home range, and patch extents using individual and pooled resource selection analyses. We predicted that moose would positively select for white birch quantity and quality given the lack of negative correlation between white birch carbon and nitrogen measures from our predictive models. Our pooled models found neutral selection by moose for the elemental estimates of quantity and quality with low explanatory power at all scales. At the individual level, however, there appeared to be quality and quantity tradeoffs, notably at the home range scale where individual selection models were also the most explanatory. Individual terrestrial herbivores appear to vary in their tactic to attain a limited nutrient.
Baltzer, Jennifer, Wilfrid Laurier University; Nicola J. Day; Xanthe J. Walker; Michelle C. Mack; Heather Alexander; Dominique Arsenault; Jennifer Barnes; Laura Bourgeau-Chavez; Carissa D. Brown; Suzanne Carrière; David Greene; Sylvie Gauthier; Marc-André Parisien; Kirsten Reid; Brendan M. Rogers; Carl Roland; Luc Sirois; Sarah Stehn; Daniel Thompson; Merritt R. Turetsky; Sander Veraverbeke; Ellen J. Whitman; Jian Yang; Jill F. Johnstone

Widespread ecological reorganization of boreal forests following severe wildfire

Intensification of wildfire regimes is driving state changes in boreal forests, from black spruce, to broad-leaved taxa or jack pine in response to deep burning and shortening fire-free periods. Such changes have dramatic implications for ecosystem functions and feedback on the regional fire regime. Understanding such changes and the generality of the underlying drivers is critical, yet to date data limitations have precluded this possibility. Using a dataset from 1538 sites across North America, we demonstrate regional variation in both the likelihood and outcome of state change following recent wildfire events. Black spruce showed a consistent loss of resilience across North America, with up to 65% of sites experiencing post-fire trajectories indicative of state change. Where black spruce resilience was compromised, post-fire trajectories included aspen, birch, and jack pine dominance in a geographically unpredictable manner. Across our models of state change, seedbed quality and regional climate were consistently important variables, indicating generality in the drivers of change. Our results suggest that black spruce, which has dominated North Americas boreal forest for millenia is being replaced and that continued warming and drying coupled with intensification of the fire regime will reinforce this trajectory.

Barbeau, Myriam, University of New Brunswick

Role of marine invertebrates in the ecology of salt marshes and mudflats along the northwest Atlantic coast

The shorelines of the Bay of Fundy (BoF) and southern Gulf of St. Lawrence (sGSL) are dominated by soft-sediment ecosystems (salt marshes and mudflats), which is not typical of north temperate coasts in North America. Rocky shores are more typical, being a result of past glacial scour. Consequently, the study of soft-sediment intertidal ecosystems at northern latitudes, where winter disturbance is substantial, is lagging behind that of such ecosystems further south (USA) or across the Atlantic (Europe). Invertebrates are often ecologically important, being trophic links between primary producers and high-level consumers or being ecosystem engineers. Examples include the ribbed mussel (Geukensia demissa), common marsh snail (Melampus bidentatus), and mudshrimp (Corophium volutator). Ribbed mussels and Melampus snails are at their northern range limit in sGSL, and may play a different ecological role than in salt marshes further south. Mudshrimps appear to be an invader in BoF mudflats dating to early European colonists, and may be opportunistic prey for higher-level consumers (e.g., shorebirds). We will explore recent results on the population and community ecology of these invertebrates and ecosystems to gain insights on how roles may be different than elsewhere, and whether winter effects could be a contributor.

Barbero, Francesca, Università di Torino; Simona Bonelli, Università di Torino

Overview of the interactions between lycaenid butterflies and ants

A successful interaction ensures stocks of trophic resources and protected niches for the several species of Lycaenid butterflies which establish commensal, mutualistic or parasitic associations with ants. Strategies developed by lycaenids to overtake the strong defenses of the ant colony involve the deception and the manipulation of workers as well as the evolution of specific morphological or behavioral adaptations. Multimodal communication is crucial to preserve the complex structure of ant societies, but its subversion is at the base of the evolution and maintenance of interspecific associations, which can be benign or detrimental for the colony fitness. I will present the amazing diversity of chemical and vibroacoustic signals used by butterfly immature stages to enter and exploit ant nests focusing primarily on the obligate-parasitic system involving Maculinea butterflies and Myrmica ants. The outstanding complexity of signaling occurring in multitrophic systems could have prompted the evolution of such specialized lifecycles thus increasing the current diversity of butterflies.
Barbosa da Costa, Naila, University of Montreal; Vincent Fugere; Marie-Pier Hebert; Charles Cong-Xu; Rowan Barrett; Beatrix Beisner; Graham Bell; Gregor Fussmann; Andrew Gonzalez; Jesse Shapiro

Indirect selection for antimicrobial resistance genes by pesticide application in a large-scale mesocosm experiment

The increasing and widespread use of pesticides is of major concern regarding their toxicity to natural communities and the introduction of a selective pressure to resistance species. Microbial freshwater communities are indirectly affected by land use contaminants which are washed away from agricultural farms and reach rivers and lakes in the watershed. Microorganisms are usually very responsive to environmental disturbances, as they have short generation times and large population sizes. In very polluted environments, it is also possible to observe an indirect selection for antimicrobial resistance (AMR) genes in the remaining microbial populations. In the present work, we describe an eight-week freshwater mesocosm experiment performed on the LEAP (Large Experimental Array of Ponds) platform, at the Gault Nature Reserve, in Mont Saint-Hilaire, Quebec. Experimental ponds received nutrients in high or low concentrations and a combination of pesticides (glyphosate and imidacloprid) in a factorial design including 8 different concentrations. We assessed changes in bacterial community functional capacities to degrade different sources of carbon and compared it to taxonomic composition along the experimental time series for different treatments. We further performed shot-gun metagenomics of ponds receiving glyphosate, which showed to be the main stressor to bacteria, to assess whether the high selective pressures led by the presence of the herbicide increased AMR genes abundance. Our results show that microbial communities are affected only by very high amounts of glyphosate in water, but they seem to be robust in terms of functional capacities, which were not affected at any concentration tested. Finally, we observed a slight increase of AMR genes abundance in the group of ponds receiving glyphosate when compared to controls, suggesting that diverse anthropogenic stressors may inadvertently select for AMR in the environment. Our ongoing work aims to determine the relative importance of evolution (mutation and HGT within species) vs. ecology (species sorting) in community responses the anthropogenic stressors.

Barreto, Carlos, Western University; Zoë Lindo, Western University

Climate change field experiment shows weak effects of warming and neutral effects of CO2 on soil microarthropod communities

Soil systems are biodiverse and responsible for important ecosystem processes such as decomposition, recycling of nutrients, and carbon storage. Understanding how global change factors affect soil biodiversity will allow us to link these changes to potential outcomes in ecosystems processes. Specifically, the effect of warming on many ecological communities is predicted to be non-linear suggesting potential tipping points. Thus, we tested the effects of warming (ambient, +2.2, +4.5, +6.7, and +9°C) and atmospheric CO2 concentration (ambient, 800 to 900 ppm) in a regression-based design on peatland microarthropod communities. Soil samples were collected from large-scaled chambers installed at the Marcell Experimental Forest, Minnesota, USA (SPRUCE experiment). Results show that total microarthropod abundance increased with warming, mostly driven by increases in both predatory mites (Mesostigmata) and fungivorous mites (Oribatida). Non-linearity in abundances in response to warming was not observed and we found no statistically significant effects of elevated CO2 on the microarthropod fauna. The implication of increased microarthropod abundances, without changes in species richness or shifts in community composition, are cascading effects to microbial communities, and decomposition and nutrient cycling processes.

Barry, Shauna, University of New Brunswick; Dr. Alexa Alexander-Trusiak

Assessment of Present and Historical Agriculture Best Management Practice Using Aquatic Indicators in Prince Edward Island

Agricultural Best Management Practices (BMPs) are integrated into land or crop management by agricultural growers and farmers in order to prevent the pollution of aquatic ecosystems. Prince Edward Island (PEI) has a strong agricultural presence, so it is likely that the quality of fresh water environments is influenced by agricultural land management. Water quality, algal community, and benthic invertebrate community data from the 2006 National Agri-Environmental Standards
Initiative (NAESI) were examined from the Dunk, West, Tryon, and Wilmot River Watersheds. Indicators such as aspect, vegetation presence, algae species, invertebrate families, and nutrients were compared within both the Atlantic Maritime ecoregion and a national context. The most influential indicators for PEI were compared to recent data to see how ecosystem health has changed since 2006. We examined the implementation of both historical and current BMPs on agricultural land near sample sites to see if they were improving the health of the aquatic environment.

Bastarache, Pierre, Université de Moncton; Pascal Dumas, Department of Chemistry and Biochemistry, Université de Moncton; Pier Jr Morin, Department of Chemistry and Biochemistry, Université de Moncton

Modulation of alpha-crystallin B in response to various challenges in the Colorado potato beetle *Leptinotarsa decemlineata*

The Colorado potato beetle, *Leptinotarsa decemlineata*, is a significant insect pest harming potato crops worldwide. Substantial efforts have been deployed in recent years to develop novel strategies to manage Colorado potato beetle populations and to understand molecular players associated with response to various stress in these insects. We hypothesized that alpha-crystallin B (CRYAB), a small molecular chaperone, could respond to temperatures and insecticides challenges in *L. decemlineata*. To test this hypothesis, alpha-crystallin B transcript levels were amplified and measured by qRT-PCR in insects exposed to chlorantraniliprole, cold or hot conditions. While alpha-crystallin B expression remained largely unchanged following exposure to the stress investigated, alpha-crystallin B transcript levels showed a substantial 54.37-fold up-regulation in insects submitted to a heat shock of 40 °C for two hours when compared with control insects housed at 25 °C. Characterization of the role, if at all, of alpha-crystallin B during heat shock response using double-stranded RNA (dsRNA)-based approaches is envisioned. Overall, this work reinforces the potential importance of alpha-crystallin B during response to select stress in Colorado potato beetles and reveals a molecular lead that warrants further investigation in the search for novel targets to control *L. decemlineata*.

Bennett, Jonathan, University of Saskatchewan; James Franklin, University of Alberta; Justine Karst, University of Alberta

Environmental and biotic drivers of plant-soil feedback in aspen

As plants grow, they affect the abundance of both beneficial and antagonistic soil microbes, with consequent effects on seedling growth (plant-soil feedback; PSF). In forests, PSF is generally positive for trees forming ectomycorrhizas and negative for trees forming arbuscular mycorrhizas. These effects, however, can be modulated by the local environment. It is less clear how the environment modulates PSF for species that form both arbuscular and ectomycorrhizas, as they can switch between mycorrhizal types depending on environmental conditions. We explored how the environment affects PSF in a dual mycorrhizal species (*Populus tremuloides*; aspen) across a 1600 km gradient spanning northwestern Alberta to southeastern Saskatchewan. We collected environmental data and soils from 27 aspen stands and used these soils to quantify PSF under controlled conditions. PSF was generally negative but became less negative when EM fungi were abundant, likely owing to increased protection from pathogens. PSF had contrasting relationships with nitrogen and rainfall, becoming most negative in dry sites and when the leaves of adult trees had the greatest nitrogen content. This suggests that site productivity has a strong, but complex effect on PSF.

Bennett, Joseph, Department of Biology, Carleton University

Value of information for threatened species management: predicting where and when we should monitor versus act

Accurate information on remaining populations of threatened species can be vital for effective management. We can undertake surveys to help find these populations, and we can build models to predict where they may exist. However, the rarer a species becomes, the harder it is to find and model. And gathering information takes time and financial resources that could be used in managing for recovery. How do we know when have we monitored enough that it makes sense to act? Where are the optimal places to monitor, so we can best inform action? Using Canadian case studies, I will present research on value of information theory that can help to solve these problems, and ultimately, better achieve recovery of
threatened species. I will also discuss theoretical problems of monitoring for immediate management needs, versus monitoring to improve overall knowledge of a system, and possible strategies to achieve a balance between these approaches.

Bergeron, Patrick, Bishop's University; Dany Garant, Université de Sherbrooke; Denis Réale, UQAM

Consumption of red maple in anticipation of beech mast-seeding drives reproduction in Eastern chipmunks

In pulsed resources environments, the reproduction and population dynamics of seed predators is driven by pulsed seed production by trees. In Southern Québec, eastern chipmunks (Tamias striatus) seem to anticipate beech mast by reproducing during early summer, so that juveniles can emerge at the time of maximum beechnut abundance during late summer. The cues allowing chipmunks to anticipate beech mast remain unknown though, and the existence of the anticipation process itself has been questioned. We investigated the links between the nutritional ecology and reproduction of adult chipmunks and compared their spring diet in mast- vs non-mast years over 11 years. We found a systematic shift in chipmunk diet towards red maple seeds in springs preceding a beech mast, with red maple seeds composing more than 77% of chipmunk diet. Surprisingly, red maple consumption was unrelated to red maple production, but it was related to beech seed production in the fall. We also found that red maple consumption, and to a lower extent red maple production, best predicted the proportion of summer females in estrus. Our results confirm that chipmunks anticipate beech mast-seeding and reveal a potential key role of red maple consumption in that anticipation.

Bernatchez, Louis, Université Laval

Harnessing the power of genomics to secure the future of fisheries and seafood production.

Best use of scientific knowledge is required to maintain the fundamental role of seafood (including fisheries and aquaculture) in human nutrition. While it is acknowledged that genomic-based methods allow the collection of powerful data, their value to inform fisheries management, and biosecurity applications remains underestimated. In this presentation I will briefly review (epi) genomic applications of relevance to the sustainable management of aquatic resources, illustrate the benefits of (from some of our own work), and identify barriers to their integration. I will conclude that the value of genomic information towards securing the future of seafood does not need to be further demonstrated. Instead, we need immediate efforts to remove structural roadblocks and focus on ways that support integration of genomic-informed methods into management and conservation practices. I will propose solutions to pave the way forward.

Beyene, Menilek, University of Toronto

Street tree canopy condition in relation to urban stress

Increasing urbanization creates environmental impacts on flora and human populations. The increase in impermeable surfaces drives increases in urban temperature, surface water runoff, pollution, and pest abundance. Urban forests provide services that may mitigate some of these impacts. Benefits provided may be maximized by understanding urban stressors that effect tree health. The study determines relationships between tree health and urban stressors; impermeable surfaces and land use. Canopy condition, as a metric of health, was expected to vary across the urban gradient and when analyzed at different spatial scales. This was explored by observing canopy condition in 300 street trees of *Tilia Americana*, *Tilia cordata*, *Acer platanoides* and *Acer saccharium* in intersecting transects along major roads of Toronto, ON. Across a gradient of urbanization, measured as the amount of impermeable surface, ArcGIS mapping tools and R programming language were used to determine landscape-level measures of impact. This study shows that impermeable surface and canopy conditions linear relationships are non-significant at small spatial scales. Characterizing tree canopy stress responses at multiple spatial scales may determine suitable predictive urban stressors informing what species and where to plant to maximize urban forest services.
Matrix for of the Laplace Kernel

Integrodifference equations (IDEs) are often used for discrete-time continuous-space models in mathematical biology. The model includes two stages: the reproduction stage, and the dispersal stage. The output of the model is the population density of a species for the next generation across the landscape, given the current population density. Most previous models for dispersal in a heterogeneous landscape approximate the landscape by a set of homogeneous patches and allow for different demographic and dispersal rates within each patch. Some work has been done designing and analyzing models which also include a patch preference at the boundaries, which is commonly referred to as the degree of bias. Individuals dispersing across a patchy landscape can detect the changes in habitat at a neighborhood of a patch boundary, and as a result, they might change the direction of their movement if they are approaching a bad patch. In our work, we derive a generalization of the classic Laplace kernel, which includes different dispersal rates in each patch as well as different degrees of bias at the patch boundaries. The simple Laplace kernel and the truncated Laplace kernel most often used in classical work appear as special cases of this general kernel. The form of this general kernel is the sum of two different terms: the classic truncated Laplace kernel within each patch, and a correction accounting for the bias at patch boundaries.

Multiple stressors and alternate states in coral reefs

Coral reefs, one of the globes most complex ecosystem types, facilitate great amounts of biodiversity and provide numerous ecosystem services to coastal communities. While coral reefs have been very well studied both empirically and theoretically, the majority of research has focused on top-down pressure due to fishing (and cascading effects on coral and macroalgae densities). While this undoubtedly influences the structure of coral reefs, it remains of interest to unfold the synergistic influences of other key drivers. With increasing nutrient loading from land development, it is unlikely that top-down pressure is the only factor determining the structure of these ecosystems, particularly in this period of global change. Here, I will expand on existing theory to incorporate bottom-up effects of nutrient loading to investigate the combined influence of multiple stressors in these important ecosystems. I will show that nutrient levels fundamentally alter the potential for top-down-driven alternate states, such that there are clear context-dependent outcomes of changes in herbivory across gradients of nutrient loading. This importantly means that management actions (e.g., reduced fishing pressure on grazers aimed at rejuvenating coral density) can have very different outcomes under different environmental conditions. Furthermore, these results suggest that nutrient enrichment can drastically alter coral reefs resilience to climate-induced perturbations.

The Effects of Varying Concentrations of Dissolved Organic Carbon on Bluegill Sunfish (Lepomis macrochirus)

Longevity and viability of Entomopathogenic Nematode products in Ontario muck and Nova Scotia mineral soils.

Entomopathogenic nematodes (EPNs) have been studied as potential biocontrol agents for various insect species since the 1940s. Several factors have been found to influence their efficacy and longevity, perhaps the most critical being soil moisture. Commercially available EPN products were sourced from BioBest and evaluated as potential biocontrol agents against carrot weevil in Ontario muck soils and Nova Scotia mineral soils. Here we report on the longevity of the nematode products from these field plots. Following application (24-36 hours) of the products, soil moisture was recorded and soil samples taken and evaluated for viability using Galleria species larvae. Soil moisture and soil samples (125 mL) were taken at 1, 3 and 6 weeks post application and again the following spring. Ten Galleria larvae were placed
on these soil samples and evaluated for mortality 1 week later. Under field conditions in Ontario and Nova Scotia, EPNs were viable for up to 6 weeks if soil moisture levels remained > 10%. Laboratory studies conducted in NS showed some EPNs to locate Galleria larvae at depths of up to 7 cm and soil moisture levels as low as 6%. Implications of these findings on use of EPNs for pest management is discussed.

Blythe, Jennifer, University of Western Ontario; Dr. Brian Branfireun

Mercury methylation along a latitudinal sulphate deposition gradient in Ontario peatlands,

Peatlands are wetlands with over 40cm of organic soil that support the growth of a variety of anaerobic microbes, including sulphate-reducing bacteria (SRB). SRB are the principal methylators of inorganic mercury (Hg) in the natural environment. Methylmercury (MeHg) is the bioaccumulating, and neurotoxic form of Hg. It is well established that increasing the supply of sulphate to nutrient-limited systems such as peatlands increases bacterial Hg methylation. This effect, however, has been shown to differ based on the legacy of sulphate deposition to the wetland. The objective was to investigate the effect of legacy sulphate deposition on bacterial Hg methylation. Peat was sampled from three Ontario peatlands along a latitudinal gradient that represents a historical sulphate deposition gradient from higher to lower: Southern, Central, and Northern Ontario. In the laboratory, the peat was packed into anaerobic columns and subjected to a range of sulphate solutions under continuous flow. Column outflow was sampled for products of sulphate reduction (MeHg and sulphide). Sulphate addition enhanced methylation in all peat, however methylation was comparatively highest in the peat from Central Ontario. Both microbial and biogeochemical explanations will be discussed. This research can inform management strategies for peatlands affected by legacy, or current sulphate deposition.

Bobiwash, Kyle, University of Manitoba

Bee holes – Filling gaps through Indigenous engagement

Studies of wild bees are spatially biased and poorly understood across Canada and notably in the Prairie Ecozone. This is especially true in northern remote regions, where the reliance of plants on their pollinator communities with which they co-evolved is especially important as this relationship can be significantly more unstable. The productivity of this relationship has direct implications to remote northern communities that rely on wild harvested food to maintain food security and sovereignty. Through community engagement and community-based research biodiversity surveys and long-term monitoring can contribute to community wellness and the filling of knowledge gaps.

Bodner, Korryn, University of Toronto Scarborough; Sara Helmuth-Paull, Environmental Health Dept, Colorado School of Public Health; Pieter Johnson, Ecology and Evolutionary Biology, University of Colorado; Christina Cobbold, Department of Mathematics and Statistics, University of Glasgow; Marie-Josée Fortin, Department of Ecology & Evolutionary Biology, University of Toronto; Péter Molnár, Department of Biological Sciences, University of Toronto Scarborough

Parasites and the Goldilocks Principle: How temperature and host stage interact to make conditions just right for *Ribeiroia ondatrae*

Temperature and the stage at which hosts are infected are both known to play critical roles in shaping dynamics of host-parasite systems. Temperature may influence disease prevalence and mean-burden by altering host immunity, parasite infectivity and virulence, as well as basic demographic rates of both parasites and their hosts. Similarly, host stage at exposure may alter disease dynamics as hosts may have stage-dependent differences in tolerance and/or resistance to infection. In the case of parasites and ectothermic hosts, there is an interaction between temperature and host-stage leading to complicated and often unexpected dynamics. To explore how both temperature and stage of infection may interact in a real host-parasite system, we developed temperature-dependent stage-structured host-parasite models for the trematode parasite, *Ribeiroia ondatrae*, and one of its primary amphibian hosts, *Pseudacris regilla*. We show that increases in temperature may result in a decline in amphibian malformations, the main negative consequence of *R. ondatrae* on its
hosts. We also find evidence that host tolerance is temperature dependent, leading to lower levels of malformations as temperatures drop below 20°C. It appears that, just like Goldilocks, R. ondatrae does best when temperatures are just right (between 20-22°C).

Bolliger, Erika, University of Toronto; Monika Havelka, University of Toronto; Christoph Richter, University of Toronto; Hugo Valdebenito, Universidad San Francisco de Quito

Illuminating Nocturnal Insect Visitation of Lantana peduncularis and Lantana camara in the Galápagos Islands

Lantana camara is one of the most invasive plant species on the Galápagos Islands and may outcompete its endemic relative, Lantana peduncularis, for resources and pollination services. There has been little investigation into the interaction between L. camara and L. peduncularis within pollination networks, particularly at night. We used camera traps to document the insect species visiting L. camara and L. peduncularis flowers and the temporal pattern (diurnal vs. nocturnal) of flower visits over a complete flowering cycle (May - June 2018) on San Cristóbal Island, Ecuador. Photos were taken every minute over ten 24-h cycles on inflorescences from 4 plants, resulting in 57,600 images evaluated for the presence and taxonomic grouping of insect visitors. Flower occupation was significantly more common at night than in the day for both L. camara and L. peduncularis (P < 0.05), and lepidopterans were the most commonly observed flower visitors overall. This study offers insight into potentially important interspecific relationships within a generalist island pollination network and highlights the need to include nocturnal observations in pollination biology analyses.

Bonar, Maegwin, Trent University; Joseph M. Northrup; Aaron B. A. Shafer

What controls animal migration behaviour? A meta-analysis

Migration is ubiquitous, and the diversity of migratory behaviours has long fascinated scientists and non-scientists alike. From the long distance migrations of wildebeest to the nocturnal migrations of small passerines, to the enigmatic migration of sea turtles, a wide range of migration behaviours occur globally. The variation in behaviour that exists across species, populations, and individuals, provides an opportunity to understand the proximate mechanisms underlying the evolution of migration. Migration is a combination of both ultimate causes and proximate cues triggering the behaviour. These proximate cues are both internal and external, and it is likely the interaction among them that results in the wide variation in migration behaviours among populations and individuals. By systematically and quantitatively reviewing the literature on migration behaviour, we aim to determine the effect of both internal and external proximate cues on variation in migration behaviour in vertebrates. First, we use partial migration systems in a comparative study to assess the effect size of drivers of migration. Then we assess the drivers of variation in four characteristic migratory behaviours (arrival time, departure time, distance travelled and direction of migration) at the individual level. These analyses provide a comprehensive quantitative assessment of the proximate drivers of migration across vertebrate taxa and advance our basic understanding of the evolution of this globally threatened phenomenon.

Boquel, Sebastien, CEROM; Alexis Latraverse, CEROM; Charles-Étienne Ferland, University of Guelph; Meghan Moran, OMAFRA; Rebecca Hallett, University of Guelph

Occurrence and parasitism rate of Synopeas myles in Quebec and Ontario

The swede midge, Contarinia nasturtii (Kieffer) is by far the biggest threat to canola production in Ontario and Quebec and causes damage through larval feeding on meristematic tissues. Synopeas myles (Walker), a parasitoid of C. nasturtii, was reported for the first time in Canada in 2016. However, it remains unknown whether the wasp is widely distributed and its efficacy at controlling C. nasturtii populations. A project conducted in Quebec and Ontario aims to determine the occurrence and parasitism rate of S. myles. Canola plants showing symptoms of infestation were collected in different regions and at different times during the season. Plants were cut and placed in containers to monitor emergence of C. nasturtii and S. myles as well as parasitism rates. Knowledge on this parasitoid will help improve current pest management practices against swede midge.
Bouchard, Pat, Agriculture and Agri-Food Canada

Weapons and other exaggerated structures in darkling beetles (Coleoptera: Tenebrionidae)

The development of disproportionately large structures in insects and other animals comes at a substantial cost. While several groups of beetles display spectacular structures, including weapons used by males during combat over critical resources, relatively little is known about their use and evolution. The diverse family Tenebrionidae includes more than 20,000 described species worldwide and contains many species with exaggerated structures. A preliminary discussion based on phylogenetic and ecological aspects will be presented.

Boudreau, Denis, Université de Moncton; Nada Hammami; Gaétan Moreau

Environmental factors affecting the phenology and occurrence of forensically important insects in New Brunswick, Canada

The larval stages of early successional species colonizing a cadaver can be used to determine the postmortem interval. However, most of the studies documenting the insect fauna associated with animal remains have been carried out for short and specific periods, generally during the summer. As a result, the phenology, occurrence and effect of environmental factors on these two metrics are largely unknown for forensically important insects. In this ongoing study, we document the early successional insect fauna of forensic importance in New Brunswick using traps rebaited twice a week with fresh pork liver. Traps were located along three transects crossing large urban, suburban and forest areas. Generalized additive modeling was used to develop species-specific models of insect occurrence. Results indicated that the complex of insect species attracted to fresh animal remains in New Brunswick is dominated by Calliphoridae and varies to a great extent according to abiotic factors, species phenology and habitat. This highlights the importance of accurately determining the life history of forensic insect species to optimize their use in police investigations.

Boudreau, Melanie, Mississippi State University

Size matters: the challenges with big data and data management in long-term research projects.

In recent decades, improvements in technology have brought researchers into the realm of big data. High resolution tracking devices paired with remote sensing data allow for the examination of fine scale animal movements and landscape choices. Bio-logging sensors can capture heart rates, body temperatures, and dynamic body accelerations elucidating activity and energy use on a second-by-second basis. Video cameras and microphones allow insights into animal decisions and interactions while trap camera arrays help define population estimates. High throughput sequencing has allowed for new insights into genomics, epigenomics, and transcriptomics. The integration of these data can even allow for an examination of population dynamics and intra- and inter-specific interactions like never before. Indeed, these new data are allowing researchers to examine a breadth of new scientific questions related to ecology and evolution however, the explosion of data volume and variety has created new challenges for information management. This is particularly true for those who participate in research spanning the course of decades. How then can long-term projects best manage big data? I present perspectives from a variety of researchers, their challenges and solutions, along with examples on the benefits of long-term projects undertaking big data for big rewards.

Bowden, Joe, Natural Resources Canada, Canadian Forest Service; Anne Eskildsen; Rikke R. Hansen; Kent Olsen; Carolyn M. Kurle; Toke T. Høye

High-Arctic butterflies become smaller with rising temperatures

The response of body size to increasing temperature constitutes a universal response to climate change that could strongly affect terrestrial ectotherms, but the magnitude and direction of such responses remain unknown in most species. The metabolic cost of increased temperature could reduce body size but long growing seasons could also increase body size as
was recently shown in an Arctic spider species. Here, we present the longest known time series on body size variation in two High-Arctic butterfly species: Boloria chariclea and Colias hecla. We measured wing length of nearly 4500 individuals collected annually between 1996 and 2013 from Zackenberg, Greenland and found that wing length significantly decreased at a similar rate in both species in response to warmer summers. Body size is strongly related to dispersal capacity and fecundity and our results suggest that these Arctic species could face severe challenges in response to ongoing rapid climate change.

Bowman, Jeff, Trent University

An introduction to the Long-term Research Section of the CSEE at this inaugural symposium of the CSEEs first ever section.

Welcome to the inaugural symposium of CSEE’s Long-Term Research Section, LTR-CSEE. We have established this first ever section of CSEE to foster collaboration among Canadian researchers and to support long-term research. We envision an open, investigator-led network of researchers interested in long-term studies. Our symposium will provide a discussion of a centrally important theme in long-term research management and accessibility of data! We will discuss issues ranging from transfer of project leadership across generations of researchers to principles of open data and database design.

Bowser, Emma, UNB/ECCC; Alexa Alexander

Stream Mesocosms: Design & Function

Stream mesocosms are used to conduct field water quality experiments using aquatic insects, specifically mayflies, to gain an understanding of multiple and cumulative perturbations in a water body. Using multiple cosms, and nutrients such as KNO3 or NaH2PO4, researchers can simulate varying nutrient gradients. A stream treatment table can hold up to eight streams and is comprised of several pieces of equipment to ensure steady mixing, temperature, and nutrient dosing. This equipment design provides increased control during the experiment, in comparison to other field experiments, yielding high-quality results of the effects of multiple stressors in aquatic ecosystems. The goal is to influence environmental guidelines to improve them and the thresholds for environmental sustainability.

Brazeau, Hannah, University of New Brunswick; Brandon Schamp, Algoma University; Amy Parachnowitsch, University of New Brunswick;

Effects of pollinator sharing on floral traits in Chamerion angustifolium

Plants are known to alter a variety of vegetative traits in response to competition for resources, such as sunlight and soil nutrients, but studies of competition-induced trait plasticity rarely treat pollinators as a distinct resource pool and tend to ignore floral traits. As floral traits play an important role in attracting pollinators and many generalist species share and potentially compete for pollinators, traits associated with advertisement and reward should be included in studies of plant-plant competition. My experiment uses a native flowering perennial, Chamerion angustifolium, grown in monoculture and with heterospecifics, to determine whether floral traits change in response to pollinator sharing. Furthermore, I use a hand pollination treatment to show whether observed changes in floral traits are due to plant-plant signaling or merely result from decreased pollen deposition due to increased community density.

Brehaut, Lucas, Memorial University; Katie Goodwin, Department of Geography, Memorial University; Kirsten Reid, Department of Geography, Memorial University; Jen Sullivan, Department of Geography, Memorial University; Anna Crofts, Département de biologie, Université de Sherbrooke; Stéphane Boudreau, Département de biologie, Université Laval; Ryan Danby, Department of Geography, Queen's University; Steven Mamet, Department of Soil Science, University of Saskatchewan; Carissa Brown, Department of Geography, Memorial University
Is pre-dispersal seed herbivory a biotic constraint across subarctic treelines?

Across altitudinal and latitudinal treeline ecotones, continued climate warming is predicted to facilitate boreal tree range expansion into novel tundra environments. Yet, where evidence of a range shift has been detected, the rate is much slower than what has been projected by temperature-based models. This lag suggests that both climate and other non-climatic mechanisms are modulating treeline range dynamics. Our research assessed how biotic factors may govern viable seed availability of eight black spruce (*Picea mariana*) dominated treelines across Canada, from the Yukon Territory to the island of Newfoundland. Specifically, we examined levels of pre-dispersal (within cone) seed herbivory by insects (*Eupithecia* spp. and *Choristoneura* spp.), and quantified site-level stand density and landscape-scale landcover (500m radius) using field methods and the Commission for Environmental Cooperation (CEC) landcover classification data set (Landsat, 30m), respectively. Contrary to our expectations based on previous case studies, early findings reveal varying, but low, levels of seed and cone herbivory across sites, suggesting site-specific herbivory rates. Results from the modelled relationship among seed viability, site-level stand density, and landscape-scale vegetation classification will lend to understanding site-level herbivory rates, as well as how treeline form (i.e., abrupt or diffuse treeline) may help further predict range expansion potential.

Brigham, Mark, Biology, University of Regina; Andrew McKechnie

Interspecific variation in the heat tolerance and evaporative cooling capacity of bats with differing roosting habits

The majority of physiological research on small mammals has focused on coping with cold. However, given the predictions of climate change models, understanding how small organisms cope with heat is important. Using methods employed for arid zone birds, we estimated heat tolerance and evaporative cooling capacity of insectivorous bats. We predicted that the ability to cope with higher ambient temperatures (Ta) would reflect the nature of roost sites, with species using external roosts (hoary bats) having more tolerance and cooling capacity than bats using cavity roosts (little brown and silver-haired bats). Our data were collected in summer in Cypress Hills Provincial Park, Saskatchewan, Canada. Gas exchange measurements were conducted the day after capture using open flow-through respirometry at a range of Tas (~ 3048° C in 2° C increments). Maximum Ta was reached before bats became hyperthermic (Ta, HT) and was significantly higher in hoary (46.5 ± 2.1° C) compared to little brown bats (44.1 ± 1.6° C). The Ta, HT of silver-haired bats (45.3 ± 1.5° C) did not significantly differ from the other species. Our findings are consistent with predictions as the species that used exposed roosts had the highest heat tolerance.

Brooks, Delaney, University of New Brunswick; Joseph Nocera, University of New Brunswick

Reproductive activity of Olive-sided Flycatchers (*Contopus cooperi*): Effects of ecological traps in forested wetlands

Ecological traps occur when a low-quality habitat is selected over available high-quality habitat, resulting in negative fitness. This phenomenon typically results in a population sink and can occur when sudden changes to the environment disrupt cues individuals use that would otherwise allow them to reliably assess suitable habitat. Olive-sided Flycatchers (*Contopus cooperi*) is an aerial insectivore with a history of occupying ecological traps. Olive-sided Flycatchers preferentially breed and forage in open forest. Within these sites, tall snags are important for foraging and defending territory. Harvested sites provide adequate substrate for perching and nesting, although such sites are often ecological traps as they lack other requirements to maintain positive fitness. NB is an ideal location to study the effects of ecological traps on Olive-sided Flycatcher as harvested sites and natural patches are abundant. We examine the degree to which habitat type acts as an ecological trap for Olive-sided Flycatchers in NB. We compare the reproductive activity, diet, and time spent in a territory of 25 individuals. Overall, 15 Olive-sided Flycatchers remained in their territory for the 2018 breeding season with eight making use of harvest sites. The presence of preferred food items and increased reproductive activity are indicators of high-quality habitat.
Brooks, Cody, UNB; Dr. Gary Saunders, UNB

The Kelp Conveyor Hypothesis: Evidence of Long-Distance Migration in the Northeast Pacific

Approximately 10% of Haida Gwaii's seaweed flora is present in California, while being absent from the intermediary Vancouver Island. Given that many of these species are non-buoyant, an explanation for their disjunct distribution presented a conundrum. One possible explanation lies in kelp rafting; large mats of kelp are known to be dislodged from the subtidal annually and subsequently drift on prevailing ocean currents for several weeks before degrading. The kelp conveyor hypothesis posits that these kelp rafts, laden with hitchhiking species of algae, drift northward from California on the winter Davidson current to Haida Gwaii resulting in long-distance, unidirectional migration of species. If the kelp conveyor hypothesis has merit, one prediction that should be met is that subtidal species with a continuous distribution along the northeast Pacific should reflect this pattern at the genetic level owing to gene flow between California and northern BC, whereas intertidal species should not. To test the kelp conveyor hypothesis, specimens of 4 low-intertidal to subtidal and 4 mid- to high-intertidal species were collected and sequenced for the mitochondrial cytochrome c oxidase region (COI-5P). Samples were collected from California, Oregon, Vancouver Island and Haida Gwaii and pairwise genetic differentiation was determined for each population pair to assess similarity of adjacent and non-adjacent populations. In support of the kelp conveyor hypothesis, the non-adjacent populations of California and Haida Gwaii tend to be more similar in their subtidal than intertidal species.

Brookson, Cole, University of Toronto & University of Alberta; Devin Kirk, University of Toronto; Chelsea Rochman, University of Toronto

A combined ecotoxicological and classical ecological modeling approach predicts microplastics may be affecting the growth and viability of Daphnia magna populations in aquatic ecosystems

Understanding how anthropogenic stressors affect the population dynamics of species at the base of aquatic food webs is important for predicting future community and food web dynamics. Plastic pollution, specifically microplastic (plastic particles < 5mm in size) pollution, is often discounted in many ecological threat assessments despite the fact that it has become a ubiquitous contaminant of concern in aquatic ecosystems around the globe. We currently know very little about the population- and community- level effects of microplastics and how they relate to aquatic ecosystems. To help begin to fill this gap, we combined an ecological model with ecotoxicological dose-response techniques to scale-up individual-level findings regarding the impacts of microplastic pollution to the population level. We constructed a density-dependent population growth model, explicitly incorporating the effects of microplastics on both reproduction and mortality, to examine the effects of microplastic exposure on the population dynamics of Daphnia magna. We show that current levels of microplastic pollution could be having an effect on natural populations of D. magna and that unless we take steps to curb ongoing pollution, future projected concentrations of microplastic pollution show the potential to cause serious declines to wild D. magna populations. We posit that these declines could have important consequences for freshwater food webs worldwide. This is an important first assessment of the potential for microplastics to have an impact on population dynamics in nature. We propose using this hybrid ecological/ecotoxicological modeling approach as a way to investigate how data on the individual effects of a particular stressor may inform studies on the ecological effects of the same stressor in nature. This approach could be used to investigate the population-level effects of microplastics in a variety of other systems, thus allowing us to gain a more holistic understanding of the impact microplastic pollution is having on aquatic ecosystems worldwide.

Brown, Joel

Cancer as an unlikely system for applying and testing evolutionary game theory

Instead of a disease of unregulated proliferation or a disease of the genes, cancer may be a speciation event where a multicellular organism gives rise to a new single celled organism. The cancer cell lineage goes from being a part of the whole organism's traits to becoming a self-defined fitness function. Cancer happens when the cell becomes the unit of selection. Within a tumor, cancer cells experience and contribute to heterogeneity; heterogeneity that selects for the evolution and coexistence of different cancer species. The cancer cells engage in public goods games, tragedies of the
commons and competition for scarce resources. Within a patient, different metastatic sites may select for different communities of cancer cells that are geographically isolated. Between patients with the same cancer, one sees a high degree of functional and morphological convergent evolution. Here I present cancer as an evolutionary game and how this can explain intra-tumoral variability and inter-patient variability. A clinical trial of advanced metastatic prostate cancer has more than doubled progression free survival by applying an evolutionary game model to conduct adaptive therapy meant to contain an otherwise incurable stage of cancer.

Brown, Grant, Concordia University; Adam L. Crane; Jack A. Goldman; Laurence E.A. Feyten

Disturbance cues: the forgotten source of risk as assessment information in aquatic prey.

Within aquatic ecosystems, prey often rely on chemosensory cues as a source of public risk assessment information. To date, the majority of studies have focused on the damage-released chemical alarm cue system and its role in acquired predator recognition, with far less attention being paid to the so-called disturbance cues. These cues are released by stressed or disturbed individuals prior to an attack (early on within the predation sequence). Using the Trinidadian guppy as a model system, we will provide an overview of our recent laboratory and field trials examining: 1) the response to conspecific and heterospecific disturbance cues; 2) their role in mediating threat-sensitive behavioural trade-offs; 3) the impact of background predation risk and donor familiarity in shaping the production and response to disturbance cues; and 4) the function of disturbance cues under fully natural conditions. Combined, our recent results suggest that disturbance cues may be a critical source of risk assessment information among aquatic prey populations and be far more than a simple early warning signal as previously argued.

Brown, Norah, University of Victoria; Ben Millard-Martin; Margot Hessing-Lewis; Rebecca Miller; Sara Wickham; Owen Fitzpatrick; Katie Davidson; Deb Obrist; Pat Hanly; Chris Ernst; John Reynolds; Chris Darimont; Brian Starzomski

Kelp forests to rainforests: nearshore marine diversity shapes island ecosystems

Cross ecosystem subsidies are an important but often overlooked driver of ecological patterns. Much of the pioneering work in this field has been conducted on coastal islands, with juxtaposed marine and terrestrial habitats. Thus far, the quantity, quality, and effect of marine subsidies have been measured only after arrival onshore. There is little known about how the diversity and production of nearshore marine ecosystems can influence terrestrial ecology. Here, we combine two datasets from the Central coast of British Columbia to understand how marine processes can shape terrestrial patterns. We explored biogeographical parameters that might influence the transfer of nutrients, likely via river otters. The marine dataset consisted of repeated beach seines, targeting fish and marine invertebrates. The terrestrial dataset consisted of transects that quantified soil and plant chemistry along with diversity and abundance of plants and animals. We found that marine diversity influenced soil and plant chemistry on nearby island transects. In particular, higher marine diversity was associated with increased δ15N in soil and two plant species. High marine diversity was also linked with declines in plant, tree, and insect diversity. These results may indicate that although marine subsidies are arriving on islands, not all species may benefit.

Brown, Charlotte, University of Alberta

Neither size-dependent competition nor competitive intensity is associated with species diversity and composition in a native grassland

The intensity of competition is thought to be a major force driving plant community structure; however, empirical evidence depicting its importance is limited and there is mixed evidence for its effects on species diversity or composition. An emerging explanation for this disjunction between theory and empirical evidence is that size-dependent competition is needed to drive changes within communities, not intensity alone. In this model, larger plants gain a disproportionate advantage over smaller individuals leading to the potential removal of smaller individuals and thus a reduction in species diversity. Here, using experimental thinning treatments to manipulate community height structure, we test the importance
of competitive intensity versus size-dependent competition on species richness, evenness, and composition in a native grassland. Overall, we found evidence that competition occurred, and it was typically size-dependent such that taller individuals had the competitive advantage; however, there was no association between competitive intensity, size-dependent competition, species diversity or composition. These results suggest that incorporating the size-dependence of competition may not improve the link between competition and plant community structure and provide further evidence that competition may not be the leading driver of community assembly.

Browne, Jessica, University of Toronto Mississauga; Darryl Gwynne, University of Toronto Mississauga

Sexual selection on female ground weta leads to post-copulatory sexual selection in males

Sexual ornaments are rare in females, likely due to their potential costs to fecundity or survival. The presence of ornaments indicates strong sexual selection on females, resulting from competition to mate frequently (polyandry) and thus acquire critical nutrition or resources that males provide. My research focuses on the evolution of female ornaments by exploring the conditions that lead to selection for these unusual traits. In addition, I investigate the seemingly paradoxical co-occurrence of strong sexual selection on females with the post-copulatory sexual selection on males that we expect to occur with increased polyandry and thus, sperm competition. I test for sexual selection on females (ornamentation) and males (paternity) using a species of New Zealand ground weta (Orthoptera: Anostostomatidae), where males provide valuable mating gifts and females possess ornaments that apparently result from intense sexual selection. Using novel molecular methods to measure female mating success and paternity patterns, I report evidence of sexual selection on both sexes, although the nature of this selection differs from our expectations. My research highlights the importance of examining exceptional systems, which are valuable tools in testing theories of sexual selection and sex differences.

Brunet, Bryan, AAFC, Canadian National Collection of Insects; Gaelan Burke, University of Georgia Department of Entomology; Robert Footit, AAFC, Canadian National Collection of Insects; Nathan Havill, USDA Forest Service Northern Research; Spencer Johnston, Texas A&M University Department of Entomology; Carol von Dohlen, Utah State University Department of Biology

Building a phylogeny for the Adelgidae using shotgun phylogenomics and genome sequences of the Hemlock and Balsam Woolly Adelgids.

The Adelgidae (Hemiptera: Sternorrhynch: Aphidomorpha) contains two regulated pest species in Canada, the Hemlock (Adelges tsugae) and Balsam (Adelges piceae) Woolly Adelgids. These species cause significant mortality and reduced growth to hemlock and true fir species, respectively, in eastern and western North America. Despite a surge in genome sequencing of non-model systems over the last decade, the genomes of these species have managed to avoid attention. Recent molecular work has focused more on characterizations of adelgid symbionts, including the genome sequences of two A. tsugae obligate endosymbionts. In an effort to bolster genomic resources for A. tsugae and A. piceae, we use a combination of Illumina short-read and 10x linked read sequences to de novo assemble the first draft genomes for these species. Subsequent alignment of low-coverage short-read data for additional adelgid species/lineages will allow for investigation of the evolutionary relationships within the Adelgidae using phylogenomic methods based on orthologous gene regions.

Bryan, Safyha

Sub-lethal effects of mercury on Leach’s storm-petrel

Mercury is a non-essential element that occurs in food webs both naturally and from human inputs. Methylmercury form is toxic, and bioaccumulates, and biomagnifies in food webs. Marine diets consisting of invertebrates and mesopelagic fish can have high levels of methylmercury. Methylmercury can affect reproductive success of both mammals and birds, but a previous study found no evidence for this in Leach’s storm-petrels, the most abundant procellariiform seabird in the North Atlantic Ocean. We are following up on that study and testing for sub-lethal effects of methylmercury on
haemoglobin and blood glucose levels. We are also continuing to test if methylmercury is associated with reproductive success (hatching and fledging success). Mean total methylmercury concentrations in hemoglobin was 158.6 g/L and mean blood glucose was 7.1 mmol/L (wet weight). Initial correlations from a preliminary sample of 26 birds suggest lower glucose and haemoglobin concentrations for birds with higher body mass (r for glucose and mass = -0.3, for hemoglobin and mass = -0.17 and for glucose and hemoglobin = -0.20). Mercury analyses are forthcoming.

Bucci, Kennedy, University of Toronto; Malak Bayoumi, University of Toronto; Kathleen Stevack, Ministry of the Environment, Conservation and Parks; Trudy Watson-Leung, Ministry of the Environment, Conservation and Parks; Chelsea Rochman, University of Toronto

Investigating the effects of microplastics and their associated chemicals to fathead minnows at multiple levels of biological organization

Due to the pervasiveness of microplastics (plastic <5 mm) in aquatic environments, the public, scientists, and decision-makers often ask whether microplastics pose an ecological threat. However, investigation into the effects of microplastics to aquatic organisms is often conducted using simplistic scenarios that do not capture the reality of microplastics as a complex contaminant. These studies generally investigate effects by exposing low trophic-level species to extremely high concentrations of pristine microspheres. The goal of my project is to investigate how environmentally relevant concentrations and types of microplastics affect fathead minnows at multiple levels of biological organization. Fathead minnows were exposed to fragments of virgin polyethylene and polyethylene collected from the shore of Lake Ontario at two concentrations: 100 and 2400 particles per L. The exposure began at the egg stage, 24 hours post-fertilization, and will last until all breeding groups from the control treatment have laid at least 1000 eggs (5-7 months). Throughout this experiment, I will be investigating effects at the suborganismal-level (e.g. histopathology, gene expression), the individual-level (e.g. survival, length, body condition), and the population level (e.g. reproductive success, sex characteristics). I will also be quantifying length, deformities, and epigenetic effects in offspring. Results to date will be presented at this conference.

Burant, Joseph, University of Guelph; Gustavo S. Betini; D. Ryan Norris

Simple signals indicate which period of the annual cycle drives declines in seasonal populations

For declining animal populations, a critical aspect of effective conservation is understanding when and where the causes of decline occur. The primary drivers of decline in migratory and seasonal populations can often be attributed to a specific period of the year. However, generic, broadly applicable indicators of these season-specific drivers of population decline remain elusive. We used a multi-generation experiment to investigate whether habitat loss in either the breeding or non-breeding period generated distinct signatures of population decline. When breeding habitat was reduced, population size remained relatively stable for several generations, before declining precipitously. When non-breeding habitat was reduced, between-season variation in population counts increased relative to control populations, and non-breeding population size declined steadily. Changes in seasonal vital rates and other indicators were predicted by the season in which habitat loss treatment occurred. Per capita reproductive output increased when non-breeding habitat was reduced and decreased with breeding habitat reduction, whereas per capita non-breeding survival showed the opposite trends. Our results reveal how simple signals inherent in counts and demographics of declining populations can indicate which period of the annual cycle is driving declines.

Burbank, Jacob, University of Waterloo; D. Andrew R Drake; Michael Power; Mary Finch

The feeding ecology of the Eastern Sand Darter (Ammocrypta pellucida) near the northern edge of its range: a test of niche specificity

Niche specificity can predispose species to population declines during periods of resource limitation, yet niche specificity from a dietary perspective is poorly known for many small-bodied freshwater fishes. Applying a two-pronged approach based on stable isotope and stomach content analysis, we examined the diet and the isotopic niche size of the Eastern Sand
Darter, a threatened species under the Canadian Species at Risk Act. Eastern Sand Darter were found to consume a variety of organisms including Chironomidae, Cladocerans, Ostracoda, Oligochaeta and Ephemeroptera, although the proportional contribution of food items differed based on the method of investigation. Stable isotope results highlighted Eastern Sand Darter exhibit a relatively narrow isotopic niche, indicating increased sensitivity to environmental and anthropogenic disturbance if prey resources become limiting. Moreover, examinations of isotopic niche overlap with other co-occurring members of the fish community highlighted Eastern Sand Darter may experience competitive interactions for food resources with other benthic fish during periods of prey scarcity. We highlight that developing an understanding of a species feeding ecology and dietary niche provides useful insight into the resilience and potential population level responses to environmental and anthropogenic disturbances that modify prey availability.

Burgess, Brock, University of British Columbia, Okanagan; Robyn Irvine, Gwaii Haanas National Park Reserve, National Marine Conservation Area Reserve and Haida Heritage Site, Parks Canada; Michael Russello, University of British Columbia, Okanagan Campus

Invasive Sitka black-tailed deer population structure and movement dynamics in Haida Gwaii to support ecosystem restoration

Bush, Alex, Environment Canada; Monk W, Environment Canada, Compson Z. Centre for Environmental Genomics Applications; Porter T., Natural Resources Canada; Hajibabaei M., University of Guelph; Peters D., Environment Canada; Baird D, Environment Canada

Metabarcoding a Metacommunity: monitoring a wetland wilderness

The complexity and inherent variability of natural ecosystems can make it hard to detect change reliably. This issue has been exacerbated by trade-offs that reduce the quality and resolution of survey data for assessments at large-scales. The Peace-Athabasca delta (PAD) is a large wetland complex in northern Alberta, Canada. Despite its isolation, the PAD is potentially threatened by the development of oil sands mining, hydroelectric dams and climate change, and methods capable of reliably evaluating ecosystem condition are needed to manage those risks. Between 2011 and 2016, aquatic macroinvertebrates were sampled at eight sites primarily distributed across a gradient of flood frequency, applying both traditional morphological identification, and DNA metabarcoding. Using multi-species occupancy models we demonstrate that DNA metabarcoding identifies far greater diversity than was previously possible, that metabarcoding is a more efficient survey method than traditional approaches, and that this information has a substantial impact on our perception of community structure. Although assemblage composition of morphologically identified samples was unrelated to their environment, models based on metabarcoding were able to detect significant environmental effects, particularly to flooding covariates. The analysis also demonstrates that inter-annual and inter-site variability was extremely high, and the composition of wetland invertebrates is consistent with neutral metacommunity dynamics. Simulations using the observed metacommunity structure show that ecological change should be interpreted for the PAD landscape as a whole, and that our statistical power is greatly enhanced, particularly at a higher taxonomic resolution, by metabarcoding.

Butterson, Skye, University of British Columbia; A.D. Roe, Great Lakes Forestry Centre; K.E. Marshall, University of British Columbia

A case for considering plasticity in cold tolerance for eastern spruce budworm management

The eastern spruce budworm, Choristoneura fumiferana, is a widely distributed native insect known for its extensive defoliation of North American boreal forests. The larvae overwinter as second instar, and low temperature stress is an important regulator of populations and outbreaks. Current models predict that the distribution of outbreaks is likely to shift northward and higher in elevation with climate change, however, it is unknown how plasticity in cold tolerance might facilitate this shift. In collaboration with the Canadian Forest Service, we aim to quantify the existence and breadth of phenotypic and transgenerational plasticity in cold tolerance using wild and lab strain spruce budworm. Here differences in overwintering capacity and measures of cold tolerance show that considering plasticity is important for validating current population growth models and accurately predicting the nuances across the species range.
Urban Rat Movement Ecology and Pathogen Prevalence

Urban Norway rats (*Rattus norvegicus*) are the source of several important pathogens that are transmissible to people. Transmission of these pathogens among rats may be determined by rat movement and social structures, suggesting that interventions (e.g., pest control) that disturb colonies could affect pathogen ecology. The aims of this project were to: 1) use population genomic structure to evaluate whether rat movement patterns align with pathogen distributions; and 2) to investigate how a simulated pest control intervention could impact pathogen prevalence. To address aim 1, we sampled 1,500 single nucleotide polymorphisms from 615 rats caught in Vancouver, Canada and used pedigree analysis to identify parent-offspring and sibling relationships among sampled individuals. Using the inferred pedigree, we described movement events for closely related individuals, and compared patterns of relatedness and movement to prevalence data for the pathogenic bacterium *Leptospira interrogans*. We found that related individuals were most often caught within the same block; where siblings were trapped in different blocks, these blocks were adjacent. Prevalence of *L. interrogans* varied by block (0–66%). The spatial clustering of related individuals and *L. interrogans* lends support to the hypothesis that rat movement promotes the heterogeneous patterns of pathogen prevalence evidenced in this population. To address aim 2, we undertook an 8 month mark-recapture study in 36 city blocks. In 5 of these blocks, we enacted a kill-trapping intervention. Rats (*N* = 513) were trapped for 2 weeks before and after a 2-week intervention. We collected urine (tested for *L. interrogans* using PCR), and fecal/oral swabs (tested for methicillin-resistant Staphylococcus aureus using culture) for each rat. Multi-level logistic regression was used to identify the impact of the intervention on pathogen carriage while controlling for confounding variables (e.g., mass, sex, bite wounds). Rats caught in the intervention blocks following an intervention had a greater odds of carrying *L. interrogans* (OR: 9.55; 95% CI: 1.757–8.31), than did rats caught before the intervention. There was no impact on carriage of MRSA. These results suggest that current, lethal rat control techniques can have unintended and paradoxical effects on pathogen prevalence, which could increase human health risks. However, these effects depend upon the mode of transmission of the pathogen.

Impacts of social context and stress on foraging decisions in the common sunflower, *Helianthus annuus*

Organisms faced with patchily distributed resources balance costs and benefits of alternative patch-use decisions as part of an overall foraging strategy. My lab utilizes the model species, *Helianthus annuus*, to determine fundamental aspects of foraging decision processes in plants. By combining image analysis with the use of behavioural arenas, we can determine how root foraging effort in soil patches varies as a function of patch value, social context, and health status. Individuals typically allocate more foraging effort to high-quality soil patches relative to low-quality patches, however, this pattern is disrupted by a discrete stress event resulting in foraging effort independent of patch quality. The chronic stressor of sharing soil space with another plant also alters patch-use decisions at very fine scales. When a plant is equidistant from a high-quality patch shared with a neighbour, the plant demonstrates reduced patch use relative to individually grown plants. However, when the plant is closer to the patch than its neighbour, it increases patch use relative to individually grown plants, suggesting anticipatory patch-use. Combined, my lab group is demonstrating complex behavioural phenomena are not restricted to seemingly complex animals. The contingency of plant root foraging suggests similarity of ultimate causes among organisms living in a patchy world, even when proximate mechanisms involved differ.
Camaclang, Abbey, University of British Columbia; Jessica Currie, WWF-Canada; Emily Giles, WWF-Canada; Simon Mitchell, WWF-Canada; James Snider, WWF-Canada; Tara Martin, University of British Columbia

Prioritizing threat management in the Saint John River watershed

Deciding what actions to take to most cost-effectively conserve and recover multiple species across a region presents an enormous challenge. Priority Threat Management tackles this challenge by identifying management strategies that will safeguard biodiversity threatened by cumulative pressures, and prioritizing these strategies for implementation based on cost, feasibility, and their expected benefit to species persistence. Based on the principles of decision science, this approach emphasizes stakeholder engagement and provides guidance for the structured elicitation and use of expert judgement along with empirical data, thus facilitating collaboration and the use of the best available information for timely decision-making. We are currently applying the Priority Threat Management approach to identify priority actions for 45 species and 1 forest community of conservation concern within the Saint John River watershed in New Brunswick. Sixteen management strategies and their estimated costs, feasibility, and benefits were elicited from 28 experts in the ecology and management of these species. This data is used in a multi-objective prioritization to identify combinations of strategies that will recover the most species for a given budget. To date, Priority Threat Management has improved decision-making for species conservation in multiple regions around the world, and is now being tested here in Canada.

Cameron, Erin, Saint Mary's University; Helen R. P. Phillips, German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig; Ines S. Martins, German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig; Carlos A. Guerra, German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig; Nico Eisenhauer, German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig

Global patterns of belowground biodiversity

Human activities are accelerating biodiversity change but understanding of global biodiversity patterns remains limited, particularly for soil organisms. We examined global patterns of soil biodiversity by mapping indices of soil (bacteria, fungi, macrofauna) and aboveground (mammals, birds, amphibians, vascular plants) biodiversity that we created using previously published data on species richness. In addition, we compiled an extensive global dataset (>7000 sites) on earthworms to further investigate patterns of local species richness. Areas of mismatch between aboveground and soil biodiversity covered 27% of the Earth's terrestrial surface. Species richness peaked at higher latitudes for soil than aboveground biodiversity in both datasets, with intermediate soil biodiversity but low aboveground biodiversity occurring in the boreal to tundra biomes. More work is needed to fill geographic and taxonomic gaps in soil biodiversity data, but these results suggest management to protect aboveground biodiversity may not sufficiently reduce threats to soil biodiversity.

Cameron, Elyssa, Université du Québec à Montréal

Using a functional approach to improve urban forest resilience

Urban trees and forests are a crucial component of the urban landscape. They provide a multitude of benefits and services to citizen quality of life and health, known as ecosystem services. In the present context of global change, humans are expected to contend with a number of adverse effects which our urban forests have the potential to help mitigate. The problem is that our urban forests worldwide are currently at risk as a result of historic management strategies favoring the use of monocultures. Tree communities therefore lack overall complexity and resilience, making them highly vulnerable to sudden disturbances. To protect our urban forests, we have developed a new management approach rooted in functional traits, rather than species identity. This approach allows us to increase the resiliency of the urban forest and maximize the ecosystem services it can produce, while simultaneously being simple, straight-forward and effective for use by city planners. Our functional approach can then be built upon to integrate different criteria including, among others, availability, acceptability, vertical diversity and canopy cover.
The Ubiquity of Pink Noise and its Application in a General Model of Evolution

Environmental variation is the medium through which evolution operates. Evolutionary models of bet-hedging often assume n-state environments, commonly two, which fluctuate by randomly switching between states. For many models these fluctuations approximate white noise, where benign events are as likely as extreme events, and act only at the level of the population. The conclusion of such models that tacitly assume white noise is the transience of bet-hedging. Studies of environmental variation have been accumulating empirical evidence of reddened or pink noise, where the average frequency of an event is inversely proportional to its severity. Pink noise is a characteristic signal of biological systems, extinction patterns, ecological variability, evolvability, climate dynamics, DNA dynamics, and more. This ubiquity of pink noise warrants the re-evaluation of previous bet-hedging models. An individual-based model with environmental variation modeled as pink noise over longer timescales will investigate the evolution of timescale dependent adaptations and resolve the purported transience of bet-hedging.

Causes and consequences of genome size variation in an invasive plant, Centaurea solstitialis

The evolutionary drivers responsible for the extraordinary genome size variation across angiosperms are still largely unknown and biological invasions may present unique opportunities to clarify the population-level processes that shape this variation. Shifts towards smaller genome sizes have occurred in association with successful colonization events in other plants, suggesting phenotypic consequences of genome size variation, possibly due to cell size effects. If genome size imposes functional constraints, a potential invader may benefit from reduced genome sizes that promote ecological traits of the ideal weed, such as faster early growth and rapid development. However, variation in genome size may also result from selection along environmental gradients regardless of where populations are in the range. Conversely, founder effects and drift in small populations may have allowed neutral or detrimental increases in genome size in recently established populations at the leading edge of expansion. Centaurea solstitialis (Asteraceae) is an invasive thistle in North America, and previous work in this system has demonstrated rapid phenotypic evolution since introduction. We investigated the causes and consequences of intraspecific genome size variation in C. solstitialis across an invasion in California to ask: (1) Is trait variation associated with genome size variation? (2) Does selection for faster growth and reproduction at the leading edge of the expansion select for smaller genomes, or do founder effects and drift in recently founded populations allow genome sizes to increase? (3) Does selection on growth and reproduction along environmental clines select for variation in genome size? We conducted a common garden and estimated genome size by flow cytometry for 333 plants across 14 populations. We found larger genomes were significantly associated with slower vegetative growth and later flowering times, with lower lifetime biomass and flower production. We also observed a negative relationship with elevation, suggesting support for a hypothesis of selection for earlier flowering time, potentially due to shorter growing seasons at higher elevations. Despite these potential ecological consequences, we found no evidence of selection for smaller genomes during range expansion. Instead, we saw a significant, negative relationship with population age, consistent with the prediction that small founding populations allowed neutral or detrimental increases in genome size to rise to high frequency. This is one of the first demonstrations that small population sizes during range expansion might impact genome architecture. Future work concerns identifying the molecular mechanisms that underlie patterns of genome size variation, such as differences in transposable element content.
(B. suckleyi), have also declined significantly there. All of these bees have been assessed at some level of endangerment by the Committee on the Status of Endangered Wildlife in Canada (COSEWIC) based on their declining populations; these declines were documented primarily through changes in their relative abundance in museum collections, decade by decade. Across most of Canada, however, there are few or no data on trends in bumble bees we really don't know whether or not their numbers are going up or down, or if they are stable. To address this lack of information, we began a series of repeatable, roadside surveys of bumblebees in the Yukon in 2017; 10 were completed in 2017 and 16 in 2018. These surveys are modelled after the successful Breeding Bird Surveys (BBS), which began in 1966 and are now carried out by thousands of observers across North America each year. Similar bee surveys have been done in some of the eastern United States in recent years, and 29 were carried out in northern Ontario in 2017. We will present the 2017 and 2018 results of these surveys and discuss potential sources of variability within and between routes. All three Yukon species at risk (Western, Gypsy Cuckoo, and Suckleys Cuckoo Bumble Bees) were encountered in these surveys.

Cantin, Ariane, University of Calgary; John Post, University of Calgary

You are where you live: How habitat shapes populations dynamics in rainbow trout populations

Density-dependent processes play an important role in structuring population dynamics as the number of organisms within a set area increases, population vital rates and life history traits will also change arising from increased competition for limited food and space. I explore how variation in the quantity of habitat available impacts size-structured animal populations using lake-dwelling rainbow trout (Oncorhynchus mykiss). First, I developed hypotheses on the biological processes by which habitat impacts population dynamics using a multi-habitat age-structured population model. This theoretical model showed that habitat limitations at any life stage can bottleneck the population and impact its dynamics, but that the timing of regulation influences population outcomes. I then compared the model predictions to empirical data from 39 wild rainbow trout populations. The field results corroborated the model predictions and showed that limited habitat in early life resulted in low overall population density of larger fish, while limited habitat in adult life led to high density of stunted fish populations.

Capurro, Gabriela, Carleton University; Felipe Dargent, University of Ottawa

Beware of ticks and mosquitoes! Coverage of emergent vector-transmitted diseases in Canadian news media

Lyme disease and West Nile virus are two vector borne diseases in which ecological interactions play a critical role in disease transmission and incidence, while presenting distinct emergence patterns and severity of disease. The recent occurrence and expanding range of both diseases in Canada provides an opportunity to explore how emerging diseases are communicated to the public in the news media, as people still rely on news outlets for public health-related information. These narratives have implications on public understanding of diseases, affecting individuals risk behaviour, and assign infection prevention responsibility to different social actors. We conducted a qualitative content analysis of coverage in ten Canadian newspapers and online news sites since 2002 to assess (1) whether the volume of coverage corresponds with the incidence and severity of these pathogens in Canada; (2) whether climate change and ecological interactions are mentioned as causes of these diseases; (3) which prevention measures are suggested; and (4) what is the role assigned to government and individuals in preventing the spread of these diseases.

Carcamo, Hector; Xiuhua Wu; Tracy Larson; Brian Beres; Timothy Schwinghamer

Can we “trick” wheat stem sawfly through manipulation of host plant quality?

Cephus cinctus can fertilize their eggs to lay female progeny depending on host quality. A number of studies have shown that wheat of higher stem diameter have female biased sex ratios relative to thinner stems. To manage this pest, farmers plant wheat with solid pith that kill juveniles and reduce female fitness. Expression of the solid pith increases with low plant populations that result in thicker diameter stems. Thus, we conducted a field cage study to test the hypothesis that female sawfly could be “tricked” into laying female eggs into apparently good (thick) hosts of a solid stem cultivar (AC Lillian). We expected that AC Lillian thick hosts would reduce female fitness by shifting sex ratios towards males.
Triticale (cultivar Pronghorn) and the wheat cultivar CDC Go were the hollow-stemmed hosts in 2009 and 2010, respectively. Treatments included a choice or no choice treatment within a cage where sawflies had a choice of stands with high or low plant densities with varying stem diameters. Only the no choice treatment with thick-stemmed solid cultivar in 2010 had an even sex ratio. Very low plant densities of solid stemmed wheat are likely required to reduce female biased sex ratios.

Caron, Anne-Sophie, Concordia University; Joshua Joseph Jarry, Université du Québec en Abitibi-Témiscamingue; Benoit Lafleur, Université du Québec en Abitibi-Témiscamingue; Emma Despland, Concordia University

Does predator- and parasitoid-caused mortality differ between defoliated and non-defoliated sites? A study of Forest Tent Caterpillar in mixedwood boreal and temperate forests of Quebec

Forest Tent Caterpillars (*Malacosoma disstria*) are early-spring defoliators attacking hardwood tree species, in the temperate and boreal mixedwood forests of Canada. The pest is present in ON, SK, MN, and AL. Outbreaks vary depending on the geographical location. In southern Quebec, outbreaks tend to be shorter and closer together, while in the north, they tend to be longer and at longer time intervals. With climate change, it is becoming increasingly difficult to predict winter temperature, which plays an important role in the survival of FTC colonies. This difficulty also comes from the challenges in conducting studies on low-density, pre-outbreak populations. At that stage populations are not present in sufficient numbers to be sampled efficiently and are less visible. While outbounding population vary dramatically in mortality rates, endemic populations are less understood. In this study, we present results that aim to understand population dynamics of FTC at low density, especially interactions with predators and parasitoids. We compare survival rates of FTC colonies in sites that were both previously defoliated and not defoliated in two forest types, temperate and boreal mixedwood. We observed differences in community assemblages of arthropod predators at the same sites. We focus on taxonomic groups that have been shown to predate on FTC such as ants, spiders and beetles and on possible parasitoid wasps and flies. By gaining a better understanding of the predator-prey interactions in those types of forests, we can gain some insight into the FTC population cycles and thus be equipped to face its threat.

Carroll, Oliver, University of Guelph; Andrew MacDougall

A devils bargain: eliminating nutrient co-limitation increases grassland productivity but elevates the risk of biomass instability

Ecosystem productivity is often co-limited by multiple nutrients such that increasing nutrient availability increases biomass production. However, the paradox of enrichment suggests short-term increases in productivity may decline over longer periods. Despite the consequences of this for ecosystem function, the effects of different nutrients on productivity over time are not clear. We assessed response ratios of biomass in plots fertilized with factorial combinations of nitrogen (N), phosphorus (P), and potassium with micronutrients (K+¼) relative to control plots in 29 globally distributed grasslands over seven years. After one year, we observed average biomass increases of 17% with N, 7% with P, 0.5% with K+¼, and 32% with simultaneous NPK+¼. After seven years, this increased to 11% with P, 7% with K, and 73% with NPK+¼. However, N and NP caused initial biomass increases to crash over time. Further, N and P produced significant and independent biomass destabilization effects (increased interannual variation), whilst K+¼ did not affect biomass stability. Diversity can maintain biomass stability but, over 7 years, different nutrient treatments produced distinct trajectories of change in community composition and species loss. Accordingly, different nutrient combinations represented paradoxes of enrichment of differing severity, with distinct effects on productivity, diversity, and stability.

Carscallen, Grace, University of Western Ontario; Zoë Lindo, University of Western Ontario

Spiders and flies: seasonality and habitat specificity of key Boreal peatland arthropod communities

Soil organisms are hyperdiverse, have high biomass, and are a vital food source for organisms in both below-ground and above-ground environments. However, soil arthropods are not well understood because they are difficult to directly
observe. Many soil-dwelling species only live in soil for part of their life cycles, emerging when they reach maturity. Along with predatory arthropods on the soil surface, these emergent arthropods connect the below-ground system to the above-ground food web. I examined the diversity of soil and soil-surface dwelling macroarthropods in two adjacent peatlands that differ in water table, nutrient level, and vegetation. I collected arthropods using insect emergence traps and pitfall traps. I found that 85% of all emergent arthropods were flies in the suborder Nematocera, and 65% of all surface-dwelling arthropods were spiders. Overall abundances declined for both emergent and surface-dwelling arthropods over the growing season in both peatlands, and the community composition of both emergent and surface-dwelling arthropods varied significantly by both peatland and sampling period. Knowledge of peatland arthropod diversity is lacking, but vital for monitoring climate change, reclamation activities, and to understand the peatland food web.

Catton, Haley, Agriculture and Agri-Food Canada; Hector Carcamo, Agriculture and Agri-Food Canada; Brian Beres Agriculture and Agri-Food Canada

Wheat stem sawfly response to intercropping in triticale

Wheat stem sawfly, *Cephus cinctus* (Hymenoptera: Cephidae) is a stem-boring pest of cereals in western North America. Triticale (*×*Triticosecale) can be affected through tissue damage in the stem during larval feeding and from stem cutting at larval maturity. Intercropping can be an effective tool for disrupting insect infestations. Here, triticale was planted in monoculture, or in intercrop with peas (each crop planted at 60% of monocrop density) for 3 years. Sawfly infestation, damage, and parasitism were measured via stem dissections and counts of cut stems. Results show that intercropped triticale had a higher proportion of stems containing sawfly larvae than monocrop triticale, but that difference did not translate to increased stem cutting. This pattern suggests that something about intercrop plants made them more prone to oviposition by female sawflies, but less prone to stem cutting by sawfly larvae. One possibility is that intercropped triticale with its reduced intraspecific competition produced plants with larger stems. Stems with greater diameter are attractive to ovipositing females, but may also be stronger and more resistant to lodging from larval damage. Future research is needed to characterize the specific behavioural responses of sawflies and morphological responses of triticale to monocrop and intercrop settings.

Chagnon, Pierre-Luc, Université de Montréal

Will mycorrhizal symbiosis make green roofs greener?

Green roofs are increasingly considered as sources of ecosystem services in urban environments. While we are well aware of the benefits plants derive from microbial symbionts in natural environments, we know virtually nothing about the microbiome of plants colonizing green urban infrastructures. Yet, the mycorrhizal symbiosis has great potential to alleviate water stress in green roofs, which are urban environments very prone to drought. Yet, for allochthonous inoculation of green roofs with mycorrhizal symbionts to be successful, it will be necessary to validate the success of symbiosis establishment in such harsh environmental conditions. Here, we report the impact of a wide water availability gradient on the early establishment of mycorrhizal symbionts in the roots of *Trifolium repens*. We show that severe drought can hamper the development of the symbiosis, suggesting that pre-inoculation of plants before installation on green infrastructures may be necessary to ensure deriving benefits from the symbiosis in urban ecosystems.

Champagne, Emily, University of Guelph; Dr. Kevin McCann, University of Guelph

Farming changes the menu for fish: A shift towards autochthonous driven food-webs in highly impacted streams

Local and regional impacts associated with agricultural activity can have drastic impacts on aquatic ecosystems. Increased nutrient inputs, channelization, reduced riparian habitat and faster hydrologic response times both upstream and locally all contribute to the degradation of stream ecosystems and their function. Here, we examine food webs, specifically fish communities, to determine the effects of agriculture on food web energy pathways and trophic structure in watersheds which feed into Lake Erie. The key players in stream fish communities were analysed using stable isotopes, including $^{13}$C $^{15}$N and $^2$H to evaluate terrestrial and aquatic energy sources as they move through the aquatic food web, as
well as trophic structure and position. These were then compared to multivariate metrics using multiple scales of environmental data to determine an agricultural impact gradient. Early results confirmed our hypothesis and show that aquatic energy input and trophic position both increase significantly with agricultural impact. These likely correspond with greater light input and nutrient levels, along with reduced in-stream habitat.

Champagne, Emilie, Département de biologie & Centre détude de la forêt, Université Laval; Alejandro A. Royo, USDA Forest Service Northern Research Station; Jean-Pierre Tremblay, Centre détudes nordiques, Université Laval; Patricia Raymond, Direction de la recherche forestière, Ministère des Forêts, de la Faune et des Parcs

Trees defence against herbivores: evaluating the resistance potential of seedlings along a latitudinal gradient

Forest composition could change in the coming century, mostly as a result of global changes. To facilitate this transition in a context of exploitation, managers are considering assisted migration, i.e. the planting of southerly sources of tree species, potentially adapted to projected climate in northern locations. The successful establishment of these seedlings, however, could be limited by herbivores. Resistance to herbivore could vary along a latitudinal gradient in plant productivity, in which seedlings from southern populations, with higher growth rates, would contain lower concentrations of defence compounds than northern seedlings. Our objective was to evaluate the resistance potential of eight species from three provenances distributed along a latitudinal gradient, based on their concentration in defence compounds (phenolics, terpenes, fibres). We observed intraspecific variation in terpene concentration among provenance for some species ($Picea$ glauca, $P.$ rubens and $Thuja$ occidentalis) and in fibre concentration among provenance of all species. Variability in defense compounds were inconsistent along the gradient, and southern populations did not consistently contain lower concentration of defense compounds, suggesting population-specific levels of resistance. Those differences could be used to select seed provenance in plantation projects. The next step will be to evaluate the link between resistance potential and realized herbivory.

Charlebois, Julia

A meta-analysis examining the relationship between inflorescence architecture and outcrossing rate in flowering plants

In flowering plants, inflorescence architecture (i.e., shape, interfloral spacing) and adaptations to separate male and female function in (e.g., dichogamy, herkogamy, dioecy) interact with pollinator morphology and behaviour to alter the flow of pollen within flowers, between flowers, between inflorescences, and between individuals. The goal of this meta-analysis is to examine the relationships between inflorescence architecture and outcrossing rates in flowering plants to understand the role of inflorescence architecture in plant mating.

Chiasson, Billie, Université de Moncton; Gaétan Moreau

Successional convergence of flying Coleoptera communities in plantations and regenerated forests

The nature of the disturbance triggering successional events in a community is known to affect the rate of succession and species occurrence at different seral stages during succession. This implies that forests originating from different silvicultural approaches may or may not converge in composition, depending whether the deterministic nature of the succession process was altered by management. Here, we test the hypothesis that with time, the deterministic processes involved in structuring species assemblages will bring about successional convergence of animal communities in extensively and intensively disturbed habitats. To this end, we evaluate how flying Coleoptera communities of coniferous plantations and naturally regenerated coniferous stands change during post-logging forest succession. Using flight intercept traps, we collected a total of 15 641 flying Coleoptera from 228 different species, genera or families in forests of New Brunswick at different seral stages. Results suggest that flying Coleoptera communities highly differ in young regeneration stands and young plantations but are similar in older seral stages. This suggests that both pathways of succession converge over time but raises concern for the conservation of early successional communities in intensively managed forest landscapes.
Chin, Andrew, University of Toronto, TRCA; Namrata Shrestha, Toronto and Region Conservation Authority; Marie-Josée Fortin, University of Toronto

Habitat suitability of avian functional groups in current and future land use scenarios in urban environments

Consequences of urbanization, such as land use conversion or intensification and natural cover loss, may have both local and regional scales of impact resulting in biodiversity loss and degradation. Therefore, understanding effects of how the current land use changes affect species may help better manage future biodiversity loss. Here we use functional trait groups of species relating to their habitat needs and requirements to assess the status of biodiversity functions in urban environments. Specifically, we focused on two avian functional groups of forest canopy foragers/nesters, and aerial insectivore foragers with data collected from 2007-2017 by the Toronto and Region Conservation Authority, Ontario. We used the amount of land use, vegetation communities, and habitat connectivity as predictors of habitat suitability in the Greater Toronto Area. We used boosted regression trees to model habitat suitability under the current landscapes capacity to identify where in the landscape support the highest capacity for each functional group. The current landscapes capacity was compared to the habitat suitability in the future landscapes capacity based on official plans that will result in land use and cover changes. We found that habitat connectivity mainly drives habitat suitability and, thus, an influential factor in current and future scenarios.

Chisholm, Sarah, University of Ottawa

Satellite-remote-sensing for the assessment of protected areas: a global application

Unprecedented rates of species extinction present serious challenges in the field of conservation biology. Although protected areas are key tools to preserve vital habitats, emphasized by the Convention on Biological Diversity (CBD) s installment of Aichi Target 11, increasing the amount of protected land does not directly translate into the protection of biodiversity. Manipulation of the surrounding landscape outside of protected area boundaries also has the potential to affect ecosystem processes that occur inside of their boundaries and, ultimately, their integrity. A global assessment of the conservation efficacy of protected areas highlights a lack of data for such a task. Under development by the Group on Earth Observations Biodiversity Observation Network (GEO BON), satellite-remote-sensing essential biodiversity variables (SRS-EBVs) seek to fill this gap. Using time series data of several ecosystem structure and function SRS-EBVs, I compared their rates of change from within and outside of protected areas worldwide to conclude whether the global network of protected areas has preserved these variables through time. I found that, although most ecosystem structure variables were preserved within protected area boundaries, indicators of ecosystem functions were not, emphasizing the need to reconsider the managerial practices of protected areas and their surrounding landscapes.

Choi, Duck-Soo, Jeonnam Agriculture research and extension service; Kyung-Cheol Ma, Hyo- Jeong Kim, Jin-Hee, Lee, Sang-A Oh

Light Responses of Riciania shanthungensis (Hemiptera: Riciiidae) Adults and Attraction Effect of Capturing Device

In order to effectively control the Riciania shanthungensis, we investigated the light response to adults and developed an adult catching device using light with superior attractiveness. The preference among six light sources such as daylight color, green, etc. for the Riciania shanthungensis adult was most favored with daylight color 97 > black 79 = red 79 = blue 79 > green 24 > yellow 13. We have developed an adult catching device using the most preferred daylight colors and behavioral habits of the Riciania shanthungensis. The capture device consisted of two daylight compact lamps (30W, 20W), a yellow plate, and a catcher using water, and caught about 700 individuals a day. The capturing device has a large amount of capturing because adult is activity at high nighttime temperatures, but the capturing amount decreased significantly when the temperature dropped below 23. More than 85% of the Riciania shanthungensis adults were trapped for 3 hours from 19:00 to 23:00. Therefore, it is considered that the adult capturing device for the control of Riciania shanthungensis is used from mid July to late August when the night temperature is over 23, and lights up from 19:00 to 23:00.
Chouinard-Thuly, Laura, UQAM CRAM; Daniel Chapdelaine, Maxime Charbonneau, François Dumont, Simon Lachance, Pierre-Olivier Montiglio

Population differences in male tarnished plant bug response to female pheromones

Pheromones are species-specific chemical signals used to communicate. Individuals are predisposed to respond, but environmental conditions might affect how they respond. The tarnished plant bug (TPB) is a prevalent polyphagous pest insect in Eastern North America. Males are attracted to a pheromone composed of more than 5 compounds emitted by females. We investigated population differences in male responsiveness to female pheromones in two TPB populations from Ontario and Quebec using a Y-olfactometer. Males from both populations spent an equal amount of time in the branches of the olfactometer. Males from Ontario spent 99% of their time in the branch with females, regardless of the population, compared to an empty branch. However, they preferred females from their own population when given the choice between females from the two populations. Males from Quebec spent 1% of their time in the branch with females, regardless of the population, compared to an empty branch. They preferred females from the Ontario population when given the choice between females from the two populations. Our results validate the olfactometer design for the TPB and suggest important population differences in the response to pheromones.

Chuard, Pierre, Bishop's University; Jade Savage, Bishop's University

eTick.ca: a Canadian citizen-science tick monitoring tool and information dissemination platform

The distribution and abundance of several tick species of medical relevance is rapidly changing in Canada. The eTick.ca citizen-science web platform is an online tool created to engage the public in tick monitoring efforts, decrease pressure on provincial identification resources, and return rapid personalized feed-back to citizens concerned with tick bites. Pictures of ticks submitted on eTick.ca are identified to species by trained personnel and results (along with relevant public health information) are communicated in less than 24 hrs. The public version of eTick.ca, originally launched in the province of Quebec, has now expanded to Ontario and New Brunswick. Preliminary data for the 2019 tick season are presented and the influence of social media to raise awareness to the etick.ca platform is discussed.

Clake, Danielle, University of Calgary; Dr. Paul Galpern, University of Calgary; Dr. Sean Rogers, University of Calgary

Bumble bee dispersal across elevation gradients: using landscape genomics to evaluate consequences of climate change

The global ranges of bumble bee species are changing globally, including a shift to higher elevation habitats in many species. These changes have consequences for these pollinator populations, especially in highly heterogeneous montane habitats which may be especially susceptible. My research uses techniques from the fields of landscape and population genomics to answer the following question: does the close geographic proximity of high and low elevation environments found in mountain landscapes allow species to utilize these different habitats, or are they specialists in either high or low elevation environments? I have sampled bumble bees at 40 different sites throughout the Rocky Mountains. Sites were chosen to cover a range of elevations while minimizing correlations between pairwise distances and elevation differences between sites. I have extracted DNA from collected Bombus melanopygus and Bombus sylvicola individuals to generate genome sequencing data. This will be used to assess gene flow and dispersal between sites, and to compare models of isolation by distance and isolation by elevation. Understanding how bees move between locations, and how they utilize habitats at varying elevations will be important in evaluating their future ability to track predicted habitat and range changes.

Clark, Catherine, Agriculture and Agri-Food Canada; Sébastien Boquel, Yvan Pelletier, Claudia Goyer

After fifteen years, is Myzus persicae (Sulzer) adapted to table beet?
Myzus persicae (Sulzer) is an important agricultural pest worldwide feeding on over 400 host plants in 50 families. This species shows considerable variation with respect to adaption to its host plants. The objective of this study was to determine if M. persicae originating on potato and reared on table beet for over 15 years had adapted to table beet. In a survival experiment, longevity and fecundity were both statistically reduced (30 and 85%, respectively) for M. persicae reared on beet than fed beet leaves compared to M. persicae reared on potato than fed potato leaves. Ethological observations showed significant differences in behavior for M. persicae reared on beet placed on beet leaves compared to M. persicae reared on potato placed on potato leaves. Probing and feeding behavior assessed with the electrical penetration graph (EPG) technique showed that for M. persicae reared on beet placed on beet, a number of behavioral response variables differed significantly from those for M. persicae reared on potato placed on potato. These results indicate that even after 15 years of being reared on table beet, M. persicae had not become well adapted to this host.

Cloonan, Kevin, Acadia University; Laura Ferguson, N. Kirk Hillier

Helicoverpa punctigera olfactory receptor neuron responses to heliothine sex pheromone components and their antennal lobe projection destinations

We challenged male Australian budworm, Helicoverpa punctigera, antennal sensilla trichodea with five heliothine pheromone components using single sensillum recordings. We then stained the olfactory sensory neurons (ORNs) housed in these sensilla with micro-Ruby (dextran, tetramethylrhodamine and biotin) and imaged their axon projections in the antennal lobe glomeruli using confocal microscopy. We found that unlike the corn earworm, Helicoverpa zea, and the cotton bollworm, Helicoverpa armigera, which have three different functional types of sensilla trichoidea (A, B, and C), H. punctigera have only two functional types of sensilla trichoidea (A and C) similar to the oriental tobacco budworm, Helicoverpa assulta. Helicoverpa punctigera type A sensilla contain one ORN that responds to the major sex pheromone component Z11-16:Ald in a dose dependent manner (0.1-10 ulg) with axons projecting to the cumulus of the macroglomerular complex (MGC). The co-compartmentalized large- and small-spiking receptor neurons in type C sensilla responds to the minor pheromone components Z11-16:OAc, Z11-16:OH, Z9-14:Ald, and Z9-16:Ald in a dose dependent manner with axons projecting to both the dorsomedial posterior glomerulus and the dorsomedial anterior glomerulus. The sex pheromone blend required to obtain optimal H. punctigera male captures is Z11-16:Ald/Z11-16:OAc/Z9-14:Ald at a ratio of 100:100:5. Axons from the large-spiking neurons in these type C sensilla responding to the behavioral agonists Z11-16:OAc and Z9-14:Ald may project to the dorsomedial posterior glomerulus. Those axons from the small-spiking neurons responding to Z9-16:Ald may project to the antagonist-sensitive dorsomedial anterior glomerulus. Future studies will investigate the role of Z9-16:Ald on male H. punctigera upwind flight behaviors to optimal pheromone blends.

Closs, Alana, University of Waterloo

Uncovering the ecological legacies of long-term landscape management in the Pacific Northwest

Landscapes have been continuously shaped and changed by long-term human interactions. Quantifying these interactions allows us to strengthen ecosystem integrity and resilience while considering humans as key drivers of ecological change. In the Great Bear Rainforest of British Columbia (BC) 14,000 years of human presence remains detectable in the landscape, providing a unique opportunity to understand long-term human-induced changes to ecosystem structure and function. Indigenous knowledge suggests that for millennia, people living along BCs Central Coast have been transplanting and cultivating economically important plants to ensure a reliable food source. My research quantifies ecological changes to coastal plant species in the Great Bear Rainforest that have resulted from long-term Indigenous plant management and cultivation techniques. The two main questions explored in this paper are 1) are the ecological legacies of Indigenous resource management techniques still detectable in present-day biodiversity patterns of shoreline plant species, and 2) has human management influenced the abundance and distribution of the economically valuable species, Pacific crab apple? The results of this study revealed differences in the richness and abundance of Shoreline plant species between sites with and without human presence, as well as significantly higher concentrations of crab apple trees on sites which people inhabited.
Cluney, Victoria, Saint Mary's University; Laura Weir

Fishery-Induced Life History Evolution in Coho Salmon

Anthropogenic exploitation is capable of inducing evolutionary changes in life histories when the phenotype selected for or against is heritable. Notably, commercial fisheries can drive evolutionary change by selecting against late-maturing individuals in a population. This study examines how the closure of an Oregon salmon fishery may exert artificial selection pressures on alternative male phenotypes in coho salmon (*Oncorhynchus kisutch*). These fish have two heritable male life histories: the majority of males mature as three-year-old fighters that compete directly with other males for access to spawning females, while the rest mature precociously after six months as sneakers, or jacks, and gain fertilizations by sneaking into spawning territories. Oregon coho were exploited by a commercial fishery that specifically targeted three-year-olds from the early 1900s until its closure in 1994. To test the prediction that artificial selection against fighter males increased survival, and thus frequency of sneaker males, sneaker frequency was calculated before and after the fishery closure for 46 populations from 14 basins. Higher mean sneaker frequencies were observed in 40 of 46 populations in the 13 years before than in the 10 years following the fishery closure. This trend is consistent with theory, and suggests an evolutionary response to fishery-induced artificial selection in exploited salmon populations.

Collins, Sydney, University of Guelph; Scott A Hatch, Institute for Seabird Research and Conservation; Kyle H. Elliott, Department of Natural Resource Sciences, McGill University; Shoshanah R. Jacobs, Department of Integrative Biology, University of Guelph

Boldness, mate choice, and reproductive success in *Rissa tridactyla*

As many long-lived seabirds are biparental and monogamous, individuals need to choose their mate wisely. While assortative mating based on physical traits is widely studied, mate choice in sexually monomorphic species based on behavioural traits remains poorly understood. We propose that personality is a possible factor on which mate choice is based and that certain personality traits within a behavioural syndrome confer a greater fitness. Here we measure boldness, a commonly explored behavioural syndrome, in black-legged kittiwakes (*Rissa tridactyla*) nesting at Middleton Island, Alaska. We measured boldness by presenting subjects with a novel object and recording the response. We considered the first principal component scores from the analysis of these responses to represent an individuals boldness. Some kittiwakes exhibited the strategy of assortative mating based on boldness, and bold birds that assortatively mate exhibited the greatest reproductive success. Within a breeding season, individuals became bolder as they reached the most critical point in the breeding season (chick hatching) which supports our finding that bolder individuals have greater reproductive success. We conclude that personality should be considered when investigating mate choice because individual personality may have an important influence on reproductive success.

Colston-Nepali, Lila, Queen's University; Jennifer Provencher, Department of Wildlife Health, Canadian Wildlife Service; Mark Mallory, Department of Biology, Acadia University; Vicki Friesen, Department of Biology, Queens University

Using genomic tools to answer conservation questions in an arctic seabird

Human activities and climate change are the largest threats to Arctic ecosystems. Canada has an international responsibility to protect species that inhabit or breed in its Arctic territories, including several seabirds. Population genetics may help conservation practitioners appropriately manage threatened species, by providing indications of genetic diversity within and between populations. The northern fulmar (*Fulmarus glacialis*) is a seabird that breeds in colonies throughout the North Atlantic and North Pacific Oceans. Though not currently considered at risk, fulmars face increased levels of toxins and ingested plastics, up to 1% of the global fulmar population is killed annually through unintentional capture in commercial fishing activities, and fulmar survival is negatively affected by climatic changes. For these reasons, we are investigating the genetic structure of fulmars in the North Atlantic to aid development of management plans. I will outline our results generated using restriction site-associated DNA sequencing (RADseq), which provided thousands of genome-wide markers for analysis. Furthermore, because northern fulmars are migratory, mortality often occurs away
from the breeding colony, and the impact of these sources of mortality on specific colonies is unknown. Therefore, I will further outline our efforts to use genomics for population assignment of birds caught in fishing activities.

Compson, Zacchaeus, Centre for Environmental Genomics Applications; (2,3) Wendy A. Monk, (4)Natalie Rideout, (5)Sonja Stefani, (1,6) Mehrdad Hajibabaei, (6,7) Teresita M. Porter, (6)Michael Wright, (2)Donald J. Baird, 1 Centre for Environmental Genomics Applications 2 Environment and Climate Change Canada @ Canadian Rivers Institute, University of New Brunswick 3 Faculty of Forestry and Environmental Management, University of New Brunswick 4 Canadian Rivers Institute, Department of Biology, University of New Brunswick, 5 Dresden University of Technology, Institute of Hydrobiology 6 Centre for Biodiversity Genomics & Department of Integrative Biology, University of Guelph 7 Natural Resources Canada, Great Lakes Forestry Centre

Exploring DNA-based food webs as rapid indicators of ecosystem change: evidence for trophic downgrading?

Trophic downgrading occurs when predator removal alters the structure and function of food webs. While evidence of top-down influences on food webs abounds, most evidence for trophic downgrading comes from studies where large vertebrate predators were extirpated from ecosystems. Further, most evidence of top-down trophic cascades comes from studies of relatively simple food webs with a single dominant food chain. Wetlands, however, are among the most biodiverse ecosystems, creating unique problems for measuring food webs. Using DNA metabarcoding to characterize aquatic communities provides a standardized, sensitive method for rapid bioassessment, but it does not yield requisite trait information for food web construction. We combined DNA metabarcoding with trait matching to create heuristic food webs for the Grand Lake Meadows, Atlantic Canadas largest freshwater wetland. We explored (1) how environmental change influences the properties of heuristic food webs, and (2) how food web properties correlate with leaf litter decomposition. Natural and anthropogenic disturbances depressed trophic height across this wetland invertebrate food web, leading to accelerated decomposition rates. We examine this evidence in the context of top-down regulation of invertebrate shredders and expound on how this pattern, together with impaired food web structure, could impact provisioning of floodplain services.

Cordero, Ruben, University of Toronto; Donald A. Jackson

Is random really random? The influence of habitat filtering on null models and species co-occurrence patterns

Abiotic factors have long been recognized to have a strong influence on the community structure at multiple scales. For example, the species-area relationship has been considered one of the few laws of ecology with area integrating various abiotic factors. Although many studies have demonstrated the direct relationship between area and species richness, it remains unclear whether and how this factor influences patterns of species co-occurrence (i.e. positive, negative or random). It has been observed that lake surface area and depth influence species richness and composition in lakes. In this study, we aim to understand how habitat filtering related to these abiotic measures affects co-occurrence patterns for 76 fish species in more than 2000 lakes in Ontario. We show the importance of considering such abiotic conditions in null model co-occurrence studies.

Cornic, Maelle, Fisheries and Oceans; Xinhua Zhu; David Cairns

Decline of American eel population: what can we do?

American eel (Anguilla rostrata) is considered as a panmictic population widely distributed from Greenland to northern South America. Recent stock assessment in Canada and the US indicated that American eel population was declining. This study investigated the abundance trends of American eels in Canada using catch per unit of effort (CPUE) as an index of relative abundance. Catch data from fisheries-independent surveys were standardized using a generalized linear mixed model to include temporal (year, month) and environmental factors (temperature, flow, water level) as potential explanatory variables. American eel abundance indices revealed regional difference with a sharp decline in abundance in Lake Ontario (-96%) while the population trends appeared to be stable, but at low abundances, in the other eastern
provinces over the last 20 years. The low abundance and the absence of a concrete population recovery plan are a concern for long-term species conservation. Therefore, it is essential to develop data-limited methods and international collaborations to better understand factors influencing American eel population to provide science advice and maintain stock at or above sustainable levels.

Corona, Cristian; Abigail C. Leeper; Jalene M. LaMontagne, Department of Biological Sciences, DePaul University

Eastern spruce budworm defoliation of white spruce over balsam fir in N. Wisconsin, USA

Eastern spruce budworm (Choristoneura fumiferana) is a defoliating insect in Canada and the northern border states of the United States. Their eggs are laid upon the needles of balsam fir and white spruce trees as primary host trees, and the larvae consume the needles during their development. Spruce budworm have been reported to typically consume approximately equal amounts of balsam fir and white spruce, or to prefer balsam fir. During an outbreak of spruce budworm at sites in northern Wisconsin, USA first detected in 2014 an observation was made that white spruce appeared more impacted than balsam fir. In summer 2019 we revisited two forested sites with the objective to quantify spruce budworm impacts on the two tree species. Based on a survey of white spruce and balsam fir trees, we found that approximately 50% of the white spruce trees and 0% of fir trees had died since 2014. We also compared characteristics of live and dead trees including diameter at breast height, crown class, and tree density; preliminary analyses indicate that tree species was the most relevant factor for defoliation.

Costamagna, Alejandro, Department of Entomology, University of Manitoba; T. Nagalingam, Department of Entomology, University of Manitoba; H. A. Cárcamo, Agriculture and Agri-Food Canada, Lethbridge Research Centre; T. Wist, Agriculture and Agri-Food Canada, Saskatoon Research Centre; J. Otani, Agriculture and Agri-Food Canada; J. Gavloski, Manitoba Agriculture; R.W. Duncan, Department of Plant Science, University of Manitoba; J. Bannermann, Department of Entomology, University of Manitoba

Management of flea beetles in Western Canada

The flea beetles Phyllotreta cruciferae (Goeze) and Phyllotreta striolata (F.) (Coleoptera: Chrysomelidae) are major pests of canola (Brassicaceae) in Western Canada. To manage flea beetles, canola growers rely on insecticide treated seeds and foliar insecticide applications when required. During 2015 to 2018, we conducted several small plot trials in Alberta (Lethbridge and Peace River regions), Manitoba and Saskatchewan. The experiments were conducted in standard agronomic small plots in a completely randomized block design with four to five replicates and under natural levels of flea beetle infestation. The treatments included an unsprayed control, a neonicotinoid-treated seed with no foliar insecticide spray, foliar insecticide spray at 15-20%, 25%, and 45% defoliation levels. We assessed defoliation by flea beetles, canola phenology, flea beetle abundance, and seedling survival. When the average defoliation of a sprayed treatment reached its threshold, the plots were sprayed with foliar insecticide, within 24 h of the assessment. The results of different defoliation spray treatments and seed treatments on defoliation levels, plant survival and yield will be discussed.

Cote, Isabelle, Simon Fraser University; Siobhan Gray, Bamfield Marine Sciences Centre Tomas J Bird, Memorial University

A class effort: Monitoring ecological shifts in a marine community across extreme disturbances

Marine communities of the shallow northeast Pacific region have experienced two large-scale disturbances: the mass mortality of many of species of large, predatory seastars in 2013, followed by a period of anomalously warm water (the blob) from 2014 to 2016, when surface waters were up to 4°C warmer than normal. The ecological effects of these events are poorly documented, particularly for subtidal communities, but they were captured in an opportunistic time-series of fish and invertebrate abundance collected at the Baeria Rocks Ecological Reserve. Since 2007, students from the Bamfield Marine Science Centre have surveyed, using standardised underwater methods, the two islets of the Reserve as the capstone project of their scientific diving course. I will present the trends in abundance of the fish and invertebrates
surveyed, and consider the coincidence of timing of these changes in community assemblages with that of major environmental disturbances. The result is a unique picture of the changes that have occurred over more than a decade at a remote site that is, by virtue of its isolation, relatively unaffected by other anthropogenic pressures, and a prime example of the power of recurring field courses in generating such a picture.

Crane, Adam, Concordia University; Laurence Feyten Grant Brown

Temporally-variable predation risk and fear retention in Trinidadian guppies

Fear is a unifying theme across animal taxa. Our work with a social fish, the fathead minnow, has demonstrated that exposure to intense predation risk induces high-risk behavioural traits (freezing, pacing, neophobia, and socially-transmitted neophobia). Conspecific models can weaken this high-risk phenotype, an outcome known as social buffering. First, we showed that exposure to risk in isolation causes stronger neophobia than risk in groups. Then, a subsequent period with a social group facilitated a weakening of the phenotype, but only when social models were calm. However, individuals that acquired the high-risk phenotype in isolation were more influenced by social models. In a second experiment, we used models in a one-on-one setting, with models being periodically replaced with new calm models after acquiring socially-transmitted neophobia. Again, the high-risk phenotype was weakened in observers, as was its social transmission. Our results may have therapeutic applications for fear recovery in other animals, and we discuss a fish model in the context of the validating criteria for animal models of Post-Traumatic Stress Disorder.

Crispo, Erika, Pace University

Underwhelming evidence for the effectiveness of Avida-ED software to teach genetic drift concepts in undergraduate classrooms

Avida-ED is a software application designed to teach evolution. The application consists of asexual digital organisms that evolve via random mutation, genetic drift, and natural selection; and includes options for users to manipulate mutation rate, population size, and selective pressures. A lab manual designed by the software developers includes four prefabricated exercises, including one each on the randomness of the mutation process and on genetic drift. I chose to explore the effectiveness of Avida-ED for learning genetic drift, a notoriously challenging topic for undergraduates, through the implementation of these two exercises under two different classroom settings. One setting was an introductory freshman biology laboratory course restricted to Honors students, and the other was an upper-year evolutionary biology elective. Students were given a genetic drift concept inventory (Price et al. 2014), both before (pre-test) and again after (post-test) completing these two exercises in class. Students were asked to either agree or disagree with a number of statements presented in the concept inventory. Although overall scores were higher on the post-test, results were discouraging in that students often performed worse on the post-test than on the pre-test. The questions that were answered most poorly differed between the two classes. In general, learning was greater in the introductory course than in the upper-year elective, despite similar scores on the pre-test.

Cross, Regan, Department of Biology, Queen's University; Christopher G. Eckert, Department of Biology, Queen's University

Long-term persistence of a species beyond its natural range

Species should be able to continuously adapt to conditions at their geographic range edges and disperse into the habitat beyond, yet most do not. Experimental planting of species within and beyond their range directly tests the mechanisms causing stable range limits, however experimental populations are rarely followed for more than one generation, providing little insight into long-term demography and potential for local adaptation beyond the range. In 2005, we transplanted eight source populations of the Pacific coastal dune plant Camissoniopsis cheiranthifolia into four sites within and one site beyond its northern range limit. During the first generation, fitness of beyond-range individuals was comparable to within-range populations, suggesting that the northern range edge is limited by dispersal rather than niche constraints. Compared to sites within the range, the beyond-range population experienced high seedling recruitment in the two seasons following
the transplant. Approximately 12 generations after planting, beyond-range individuals remained as abundant and reproductively successful as within-range individuals, providing compelling support for a role of dispersal in limiting the northern range edge for this species. Long-term experiments provide robust conclusions in the face of environmental stochasticity, and allow for a better understanding of how species respond to novel habitats.

Crowley, Samantha, Department of Ocean Sciences, Memorial University; Ian R. Fisheries and Oceans Canada, Northwest Atlantic Fisheries Centre; Amber M. Messmer, Fisheries and Oceans Canada, Northwest Atlantic Fisheries Centre; Shahinur S. Islam, Department of Ocean Sciences, Memorial University of Newfoundland; Ian A. Fleming, Department of Ocean Sciences, Memorial University of Newfoundland

Assessing genetic influence on growth and survival of juvenile farmed, wild, and hybrid Atlantic salmon (Salmo salar) in nature

Farmed Atlantic salmon have experienced multiple generations of both intentional and unintentional domestication selection, generally reducing their fitness in the wild. When farmed salmon escape and interbreed with wild populations, these differences can lower wild population productivity and alter key life history traits. Understanding the genetic basis of relative survival and fitness related traits (i.e. growth) of farmed, wild, and hybrid salmon is critical to predicting population impacts from farm escapees. To date, only a few European studies have considered all cross-types under common conditions in the wild, which are not necessarily applicable to North American populations. This study assesses differences in growth and survival of experimentally derived Atlantic salmon fry from four cross-types (wild, farmed, and reciprocal F1 hybrids) during the first summer of growth at three replicate locations in a southern Newfoundland river. Preliminary analyses indicate differences in size (weight and length) and survival based on cross-type, with wild fish having lower growth but greater survival than farmed fish, and cross direction influencing the performance of hybrids. These findings extend existing studies of wild, farm, and hybrid Atlantic salmon growth and survival in the wild, and inform predictions of population responses to escaped farmed salmon in Atlantic Canada.

Culjak Mathieu, Vinko, McGill University

Temporal dynamics of plant-pollinator networks in the Canadian Arctic Archipelago

In the Canadian Arctic, climate change is disrupting pollination services and reducing plant community robustness by diminishing pollinator diversity, shifting flowering phenology, and rearranging plant-pollinator networks. This study aims to describe the properties and temporal dynamics of an arctic plant-pollinator network across a flowering season. Thus, we actively sampled 2,346 pollinators in two habitats types, recorded 4,002 plant-insect interactions, and measured the flowering phenology of 20 plant species on Victoria Island, Nunavut, in summer 2018. Preliminary results suggest the presence of pollination syndromes across major pollinator groups and generalisation within groups. Next, we will ID insect specimens to improve the resolution of the plant-pollinator network and to determine the properties of the network. Describing this network will facilitate making testable predictions of climate change effects on plant and insect communities in the Arctic.

Cullingham, Catherine, Carleton University; Joshua Miller, University of Alberta; Rhiannon Peery, University of Alberta; Julian Dupuis, University of Hawai'I; Rene Malenfant, University of New Brunswick; Jamie Gorrell, Vancouver Island University; Rose Andrew, University of New England; Jasmine Janes, Vancouver Island University

When does K=2, and what does it mean?

Delineating populations from genetic data is commonly used for wildlife conservation and management. Many studies use the program STRUCTURE, combined with the “K method to identify the most probable number of genetic populations (K). We recently found that K=2 was identified more often as the optimal solution using the “K method compared to studies that did not use the method. There are two reasons for this, first is hierarchical population structure leading to underestimating the actual number of populations. While the second, is the inability to assess K=1, leading to
overestimating the actual number of populations. Our current work aims to provide guidance for authors finding K=2, and to develop a better understanding of the " K statistic. We simulated two populations, and varied the migration rate between them (m=0.0001 to 0.5). From these simulations we calculated the " K statistic for K=2 and FST. Our findings show that the magnitude of " K corresponds to the level of divergence between the populations, and this method quickly breaks down once m=0.005. This highlights the need for studies to report all relevant statistics, but more importantly from a conservation and management perspective, genetic populations may not be identified at relatively low migration levels.

Cumming, Heather, Canadian Food Inspection Agency

Introduction to Plant Health Risk Assessment

An introduction to the work performed by the Plant Health Risk Assessment Unit of the Canadian Food Inspection Agency (CFIA) will be given. In addition, the plant health risk assessment process will be explained with specific examples of invasive insect species that are of concern to the CFIA.

Currie, Jessica, WWF-Canada, Valentina Marconi, Zoological Society of London; Scott Findlay, University of Ottawa

An analysis of threats and factors which predict trends in Canadian vertebrate populations

The identification of threats to native flora and fauna is critical in the formulation of strategies to successfully combat biodiversity loss. In Canada, threats to at-risk populations are systematically identified by the Committee on the Status of Wildlife in Canada (COSEWIC). Here we investigate the leading threats to 180 COSEWIC-assessed at-risk vertebrate populations, which also contain long-term abundance data available from the Living Planet Index Data Portal. We investigated threat profile the combination of threats for a given population as a predictor of population trends exclusively, and in combination with additional biotic and abiotic factors. Biological resource use was the most frequently cited threat to at-risk vertebrate populations, while herpetofauna were largely considered the most threatened taxonomic group. Moreover, our analysis revealed a strong association between taxonomic group and population trends. Threat profile, however, was not a strong predictor of the likelihood of annual increasing population trends for the analyzed sample. Given the cumulative and compounding nature of biodiversity threats, it is important to gain an understanding of threat profiles and factors which do or do not predispose Canadian-assessed at-risk vertebrates to declining trends in population abundance. This evidence base can aid in more appropriately prioritizing conservation action.

Curry, Colin, Wolastoqey Nation in New Brunswick

Expanding the role of Indigenous peoples in next-generation ecosystem biomonitoring

Across Canada, Indigenous peoples hold rights to harvest natural resources that are protected by both the constitution and treaties with Canada or the British Crown. Due to strong legal and cultural ties to the land and water, Indigenous peoples seek to take leadership roles in ecosystem monitoring to safeguard their rights. By permitting work to be conducted in more remote areas by users without extensive scientific training and potentially at a lower cost than established methods, next-generation ecosystem biomonitoring tools will be valuable in supporting their role. Novel tools could also affect the regulatory environment, providing Indigenous peoples with more effective ways to document the impact of development on the ecosystems that support their rights (e.g. through more effective documentation of cumulative effects). Successful partnerships among Indigenous communities, academia, government and industry requires a shift in practice. Early engagement, capacity building, sustained communication and respect for Indigenous knowledge systems will all be necessary for collaborators who seek to work with Indigenous communities on next-generation ecosystem monitoring.
DNA-based diagnostic tools targeting the spruce budworms natural enemies

Annual monitoring of mortality agents in the course of a spruce budworm (SBW; *Choristoneura fumiferana*) population cycle is an essential component of any study aimed at identifying the factors governing the rise and decline of outbreaks. To date, assessments of causes of SBW mortality have relied on laboratory rearing of field-collected larvae, followed by visual identification of emerging parasitoids and/or microscopic analysis of fungal pathogens in larval carcasses. Although this approach has so far provided vital information on the abundance and identity of mortality agents, the procedure is labour-intensive, costly, and can show limits in terms of accuracy. In an effort to overcome these shortcomings, we undertook the development of a suite of molecular assays that make use of real-time quantitative PCR (qPCR) and TaqMan® technologies. The assays rely on the identification of species-specific molecular variants (single nucleotide polymorphisms [SNP] markers) in mitochondrial (COI) and nuclear (28S rDNA) genes, which are then targeted by qPCR primers and TaqMan probes. The suite of assays works like an insect identification key, where molecular signatures substitute for morphological characters. The tool we have developed has four modules that can be used in combination or independently, depending on the level of diagnostic precision required.

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Effets de l'inoculation de champignons mycorhiziens arbusculaires en milieu agricole sur les insectes phytophages du soja

Outre leurs effets bénéfiques sur la nutrition et la croissance des plantes, les champignons mycorhiziens arbusculaires (CMA) peuvent influer indirectement sur les performances des insectes phytophages. Par exemple, les populations de tels insectes peuvent être favorisées ou désavantagées par la présence du CMA selon leur biologie particulière. En effet, l'utilisation d'inoculants introduits de CMA dans les systèmes agricoles est en développement et il est difficile de prédire les conséquences écologiques surtout sur la communauté des insectes. Notre étude vise à appréhender les effets d'une souche de CMA, *Rhizophagus irregularis* sur la diversité des pucerons et autres insectes associés au soja au champ. Dans deux localités du Québec (Varennes et Saint-Simon), un même dispositif en blocs complets randomisés avec divers traitements d'inoculant et engrais a été mis en place. Nous avions effectué ensuite un inventaire des insectes dans les parcelles avec trois types de pièges (Aspirateur-DVAC, bols jaunes et pièges fossés). La comparaison de l'entomofaune des parcelles avec et sans inoculants, sera discutée. Mots clés : Mycorhize arbusculaire, inoculant, symbiose, insectes, soja

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Local adaptation of an anadromous salmonid fish to marine conditions of the Arctic ocean

The importance of natural selection and adaptation in the genetic differentiation of populations across a species range is a fundamental question in evolutionary biology. Local adaptation to riverine conditions has been detected in many salmonid species. Arctic Char (*Salvelinus alpinus*) is an anadromous salmonid known to migrate to coastal feeding areas in proximity to their natal rivers, which could indicate a potential for local adaptation to the marine as well as the freshwater environment. We assessed neutral genetic population structure at a local and regional scale and detected potential targets for selection in the southwestern Canadian Arctic, an environmentally heterogenous marine region. We sampled 800 individuals from 25 localities in Nunavik (Quebec), Baffin Island (Nunavut) and northern Labrador, and over 25,000 SNP markers were obtained using genotyping-by-sequencing. Patterns of genetic diversity show signs of neutral structure, with pairwise Fst values ranging from 0.07 to 0.16 for populations of a common glacial lineage. Both monogenic (e.g. Bayenv, LFMM) and polygenic (e.g. RDA) methods were used to test the association between genetic markers and a wide range of environmental. These results will give insight into the adaptation of anadromous fishes to their environment during the entirety of their life cycle.
D'Aloia, Cassidy, University of New Brunswick; Jose Andres, Cornell University; Steven Bogdanowicz, Cornell University; Peter Buston, Boston University

Intensive geographic and genomic sampling are both required to uncover fine-scale genetic structure in a marine metapopulation.

Marine populations often exhibit subtle population structure that can be difficult to detect at fine spatial scales. Given recent advances in high-throughput sequencing, an emerging question is whether various genomic approaches will substantially improve our understanding of genetic structure in the sea. We explored hierarchical patterns of structure in the reef fish Elacatinus lori using a high-resolution approach with respect to both geographic and genomic sampling. We systematically sampled individuals at ~10 km intervals across the entire Belize barrier reef. We then sequenced all individuals at four sets of markers: 57 anonymous nuclear loci; 2,418 ddRAD-derived SNPs; 89 microsatellites; and ~12 kb of the mitochondrial genome. There was mito-nuclear discordance: mtDNA displayed no discernible pattern, whereas all three the nuclear data sets resolved genetic breaks at small spatial scales (d 10 km). More broadly

Daniel, Jody, University of Waterloo; Rebecca C Rooney

Aquatic macroinvertebrates, but not wetland birds or plants, exhibit reduced niche partitioning in permanently-ponded marshes

Both hydroperiod and cross-taxon interactions are important drivers of biotic community composition in marshes, but their relative magnitude of influence on community functional diversity is understudied. Because prior research revealed that species turnover is lower in permanently-ponded marshes, we asked: could increased niche partitioning (i.e., species segregation in functional traits) explain this lower turnover? We used structural equation modeling to compare the relative influence of biological interactions and hydroperiod on the niche partitioning of birds, plants and aquatic macroinvertebrates in southern Albertan marshes. We compared the fit of six models, which explored ways that: 1) hydroperiod structures communities and 2) communities may influence each other. The best fitting model was the one in which hydroperiod had the strongest influence on macroinvertebrate niche partitioning, which was highest in less permanently-ponded marshes. In contrast, niche partitioning for birds and plants was lowest in less permanently-ponded marshes. Additionally, niche partitioning among birds and macroinvertebrates was influenced by plants. We show that: 1) the sustained presence of ponded water may increase niche overlap for some taxa (i.e., macroinvertebrates) but cause declines among others (i.e., birds and plants), and 2) taxa lower on the food chain (i.e., plants) have the strongest relationships with other taxa.

Dankworth, Marie; Dr. Gary Saunders

The relative abundance of hedophyllum nigripes in the bay of fundy over time

Since the early 1980s, the sea surface temperature (SST) in the Bay of Fundy has risen on average 1°C per decade, particularly during spring and autumn. It is likely that cold water adapted kelps will no longer survive if SST in the Bay of Fundy continues rise. For the seaweed species Hedophyllum nigripes it was hypothesized that an initial decline recorded in 2012 in the Bay of Fundy was correlated to a winter of unusually warm SST. During the investigated period between 2010 and 2012, the relative abundance of H. nigripes dramatically declined and did not fully recover to 2010 values by the end of their study in 2014. Therefore, I have completed a local ecological survey of H. nigripes, Laminaria digitata and Saccharina latissima to provide new insights on biogeography and survivorship of kelp species in a warming Bay of Fundy. Recent data from 2018 has revealed a rebound of H. nigripes at Lepreau (Bay of Fundy), which is again the dominant contributor in the intertidal kelp community. No S. latissima specimens were detected at the investigated sample site in 2018. An inverse correlation of the relative abundance of H. nigripes and L. digitata is observed. H. nigripes was highly abundant (70-80%) in 2010-2011 and in 2018 compared to L. digitata, which had a low abundance (20%) in 2010 and 2018. The low relative abundance of H. nigripes in 2012 resulted in enhanced relative abundance of L. digitata (64%). SST in Bay of Fundy is a major factor that varied and was approximately 4°C warmer in 2012-2013 (8°C) compared with 2010 (2-5°C), 2011 (3-5°C) and 2018 (3-5°C). Thus my preliminary data continue to support the hypothesis that unusually high SST contributed to the relative decline in H. nigripes.
Dargent, Felipe, University of Ottawa

Integrating parasite communities into infection-diversity research

The study of infection dynamics and host-parasite interactions has been crucial to understanding the pervasive role that disease has on ecosystems. These studies have traditionally focused on single-host single pathogen species interactions. Recent interest in integrating a community-wide perspective shows that the diversity of co-existing species often influence disease dynamics leading to positive or negative infection-diversity correlations, and challenges predictions derived from single host-single parasite studies. This expanding view of disease and community interactions, although useful, has some important limitations, one of them is that it neglects among-parasite and vector species interactions and their links to host species dynamics. I present a conceptual model outlining the effects of parasite communities in shaping broader infection-diversity patterns, and contrast its predictions to data from recent publications.

De Heij, Stefanie, University of Saskatchewan; Christian Willenborg, University of Saskatchewan

Patterns in Carabid weed seed consumption in Pulse crops

Carabids (Carabidea: Coleoptera) can be beneficial insects in agriculture by consuming pests and weed seeds. But, weed seed consumption is found to be variable, and correlations between seed predation and carabid activity density are not always found. Why? We are exploring the role of carabid seed predation in weed seed reduction and the factors that could explain variations herein. This work can aid in the understanding and design of carabid biocontrol efforts. We found an overall low, but highly variable, correlation between carabid activity-density and seed consumption. Field factors like, crop type, crop history, and soil type played an important role in carabid community differences, but not in seed consumption. Our future work will explore whether carabid foraging behavior can explain discrepancies between carabid activity-density and seed consumption.

De Keyzer, Charlotte, University of Toronto; James D. Thomson, University of Toronto; Thomas M. Onuferko, Canadian Museum of Nature; J. Scott MacIvor, University of Toronto

Spatiotemporal variability in bloom period supports greater bee diversity in cities

Shifts to earlier flowering and leaf-out phenology have been observed in cities around the world. Drivers include increased temperature due to urban heat island effects and increased photoperiod due to artificial light at night. Phenological responses along rural-urban gradients have been predicted using linear relationships with distance to city core, but this simplifies much of the heterogeneity found within cities. Indeed, few studies consider the ecological importance of intra-urban flowering time variation. At spatial scales relevant to plant-pollinator interactions, floral resource phenology is hypothesized to be an important filter on wild bee communities. In this study we characterize floral resource phenology of an early flowering, bee-pollinated tree, the eastern redbud (Cercis canadensis) across Toronto, Ontario. We surveyed 24 sites to assess composition and turnover in the wild bee community during the bloom period. In 2018, this lasted 33 days, with each individual tree flowering for an average of 16 days. We found that intra-urban variation in bloom period was correlated to microclimate conditions, specifically the average daytime air temperature in May. The bee community shifted from Andrena-Osmia to Lasioglossum-Agapostemon dominated. High spatiotemporal variability in flowering meant that this resource was available to a greater diversity of bees through time.

Deakin, Samuel, University of Alberta

Development and validation of a high density SNP array for genomic studies of Rocky Mountain bighorn sheep

When using molecular markers to investigate genetic architecture of phenotypic traits greater densities of markers improve both the accuracy and reliability of the conclusions. Here we document the development and testing of a high-
density single nucleotide polymorphism array, for genotyping Rocky Mountain bighorn sheep at ~50,000 loci. Following an initial database search, we identified ~4.5 million variant sites in the Rocky Mountain bighorn sheep genome, from multiple sources. Utilizing several bioinformatic tools we filtered these initial variant sites to retain ~50,000 high quality, highly variant SNP loci suitable for genotyping through single primer enrichment technology (SPET). The purpose of this array is to enable us to characterise the genetic basis of phenotypic traits in Rocky Mountain bighorn sheep. Prior attempts have been made to examine the effect of loci on phenotype in bighorn sheep, however these studies lacked the resolution to detect any loci of significant effect. Utilizing life-history data, morphometric measurements, and genotypic data from the ~50,000 loci, we will perform genome wide association surveys (GWAS) in an attempt to characterise the genetic basis of horn-size, body mass, and reproductive success in Rocky Mountain bighorn sheep.

Deb, Jiban Chandra, University of New Brunswick; Graham Forbes, University of New Brunswick; David A. MacLean, University of New Brunswick

Modelling spatial distribution of North American woodland mammals under changing climates for conservation prioritization

North America encompasses most of the ecological zones of the world and has a diverse array of mammal species. Model projections indicate significant variations in future climates of North America and the habitats of woodland mammals of this continent may be particularly sensitive to changes in climate. We modelled the spatial distribution of thirteen North American woodland mammals under changing climates and examined the potential influence of the mean and seasonal climate, topography and land use/land cover variables on the distribution of species. Presence-only occurrence records of species, six predictor variables, two future climate scenarios (RCP4.5 and RCP8.5), and two time steps (current and 2070) were used to build species distribution models using a maximum entropy algorithm (MaxEnt). Our results suggest that overall, most of the mammals are likely to gain suitable climate space across the continent except for *Lepus arcticus*, *Ursus americanus* and *Rangifer tarandus*, which are likely to lose suitable habitat by 2070. Furthermore, habitat suitability is likely to be expanding northwards under future climate scenarios for most of the mammals. We recommend managing in situ and ex situ climate refugia as a potential strategy for conservation planning of the mammals.

DeClerck-Floate, Rose 1, S. Blatt 2; D. Ostrander 3; B. Dunlop 4; P. Mason 5; Agriculture and Agri-Food Canada; 1 Lethbridge, AB, 2 Kentville, NS, 3 Swift Current, SK, 4 Brandon, MB, 5 Ottawa, ON

Early exploration of the establishment limits of a new weed biocontrol insect in Canada

The stem-galling weevil, *Rhinusa pilosa* Gyllenhal (Coleoptera: Curculionidae) was recently approved for biocontrol of the invasive perennial, yellow toadflax (*Linaria vulgaris* Mill.; Plantaginaceae) in Canada. Initial releases were made across Canada in 2014-16 (average 155 weevils/site, n=31) to obtain a preliminary sense of the geographic limits of *R. pilosa*’s establishment, as measured by its persistence and increase at repeatedly monitored sites. As of 2018, *R. pilosa* had colonized 68% (21/31) of release sites (BC, AB, SK, MB), and population increases had occurred at 57% (12/21) of these. The strongest increases occurred at higher elevations in BC and AB, perhaps associated with greater moisture. No releases persisted in ON or NS. To explore the limits of when *R. pilosa* (univoltine) could be released to initiate populations, two AB studies investigated galling success upon release of adults: 1) in early versus later spring; i.e. in relation to shoot availability for galling (n=3 sites/gp), and 2) in fall (pre-diapause) versus spring (reproductive) (n=4 sites/gp). More galls were produced when weevils were released in later versus early spring, and fall-released weevils survived the winter to produce as many galls as spring-released weevils. Results are shaping strategies for future use of *R. pilosa*.

Delgado Aquije, Maria Lisette, Dalhousie University; Aliro Manosalva, Universidad de Concepción; Evelyn Habit, Universidad de Concepción; Mauricio Urbina, Universidad de Concepción; Anne C. Dalziel, Saint Mary's University; Konrad Górski, Universidad Católica de la Santísima Concepción; Oscar Link, Universidad de Concepción; Daniel E. Ruzzante, Dalhousie University

Genomic and plastic differences between diadromous and resident galaxias maculatus populations in chile
Diadromy, the ability to migrate between fresh- and seawater, is a life history trait suitable for the study of local adaptation and adaptation to salinity changes. Here, we focus on Galaxias maculatus, one of the most widespread fishes in the Southern Hemisphere. We first compare 10 diadromous and resident population pairs across the species distribution in Chile using genome-wide SNP markers. Diadromous populations exhibit high gene flow, while most resident populations were strongly genetically distinguishable by both neutral and selective factors, forming their own genetic group. We then examine how diadromous and resident populations respond to salinity changes. We reared from two pairs of diadromous and resident populations under a common garden setting. Diadromous adults were highly plastic consistently enduring abrupt changes in salinity. Resident adults instead varied in their response as a function of river of origin. Resident G. maculatus from the first river showed no plastic response and an inability to survive abrupt increases in salinity, while resident individuals from the second river exhibited a plastic response similar to diadromous individuals. These findings suggest that resident populations differ in their ability to survive in estuarine and marine environments pointing to differences in local adaptation and suggesting independent colonizations.

Demers, Jacob, Mount Allison University; Dr. Joshua Kurek

Aquatic Ecosystem Senescence of Wetland Impoundments in the Upper Bay of Fundy, Canada

The loss of wetlands through human activities has raised the importance of preserving these habitats. Wetlands provide ecosystem services to humans and to the species of wildlife that use them. We are investigating observed declines in primary productivity in 30 freshwater wetland impoundments in the Upper Bay of Fundy. This phenomena is commonly referred to as senescence and supported by recently published research and observations from wetland managers. Impoundments vary from newly flooded (<2yrs) to 50 years old. Each impoundment was sampled for macroinvertebrates in its emergent vegetation, submerged vegetation, and open water habitats in the spring, summer and fall of 2018. Water chemistry and soil organic content measurements were collected for each site. Water quality demonstrates pH, total organic carbon, total inorganic carbon, ammonium and total nitrogen levels to be highest among newly restored impoundments. Macroinvertebrate assemblages displayed shifts in species composition in relation to impoundment age. Ephemeroptera, Hemiptera and Diptera taxa were most abundant in younger sites (<10yrs) while Coleoptera and Trichoptera were most abundant in older sites (>10yrs). This research is ongoing and the findings will deepen the understanding of how wetland senescence may structure the aquatic environments of impoundments and the ecosystems services that they support.

Demers, Ebony Elizabeth, Concordia University; Jean-Michel Matte, Concordia University; Grant E. Brown-Concordia University

Ecological Uncertainty Delays Learning of Novel Foraging Tasks

The variability of predation risk in time and space means prey cannot always recognize imminent threats. This ecological uncertainty can lead to prey making behaviourally inappropriate and potentially costly decisions. Uncertain conditions are known to induce avoidance behaviours towards novel stimuli (i.e. neophobia) as a means of protection from unknown risks. While neophobia can reduce the predation costs associated with uncertainty, we might expect it to have costs associated with other fitness related activities, such as foraging. Here, our goal was to determine whether ecological uncertainty negatively impacts the learning of a novel foraging task. Manipulating predation risk as a proxy for uncertainty, we pre-exposed Trinidadian guppies (*Poecilia reticulata*) to conditions of high or low risk. We then used operant training methods to form an association between one of two coloured objects and a food reward. During the training phase, a reinforcement stimulus of high vs. low risk was administered twice daily. Individuals exposed to uncertain reinforcement stimuli were significantly slower to learn the food association than those exposed to the low risk. Our data suggests that uncertainty delays the learning of a novel foraging tasks and highlights the potential costs of neophobia.
Dennert, Allison, Simon Fraser University; Dr. Elizabeth Elle; Dr. John Reynolds

An experiment in marine-derived nutrients: salmon carcasses and marine algae alter coastal plant traits

Nutrient deposition can change terrestrial plant biomass, floral rewards, flower size, and inflorescence number. While studied extensively in agricultural contexts, nutrients at the boundary of two ecosystems such as land and sea are less commonly studied. For example, Pacific salmon (Oncorhynchus spp.) influence many coastal organisms due to their role in aquatic nutrient cycling, which make salmon streams important ecosystems in which to study nutrient dynamics. Despite work illustrating the importance of salmon to terrestrial ecosystems, the extent to which species traits are altered by marine nutrient deposition is unresolved. Through a three-year field experiment, we tested the relationship between pink salmon (O. gorbuscha) carcass and/or marine algae (Fucus distichus) deposition and terrestrial plant reproductive allocation, leaf nutrient content, and floral visits by pollinators. Treatments with both a salmon carcass and algae showed an increase in leaf size across all flower species measured, and only treatments with algae had larger floral display than the control. However, there were no differences in leaf nitrogen content across treatments. This work is some of the first experimental evidence linking marine-derived nutrients to changes in organismal traits and demonstrates the importance of the land-sea interface to coastal plants in the Pacific Northwest.

Déry, Florent, Université Laval & Centre d'études nordiques; Sandra Hamel, Université Laval; Steeve D. Côté, Université Laval & Centre d'études nordiques

Fitness benefits of vigilance: offspring from more vigilant mothers survive better

Vigilance is a behaviour aiming at detecting threats from predators and conspecifics. Although it is costly in terms of time, early detection can improve survival and allow avoidance of risky interactions, therefore, vigilance can potentially provide fitness returns. Even though drivers of vigilance have been extensively studied, whether vigilance increases fitness remains largely unexplored. We investigated this relationship in adult female mountain goats in west-central Alberta (Canada). Using focal observations collected over 12 years, we first evaluated which intrinsic and extrinsic factors influenced vigilance in terms of alert frequency and duration. We used a joint modelling approach to simultaneously model multiple response variables, including alert frequency, alert duration, total time spent vigilant, kid survival and female survival, while accounting for explanatory variables influencing each response variable. This allowed to estimate the latent correlation among vigilance and fitness responses due to female identity. We found that all correlations between vigilance and fitness responses were positive. Nonetheless, only correlations between kid survival and alert frequency and total time spent vigilant were strong and clear. This suggests that mothers allocating more time to vigilance improved their fitness by increasing offspring survival.

Deschodt, Pauline, Simon Fraser University; Olivia J. H. Walker, Simon Fraser University; Jenny S. Cory

Effect of mixed pathogen infections on pathogen transmission in the field

Mixed pathogen infections are common. Pathogens co-infecting a host may compete for resources or through the host immune system or interfere directly with each other. These competitive interactions could alter pathogen transmission via changes in behaviour, timing, replication or alterations in virulence. Yet, there are little empirical data on how mixed infections affect pathogen replication and subsequent transmission. Moreover, traits that enable a pathogen to be a good competitor within the host might not be the same as those that are needed for its successful transmission. Using the cabbage looper Trichoplusia ni larva, its nucleopolyhedrovirus (TnSNPV) and the entomopathogenic fungus, Beauveria bassiana, we are exploring how mixed pathogen infections alter replication and pathogen transmission. We will present data from a semi-field experiment where transmission from a single pathogen species is compared with transmission from insects challenged with two pathogens simultaneously or asynchronously. Lab data showed that the number of viral transmission stages produced is higher in mixed infections; however, mortality is increased in mixed infections but the proportion killed by virus declines in the presence of fungus. Thus the outcome in the field, where host behaviour, pathogen persistence and host plant quality also play important roles, is hard to predict.
Dettlaff, Margarete, University of Alberta; Jonathan A, University of Alberta; Nadir Erbilgin, University of Alberta; James F Cahill Jr, University of Alberta

Aspen chemotype patterns suggest local chemical diversity.

Understanding the production and distribution of plant secondary chemicals is crucial to our understanding of how plants respond to external stressors. One approach to understand these responses is to look for plant chemical phenotypes (chemotypes) and determine whether regional or local processes drive chemotype patterns, as this can have broader impacts on ecosystem health. For example, if patterns are driven regionally, then large-scale stressors could have a single widespread impact, potentially affecting ecosystem resilience. Using a survey of natural aspen stands across central Alberta we asked if chemotypes were present, how they were distributed, and if they were associated with regional climate variables, stand structural characteristics, or individual tree measures. We identified two chemotypes; one characterized by high concentrations of condensed tannins and one with high phenolic glycosides. Despite predictions that aspen stands should have low local chemical diversity due to clonal growth patterns, more than 50% of stands exhibited both chemotypes. Neither regional climate factors nor individual tree size was associated with chemotype; however, a combination of stand attributes was significant. These results suggest that local processes are the major driver of aspen chemotypes and that these systems may be resilient to wide-scale stressors.

Dey, Cody; Semeniuk, CAD; Iverson, SA; Gilchrist, HG

Have nesting common eiders redistributed in response to polar bear predation?

Losses of Arctic sea ice are causing polar bears to increasingly forage on colonial seaduck eggs in lieu of ice-based hunting of marine mammals. While polar bear predation of bird eggs has been widely documented, it is unclear whether this change in predator behavior is having population-level consequences for Arctic breeding birds. Here, we analyze the spatial distribution of polar bear sign observed during common eider breeding surveys in Hudson Strait, Canada, and the spatial response of the eider nesting population to variation in polar bear presence. We found that polar bear sign was more likely to occur on islands far from human communities and on islands with more eider nests. However, the spatial response of common eider nests to variation in polar bear presence was statistically unclear. In our analysis, the distribution of eider nests did not clearly shift closer to human communities or towards more onshore locations, nor did we find that eiders tended to disaggregate (i.e. spread out among islands) in areas with high polar bear presence. This study suggests that the spatial overlap between eiders and polar bears varies across the landscape, but patterns of polar bear spatial variation have not driven large-scale redistribution of nesting common eiders.

Diamond, Tony

Launching, maintenance and succession of a long-term field research programme; experiences and lessons.

I describe the establishment and maturation of a long-term ecological study of the seabird community of Machias Seal Island in the Bay of Fundy, begun in 1995 and now in year 4 of a 5-year handover period to Dr Heather Major of UNB Saint John. Funding was initially through a renewable 5-year discretionary grant under NSERC-Government Research Chair program (a Mulroney-era Green Plan initiative) mirroring one at Simon Fraser University. Research structure was a core of monitoring contributed to by a mixture of research techs hired for the summer, and graduate students carrying out their own projects. The overall focus was broad - detecting change (however caused) and interpreting in terms of change in marine environment with emphasis on demography and diet. An unique advantage was proximity to other colonies in the Gulf of Maine and collaborations with researchers at those colonies, allowing a metapopulation approach that is rarely feasible at this scale. Guaranteed funding ceased after 15 years, requiring frequent negotiations with funders especially on the issue of multi-year support, and was extremely stressful. Strong support by UNB administration was critical especially at this stage.
Dickey, Alex, University of New Brunswick

Food web structure of the Bay of Fundy

The Bay of Fundy, situated on Canada’s eastern coast, is a highly productive marine ecosystem which supports a high biodiversity of invertebrates, fishes, marine mammals and birds. Comparatively little is known about resource pathways which fuel this important ecosystem and how the relative importance of these pathways differs between depths. We used stable isotopes of carbon (d\(^{13}\)C) and nitrogen (d\(^{15}\)N) to investigate the food web structure within the Bay and assess spatial and depth related variation in the resource use of prevalent fish and invertebrate species. We identified distinct pelagic and benthic food chains within the Bay of Fundy food web. Pelagic primary production supports sponges, squid and pelagic fishes, whereas most benthic invertebrates and fishes are reliant on benthic production. These distinct food chains are coupled by generalist fishes, notably silver hake. We observed minimal differences in stable isotopic ratios of fish or invertebrates between regions, but fishes showed significant changes in resource use between depths. Fish within the Bay of Fundy obtain their resources from both benthic and pelagic sources suggesting that pelagic detritus that would normally fall to the benthos may be captured by these fishes and re-assimilated into the pelagic food web.

Dixon, Peggy L.; David J. Ensing 1; Robert Bourchier 2; Rose De Clerck-Floate 2; Val Miller 3; Chandra E. Moffat 1; 1 Summerland Research and Development Centre, Agriculture and Agri-Food Canada; 2 Lethbridge Research Centre, Agriculture and Agri-Food Canada; 3 British Columbia Ministry of Forests, Lands, Natural Resource Operations and Rural Development, Range Branch, Operations Division

Evaluating biological control of invasive spotted knapweed in British Columbia

Spotted knapweed (Centaurea stoebe ssp. micranthos) is a widespread and problematic invader of rangelands in southern British Columbia and much of the Pacific Northwest. Together with diffuse knapweed (C. diffusa), spotted knapweed has been the subject of a North American biocontrol programme since the 1970s, resulting in the release of 13 insect agents. Despite effective biocontrol of diffuse knapweed in BC, and widespread reductions in the density and fecundity of spotted knapweed across the province, pockets of abundant spotted knapweed remain with considerable costs to rangeland tenure holders. Here we present factors we hypothesize to influence control of spotted knapweed across BC, and highlight contrasts between locations with effective management and those where problems persist. We outline plans to assess longitudinal field studies (>20 years) of spotted knapweed demography, control agent abundance and efficacy, and plant community compositional changes in spotted knapweed sites across BC. Finally, we aim to evaluate the potential for phenological mismatches between control agents and spotted knapweed as a result of ongoing climate change with a common garden study. Our research will clarify the factors influencing spotted knapweed control while also generating methods to guide post release monitoring of weed biocontrol agents more generally.

Dogantzis, Kathleen, York University Department of Biology; Harshil Patel; Tanushree Tiwari; Stephen Rose; Ida Conflitti; Alivia Dey; Amro Zayed

Improving genomics tools to identify Africanized honey bees

The honey bee, Apis mellifera, is an ecologically and economically important species contributing to pollination services worldwide. Consequently, it is essential that potential threats to honey bee populations are identified, and mitigated, to prevent losses to the beekeeping industry. Africanized honey bees (AHB) are a hybrid population composed of European and African ancestry and are considered undesirable for beekeeping due to their aggressive defensive behaviour. Given the large-scale trade and movement of honey bees, there is a concern that AHBs will spread from South America and the southern United States to the rest of North America, Australia, New Zealand, and Hawaii. Developing an accurate and cost-effective assay to detect AHB is an important first step towards restricting the accidental importation of AHBs. Here, we used an extensive population genomic dataset, including over 150 newly sequenced individuals from all known evolutionary lineages, to assess the genomic composition of Apis mellifera populations, and patterns of genetic admixture in North and South American commercial honey bee colonies. Using assisted machine learning we were able to estimate the importance of SNPs for differentiating Africanized bees and developed a SNP assay, consisting of 80 curated markers, that shows high accuracy in assigning bees of unknown genetics as either African or non-African. Our SNP assay has
been validated on over 2000 individuals from commercial colonies located in Canada, Texas, and Australia, as well as feral colonies from Texas, and Brazil.

Doherty, Kristin, University of Guelph; Dr. Ellen Esch, University of Guelph; Dr. Andrew MacDougall

Optimal resource allocation theory predicts canola production under drought and nutrient stress

Agricultural practices aim to maximize aboveground biomass production, often through the addition of mineral nutrients. However, in the face of increasing drought frequency and severity, the interaction between mineral nutrient additions and water resource availability may poise crops to experience yield losses due to shifting plant allocation patterns. Using a multifactorial experimental design, we grew 400 unique treatments of phosphorus and nitrogen crossed with four drought regimes. Plant height and soil moisture were measured monthly, with final below- and above-ground biomass quantified to assess plant allocation patterns. With all measurements, we found that plants had restricted growth when subjected to early season drought ($P<0.05$). Additionally, intermediate levels of nutrients additions optimized plant growth as high nutrient levels reduced root allocation, thereby leaving the plants vulnerable to drought. This work suggests that intermediate levels of nutrient addition can buffer plant growth responses in an increasingly variable climate as well as suggests that in the presence of drought, higher nutrient additions may not be utilized by plants resulting in negative economic and environmental consequences.

Dolezal, Aleksandra, University of Guelph; Ellen Esch Andrew MacDougall

Habitat-based drivers of arthropod abundance and richness in an intensively farmed agricultural landscape

Habitat is critical to arthropod populations, but knowledge of habitat-based drivers in agricultural landscapes is lacking. I examined drivers of habitat on arthropod abundance and richness in an agricultural region of Southern Ontario at two scales: landscape, based on the isolation of habitat and local, based on farm cover type (crop, prairie, forest). Additional analyses were conducted on arthropod communities among cover types, prairie addition affects on crop damage, the effect of crop type on arthropods, and arthropod richness between farm and non-farm sites. I found that locally, prairie produced greater arthropod abundance than crop or forest. Prairie addition did not affect crop damage but influenced the spatial distribution of herbivores in crops. Crop type influenced arthropod groups, especially herbivores, which preferred the mixed organic crop. Lastly, farm sites had similar arthropod richness as non-farm sites, suggesting that even conventional farms can support arthropod biodiversity if habitat is not limiting.

Driver, Hannah, Queen's University; Rute Clemente-Carvalho, Queen's University; Virginia K. Walker, Queen's University; Peter V.C. de Groot, Queen's University; Geraint Element, Queen's University; Stephen C. Lougheed, Queen's University

Establishing a sustainable arctic fishery: Population genomics of lake whitefish in a hybrid species complex

Genetic variation is an important predictor of population persistence under changing or stressful environmental conditions. Consequentially, efforts to preserve genetic variation by identifying genetically distinct populations and delineating management units are primary goals of conservation genetics and fisheries management. Accelerated melting of sea ice in the lower Northwest Passage (LNWP) in Nunavut has provided the opportunity to establish a fishery in an underexploited area, where food insecurity rates are high. Sustainable fishery management in the LNWP requires the characterization of genetic structure in focal species such as the lake whitefish (Coregonus clupeaformis). Using genome-wide panels of single nucleotide polymorphisms, we find evidence for two genetic populations of lake whitefish with overlapping ranges in the region. Further, we find evidence of hybridization and introgression between lake whitefish and two other coregonid species (C. sardinella and C. autumnalis). Admixture between these species makes setting sustainable catch limits for lake whitefish challenging, since fishing pressures will decrease the genetic diversity of each species. Our work aims to preserve biodiversity in the LNWP, by informing fishing regulations that reduce the relative exploitation of genetically distinct populations, and ultimately allow lake whitefish to become a sustainable resource for the people of Nunavut.
Du, Trina, University of Ottawa; Hans Larsson, McGill University

Modelling morphological evolution with geometric constraints: a case study of disparity and morphospace occupation in theropod dinosaurs

Geometric morphometrics in combination with analyses of disparity and morphospace occupation are often used to explore trends in morphological evolution. The interpretation of patterns of morphological change through time and across phylogeny is complicated by the ability of random processes to produce seemingly non-random patterns in morphospace, necessitating the comparison of observed variation to appropriate null models. Using the skull shapes of theropod dinosaurs as a case study, we introduce a modified Brownian motion model for geometric morphometric data that incorporates some simple constraints on morphology. We find that diet is an important factor on disparity within theropod clades, with non-carnivorous clades having greater disparity than carnivorous clades. Relative to simulated data, carnivorous clades have lower disparity and higher lineage density, suggesting morphological convergence. Several non-carnivorous taxa, particularly oviraptorosaurs and avians, occupy regions of morphospace not predicted by the null model, supporting the appearance of morphological innovations at the origins of these clades. Our model can be easily applied to any geometric morphometric dataset, and may be useful in a wide variety of systems.

Dubois, Raphaelle, Université de Montréal; Stéphanie Pellerin; Raphaël Proulx

Ecological uniqueness of plant communities as a conservation criterion in lacustrine wetlands

The intensification of human activities and their increasing impact on natural areas call for the implementation of conservation measures. To maximize benefits, one must select areas where conservation efforts are to be invested in priority. To do so, several criteria can be used, such as taxonomic diversity, incidence of range-restricted species, spatial extent or connectivity. Employing different criteria to select sites will yield variable outcomes. An alternative tool, ecological uniqueness, is based on the rarity of whole species assemblages, making them irreplaceable. This study aims to determine whether the ecological uniqueness of plant communities is an adequate criterion for assessing the conservation value of lacustrine wetlands. We sampled the vegetation of 38 wetlands (swamps and peatlands) surrounding Lake Papineau, Québec (Canada) and used past plant survey data from 40 peatlands in La Mauricie National Park, Québec (Canada). We computed the local contribution to beta diversity (LCBD) as a measure of uniqueness and evaluated its relationship to more commonly used conservation criteria. Uniqueness decreased with increasing plant species richness, suggesting a conservation trade-off, whereas it increased with the percentage of rare and disturbance-sensitive species. Overall, ecological uniqueness selected sites of high conservation value, indicating its potential as a conservation tool.

Dumas, Pascal, Université de Moncton; Mathieu D. Morin, Department of Chemistry and Biochemistry, Université de Moncton; Sébastien Boquel, Fredericton Research and Development Centre, Agriculture and Agri-Food Canada; Chandra E. Moffat, Fredericton Research and Development Centre, Agriculture and Agri-Food Canada; Pier Jr Morin, Department of Chemistry and Biochemistry, Université de Moncton

Quantification and dsRNA-based targeting of heat shock proteins in Colorado potato beetles (Leptinotarsa decemlineata) submitted to temperature or insecticide stress.

The Colorado potato beetle (Leptinotarsa decemlineata (Say)) is a threat to the potato industry. This pest's control is challenging as it tolerates harsh temperatures and routinely develops resistance towards insecticides. The understanding of molecular bases associated with these stresses is lacking in L. decemlineata. Heat shock proteins (HSPs) study in response to stress has been conducted in several species but data in L. decemlineata is lacking. Our objective is to evaluate the expression of HSPs in L. decemlineata exposed to a temperature stress or treated with select insecticides. Expression levels of four HSPs were measured by qRT-PCR and insect mortality was monitored using dsRNAs targeting select HSPs. Elevated HSP70 and HSP90 transcript levels (119.62-fold and 6.93-fold, respectively) were observed in heat-exposed beetles while downregulation of HSP70 transcript levels (0.25-fold) was measured in cold-exposed insects. Chlorantraniliprole exposure was associated with reduced HSP Beta-1 transcript levels (0.31-fold) while no significant
results were found in imidacloprid-exposed insects. RNAi-based knockdown of HSP60 levels induced significantly high mortality 14 days following dsRNA injection. These results show the importance of HSPs in *L. decemlineata* for stress coping and place the HSPs as interesting candidates in the search for new ways to control this insect.

Dumont, François, Centre de recherche agroalimentaire de Mirabel; Mireia Solà; Geneviève Labrie; Caroline Provost; Eric Lucas

Potential of damsel bugs for biological control of the tarnished plant bugs in fields and greenhouses.

The tarnished plant bug (TPB), *Lygus lineolaris* (Hemiptera: Miridae) is a polyphagous pest that causes important economic damages in several crops. This phytophagous insect feeds on more than 350 hosts, of which about 120 are economically relevant. Organic strawberry and greenhouse growers have few tools to fight the TPB, and so up to 100% of their yield can be lost due to this pest. The TPB is the main barrier that prevents transitioning from conventional management to organic strawberry farming. The TPB has several predators that can reduce its density in agroecosystems (e.g. predatory bugs, ladybeetles, spiders). However, these predators are not used in classical or inundative biological control because their potential is not yet determined. In a recent study on the effect of trap crops on TPB in strawberry fields, we observed that the damsel bug *Nabis americoferus* (Hemiptera: Nabidae) naturally colonize plots exploited by the TPB and are suspected to be the main contributors to the TPB's mortality (about 50% from large nymphs to adults). The damsel bug feeds on every one of the TPB's developmental stages and has a life cycle that matches the TPB (besides having high fertility). The aim of this project is to determine the potential of *N. americoferus* bugs against the TPB and optimize their role in organic strawberry fields and cucumber greenhouses. Laboratory results (voracity, functional response, microcosm), strawberry fields and cucumber greenhouse will be presented.

Eckert, Christopher, Department of Biology, Queens University

Inconsistent local adaptation despite strong genetic differentiation across a steep elevational gradient in growing season length

When species colonize latitudinal or elevational gradients of growing season length, natural selection should promote local adaptation in reproductive timing. In the Canadian Rocky Mountains, the annual Rhinanthus minor exhibits steep phenotypic clines in phenology across elevation due, in part, to what seems like adaptive genetic differentiation in the timing of flowering and fruit maturation. However, the species also responds to variation in season length with striking co-gradient plasticity that could erode local adaptation by facilitating gene flow. In each of two generations, we quantified local adaptation by reciprocally transplanting seeds among nine sites spanning ~1000m elevation and 2-fold variation in season length. Based on lifetime fitness, local adaptation was inconsistent, varying from strong local adaptation to strong local maladaptation. The hypothesis that rampant gene flow eroded adaptation among *R. minor* populations is inconsistent with substantial variation in fitness among source populations when planted at common sites, and with strong genetic differentiation (Fst = 0.31) at genome-wide SNPs. Although local adaptation is widely viewed as common, especially in sessile organisms, our results join growing evidence of inconsistent adaptation to variation in climate. What constrains climatic adaptation is emerging as a key question in this era of rapid global change.

Edge, Chris, Natural Resources Canada - Canadian Forest Service, Marie-Josee Fortin, University of Toronto

The effect of ecological traps on metapopulation dynamics varies in different network topologies

Metapopulation dynamics are controlled by the vital rates of local populations, dispersal among different populations, and interactions between vital rates and dispersal. Vital rates are influenced by local environmental characteristics that determine habitat quality and control local extinction probabilities. Whereas dispersal among populations is influenced by the topology of the habitat network and control recolonization probability. When disturbances occur within individual habitat patches the patch becomes a population sink, or an ecological traps if the poor quality habitat patch is are preferred to high quality patches. Using a spatially explicit, stochastic, stage-based metapopulation model based on amphibian life-history, we investigate how the number of disturbances, fitness cost, dispersal, and attractiveness affect the persistence of
metapopulations in different network topologies. We find that habitat network topology influences the relative importance of all variables, likely due to its effect on recolonization. Overall dispersal, the number of disturbances, and the fitness penalty of the disturbance are the most important factors, with ecological traps having the largest effects and occurring most commonly in tree network topologies. The effects of disturbances are greater when they occur in habitat patches that are centrally located in networks, and these effects are magnified in tree networks. Overall, the effect of patch attractiveness had a relatively small effect on metapopulation persistence compared to the other variables indicating the ecological traps can occur and have consequences for metapopulations, but these effects are relatively small compared to other factors.

Edwards, Sara, Forest Protection Ltd; Rob Johns; Veronique Martel; Emily Owens; Deepa Pureswaran

Early Intervention Strategy for spruce budworm: Can we contain outbreak spread?

Spruce budworm (Choristoneura fumiferana Clemens) (Lepidoptera: Tortricidae) is the major defoliating pest of spruce (Picea sp.) and balsam fir (Abies balsamea (L.) Mill) in northeastern North America. The recent resurgence of a budworm outbreak in northeastern North America has rekindled interest and discussion around how best to manage its potential impact across the region. Early Intervention Strategy (EIS) is an area-wide management program aimed at containing the spread of spruce budworm in Atlantic Canada. In brief, intensive regional monitoring is used to help identify emerging hot spots along the leading edge of outbreak, which are then treated with relatively narrow-spectrum insecticides (i.e., Btk or tebufenozide) to slow or prevent further population expansion. Our research represents a large-scale test of the efficacy of the EIS approach and has many key features, including work on population and community ecology, pest monitoring, public outreach, and citizen science (i.e., Budworm Tracker). Results from the first 5 years of this program indicate that under the right conditions the EIS approach has strong potential for containing budworm outbreaks with minimal impacts on non-target species.

Einfeldt, Anthony, Dalhousie University; Tony Kess; Paul Bentzen; Daniel E Ruzzante; Ian R Bradbury

Genomic architecture underlying recent evolution of XY sex determination in Atlantic Halibut

Transitions between sex determining mechanisms have occurred across vertebrates, but the genomic features underlying these transitions are poorly understood. We investigated the recent evolution of sex chromosomes in Atlantic Halibut, which have an XY sex determination system and are thought to have diverged from Pacific Halibut which have a ZW sex determination system less than 5 million years ago. Using a chromosome-level genome assembly and >500,000 SNPs from >700 samples, we identify unique features of the Atlantic Halibut sex chromosomes, including an inversion, a large pseudo-autosomal region with unsuppressed recombination, male-linked deletions indicating rapid decay, and retrotransposons that may have played a role in facilitating genomic rearrangements. Sex-linked markers in Pacific Halibut align to a single autosome in Atlantic Halibut, indicating that the ancestral sex chromosomes have reverted to autosomal function.

Ensing, David

Evaluating biological control of invasive spotted knapweed in British Columbia

Ernst, Christopher, University of British Columbia, Hakai Institute; Christopher M. Ernst, Hakai Institute/University of British Columbia; John Reynolds, Simon Fraser University

Bridging the intertidal: insects and wrack influence sand nutrients and plant growth on coastal beaches

Supratidal beaches support unique communities that are sensitive to seaweed wrack deposits. Insects that forage in wrack are thought to link marine and terrestrial systems by releasing into sand nutrients that can be used by plants. We used field and greenhouse experiments to quantify: 1) the effects of wrack (control, moderate, high deposits), with and without
insects, on sand properties, and 2) subsequent effects on plants grown in that sand. In the field, wrack biomass loss was
greater when insects were present (open plots), compared to plots with insect exclosures, but sand OM and moisture did
differ. Sand from high wrack/open plots accumulated less NO₃ and Pext over time. In the greenhouse, seeds
successfully germinated in sand from all treatments, but took longer in sand from control/exclosure plots, and in
wrack/open plots. Seedling mortality was higher in open plots but was moderated at high wrack levels. Seedling biomass
responded positively to wrack, but biomass allocation depended on interactions between wrack and insects. Insects can
influence beach plant growth by changing sand properties, depending on the size of wrack deposits. Further study is
needed to understand this marine-to-terrestrial nutrient pathway and how changing ocean conditions might affect it.

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Esch, Ellen, University of Guelph; Andrew S. MacDougall, University of Guelph

Nitrogen addition enhances terrestrial phosphorous retention

Nutrient availability influences ecosystem function ranging from biomass production to nutrient retention. In tandem,
nitrogen (N) and phosphorus (P) availability may be particularly influential on ecosystem function given widespread
prevalence of colimitation dynamics. Within 200 experimental mesocosms, variable amounts of N and P were applied to
plant communities consisting of either 1 or 2 functional groups, with leachate collected for 3 months following
fertilization. We found (i) that N fertilizer additions reduced P leaching losses, but there was no reciprocal effect of P
fertilizer enhancing N retention. Mechanistically, increased plant biomass under N fertilization mediated this effect,
pointing towards higher biotic demand for P in the absence of N limitation. (ii) Retention levels were in excess of 95% for
N and P across all treatments, and (iii) despite high retention, nutrient runoff was in excess of recommended guidelines for
safe drinking water and above levels known to support harmful algal blooms. While our results that adding N can promote
P uptake, and hence reduce P leaching, are in line with resource limitation theories, we stress that more research should
refine the interactions between N and P availability and leaching at low levels of P addition.

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Etzler, Erik, University of Toronto Mississauga; Darryl Gwynne, University of Toronto Mississauga

Sex and death in Southern Ontario: Impact of newly discovered cricket-parasitoid interaction.

*Stylogaster neglecta* (Conopidae) are fly parasitoids of juvenile Oecanthus nigricornis tree crickets (Orthoptera:
Gryllidae). Parasitoids are predicted to favour larger hosts as they provide more resources. Theoretical models predict that
high juvenile mortality will also favour smaller individuals at maturity. Body size has large impacts on mating and
fecundity in tree crickets and selection for changes in body size could thus change mating dynamics. I measured body size
in juvenile male and female tree crickets and determined if sex and body size affected probability of parasitism. Although
I predicted that larger crickets would be more likely to be parasitized, I found instead that smaller and intermediate size
crickets were more likely to be victims. There was significant linear for larger body size and non-linear selection for
intermediate body sizes. Males were significantly more likely to be parasitized than females. Size biased selection could
be due to parasitoids preferring a narrow size of crickets. Alternatively, larger crickets may be in better condition and
better able to fend off attempts at parasitism. Males may be more likely to be parasitized due to higher risk-taking
behaviour when foraging.

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Evenden, Maya, University of Alberta; Jessamyn Manson, University of Virginia

Bumble bee (Hymenoptera: Apidae) bycatch in semiochemical-baited traps targeting moth pests (Lepidoptera: Noctuidae)
in Alberta,

Unintentional bycatch of bees in monitoring traps that target moth pests occurs in many agroecosystems. Bee capture can
substantially effect the efficiency of monitoring systems and may negatively impact bee biodiversity and pollination
services for both crops and wild flowering plants. We measured the abundance and diversity of bumble bee bycatch in
moth traps targeting cutworm and armyworm moth pests in canola and wheat agroecosytems in Alberta. Moth
pheromone lures attracted bumble bees and bycatch was dominated by one species, Bombus rufocinctus.
Electrophysiological studies confirm that B. rufocinctus can detect moth pheromones. Foodbait lures did not attract bumble bees and may be a good alternative to pheromones for monitoring moth pests.

Fairweather, Aaron, University of Guelph; Donald McAlpine, M. Alex Smith

Ant Species in New Brunswick: A first comprehensive look at ant diversity across the province from key parks and protected natural areas

New Brunswick is a diverse landscape of 72,908 square kilometres, with a variety of habitats, various climatic profiles, and in some cases poorly known taxa. Based on our 8079 ant (Hymenoptera: Formicidae) samples from five protected natural areas, two parks, several additional locales, and including historical taxonomic occurrence data, we present the first comprehensive dataset to examine ant species across New Brunswick. In order to obtain an accurate representation of ant richness, all locations were sampled using a standard method for collecting soil dwelling arthropods. Sampling was conducted in a variety of habitats, including: mountain rock outcrops, deciduous, coniferous, and mixed forests, bog/wetland, grassy fields, disturbed forests, and coastal areas. We collected 86 ant species from 5 subfamilies and 19 genera. These collections included two species only collected once previously (Leptothorax sphagnicolus and L. retractus; Quebec, Francoeur, 1986) and one European invasive (Myrmica rubra, The European Fire Ant). In addition, we paired our morphological taxonomic data with a first look at the genetic diversity of ant species in the province, with 882 DNA barcoded specimens across species, paired with specimen information and photographs uploaded to the Barcode of Life Datasystem.

Faraone, Nicoletta, Acadia University; Samantha MacPherson; N Kirk Hillier

Behavioral responses of Ixodes scapularis to natural products: role of chemosensory organs in volatile detection

The spread of blacklegged ticks (Ixodes scapularis) and growing threat of Lyme disease transmission has increased demand for effective, safe and environmentally-friendly repellent products. Plant-derived essential oils are natural products that exhibit insecticidal and repellent activities and represent a promising alternative to synthetic repellants. However, mechanisms by which ticks detect odor stimuli and how such stimuli may function as repellents is not well understood. We examined the repellent activity of selected essential oil components towards I. scapularis in short- and long-term dose-response trials. To determine the specific olfactory organs involved in detection of chemical stimuli, we tested tick behavioral response in repellency bioassays after removing appendages that house chemosensory sensilla (e.g., foretarsi or pedipalps). New prototype formulas were tested in longevity trials repelling up to 95% of tested ticks after 1h post-application. This study provides new insight regarding tick olfaction and behavior, and innovative methods for selecting appropriate chemicals for development of novel plant-based repellent products for protection from ticks.
Keywords: tick olfaction; repellent; essential oils; Hallers organ; palps; terpenoids

Fernandes, Timothy, University of Toronto Mississauga; Bailey McMeans, University of Toronto Mississauga

The Role of Risk: Exploring Seasonal Strategies in Temperate Fishes

Aquatic organisms exposed to predictable shifts in environmental conditions have commonly exhibited phenological adaptations via behavioural and physiological cycles. In the face of a rapidly changing climate and seasonal landscape, we must work quickly to better understand the dynamics of these cycles if we are to predict ecological outcomes in aquatic systems and better manage high-risk areas. We conducted a comprehensive review of the current literature on seasonal lipid cycling in north-temperate freshwater fish to determine the predominant mediators of lipid cycling, across species. As environmental variables were not found to have any significant effect on lipid cycling, we focused on two factors: thermal preferences and maximum body size. Contrary to our expectations, cold-water fish (thermal optima below 19oC) commonly exhibited greater levels of seasonal lipid cycling than cool-water species (thermal optima between 19oC and 25oC). We also identified, for the first time, significant, across-species scaling of seasonal lipid cycling with body size; as maximum body length increased, the magnitude of seasonal lipid cycling decreased. We contend that the risk associated with body size at both the species and population level may shape the propensity and capacity to cycle lipids seasonally.
Fernandez, Diana, University of Windsor; Sherah Vanlaehoven Roselyne Labbé

Genetic diversity of Anthonomus eugenii in North America through COI gene barcode analysis.

The pepper weevil (Anthonomus eugenii Cano) is a pest of cultivated pepper (Capsicum spp.) causing important damage in Central America, the southern United States, the Caribbean, and Mexico. The insect is originally from Mexico and outbreaks of the pepper weevil were recently reported in southern Ontario, Canada. We present preliminary results on the genetic diversity of A. eugenii populations from Mexico, United States, and Canada through the analysis of the COI mitochondrial gene sequences from individuals from each of these three source countries. The results of this analysis will provide information on the population structure of the pepper weevil in North America, which may reveal variations in their ecology that can be applied in pest management programs. In addition, the results will contribute to understand the occurrence of A. eugenii in a temperate country as it is the case of Canada.

Fernandez-Fournier, Philippe, Simon Fraser University; Jayme Lewthwaite, Simon Fraser University

Do we need to identify adaptive genetic variation when we prioritize populations for conservation?

Defining candidate populations to prioritize for conservation is important but difficult. These populations can be geographically or genetically isolated populations, and higher priority is often given to more distinctive ones. However, recent studies, using recent advancements in genomic tools, rarely identify the extent to which populations are distinct due to local adaptation. To preserve adaptive variation, maintaining populations isolated would safeguard locally adapted characters. On the other hand, when populations become distinct through drift, the proposed solution is to restore gene flow via translocation. Thus, because the prevalence or scarcity of adaptive variation among populations may result in widely different conservation strategies, the question arises: is it necessary to identify adaptive genetic variation when prioritizing populations? Here we offer a simple test of this question as we test if indiscriminately measuring genetic distinctiveness captures adaptive variation by testing if similar populations are prioritized when ranking them based on putatively adaptive vs. standing genetic variation. We used the genomic database of the Yellow Warbler and ranked populations by genetic distinctiveness using multivariate and allelic differentiation metrics. We present and compare the results between the two methods and evaluate whether identifying adaptive variation is valuable or not in conservation efforts.

Ferzoco, Ilia Maria, University of Toronto Mississauga; Shannon McCauley

Trade-offs in dispersal and competitive abilities in a guild of semi-aquatic insects

How species coexist is a longstanding question in ecology. A potential coexistence mechanism occurring in metacommunities is the competition-colonization trade-off, wherein competitive abilities and dispersal abilities of interacting species are inversely related. Most empirical studies testing the competition-colonization trade-off are in systems of passively dispersing organisms and are measuring single aspects of competition. We lack a clear understanding of how this trade-off between dispersal and competitive abilities operates in active dispersers - organisms that make their own dispersal decisions. Using a combination of mesocosm and laboratory experiments, we empirically tested whether semi-aquatic backswimmer congeners (Notonecta undulata and Notonecta irrata) differ in components of competitive ability and dispersal ability using multiple assays. Here, we provide partial support for the competition-colonization trade-off. In this system, competition and dispersal are negatively correlated in some ways, eg. dispersal rates traded off with resource capture. However, competitive abilities are not perfectly asymmetrical in this system and context-dependent competitive relationships exist. Our results suggest that in actively dispersing organisms, the competition-colonization trade-off may be more multi-faceted and messier than previously thought.
Feyten, Laurence, Concordia University; Adam L. Crane; Grant E. Brown

Shoal in a Bottle: the use of conflicting social and private information is shaped by uncertainty of risk

According to the costly information hypothesis, prey should rely on social information when the cost of acquiring private information is high. Here, we tested the prediction that the use of conflicting social vs. private information varies based on certainty of risk, dictated by ambient predation risk levels and the reliability of information. We presented high and low predation populations of Trinidadian guppies (*Poecilia reticulata*) with novel foraging arenas, in situ, paired with one of three sources of private information (alarm cue = reliable indicator of risk, novel cue = unreliable, or a stream water control). Social information was manipulated by presenting a clear plastic bottle containing either nothing or a shoal of guppies. We found a three-way interaction between the level of risk, presence of stimulus shoal, and chemical cue on the latencies to enter the arena and to forage. When social and private information conflicted, high predation fish utilized reliable private information, but shifted to social information when private information was unreliable. Conversely, low predation fish utilized social information regardless of private information reliability. Our results suggest that the use of private vs. social information is dependent upon the level of certainty of predation risk among prey populations.

Fields, Paul, AAFC; Kevin Floate, Lethbridge Research Centre, AAFC; Robert Laird, Dept. of Biology, University of Lethbridge; Paul Fields, Morden Research Centre, AAFC

Cross tolerance to desiccation and cold in khapra beetle, *Trogoderma granarium*

Khapra beetle enter a larval diapause in response to crowding. This diapause increases cold-tolerance to make khapra beetle among the most cold-hardy of stored-product insect pests. This finding is non-intuitive, given that the beetle is only common in hot dry regions in the Middle East. Because desiccation-tolerance and cold-tolerance are positively correlated in several different species of plants and insects, we tested for a similar cross tolerance in khapra beetle. Khapra beetles were reared from the egg stage to first instar larvae at 30 ± 2 °C and 20 ± 10% RH. From then onwards, larvae were reared at different relative humidities (3, 28, 49 and 79%) either in non-diapausing conditions (not crowded) or diapausing conditions (crowded). Then their cold-tolerance was measured (survival at -10°C). For non-diapausing larvae, rearing conditions had little effect on cold tolerance with the lethal time to 50% mortality (LT50) occurring between 2-4 days. For diapausing larvae, cold tolerance increased with greater desiccation stress with LT50s of 5, 7, 10 and 18 days at 79, 49, 28 and 3% RH respectively. This indicates that the physiological mechanisms that protect diapausing larvae from desiccation, may also increase cold-tolerance, even though these insects may rarely be exposed to low temperatures.

Filbee-Dexter, Karen, University Laval; C Feehan, Mont Clair State University; D Smale, South Hampton; K Krumhansl, DFO Halifax; B Konar, University of Alaska; M. Pedersen, Roskilde University; T Wernberg, University of Western Australia

Hotspots of slow carbon turnover in high latitude kelp forests

Understanding carbon turnover and transfer in marine ecosystems is essential to predict and mitigate human impacts on the global carbon cycle. Compelling evidence suggests that macroalgae represent an important flux of carbon in the global ocean, yet the fate of this material is largely unknown. Here, we show exceptionally slow kelp carbon turnover rates occur in high latitude regions, suggesting geographic hotspots of potential carbon storage at the cooler, northern ranges of kelp forests. We used a broadly replicated litter bag experiment spanning 10 ecoregions in the northern hemisphere to measure in situ rates of biomass loss and degradation of kelp. Latitude and ocean temperature explained the most variability in turnover rates. In general, turnover rates were slower compared to other dominant forms of marine carbon. The slower carbon turnover at higher latitudes suggest kelp forests along subarctic and cold temperate coasts have higher potential for long-term carbon residence time and storage. These regions are predicted to expand with sea ice retreat and could be targeted by climate mitigation strategies to increase organic carbon sinks globally.
Filice, David, McMaster University; Reuven Dukas, McMaster University

Can losers still be winners? The evolutionary biology of winner-loser effects

In many animals, the outcomes of competitive interactions can have lasting effects that influence an individual's reproductive success and have important consequences for the strength and direction of evolution via sexual selection. In the fruit fly, Drosophila melanogaster, males that have won previous contests are more likely to win in subsequent conflicts and losers are more likely to lose (winner-loser effects), but the direct fitness consequences and genetic underpinnings of this plasticity are poorly understood. Here, we tested how male genotype and the outcomes of previous male-male conflicts influence male pre- and post-copulatory success. We quantified pre-copulatory success in a choice and no-choice context, and post-copulatory success by quantifying ejaculate offensive and defensive ability. We found that winners have higher reproductive success compared to losers in both pre-copulatory scenarios. However, losers consistently mated for a longer duration, boosted female fecundity and had an increased paternity share when they were the first males to mate, suggesting increased investment into post-copulatory mechanisms. Our results place the behavioural data on winner-loser effects in an evolutionary context by documenting the potential fitness gain to males from altering their reproductive strategy based on fighting experience.

Finley, Jenna, Queen's University; Lonnie Aarssen, Queen's University

Do species with smaller leaves have the ability to better compensate for the loss of apical dominance?

Apical dominance in angiosperms confers a number of adaptive advantages. But the disruption of apical dominance resulting from damage or removal of the terminal shoot apical meristem (e.g. by consumers) has been commonly shown to have no resultant net loss for the plant in terms of fecundity and/or biomass production. And some studies have reported overcompensation—an increased fecundity and/or biomass, representing a cost of apical dominance. Apical meristem damage limits the effects of the hormone auxin in suppressing the lower axillary meristems, which can subsequently develop further into additional lateral shoots, and hence possibly result in greater flower/fruit production per plant. Using a variety of herbaceous angiosperms sampled from natural populations in the region of Kingston, Ontario, we examined the relationship between fecundity allocation (seed count as a ratio of body mass) versus leafing intensity (total number of leaves as a ratio of body mass). Species with smaller leaves hypothetically have a greater compensatory response, as smaller leaves generally enable a higher leafing intensity, and thus release of a larger bud bank of previously suppressed axillary meristems and consequently more total meristems (per unit body mass) available for deployment in sexual reproduction.

Firth, Britney, University of Waterloo; Drake, D.A.R.; Power, M., Department of Biology, University of Waterloo

Diet overlap of common and at-risk riverine benthic fishes before and after Round Goby (Neogobius melanostomus) invasion

The Round Goby (Neogobius melanostomus) invaded high diversity tributaries of the Laurentian Great Lakes that are also species-at-risk hotspots. This is of concern as the Round Goby is a threat to similar benthic species and can accelerate abundance declines in species at-risk. This study examines the first ever-realized impact of the Round Goby on native benthic riverine fishes including the federally threatened Eastern Sand Darter (ESD; Ammocrypta pellucida) in the Sydenham River, a high diversity species-at-risk hotspot. Fish were collected by electrofishing and seine netting in 2002/2003 and 2009 to obtain and compare pre- and post-invasion diet overlap samples and feeding strategies of the entire community. Direct and potential indirect realized impacts of this invasion were assessed. Between 2002/2003 and 2009, there was a significant increase in diet overlap in the entire benthic community. The community shifted their feeding strategies to become more generalists, with Stonecat (Noturus flavus), Fantail Darter (Etheostoma flabellare), Greenside Darter (Etheostoma blennioides) and Logperch (Percina caprodes) having a significant shift. All benthic species sampled in the community other than Stonecat and Fantail Darter had a significant diet overlap with the Round Goby. ESD did not have a significant change in diet overlap with the community and feeding strategy; therefore, it appears to not be direct or indirectly affected by the Round Goby invasion. Sampling should be conducted again at the
Sydenham River to assess long-term impacts as a further increase in community diet overlap could lead to an increase in indirect affects on ESD and the native benthic fishes.

Fischer-Rush, Jonathan, CSEE; Dr. Karen Kidd; Dr. Heather Hunt

Salmon Aquaculture-Derived Nutrients and Metals in Biota from Rocky Habitats in the Bay of Fundy

Few studies have examined the impact of metal and nutrient loading from aquaculture in rocky bottom habitats or quantified effects at distances greater than 200 m from salmon pens. I assessed metal contamination and feed reliance at two distances from salmon pens, in 2016 and 2017. I deployed 7 bio-collectors at 8 pairs of sites, near (68-441 m) and away (260-2750 m) from salmon pens, across three Bay Management Areas in the Bay of Fundy to assess exposure to copper, zinc and nutrients (using stable isotopes) in five benthic species, including the American lobster (*Homarus americanus*). PCA analysis indicated no consistent separation in metal content between near and away sites. Moreover, 41 species-site pair combinations for both metals across both years were compared using t-tests, 8 and 6 showed significant differences in copper and zinc, respectively, between near and away sites, but the direction of difference was inconsistent. Some species-site pair combinations showed differences in isotope values, but only sulfur isotopes suggested a small shift towards reliance on aquaculture nutrients. Overall, my results suggest limited impacts of aquaculture in terms of metal contamination and feed use in animals in rocky bottom habitats greater than 200 m from aquaculture pens.

Forsythe, Adrian, McMaster University; Jianping Xu,

Using public data to track the spread of a fungal epizoonotic: Is human activity contributing to the spread of White-nose Syndrome?

White-nose Syndrome (WNS) is an ongoing fungal epizootic caused by epidermal infections of the fungus, *Pseudogymnoascus destructans* (Pd), affecting multiple bat species in North America and is now considered the deadliest disease affecting any non-human mammal species in history. Emerging sometime around 2006 in New York State, WNS has clonally spread into Eastern Canadian provinces sometime before 2012. Using molecular and genomic markers, we have investigated isolates from the Canadian Maritimes to understand the population dynamics of Pd at the local and regional scales. Our analyses revealed high genotype diversity and a lack of local population structuring: both are consistent with frequent transfers of Pd between caves. Human activity has the potential to influence the spread potential of WNS. Our influence on the transmission of Pd has never been quantitatively measured at bat hibernacula. Here we use online Geocaching records at sampling sites as a proxy for human activity in these areas. Our results suggest that sites with a greater number of unique visitors are correlated with higher genotype diversity at these caves. Considering the impact that humans could have on the spread of WNS, further precautions need to be made to prevent and manage the further spread of WNS.

Fortier, Anne-Marie

A new HRM-based assay suggests a different temporal distribution pattern between genetic lines 2511 and 3453 of *Delia platura*

The seedcorn maggot *Delia platura* (Meigen), and the bean seed maggot *Delia florilega* (Zetterstedt) can cause considerable feeding damage to almost all cultivated crops. The recent discovery of two distinct genetic lines of *D. platura* with unique distribution patterns suggests the presence of a new cryptic species for the group that could be native to the Americas. These two lines have more than 4% polymorphism in the Folmer region of the DNA barcoding gene cytochrome c oxidase 1 (COI) and form two distinct BINs (barcode index number). Based on thousands of records in the Barcoding of Life Data System (BOLD), the H-line (BOLD: AAG2511) has a Holarctic distribution while the N-line (BOLD: AAA3453) is restricted to Northern and central America. Currently, eastern Canada (ON, QC and the Maritime Provinces) is the only area in the world where the distributions of these two lines overlap. As each may present a different distribution pattern in time or space, reliable identification of these species and genotypes is crucial to understand their respective contribution to crop damage and develop specific integrated pest management approaches such as sterile insect
releases (SIR). The recent development of a combined real-time PCR assay with a high-resolution melting curve analysis (HRM) to differentiate between D. florilega and both genetic lines of D. platura suggests a different temporal distribution pattern between the two D. platura lines in southwestern Quebec, where about 90% of onions and more than 50% of cruciferous crops of the province are grown.

Fortin, Marie-Josée, Ecology and Evolution, University of Toronto; Andrew Chin, Ecology and Evolution, University of Toronto; Christopher Edge, Canadian Forest Service, Atlantic Forestry Centre - Natural Resources Canada

Landscape-Aquatic networks at the watershed scale

The functional interactions between terrestrial and aquatic ecosystems occur due to species movement and nutrient exchanges between these ecosystems that constitute a meta-ecosystem. Yet, both terrestrial and aquatic ecosystems are acting at different spatial and temporal scales making it paramount to determine how land-use and climate change will affect the spatiotemporal dynamic ecological processes. It is therefore important to integrate knowledge and develop management planning at the interface of terrestrial and aquatic ecosystems (e.g. forest-stream, lake-stream-riparian zones, wetland-land) that may amplify the fluctuations and mismatch of ecological processes between terrestrial and aquatic ecosystems. Given the synergy among natural fluctuations, natural and anthropogenic disturbances, and climate change, novel analytical methods are needed to generate early detection of changes in these ecosystems that might impair the delivery of ecosystem services. The development of conceptual frameworks and analytical tools also need to be built upon quantitative indicators of ecosystem health and functions provided by these ecosystems at multiple spatial scales to better manage the interactions of ecosystem services. Here, we present how to quantify terrestrial variability at the watershed-level that can influence aquatic fish communities along a north-south gradient in two regions (Toronto and New Brunswick).

Fox, Janay, McGill University; Madlen Stange, McGill University

Dietary change in an invasive sea catfish species from Panama

Invasion of a new habitat can lead to rapid adaptation of a species. The coastal brackish sea catfish species Cathorops tuyra (Ariidae) from the Eastern coast of Panama has reportedly been found reproductively active in the freshwater rivers and lakes of the Panama Canal. Habitat transitions require various adaptations to different environmental conditions including changes in feeding ecology. Stomach content analysis is the most convenient and often the only way available of researching the feeding habits of a non-model species cost-effectively. We collected 101 C. tuyra specimens from two different habitats that differed in salinity; the freshwater Rio Chagres and the brackish estuary of Rio Santa Maria. Fish were dissected and information was collected on various internal and external features. A stomach content analysis was carried out identifying prey to the lowest possible taxonomic group then categorized into fish, bivalves, crustaceans, gastropods, insects, other invertebrates, and plants. This study provides information on a largely unstudied species but will also provide insight into the ways in which C. tuyra has been able to adapt to a drastically different habitat. Additionally, results from this study may also have implications regarding the invasive impacts of C. turya on freshwater ecosystems.

Franckowiak, Ryan, Queen's University; Anna Tigano, Department of Molecular, Cellular and Biomedical Sciences, University of New Hampshire; Gregory J Robertson, Wildlife Research Division, Environment and Climate Change Canada; Marie-Josée Fortin, Department of Ecology and Evolution, University of Toronto; Vicki L Friesen, Department of Biology, Queens University

Arctic seabird conservation and management in the genomics era: a murre story

Advancements in genomic methods have provided increasingly accurate and versatile approaches for addressing conservation and management issues. In Arctic seabirds, this has been important because nuclear and mitochondrial markers often lack sufficient power. Thick-billed Murre (Uria lomvia) are a numerically dominant apex predator that are hunted throughout the eastern Canadian Arctic and Greenland. Populations are large and generally stable in the western
Atlantic but are declining elsewhere. Thus, murres have been identified as the highest conservation priority of any marine bird in the Arctic region. Using restriction site-associated DNA sequencing, we characterized genome-wide levels of standing variation, population genetic structure, and the degree of connectivity among colonies throughout the North Atlantic. Despite weak population structure, we were able to assign birds hunted off the coast of Newfoundland to their respective colonies in the Canadian high Arctic. We also used environmental association analysis to assess the correlation between putatively adaptive genetic variation and various oceanographic variables to help identify colonies with the greatest sensitivity to environmental change. Our on-going research addresses critical issues outlined in the International Murre Conservation Strategy and Action Plan, and can be used to mitigate anthropogenic and climate related threats to the long-term persistence of Thick-billed Murre.

Frederickson, Megan, University of Toronto; Jason Laurich, University of Toronto; Anna O'Brien, University of Toronto

Using a small symbiosis to answer big questions about mutualism ecology and evolution

Many hosts, including humans, are teeming with beneficial microbes, but host interactions with their microbiota can be hard to manipulate experimentally. We developed a new experimental system to test the outcome of host-microbiome interactions for both partners across many combinations of different host genotypes, microbes, and environments. We used one of the worlds smallest angiosperms, the duckweed Lemna minor, and the culturable portion of the L. minor microbiome, sampling hosts and microbiota from more than 80 field sites. By mixing and matching host isogenic lines with both single- and multi-strain microbial inocula in experiments, we tested three important questions about host-associated microbiomes: 1) Are microbiomes more than the sum of their parts? In other words, do microbial communities have non-additive effects on hosts that cannot be predicted from testing each microbe in a community individually? 2) Are hosts locally adapted to their microbiome? And 3) can we experimentally evolve microbiomes to improve host stress tolerance? I will explain why duckweeds and their microbiota are a powerful system in which to answer these and other big questions about mutualisms between hosts and their associated microbiomes.

French, Sarah, University of Waterloo; James H. Devries, Ducks Unlimited Canada; Dale A. Wrubleski, Ducks Unlimited Canada; David McLaughlin, Ducks Unlimited Canada; Daniel R. McIsaac, University of Waterloo; Rebecca C. Rooney, University of Waterloo

Are agricultural wetlands ecological traps for aquatic communities?

Wetlands provide critical habitat and valuable ecosystem services. Land use conversion in Ontario, however, has led to substantial wetland loss. The creation of wetlands on agricultural properties has the potential to offset wetland loss, yet these wetlands are also susceptible to contamination by pesticides, which may accumulate to toxic levels. Our research will establish whether pesticide contamination affects aquatic invertebrates in created wetlands. Pesticides could create ecological traps if invertebrates choose inferior over high quality habitats and experience a reduction in fitness. We expect that created wetlands that are surrounded by substantial agricultural activity will accumulate pesticides and will be low quality habitat for sensitive invertebrate species, potentially acting as sinks for populations. However, less pesticide-sensitive species may benefit from these created habitats. We will sample 32 wetlands in southwestern Ontario that were created by Ducks Unlimited Canada in partnership with local landowners. We will measure pesticides, aquatic invertebrates, and emerging insects. If aquatic invertebrate densities or emerging insect biomass are inversely related to pesticide load, we will conclude that they provide inferior habitat. Our research will help to ensure that efforts to offset historic and continuing wetland loss in Ontario achieve the desired result of bolstering wetland-dependent species.

French, Rowan, University of Alberta; Aaron J. Bell, University of Saskatchewan; Kiara S. Calladine, University of Saskatchewan; John H. Acorn, University of Alberta; Felix A. H. Sperling, University of Alberta

Seeing past the shell: Discordance between morphology and molecules complicates taxonomy and conservation of *Cicindela formosa* Say (Coleoptera: Carabidae)
Accurate taxonomy is essential to biodiversity management, yet many taxonomic delimitations are supported by very few characters. One example is *Cicindela formosa gibsoni*, a Canadian nationally threatened tiger beetle whose subspecies status is based on morphological criteria. We sampled C. f. gibsoni populations throughout their North American range and assessed their genetic and morphological distinctiveness from sympatric *C. f. formosa* and *C. f. fletcheri*. Analyses of elytral (forewing) patterns showed that *C. f. gibsoni* and *C. f. fletcheri* are present in Saskatchewan while *C. f. gibsoni* and *C. f. formosa* are present in Colorado, as reported in previous studies. However, *C. f. gibsoni* is not an evolutionarily distinct unit based on either genome-wide SNPs or mitochondrial COI haplotypes. Saskatchewan populations of *C. formosa* are genetically distinct from Colorado populations, but different morphotypes inhabiting the same geographic region are genetically similar. Thus, the elytral pattern characteristic of *C. f. gibsoni* likely evolved independently in Saskatchewan and Colorado. Our results highlight congruence between phylogeographic and genomic data types and conflict with morphology, the conventional basis for subspecies designations. This study also represents the first intraspecific genetic analysis of *C. formosa* and can inform future conservation of the species.

Friedman, Jannice, Queen's University; Abrar Aljiboury, Syracuse University

Sex allocation, siring success and mating portfolios in a wind pollinated plant

Sexual selection in plants may act on male fitness by favoring traits that improve their reproductive and mating success. In wind-pollinated plants, sex allocation theory predicts that male fitness increases linearly with investment of resources into male function, because the air is unlikely to become saturated with pollen. Furthermore, architectural traits such as plant height or long branches, and the timing of flowering, may influence pollen liberation, pollen dispersal, and access to a greater number of different mates. To test these predictions, we experimentally manipulated allocation to male function, recorded the onset of female and male flowering time and measured architectural traits, in three experimental field arrays of *Ambrosia artemisiifolia* (common ragweed). We estimated siring success and mating portfolios using seven polymorphic microsatellite markers. We found a linear relationship between allocation to male function and male fitness. In addition, we observed a positive association between plant width and siring success. The start of male flowering positively affected the number of different mates on which a plant sired offspring, and conversely the start of female flowering was associated with a greater diversity of fathers siring seed on a given plant. Our results show the fitness consequences of high male allocation in wind-pollinated plants, providing an explanation for the large quantities of pollen produced by wind-pollinated plants. In addition it points to the importance of architectural traits for male fitness and the implications of protandry on siring success and mating portfolios.

Frost, Carol, University of Alberta

Species traits can predict host and parasitoid contributions to apparent competition

Apparent competition is an important indirect interaction mechanism that structures host-parasitoid communities. In several applied scenarios it would be useful to be able to use traits to predict which host species will cause and be affected by apparent competition, and which parasitoid species will mediate apparent competition between host species. Using temperate forest plant-caterpillar-parasitoid quantitative food web data we tested whether there are traits, including trophic traits related to network position, which can predict species-involvement in apparent competition. We identified three host traits that were related to the strength and direction of apparent competition between pairs of host species. We also identified one parasitoid trait that was associated with how likely a parasitoid species was to mediate apparent competition between two host species. These results could be useful in planning the provision of alternative hosts for conservation of natural enemies for biological control, in predicting food-web impacts of introduced species, and in modeling community-wide responses to disturbance.

Fuentes-Pardo, Angela, Dalhousie University

Adaptive and neutral genetic variation in spring- and fall-spawning herring (*Clupea harengus* L.) in the northwest Atlantic
While intraspecific diversity is crucial for species persistence, its accurate assessment is sparse, which compromises speciessevolutionary potential and the effectiveness of conservation plans. In this thesis, I used Atlantic herring as a model system to (i) identify patterns, genomic regions, evolutionary processes and environmental variables involved in the origin and maintenance of population divergence, and (ii) develop a genetic tool for management purposes. By integrating whole-genome and oceanographic data, bioinformatics, and statistics, I successfully disentangled an intricate pattern of fine-scale population divergence in herring at putatively adaptive loci, despite low differentiation at neutral loci. Such divergence is defined by seasonal reproduction and a climate-related cline in which disruptive selection may lead to local adaptation. I identified genomic regions and candidate genes underlying divergence and disclosed that many seasonal reproduction-related loci are shared among populations across the Atlantic. I also developed and evaluated the efficacy of two SNP-panels diagnostic of spawning season and geographic origin. Mixture samples analysis revealed a dynamic composition of aggregations outside of the breeding season and demonstrated the SNP-panels utility for stock assessment. Together, this research contributes to an increased understanding of how population divergence arises in the sea and provides genetic tools for effective management.

Gagne, Chase, University of Maine; Dr. Hamish S. Greig

Environmental Drivers of Aquatic Invertebrate Communities in Riverine Rock Pools

Small pools are common in the cracks and depressions of rock outcrops adjacent to large Maine rivers. However, the aquatic invertebrate communities of these rock pools have been little studied. This lack of knowledge is problematic, as climate-driven changes in rainfall and river flows will likely alter pool hydrology and impact their unique invertebrate communities. We surveyed aquatic invertebrate diversity and abundance in 40 rock pools across four sites along the Penobscot River near Bangor, Maine. Invertebrate surveys were repeated in summer and fall, and over this period we also monitored a suite of habitat variables including pool size, hydrology, and resource availability. Pools supported surprisingly diverse aquatic invertebrate assemblages comprising 55 genera of both lentic and lotic fauna. Invertebrate diversity and abundance decreased across all sites between summer and fall, and invertebrate community composition varied between different rock outcrops, and among pools of differing hydrology within an outcrop. These results suggest processes operating at multiple spatial and temporal scales structuring rock pool communities, and that changes in pool hydrology will likely impact invertebrate assemblages.

Gagnon, Annie-Eve, Agriculture and Agri-Food Canada; Gaetan Bourgeois, Agriculture and Agri-Food Canada

Increased voltinism in carrot weevil under a warmer climate

The carrot weevil, Listronotus oregonensis, is an important pest of carrots that causes yield losses of up to 50%. In recent years, control of this pest has become more complex in carrot-producing areas of Quebec, Canada. This situation is explained mainly by an extension of the activity period of adults, which complicates pest control management strategies. The objective of this study was to evaluate the impact of temperature increases on the phenology of carrot weevil. In a field experiment, we observed the activity period of adults, egg-laying duration, and larval development in carrot plots exposed to two different climatic conditions. A plot of carrots was set up under a tunnel to increase the temperature by 1°C in comparison with a control plot without any shelter. Weevil phenology was affected greatly by the increased temperature, as shown mainly by the extension of the egg-laying period. The proportion of mated and sexually mature females was higher at the end of the season under the warmer climatic conditions than under the ambient temperatures. The inhibition of reproductive diapause under warmer conditions can explain why females were still active in the field at the end of the season. In addition, the abundance of the four larval stages of carrot weevil during the growing season demonstrates that two cohorts were present, thus confirming the presence of two generations in northern regions. These results concretely show that the recent increase in temperature is changing the phenology of this pest and will require modifications to pest management strategies.
Ganesan, Lavanya; Miss Digvir Jayas, Department of Biosystems Engineering, University of Manitoba; Paul Fields, Morden Research Centre, AAFC

Survival of life stages of three species of flat grain beetles at cold temperatures

We compared the cold tolerance of different life stages of flat grain beetles (Laemophloeidae; Coleoptera) like *Cryptolestes ferrugineus* (Stephens), *Cryptolestes turcicus* (Grouvelle) and *Cryptolestes pusillus* (Schönherr). These insects do not undergo diapause, but their cold tolerance can increase with exposure to cold temperatures. With the effect of acclimation (18 to 5°C) and non-acclimation (30°C), cold tolerance was measured by survival of the life stages at -10°C after various durations. Acclimation increased cold tolerance by as much as 8-fold. For acclimated insects, adults were more cold hardy than other stages. *Cryptolestes ferrugineus* was more cold tolerant than *C. turcicus* and *C. pusillus* was the least cold tolerant.

Garcia, Matthew, University of Wisconsin; Madison, B.R. Sturtevant; J. Régnière; Y. Boulanger; R. St-Amant; B. Cooke; G.L. Achtemeier; J.J. Charney; P.A. Townsend

Modeling Aerial Dispersal of Eastern Spruce Budworm Moths During Summer Migration

Unlike passive aerial transport that depends only on wind speed and direction, the aerial dispersal of insects and animals is an interactive process in which the individual expresses agency, both acting on and driven by its environment. Dispersal of birds, bats, and insects may frequently occur in numbers and at scales that are observed with weather radar. Using an individual-based model of dispersal behavior, combined with independent weather model outputs at high spatial and temporal resolution, we developed a methodology by which the resulting flight trajectories are then compared with weather radar observations to calibrate dispersal model parameters. Applied to numerous individuals on a regional domain, the calibrated model can then express emergent results indicating collective aerial migration across a landscape. We applied this approach to model eastern spruce budworm (*Choristoneura fumiferana* [Clem.]) migration events during the current outbreak period in Québec. Our rule-based flight model was developed from decades of empirical aerobiological research and is coupled with an established phenological model, BioSIM. We used the Weather Research and Forecasting (WRF) model to drive high-density agent-based simulations of spruce budworm moth nocturnal dispersal activity over a three-week period in July 2013. Flight model results were calibrated and validated using available weather radar observations in an area centered on the St. Lawrence River. Overall results are consistent with observed regional patterns of spruce budworm dispersal from defoliated areas with known spring feeding activity, and significantly advance our understanding of the spatiotemporal variability and interannual dynamics of the current spruce budworm outbreak in the eastern North American boreal forest. Our quantitative parameter-estimation methodology reduced uncertainty in several flight-oriented biophysical parameters and may have broader application to other species where weather radar observations of dispersal events are available.

Gaudreau, Mathilde, Université de Montréal; Paul Abram, Agriculture and Agri-Food Canada; Jacques Brodeur, Université de Montréal

Parasitoids walking in the (UV) light: variability in individual locomotor activity and circadian rhythm

Since many parasitoid wasps forage for hosts by walking on plant surfaces, studying this short distance mode of locomotion in response to abiotic factors can provide insight as to their efficiency as biological control agents. Little work has been done to characterize how parasitoid walking activity could be influenced by different light environments, despite their importance as to visual foraging cues and the negative effects of exposure to ultraviolet (UV) wavelengths on parasitoid fitness. By stimulating host location or avoidance behaviors, UV radiation could increase parasitoid activity levels or alter the expression of their circadian rhythms. To test these hypotheses, two scelionid egg parasitoid species - *Telenomus podisi* and *Trissolcus cosmopepla* - were placed in an infrared-based locomotor activity monitor system and exposed to ultraviolet and visible light under UV-blocking or UV-transmitting filters for different time periods and intervals. While overall daily activity levels remained the same regardless of the presence of UV, we observed a species-specific increased variability in individual circadian rhythms associated with our light environment treatments. These
unexpected results suggest that the highly variable UV levels found in natural settings favor variable parasitoid response, and will be discussed in the context of their host exploitation behaviors.

Gauthier, Gabriel, University of Ottawa; Jessica Forrest, University of Ottawa

Temperature-mediated beeplant synchronization and its consequences for a pollen-specialist solitary bee

Rising temperatures are advancing the timing of flowering and pollinator emergence in numerous systems. If phenological shifts do not occur in parallel, a change in temporal overlap between mutualistic partners may arise. We know that experimental beeplant mismatch reduces solitary bee fitness, but we remain unaware whether such mismatch occurs in nature. We studied populations of Osmia iridis, a specialist solitary bee dependent on the flowering plant Lathyrus lanszwertii in the Colorado Rocky Mountains. We collected data on bee emergence, bee reproductive output, flowering phenology, and site-level temperatures between 2008 and 2018. We found a significant effect of spring temperatures on overlap due to greater temperature sensitivity in Lathyrus. The degree of overlap does not predict bee per-capita reproductive output but is a good predictor of population-level reproductive output. Our results suggest that moderate increases in temperature may lead to increased population-level reproductive output through improved synchrony. However, further temperature increases could result in bees emerging after the flowering period and an outcome that could be devastating for bee reproduction. Understanding the extent to which bees can tolerate shifts in synchrony is paramount given that regional mean spring temperature increases are projected to reach 3°C by 2050.

Gavloski, John, Manitoba Agriculture

Techniques for Incorporating Natural Enemies into Insect Management Programs

Natural enemies of crop feeding insects can often be a large component of the insect fauna in an agroecosystem. Yet they can often be overlooked when assessing the threat of insects to a crop. Three steps will be discussed that can aid in making predaceous insects and parasitoids a more practical component of insect management programs. Step 1 is enhanced identification of natural enemies. Good factsheets and guides are helpful, although many leave out key groups, often because identification in the field is difficult. A program in western Canada targeting those growing and scouting field crops has used creative techniques to help associate key natural enemies with some of the primary pests of field crops. Entertaining and eye-catching videos, posters and factsheet inform on identification, and where data exists the voracity of key predators and parasitoids. Parasitoid recognition remains a challenge. Step two is demonstrating the value of natural enemies. Voracity studies are available for some natural enemies, but lacking for many. This information is necessary to fully integrate natural enemies into our decision-making process. Step three is the development of natural enemy units, or some similar process, to fully integrate natural enemy levels into the decision-making process. A broad enough knowledge of the voracity of several natural enemies has resulted in the development of the apps Aphid Advisor and Cereal Aphid Manager. Creative methods are needed to incorporate natural enemies of a broader range of potential pest insects into the management decision process.

Giles, Rachel, University of Toronto; Jonathan Ruppert2; Angela Wallace3; Chelsea Rochman1. 1 Department of Ecology and Evolutionary Biology, University of Toronto, 2 Research and Knowledge Management, Planning Policy, Toronto and Region Conservation Authority, 3 Palmer Environmental Consulting Group Inc.

Impacts of road runoff: a cocktail of multiple anthropogenic stressors and the subsequent response of macroinvertebrate communities

Globally, urbanization continues to increase and produce elevated levels of contaminants in the air, soil, and water within and around urban centers. In particular, heavily trafficked roads are a major source of anthropogenic contaminants, including polycyclic aromatic hydrocarbons, heavy metals, tire dust, and road salt. This mixture, herein referred to as road runoff, represents one of the largest contributors of diffuse-source toxicants in urban areas, and yet is seldom studied as a contaminant mixture. Here we investigate how road runoff could impact ecosystem structure and function in urban stream ecosystems. Specifically, we (1) investigate contaminant fluctuations over the winter, a time of intense road salt
application, and (2) assess community-level invertebrate responses to contamination loads in urban streams. Preliminary results demonstrate that chloride concentrations in urban sites are an order of magnitude greater than rural sites. Additionally, the amount of chloride has a strong relationship with temperature, where chloride concentrations increase with air temperature during the winter season. Last, we detected differences in community composition of benthic macroinvertebrates between rural and urban sites. Such work builds on our understanding of how multiple anthropogenic stressors impact stream communities as a mixture, and has the potential to help inform future policy and urban development decisions.

Gillis, Daniel, University Of Toronto; Ken Minns, University of Toronto & Fisheries and Oceans Canada; Brian Shuter, University of Toronto and Ontario Ministry of Natural Resources

Forecasting the effects of climate change on fish thermal habitat in North American lakes

Temperature is a key characteristic of lakes profoundly affecting their physical, chemical, and biological processes. Fish habitat availability is constrained by a lakes suitable thermal habitat supply, a result of its thermal regime. Several abiotic factors influence thermal regimes; therefore, to predict the influence of climate warming on fish thermal habitat supply, we must understand the relationship between climate and other abiotic factors with lake temperature patterns across a wide geographic scale. We fit a semi-mechanistic seasonal temperature-profile model (STM) to datasets of 431 morphometrically diverse North American lakes (1971-2016). Using the STMs fitted parameters for these lake thermal characteristics (e.g. onset date of stratification, peak summer surface temperature), we use mixed modelling to create a set of sub-models for predicting STM parameters of any lake based on abiotic factors, including climate. We will use these results to assess changes in fish thermal habitat supply over the sampling period and the sub-models to forecast future thermal habitat supply under climate change. These findings will strengthen our understanding of the factors that influence lake thermal regimes across regional gradients, and help identify lake types and regions that may be especially susceptible to climate change.

Gillott, Cedric

Goldman, Jack, Concordia University; Laurence E.A. Feyten, Concordia University; Grant E. Brown, Concordia University

Quality over quantity: sender diet quality but not quantity shapes the production of disturbance cues

Disturbance cues are widely distributed among aquatic prey and are thought to function as early indicators of risks. They are believed to be metabolic by-products; released in urine or across the gills of stressed or disturbed prey. Recent studies suggest that disturbance cues are plastic and can relay differential information based on predation experience of senders. We hypothesized that diet quantity and quality may alter the production of disturbance cues and that the response to these cues is dependent upon receiver experience. In laboratory experiments, we tested whether receivers with different background risk experience alter their response to disturbance cues from senders fed diets differing in quality (high vs. low protein) and quantity. In our first experiment, receivers exhibited increased antipredator behaviors to cues from high protein senders compared to cues from low-protein senders and that this effect was most pronounced among high predation risk receivers. In our second experiment, we manipulated the quantity of food, and found that receivers did not significantly increase antipredator behaviors towards cues from senders fed a high- but not low-quantity diets. We found an effect of receiver background risk, but this effect was similar across diet treatments. Combined, our results suggest that diet quality and not quantity shapes the production of disturbance cues.

Goodwin, Katie, Memorial University of Newfoundland; Carissa Brown, Memorial University of Newfoundland

Integrating demographic niche shifts and northern black spruce range expansion
When assessing how species' distributions will respond to climate change, many studies assume a species' niche will remain the same throughout its life span. However, species niches can be broken up demographically, with unique dimensions representing different life stages, resulting in a changing niche throughout the life cycle. This approach can identify demographic bottlenecks on climate-induced range expansion. We quantified microsites inhabited by four life stages of black spruce (Picea mariana) at treeline in Yukon Territory to characterize demographic niches and assess how observed ontogenetic niche shifts may impact climate-induced changes in the distribution of this conifer species. Microsite characteristics were compared to treeless tundra substrates to identify which factors limit establishment. Black spruce exhibited consecutive niche shifts and microsite preferences from emergence to reproductive maturity, which was mainly driven by changes in plant community composition and soil moisture preferences. Overall, we found that (1) many black spruce seedlings at the range edge occupied unsuitable conditions for transitioning to the next life stage; and (2) reproductive adults have a narrow niche, limiting cone production where suitable niche space is limited. Our results suggest that demographic niches can provide a better understanding of how species distributions will respond to climate change.

Gormley, Ty, University of New Brunswick; Dr. Scott Pavey, University of New Brunswick; Dr. Sherrylynn Rowe; Dr. Greg Puncher, University of New Brunswick

Comparing genetic variation among Atlantic cod (Gadus morhua) populations following the collapse of the Northern cod stock

Atlantic cod (Gadus morhua), within the Northern cod stock, once served as the economic pillar for Newfoundland and Labrador. Following the stock collapse and over twenty years of moratoria, the genetic structure of the stock remains at question. Learning about past and present genetic structure of the stock is important because it may allow the testing of two hypotheses; metapopulation vs. isolation, both of which have support from past studies. We performed a double-digest RAD-seq technique on 130 historic adults captured in 2001-2003 from 4 regions (Hawke Channel, Bonavista Corridor, Smith Sound, Placentia Bay) to assess the genetic structure of the Northern cod stock following the collapse. A total of 4654 single nucleotide polymorphisms (SNPs) indicated a significant but very small genetic difference between Hawke Channel and Smith Sound and no differences among the remaining populations. Based on these findings of these historic samples, our conclusions support the metapopulation hypothesis, where substantial migration was pivotal to the recovering Northern cod stock.

Gorrell, Jamie, Vancouver Island University; Malcolm McAdie; Jasmine Janes; Corey Davis; Axel Moehrensclager

Genetic diversity and relatedness in the endangered Vancouver Island marmot captive breeding program

The Vancouver Island marmot (Marmota vancouverensis) is the most endangered mammal in Canada. The wild population declined to 30 individuals in the early 2000s but through captive breeding the current population has rebounded to 150 animals. However, a previous study found low genetic diversity in the recovering population. Here >10 years later, we used next-generation sequencing to reassess the genetic diversity in the wild. Additionally, we provide the first estimates of genetic diversity in the captive population at a critical time in the management of the captive breeding program. Studbook and molecular estimates of relatedness among captive marmots were compared to determine how well studbooks can predict genetic similarity and avoid inbreeding when selecting mating pairs. Surprisingly, our next-generation sequencing technique provided little increase in resolution among individuals which limits the potential of this approach to aid in the conservation of endangered species experiencing population bottlenecks.

Goud, Ellie, Cornell University; Jed Sparks

The role of metabolic diversity in ecological communities revealed by leaf carbon and oxygen stable isotopes

Variation in metabolism may be an important mechanism that sustains biological diversity, but the extent and role of metabolic diversity in structuring community composition is largely unknown for many plant communities. We
demonstrate variation in metabolic strategies, as defined by carbon and oxygen stable isotopes of leaf cellulose, among 18 co-occurring plant species in a mid-successional old field in Ithaca, NY. Changes in species abundance over two years suggest that temporal variation in water availability (i.e., inter-annual precipitation), rather than spatial variation, may be an important mechanism structuring functional diversity and species composition in this community. We extend the current carbon and oxygen dual-isotope model to predict inter-specific responses under variable resources. Across-biome comparisons suggest that variation in temperature, water availability, and light can promote functional diversity via variation in carbon and oxygen stable isotopes. Future studies that measure carbon and oxygen stable isotopes in other communities and along additional resource gradients (e.g., nitrogen, CO2) may reveal a previously underappreciated role of metabolic diversity in structural ecological communities.

Goudis, Lindsey, BASF Canada Inc.; Alejandro Arevalo, BASF Corporation; Justin Clark, BASF Corporation; Christine Noronha, Agriculture and Agri-Food Canada; Wim van Herk, Agriculture and Agri-Food Canada; Bob Vernon Rebecca Willis, BASF Corporation

Broflanilide Insecticide In-Furrow Treatment: a new active ingredient to control wireworms (Coleoptera: Elateridae) in potatoes

Broflanilide Insecticide In-Furrow Treatment, a new meta-diamide active ingredient that was evaluated for efficacy against wireworms infesting potatoes in the US and Canada in 2014 - 2018. Broflanilide consistently decreased damage caused by wireworm feeding under moderate to heavy pressure, resulting in increased marketable yield. Broflanilide was submitted to the US EPA and Canadian PMRA by BASF in 2017.

Gounand, Isabelle, University of Zürich; Eawag, Chelsea J., Little Eric Harvey Claire Jacquet Florian Altermatt

Indirect spatial effects and meta-ecosystem resilience in a changing world

Recent syntheses on cross-ecosystem flows of resources have highlighted the ubiquity of spatial flows, as well as common ecosystem interdependencies. Production in one ecosystem is partly conveyed through spatial flows, which serves as resources in other ecosystems. In a context of increasing perturbations, these transports potentially drive spatial cascades among ecosystems, with local perturbations propagating across landscapes. Spatial cascades and feedbacks likely play an important role in ecosystem response to perturbations and might strongly depend on climatic zones due to variation in productivity. To understand how meta-ecosystem dynamics influence ecosystem stability and response to local perturbations, we developed a general meta-ecosystem model connecting a terrestrial and an aquatic ecosystem through cross-ecosystem resource flows. We defined a realistic parameter space to be explored based on a global empirical dataset on ecosystem carbon stocks and fluxes. With this empirically-based model settings, we analyze the spatial cascade effects of local perturbations on ecosystem stability at the aquatic-terrestrial interface for different climates. We characterize the strength of spatial cascades according to perturbation magnitude and connectivity context, and perturbation amplification due to spatial feedbacks. We identify the impact of climate on these dynamics and discuss the implications in the current context of global changes.

Gowton, Chelsea, University of British Columbia; Michal Reut; Juli Carrillo

Peppermint essential oil inhibits Drosophila suzukii emergence but reduces efficacy of a native parasitoid

Spotted Wing Drosophila (Drosophila suzukii) is an invasive fruit fly with the ability to oviposit in a broad range of agriculturally valuable fruits. Volatile organic compounds (VOCs) produced by botanical oils may reduce D. suzukii attraction to hosts and decrease survival, but it is unknown how their efficacy varies across D. suzukii life stages and whether VOCs produced by botanical oils reduce the survival and success of higher trophic levels. Through a series of laboratory bioassays, we evaluated the joint effects of peppermint oil VOCs on D. suzukii survival and the survival of and parasitism rates by a pupal parasitoid wasp, Pachycrepoideus vindemiae. First, we determined whether exposure to peppermint oil VOCs at the pupal stage reduced adult emergence, and whether this depended on environmental conditions (i.e. soil moisture). Secondly, we evaluated whether exposure to peppermint oil VOCs reduced or enhanced parasitism by
the pupal parasitoid and whether this depended on the timing of peppermint oil VOC exposure (i.e. before, during, or after parasitoid access). Exposure to the volatiles of higher concentrations of peppermint oil reduced *D. suzukii* emergence under moist soil conditions but dry soil had a similar effect on reducing adult emergence. Peppermint oil VOCs were toxic to adult *P. vindemiae*, but developing *P. vindemiae* were unaffected by peppermint oil VOC exposure. Using peppermint essential oil may reduce *D. suzukii* emergence from the pupal stage. However, this could negatively impact populations of *P. vindemiae* dependent on the timing of application.

Graham, Brandon, University of Guelph; Kevin McCann; Matthew Guzzo

Setting the Pace: Resource Availability Influences Lake Trouts Pace of Life Syndrome

The Pace of Life Syndrome (POLS), an extension of life history theory, is seen along a slow to fast continuum where trade-offs are introduced due to the investment of finite resources to current versus future reproduction. POLS postulates life history, behavioral, and physiological traits should co-vary and create strategies that position a species or population along the slow-fast continuum. For example, a fast-paced individual invests in early reproduction, has a shorter lifespan, higher metabolic rate and higher activity levels. Ecological and environmental conditions can alter the expression of these co-varying traits; however, the current understanding of POLS is constrained by the lack of field experiments incorporating varying ecological/environmental conditions. Lake Trout (*Salvelinus namaycush*), a cold-adapted predator, is well studied and known to exhibit variation in life history, behavioral and physiological traits. Here, we investigate Lake Trout and the impact of ecological variation on POLS by sampling lakes with and without a preferred pelagic prey, Cisco (*Coregonus artedi*). Measurements of in-field standard metabolic rate, feeding behavior, and life history traits determines across population POLS variation. This study will inform future POLS studies and fisheries management to the impact of resource availability on a suite of quantifiable traits associated with POLS.

Greig, Hamish, University of Maine; Scott Wissinger, Allegheny College; Amanda DelVecchia, North Carolina State University; Isaac Shepard, University of Maine; Brad Taylor, North Carolina State University

Ecosystem consequences of species range shifts: a test with caddisflies in alpine ponds

Shifts in species distributions poleward in latitude and upslope in elevation are among the most commonly reported ecological responses to climate change, yet few studies have explored the impacts of these shifts on ecosystem function. We investigated the ecosystem-level impacts of observed elevational range shifts in a guild of detritivorous caddisflies (*Trichoptera: Limnephilidae*) in alpine ponds in the Colorado Rockies. We manipulated caddisfly assemblages in microcosms, mesocosms, and cages within ponds to reflect changes in species relative abundance as high elevation resident taxa are replaced by range-expanding taxa from lower elevations. These replacements altered a suite of ecosystem processes linked to detritus decomposition including rates of detritus breakdown and fine particle production, and the release of detritus-sourced nutrients into the water column. Moreover, outcomes for particulate detritus dynamics were consistent across experimental units differing in spatial scale and ecological context. These results suggest that species range shifts can alter carbon and nutrient dynamics, which could have broader ramifications for the provision of ecosystem services.

Greiner, Ariel, University of Toronto; Marco Andrello, MARBEC, Univ. Montpellier, CNRS, Ifremer, IRD; Emily Darling, Wildlife Conservation Society; Martin Krockaek, University of Toronto; Marie-Josée Fortin, University of Toronto

Impact of Climate Change on Global Coral Reef Networks

Climate change threatens the existence of coral reefs around the world through mass mortality of corals following bleaching. Coral reefs, like many other marine ecosystems, are connected through the dispersal of pelagic larvae that travel along ocean currents, creating reef networks. Loss of reefs due to coral bleaching will lead to unexpected changes in the characteristics of coral reef networks, threatening network persistence and reducing the availability of source reefs. Using a larval dispersal model and existing global datasets of hypothesized reef climate refuges, we identified how reefs
worldwide are connected in networks and how those networks may be affected by reef loss induced by climate change. We explored different scenarios of reef loss, removing reefs in increments comparable to the percentage lost in the mass bleaching event of 2016, but differing in the order of reef loss. We also explored the dynamics of recolonization from the remaining living reefs to the former reef sites. We found that the pattern of loss and the recovery potential changed markedly depending on the timing of the loss of these hypothesized reef climate refuges, demonstrating their importance for maintaining global coral reef connectivity.

Gridzak, Riley, University of New Brunswick; Michael Lavender, Queen's University; Anusha Kunasingam, Algoma University; Joanna Murtha, Algoma University; Ashley Jensen, Algoma University; Aksel Pollari, Algoma University; Lidi anne Santos, Algoma University; David Ensing, Queen's University; Jason Pither, University of British Columbia

Exploring the relative influence of dispersal and competition on co-occurrence patterns in response to two disturbance regimes

Negative co-occurrence patterns are a regular feature of natural systems; however, the circumstances under which different mechanisms drive these patterns remain unclear. While competition remains a compelling potential driver of co-occurrence patterns, recent research has highlighted the role of dispersal, which is expected to have the most pronounced effect when disturbance creates gaps in the community. Here, we use two different disturbance treatments to investigate the relative roles of dispersal and competition in driving co-occurrence patterns. We use three sites with two different disturbance treatments (herbicide application and grazing) to investigate the relative roles of dispersal and competition in driving co-occurrence patterns. We found that negative co-occurrence patterns were most pronounced in plots disturbed by herbicide application, and negative co-occurrence patterns in grazed plots were most pronounced in communities with greater species evenness and lower productivity. These results highlight how dispersal into disturbance-generated gaps can create pronounced patterns of negative co-occurrence, but such an effect may be short lived post-disturbance. Furthermore, our results suggest that both dispersal and competition can generate negative co-occurrence.

Differential colonization by ecto-, arbuscular and ericoid mycorrhizal fungi in forested wetland plants.

The roots of most plants are colonized by mycorrhizal fungi under normal soil conditions, yet the influence of soil moisture on different types of mycorrhizal symbioses is poorly understood. In wet soils, colonization of woody plants by ectomycorrhizal (ECM) fungi tends to be poor, and colonization of herbaceous plants by arbuscular mycorrhizal (AM) is highly variable. However, little information is available on the influence of soil moisture on the colonization of ericaceous roots by ericoid mycorrhizal (ERM) fungi. We studied the colonization patterns of these three mycorrhizal types along soil moisture gradients from upland forests to forested wetlands in Nova Scotia. Colonization was assessed microscopically in the ECM plant Pinus strobus, two AM plants (Cornus canadensis and Lysimachia borealis) and two ERM plants (Kalmia angustifolia and Gaultheria hispidula). For the two ERM plants, fungal community structure was also assessed along the soil moisture gradient by sequencing fungal ITS. Our data agrees with previous reports on the influence of soil moisture on colonization patterns of ECM and AM mycorrhizae, but indicates that ERM colonization increases with soil moisture in forested wetlands.

Evolutionary divergence of sympatric rainbow trout ecotypes in a large British Columbia lake

Whereas allopatric population divergence is driven by geological processes, sympatric divergence is in many cases due to intrinsic biological factors that makes the process of population differentiation more difficult to understand. In Kootenay Lake of southeastern British Columbia, two genetically distinct rainbow trout (Oncorhynchus mykiss) ecotypes co-occur...
and are distinguished by diet and size-at-maturity: "Gerrards" are large-bodied piscivorous specialists whereas individuals from the other populations are smaller bodied and feed mainly on insects. Using a pooled sequencing approach, we identified ~11 million SNPs to determine the level of population genomic divergence (Fst) and identify genomic regions that may have functional importance in the divergence of these populations. A sliding-window analysis revealed the average genome-wide Fst = 0.19, with > 1,300 fixed SNPs. Our interrogation of the most divergent loci suggest mechanistic hypotheses involved in the divergence of these sympatric populations.

Gutgesell, Marie, University of Guelph; Dr. Kevin McCann, University of Guelph

Timing is Everything: Temporal Restructuring of Agriculturally Impacted Stream-Riparian Food Webs

Agricultural landscapes are intersected by complex patterns of streams, whose structure and function are tightly linked to the structure of their neighbouring riparian zone. Increasing agricultural production has the potential to alter the structure and function of these adjacent stream-riparian ecosystems through land-use changes that can temporally alter stream-riparian consumer-resource dynamics. Here, I will demonstrate how agricultural land-use change is temporally redistributing resource dynamics in adjacent stream-riparian ecosystems across 3 streams, with varying agricultural intensity (conservation area, mid-impact, conventional farm) in the Lake Erie Watershed. Specifically, I will determine i) the influence of agricultural land-use on the seasonal temporal dynamics of insect resources within riparian, stream, and in-flux (i.e., emerging and in-falling) communities, ii) how the diet of generalist consumers (fish) responds to these seasonal changes, and iii) how this is altering stream-riparian food web structure. Preliminary stable isotope results looking at stream food web structure suggest there are differences in temporal structure between highly impacted and pristine stream-riparian food webs, where high agriculturally impacted food webs demonstrate less asynchrony and heavier reliance on aquatic energy pathway across seasons. This preliminary evidence suggests agricultural land-use is indeed altering the structure of adjacent stream food webs, which has the potential to influence whole ecosystem function and stability.

Guy, Cylita, University of Toronto; John M. Ratcliffe, Department of Ecology and Evolutionary Biology, University of Toronto

Understanding urban bat behaviour for conservation & disease management: a case study on sex specific habitat use in big brown bats

Some animal species show great capacity to adapt to urbanized landscapes. However, we have a limited understanding of demography and habitat use within cities for many synurbic species. Using a combination of captures to obtain demographic data, radio-telemetry to examine foraging and roosting behaviour, and data on diet and prey availability, we examined how big brown bats (Eptesicus fuscus) use an urban green space (High Park) in Canada's largest city (Toronto). We found that adult males outnumbered adult females more than two to one. While males were found throughout the park, females were concentrated in an area with more water, but lower prey availability. We also found that bats of both sexes were in poorer body condition than reported for other non-urban areas. Finally, no bats roosted in the park, but were found roosting on residential properties. While previous studies based on acoustic surveys have suggested that urban green spaces may offer refuge to bats, our data suggest that High Park may be a suboptimal patch in the landscape, particularly for reproductive females. These results highlight the importance of considering sex-specific patterns of habitat use in cities and motivate future work that looks to understand bat movement in the broader landscape.

Guzman, Laura Melissa, Simon Fraser University

Trophic Metacommunities: Lessons from the bromeliad system, Presenting at the graduate student phd award symposium.

Haines, Jessica, MacEwan University; Sarah E. Nason; Alyshia M. M. Skurdal; Tenal Bourchier; Stan Boutin; Ryan W. Taylor; Andrew G. McAdam; Jeffrey E. Lane; Amanda D. Kelley; Murray M. Humphries; Jamieson C. Gorrell; Ben Dantzer; David W. Coltman; Anni Hämäläinen
No link between personality and life history in red squirrels despite accounting for sex and environment

The pace of life syndrome hypothesis posits that personality traits (i.e., consistent individual differences in behaviour) are linked to life history traits. Specifically, fast-paced individuals are predicted to be proactive (i.e., bold, active, and aggressive) with an earlier age at first reproduction and a shorter longevity than slow-paced individuals. Environmental conditions and sex differences are important in maintaining behavioural and life history variation in populations and may influence the covariation of personality with life history. However, these effects are rarely tested together. We investigated whether the occurrence of a resource pulse (called a mast year) during adulthood altered the associations between personality and life history (age at first reproduction and longevity) in adult male and female North American red squirrels (*Tamiasciurus hudsonicus*). Males and females had similar activity levels, but females were more aggressive. Despite accounting for environmental context during adulthood, we found no evidence of an overall pace-of-life syndrome in this population as personality was not associated with life history traits in either sex.

Hajibabaei, Mehrdad

Will Environmental DNA metabarcoding stand the test of time?

DNA metabarcoding relies on next generation sequencing analysis of marker genes such as CO1 DNA barcode to provide biodiversity analysis directly from environmental samples. Given the need for biodiversity information for various ecological investigations from biomonitoring to detection of rare/endangered species, DNA metabarcoding has gained significant momentum. However, the use of this approach for long term and large-scale studies of ecosystem dynamics has not been sufficiently demonstrated. Given rapid advances in HTS technology and bioinformatics approaches, DNA metabarcoding methodologies require careful optimization and testing to successfully operationalize them for scientific and socio-economic applications. This is especially important for applying DNA metabarcoding in biomonitoring and environmental impact assessment programs where ecosystems status are examined over time and space and in linkage to various anthropogenic activities.

Halloway, Abdel, University of Illinois; Joel S. Brown, Moffitt Cancer Center and the University of Illinois; Katerina Stankova, Maastricht University

Non-Equilibrial Dynamics in Under-Saturated Communities,

Integral to the development of evolutionary game theory was the unification of the evolutionary stable strategy (ESS), an equilibrial evolutionary state in which no rare invader can establish, with other stability concepts to create a larger evolutionary stability framework. However, some work on evolutionary dynamics shows the possibility of unstable and/or non-equilibrial pathologies such as limit cycles and evolutionary suicide which remain outside of this current stability framework. One possible reconciliation is that non-equilibrial dynamics are more likely in species poor communities "far" from the ESS and that being "closer" to the ESS by being species rich stabilizes co-evolutionary communities. To that end, we analyzed three models of evolution, two predator-prey models and one competition-based evolutionary suicide model, to see how degree of community saturation affects the evolutionary stability. In the predator-prey models, stability is linked to degree of saturation, and the competition model is shown to be permanently under-saturated, likely showing such extreme dynamics for this reason. Our analysis provides support for a link between community saturation and evolutionary dynamics and offers a possible placement of unstable and non-equilibrial dynamics into a wider stability framework.

Harder, Lawrence, University of Calgary; Shane Richards, School of Natural Sciences, University of Tasmania

Life-history consequences of stochastic pollen limitation for dynamically optimal annual plants

Owing to their immobility, plants must contend with the vagaries of mortality risk and resource, pollinator and mate availability at their establishment site. Given such uncertainty, making the best of prevailing circumstances will often
promote performance better than fixed allocation of effort (e.g., resources, time). We assess theoretically the consequences of stochastic availability of resources for growth and reproduction, and of pollination for variation in the size, phenology, flower production and reproductive success of a population of genetically identical plants. Our adaptive dynamic programming model determines the optimal daily responses (e.g., grow, produce new flowers, increment fruit, store resources) by individual plants based on their current states and the probabilities of resource increments, pollination and death. Because of their stochastic histories, plants differ in their states and optimal responses on a given day, despite having identical capabilities. Consequently, lucky plants grow faster, become reproductive earlier, but at a larger size, and are more fecund than unlucky plants. Because of fruit-production costs, poorly-pollinated plants produce more flowers than well-pollinated plants, partially compensating for low pollination probabilities. Together, these results illustrate pervasive implications of environmental stochasticity for plant size (vegetative and reproductive) and phenological distributions, as well as general life-history characteristics.

Hargreaves, Anna, McGill University

Local adaptation, biotic interactions, and species distributions

Understanding species distributions is a fundamental goal of ecology and evolutionary biology, and increasingly relevant to conservation. Dr Anna Hargreaves will share results from experiments and syntheses testing patterns proposed to broadly influence species distributions, including local adaptation in range-edge populations and global patterns in the importance of species interactions.

Harris, Erin, AAFC/Acadia; N. Kirk Hillier, Acadia University; Suzanne Blatt, AAFC

Abundance Versus Precision: An Oviposition Analysis of Delia platura and Delia radicum on Crucifer Crops in Nova Scotia

Delia radicum (Diptera: Anthomyiidae), cabbage maggot, is a specialist on crucifers such as cabbage and broccoli. A generalist species, Delia platura (seedcorn maggot) is reported to feed on crops such as bean, rutabaga and cabbage. Competition between these species has not been studied. Laboratory studies evaluated D. platura and D. radicum for oviposition on cabbage, broccoli and radish. Experiments were done at four plant stages (germination, cotyledon, first true leaf, second true leaf), with two mating pairs of a species placed on a single plant, covered with a 2 L plastic bottle dome and placed in a growth chamber for 48 hours. Each trial had 6 plants with D. platura, 6 with D. radicum, and 4 controls (no plant). Each trial was repeated 5 times for each plant stage. Eggs were counted and recorded. Preliminary laboratory results show D. platura to be attracted to soil, and will oviposit on controls, while having only slight preference to the germination and cotyledon stages. D. radicum will only oviposit on plants, preferring the later stages.

Harvey, Eric, Université de Montréal

Reconciling community and ecosystem functioning across scales with landscape stoichiometry

Metaecosystem has great empirical potential but 10 years after its inception it is still almost entirely theoretical. This issue stems in part from the fact that most metaecosystem theory is too abstract to lead to clear and testable predictions. Here, we propose that the analysis of spatial patterns in the fundamental building blocks of all life elements - can pave the way for an empirically-based metaecosystem framework.

Haworth, Sarah, Trent University

Mapping the susceptibility of Ontario's white-tailed deer (Odocoileus virginianus) to chronic wasting disease

Effective and well-informed surveillance is essential to early detection and efficient containment of new and rare wildlife diseases, especially in the face of increasingly frequent transmission of wildlife diseases to humans. One of these potential
zoonotic pathogens is chronic wasting disease (CWD). CWD is a highly contagious and fatal neurodegenerative prion disease of wild and captive cervids (species of deer, elk, caribou, and moose) with no treatment, cure, or live test. Recent work has also demonstrated CWD infecting non-human primates via consumption of CWD-positive deer meat, prompting stricter regulations to prevent zoonotic spillover. White-tailed deer (WTD; Odocoileus virginianus) are the most abundant cervid species in North America and experiencing northward range expansions as a result of climate change. This expansion facilitates the spread of pathogens and thus pose a zoonotic threat. Although not yet reported in Ontario, the Ontario Ministry of Natural Resources and Forestry (OMNRF) regularly screens for CWD and produced an extensive database of tissue and auxiliary data available for research. This screening is more important than ever since Quebec confirmed its first three cases October 2018, only a few kilometers from Ontario. PRNP (prion) gene variations cause two substantially different progressions of CWD with major implications for potential spread pathways. About 1000 samples and linked auxiliary data from above database will be used to understand the population demographics of WTD in Ontario and screen the PRNP gene variation across the province to inform the OMNRF CWD risk model. This will be integrated to develop better-informed management practices and policies in the face of CWD entering Ontario.

Hayden, Brian, University of New Brunswick; Chris Harrod, Universidad de Antofagasta; Chile Stephen Thomas, EAWAG; Kimmo Kahlainen, Inland Norway University of Applied Sciences

Seasonal variation in the food web structure of subarctic lakes

Subarctic lakes are predominantly fuelled by benthic primary production, however seasonal phyto- and zoo-plankton blooms offer a temporary but highly nutritious additional food source to consumers within these lakes. Research in these systems is generally restricted the summer ice-off period, possibly biasing our interpretation of annual trends in consumer trophic ecology and overall ecosystem function. We combined stable isotopes of carbon and nitrogen with stomach content data to assess food web structure during the ice-off (September) and ice-on (March) phases in nine subarctic lakes in Finnish Lapland. We observed a seasonal change in resource use of most fishes from pelagic and generalist in summer to benthic specialist in winter, this was accompanied by a decrease in dietary and isotopic niche width in most species and an overall reduction in food web breadth. Characterisation of lake food web structure solely using data derived from summer sampling fails to account for the trophic dynamics within these systems during the winter ice-on

Hayward, Kristen, Queen’s University; Evelyn L. Jensen, Yale University; Christina Tollett, Queen’s University; Rute Clemente-Carvalho, Queen’s University; Zhengxin Sun, Queen’s University; Peter V.C. de Groot, Queen’s University; Stephen C. Lougheed, Queen’s University

A SNP GT-seq assay for polar bear fecal and degraded DNA

In the context of rapid climate change, a new polar bear (Ursus maritimus) monitoring program that is continuous, cost-effective, and community-based will be paramount for informed conservation efforts. To address this need, the BEARWATCH project aims to develop a new monitoring program based on non-invasively collected samples. As part of this collaborative effort, we are developing and validating a Genotyping-in-Thousands (GT-seq) assay to genotype a SNP panel optimized for individual and subpopulation differentiation based on field-collected fecal samples. GT-seq is a multiplex amplicon sequencing approach that will enable genotyping of low quantity and quality DNA and reduce the cost of genotyping hundreds to thousands of samples. In tandem with our GT-seq assay, we have developed a qPCR assay to specifically target polar bear DNA and screen for DNA extracts likely to be successfully genotyped with GT-seq. Other biomarkers will be assessed after genotyping, including diet and environmental contaminants. GT-seq will also be used to create a catalog of SNP data based on muscle samples with DNA too degraded for use with double-digest RAD sequencing. Thus, our assay will provide baseline population genetic data and the foundation for a new, cost-effective polar bear monitoring program based on non-invasively collected samples.

Heim, Amy, Saint Mary's University; Jeremy Lundholm, Saint Mary's University

Soil Depth Heterogeneity and Functional Trait Diversity in a Green Roof System
Since different plant traits are associated with different ecosystem services, increasing the functional diversity of green roofs may lead to an increase in multifunctionality. One way in which functional diversity (FD) could be increased, is through soil depth heterogeneity, which would lead to an increase in microsites favorable to functionally different plant species. In this five year green roof study, we created four soil depth treatments; three homogenous treatments with a soil depth of 5, 10, and 15cm and one heterogeneous treatment with a mixed soil depth of 5 and 15cm. The quantity of soil in the 10cm and 5/15cm treatment was equal. 18 different plant species, including grasses, forbs, creeping shrubs, and succulents were evenly distributed into each treatment. For each species, six functional traits were measured, and all aboveground biomass was harvested at the end of year 5. Overall, Functional diversity was not significantly different between the 10cm and 5/15cm treatment. However, the 5/15cm treatment had FD values overlapping with those of the 15cm treatment, suggesting a slight increase in functional diversity attributable to soil depth heterogeneity.

Helmond, Erika, University of Regina; Kerri Finlay, University of Regina; Mel Hart, University of Regina; Jennifer Heron British Columbia Ministry of Environment and Climate Change Strategy; Cory Sheffield, Royal Saskatchewan Museum

In Hot Water Thermal Tolerances of the Endemic Hot Spring Snail *Physella wrighti*

*Physella wrighti* is an endangered freshwater snail endemic to the Liard Hot Springs in British Columbia. Despite its conservation status, little is known about this species aside from it inhabiting water temperatures ranging from 23.5°C to 36°C and remaining active during winter air temperatures dropping to -40°C. To investigate the effects of temperature on this species, I determined their preferred water temperature by exposing snails to a gradient of temperatures. I then examined effects of water temperatures on behaviour, mortality, number of egg masses produced, number of eggs per mass, egg viability, and duration of embryo development by rearing snails in 13°C, 23°C, and 33°C aquariums. I determined *P. wrighti* prefers 23°C. Their behaviour was not different among temperatures; however, snails did not survive in the 33°C tanks. Snails in the 23°C tanks produced more egg masses, while those in the 13°C tanks produced more eggs per mass. Egg viability was higher, and embryo development fastest in the 23°C tanks. These data suggest that *P. wrighti* grows and survives better at temperatures lower than their natural environment and may only tolerate the warmer hot spring water.

Hemming, Victoria, Martin Conservation Decision Lab

How to derive good judgments from experts when the data eludes? The IDEA protocol

Conservation scientists often find there is insufficient data to inform critical decisions and assessments. In such circumstances, subjective judgments of experts are often required. Given that such judgments are used no differently to data, it's important to ensure these judgments represent the best possible judgments from which to make decisions and assessments. But how? In this talk, I introduce structured elicitation protocols, which are promoted as a means to improve the judgments of experts in science. I focus on the IDEA protocol ("Investigate", "Discuss", "Estimate", and "Aggregate") which is rapidly becoming used in conservation science as a best-practice means to improve expert judgment for critical decisions and assessments. Using two case studies I present evidence that basic steps of the protocol improve judgments of experts, and demonstrate the extent to which these can be implemented within the practical and financial constraints of most contexts in conservation.

Hendricks, Sarah, University of Idaho; Rena Schweizer, University of Montana; Paul Hohenlohe, University of Idaho; Robert Wayne, University of California

Natural re-colonization and admixture of wolves (*Canis lupus*) in the US Pacific Northwest: challenges for the protection and management of rare and endangered taxa

Admixture can potentially generate novel phenotypic variation that may facilitate persistence in changing novel environments or can result in the loss of population-specific adaptations. Therefore, ad.
Hendry, Andrew, McGill University

Eco-Evolutionary Dynamics In the Wild

I will argue that understanding eco-evolutionary dynamics requires experimental manipulations in nature. I will then describe two such experimental manipulations we have recently performed - one to study finch-plant interactions in Galapagos and the other to study stickleback-plankton interactions in Alaska.

Heron, Jennifer, BC Ministry of Environment

Taylor's Checkerspot: successes, challenges and future work for an endangered butterfly in British Columbia

Taylors Checkerspot butterfly (Euphydryas editha taylori) is nationally Endangered and listed under the federal Species At Risk Act. Historically, the species was found in approximately 20 sites throughout southeastern Vancouver Island, British Columbia. Cumulative threats from urbanization, agricultural conversion, invasive species and pesticides have reduced the species to two known subpopulations, one on Denman Island and the other outside of Oyster River on Vancouver Island. A group of dedicated biologists have been collaborating on recovery actions for this species for the past 15 years, including inventory, habitat restoration, outreach and stewardship, research and a captive rearing program. Most recently, the recovery team has been working on habitat restoration within Helliwell Provincial Park, a formerly occupied site on Hornby Island. Our objective is to release larvae into the park in March 2020 and ultimately establish a third self-sustaining subpopulation. A summary of the recovery teams ongoing efforts, challenges, collaborations, further research opportunities and future work will be outlined in this talk.

Hervet, Vincent, Agriculture and Agri-Food Canada; Rob Bourchier; Sandy Smith

Artificial diet for the rearing of Archanara neurica (Lepidoptera: Noctuidae), a potential biocontrol agent of European common reed, Phragmites australis australis (Poaceae)

Archanara neurica and Lensia (Archanara) geminipuncta are two European moth species that are under consideration as biocontrol agents for introduced Phragmites in North America. A key step in the successful establishment of any weed biocontrol agent is the ability to mass-rear the agents for release. Current rearing methods for Archanara neurica are very labor intensive, requiring hand-transferring of larvae between multiple Phragmites stems to achieve successful pupation. To facilitate rearing of A. neurica, we tested four artificial-diet recipes: 1) the McMorran Lepidoptera diet and the McMorran diet supplemented with either 2) dried Phragmites shoots, 3) fresh Phragmites stems and leaves or 4) fresh growing tips of stems. Plant material was added to the base diet because we expected it to be required to stimulate feeding. Archanara neurica was successfully reared from egg to adult and the adults produced viable eggs on all diets. Contrary to our expectations the best results were obtained on base McMorran diet for all parameters of fitness measured (survival, development times of larvae and pupae, pupal mass and length) compared to the plant-supplemented diets. The McMorran diet can now be used to replace or complement labour intensive rearing of Archanara neurica on Phragmites.

Hillier, N. Kirk, Biology, Acadia University; Laura MacVicar, Biology, Acadia University; Kevin Cloonan, Biology, Acadia University; Ersa Gjelaj, Biology, Acadia University; Taylor Swanburg, Biology, Acadia University; Leah MacLean, Biology, Acadia University; Russell Easy, Biology, Acadia University; Rebecca Rizzato, Biology, Acadia University

Investigating moth pheromone receptor plasticity

We are investigating the potential for pheromone pre-exposure to modify olfactory receptor expression at the antennal level, comparing effects in males and females, documenting temporal and dosage-dependency, and selective downregulation using key compounds from Heliothine species.
Hines, Jeff, University of New Brunswick; Jeff Houlahan

A Method of Training Software to Monitor Bird Diversity and a Comparison to Expert-level Human Sampling

Kaleidoscope is a new software program by Wildlife Acoustics that uses machine learning to identify bird vocalizations within audio recordings but there has not yet been a method published which uses this software to monitor bird diversity or any comparisons of its results to more traditional methods. Here we present a method for a non-expert in bird identification to be able to train the program and apply it to field recordings to determine which bird species are present in the area. To test the effectiveness of the new method, we used it on field recordings generated over 21 sites at CFB Gagetown, NB, from April-September, 2014. We verified a portion of the vocalizations detected by Kaleidoscope and compared the total number of (verified) species detected per site against those detected by an expert sampling the same audio. The new method of using software to pick out and identify target vocalizations typically found 50%-100% more species and more species at every site tested (mean: 28 species/site vs. 18 species/site). Leaving audio recorders at a site over the field season can greatly increase the amount of data collected and using software to analyze the data can detect more than what an expert typically has time to find. The better-focused sampling effort and the lower amount of expertise identifying birds required by the Kaleidoscope-guided approach greatly improved our ability to monitor bird diversity. However, the difficulty the software has detecting/identifying certain bird species and the effort required to verify its identifications makes the approach a supplement, rather than a replacement, for experienced bird-sampling experts.

Hitsman, Harry, Carleton University; Andrew Simons

Latitudinal trends in timing of a life-history trait in the greater duckweed *Spirodela polyrhiza*

The timing of life-history traits is vital to the fitness of organisms. An example of this is in the aquatic plant the greater duckweed, *Spirodela polyrhiza*. *S. polyrhiza* produces dormant structures called turions prior to the end of the season that allow it to overwinter. If turions are produced too early, time for growth is lost. If, however turion production does not occur before pond freeze-over, duckweed plants may risk complete reproductive. Turion production shows phenotypic plasticity to environmental factors including a decrease in temperature associated with the end of the growing season. The evolution of the timing of turion production can be studied using a latitudinal gradient where season length is negatively correlated with latitude. Here, duckweed populations have been collected from a gradient spanning from Ontario to Florida. We hypothesise that there will be divergent norms of reaction in populations from different latitudes with those from higher latitudes producing turions earlier. This is tested by placing plants from each population in a temperature gradient and monitoring turion formation. Initial results suggest that populations from Ontario produce turions sooner than those from more southern latitudes.

Hoeg, Rielle, Acadia University; Dave Shutler, Acadia University; Ingrid Pollet, Justus Liebig University

Within breeding-colony predation of Leach's storm-petrels (*Oceanodroma leucorhoa*)

Many seabirds nest on islands free of mammalian predators, and some nest underground and move to and from colonies at night to avoid diurnal avian predators; many species are experiencing population declines. Leachs storm-petrels (*Oceanodroma leucorhoa*) are declining colonial seabirds that nest underground on offshore islands; causes of declines are unclear. We are quantifying predation at three breeding colonies in Atlantic Canada, and determining whether presumed herbivorous meadow voles (*Microtus pennsylvanicus*) are contributing to egg and nestling mortality. Transects and plots were monitored approximately biweekly on Bon Portage Island in 2018 and 2019, and less frequently on Country and Kent Islands in 2019. Carcasses, as well as gull and owl pellets, were counted and removed from transects on each visit, with pellets subsequently dissected for content analysis. In 2019, meadow voles were live-trapped during storm-petrel incubation and chick-rearing. Samples of vole fur and faeces from storm-petrel colonies and adjacent mainland were collected for stable isotope analysis of vole diet. VHF tags were deployed on voles to monitor movements around nest burrows. In 2018, 1.7-5.3% of breeding adults were depredated on Bon Portage Island. Ongoing analyses will aid in partitioning causes of population declines.
Hoi, Amber, University of Toronto; Benjamin Gilbert, University of Toronto; Nicole Mideo, University of Toronto

Using structural equation models to understand mechanistic causes of disease-diversity relationships.

Mosquitoes exist in communities in their natural habitats, and these communities vary in their absolute size, and species composition and richness through time and space. Mosquito species differ in life history, behaviour, niche preferences, the range of parasites they carry, and vector competence. As such, mosquito community structure is expected to be an important driver of variation in disease transmission patterns across the globe. Surprisingly, there has been little research into the relationship between mosquito diversity and disease dynamics, and existing data and theory tend to generate mixed results and predictions. To shed light on this important question, we analyzed publicly-available data on global mosquito and malaria prevalence gathered under the Malaria Atlas Project using structural equation models. These systematically-compiled datasets allowed for a thorough examination of 1) the effects of the biotic (e.g. presence of non-human hosts) and abiotic (e.g. landuse types) environment on various indexes of mosquito diversity, and 2) the effect of mosquito diversity on Malaria risk, which are factors that often covary and thus difficult to model using simple regressions. Results from preliminary analyses and implications to disease control are discussed.

Howland, Julia, University of New Brunswick; Alexa Alexander, Environment and Climate Change Canada

Chronic responses of Hexagenia mayflies to oil sands process water mixtures

Tailings ponds in Alberta, Canada contain massive amounts of oil sands process water (OSPW) that is currently stored on site, due to the toxicity of some components. Limited space and the need for reclamation of oil sands operation sites necessitates release of OSPW in the near future. Knowledge of the composition and toxicity of OSPW is often lacking yet is crucial for both risk assessment and management planning. This study examines the chronic toxicity of OSPW components (sodium naphthenate and naphthenic acids: NA) to nymphs of the mayfly Hexagenia limbata in either control or PAH-spiked sediment. The objective of this study was to determine whether the addition of the PAH-spiked sediment contributed to, or masked, the responses of these sensitive mayflies to OSPW components. Both lethal and sublethal responses to treatment were observed. Sublethal effects suggest that mayflies exposed to NA and PAH-spiked sediment may favour development over size to escape stress. These results reveal that the planned release of OSPW to the surrounding environment at concentrations currently thought to be safe would likely cause a reduction in sensitive mayfly populations and potentially other insect communities.

Huber, Dezene, Faculty of Environment, University of Northern BC; Lisa M. Poirier; Alicja M. Muir

Ground-dwelling invertebrate biodiversity patterns in a small, central British Columbia city support the intermediate disturbance hypothesis

We surveyed industrial, residential, and greenbelt sites spread across an urban landscape in the central interior of British Columbia. Over the course of four one-week sampling periods in Prince George, BC in July and August (2015) we collected substantially more than one-hundred species of Insecta, Arachnida, Crustacea, Myriapoda, Annelida, and Mollusca. Biodiversity patterns supported the intermediate disturbance hypothesis with the highest \( \pm \) diversity and richness found in industrial areas, followed closely by residential areas. Greenbelt sites exhibited the lowest richness, and both greenbelt and residential areas tended towards lower \( \pm \) diversity than industrial sites. Industrial areas exhibited a distinct community, while residential areas were somewhat differentiated from the other areas. Our work is foundational for new research into ecosystem service preservation and enhancement, and for the development of data-based conservation policy in central interior urban ecosystems. This work also provides a baseline invertebrate checklist including data on urban habitat use by native and introduced species in a poorly surveyed region.

Hughes, Josie, Environment and Climate Change Canada; Colin Daniel, Apex Resource Management Solutions Ltd.

Projecting the cumulative effects of harvest, fire and roads on forests and boreal caribou: a northwestern Ontario example
An important factor in the decline of boreal woodland caribou is disturbance mediated apparent competition; disturbance improves conditions for predators and alternate prey. We use a spatial stochastic model of forest harvest, fire, succession, and road development to project the cumulative effects of ongoing disturbance in the Churchill range (Northwestern Ontario). Succession and harvest parameters are derived from inputs and outputs of operational planning models (2008/09 plans). Without fire or roads our model matches operational plans, and projects an increase from 18% to between 30 and 37% of the landscape within 500m of a cutblock after 40 years. Adding initial roads and fires increases total disturbance to between 59 and 66% after 40 years. Most trunk roads have already been built, so road projections have little impact. A dynamic caribou habitat supply policy and a natural disturbance emulation policy both aggregate harvest. Removing either policy alone has little effect but dispersing small (<100 ha) cutblocks would increase the total disturbance footprint to between 80 and 85%. Climate change is expected to further increase fire disturbance. Spatial stochastic projections derived from operational planning models allow us to assess the implications of plans for caribou using the language of management.

Humphries, Murray, McGill University; Allyson Menzies, McGill University; Emily Studd, McGill University; Stan Boutin, University of Alberta

Warm bodies in cold places: the winter behavior and physiology of northern boreal endotherms

The northern boreal forest is the world’s most seasonal environment, defined by winters that are long, cold, snowy, dark, and unproductive. Homeostasis—the maintenance of a constant internal state—is a unifying principle in organismal physiology. However, in variable environments, homeostasis requires allostasis, the process of achieving balance through change, meaning that constancy and variation are co-requisites to surviving environmental variation. The study of warm bodies in cold places—homeothermic endotherms that remain resident and active throughout boreal winters offers a case study in how trait constancy and variation coalesce to define winter behaviour, energetics, and trophic interactions. And recent technological advances enabling simultaneous biologging of temperature, heart rate, and activity of free-ranging animals provides unprecedented opportunity to reveal these responses. Combining winter biologging data from red squirrels, snowshoe hares, and lynx in south-western Yukon with the described natural history of other boreal heterotrophs and autotrophs, reveals how winter, combined with endotherms need and capacity for homeostasis, flips boreal food webs upside down and creates keystone species.

Hunt, Heather, University of New Brunswick; Marie-Josée; Krystal Woodard; Rémy Rochette, University of New Brunswick

Cobble-filled bio-collectors: a tool for monitoring biodiversity and detecting human impacts in the rocky subtidal zone

In the Outer Bay of Fundy, shallow cobble habitat harbours a diversity of species, and serves a nursery function for commercially important species such as the American lobster. However, conventional methods do not sample this habitat effectively. Cobble-filled bio-collectors were developed to monitor settlement of American lobster in cobble habitat, but are colonized by a wide variety of invertebrates and fishes. We have a 10-year dataset of decapod crustacean and fish abundance (and for some years, data for all invertebrates; >500 species detected) from bio-collectors deployed in the southwest Bay of Fundy, which is considered a biodiversity hotspot and is among the fastest warming regions globally. Our dataset provides the first record (2012) of juvenile cunner Tautogolabrus adspersus in this region and recent research motivated by this finding suggests the species is undergoing range expansion driven by increasing water temperature during embryo development. We have also used bio-collectors to quantify impacts of salmon aquaculture. Effects of proximity to aquaculture on biodiversity patterns were detected but were smaller than spatial differences among Bay Management Areas. Our data demonstrate that cobble-filled bio-collectors are a useful tool to detect changes in biodiversity in shallow cobble habitat in response to anthropogenic impacts.
Hurford, Amy, Memorial University; Xiunan Wang, Department of Mathematical and Statistical Sciences, University of Alberta; Xiao-Qiang Zhao, Department of Mathematics and Statistics, Memorial University

Regional climate affects salmon lice dynamics, stage structure, and management

Regional variation in climate can generate differences in population dynamics and stage structure. Where regional differences exist, the best approach to pest management may be region specific. Salmon lice are a stage structured marine copepod that parasitizes salmonids at aquaculture sites worldwide, and have fecundity, development, and mortality rates that depend on temperature and salinity. We show that in Atlantic Canada and Norway, where the oceans are relatively cold, salmon lice abundance decreases during the winter months, but ultimately increases from year-to-year, while in Ireland and Chile, where the oceans are warmer, the population size grows monotonically without any seasonal declines. In colder regions, during the winter the stage structure is dominated by the adult stage, which is in contrast to warmer regions where all stages are abundant year round. These differences translate into region specific recommendations for management: regions with slower population growth have lower critical stocking densities, and regions with cold winters have a seasonal dependence in the timing of follow-up chemotherapeutic treatments. Predictions of our salmon lice model agree with empirical data, and our approach provides a method to understand the effects of regional differences in climate on salmon lice dynamics and management.

Hutchison, Chantal, McGill University; F. Guichard, McGill University; G. Gauthier, Université Laval; P. Legagneux, Université Laval; J. Bety, Université de Québec; Rimouski D. Berteaux, Université de Québec; Rimouski D. Gravel, Université de Sherbrooke

Including migrants in a high-Arctic food web model reveals indirect interactions between species are strongly driven by seasonality

To fully assess the impact of global warming on Arctic communities, theoretical models with a multi-season perspective are necessary. Migrating species are a key component of Arctic food webs that cannot be modelled with a single equilibrium. We optimize a multiple equilibrium, hybrid dynamical systems model of a tundra food web, parametrized by data from long-term high-Arctic terrestrial ecosystem monitoring, to reproduce known qualitative dynamics. We show that species persistence and their coexistence strongly depend on winter growth and interaction strengths. We further show that causal relationships between species are better characterized when seasonality is included. Our work demonstrates that multi-season models are crucial for understanding cross-ecosystem interactions in Arctic communities and are an invaluable tool for any community ecologist.

Ileperuma Arachchi, Ilesha Sandunika, Department of Biology, University of New Brunswick; Ilesha S. Ileperuma Arachchi1; Deepa Pureswaran 2; Stephen Heard1; 1 Department of Biology, University of New Brunswick, 2 Natural Resources Canada, Canadian Forest Service, Laurentian Forestry Centre

Invasive farmers in the woods: Invasion potential of Xyleborine ambrosia beetles in North America and Europe (Coleoptera: Curculionidae, Scolytinae)

Ambrosia beetles (Scolytinae) in tribe Xyleborini are a successfully established and rapidly expanding group of Coleoptera with invasive members in non-native biogeographic regions. Being introduced and well-established in North America and Europe, ambrosia beetles have overcome various challenges associated through mutualistic interactions with their ambrosia fungi. Factors that cause differences in invasion potential of successful insect invaders like ambrosia beetles are poorly known. Moreover, possibilities of their shifts in niches and range expansions are experienced and predicted with climate change during the past few decades. Thus, I will investigate the invasion potential of five candidate ambrosia beetle species present in both North America and Europe. I will address variation in invasion potential of selected ambrosia beetles as a function of trophic interactions and climate (temperature). I will test the extent to which non-native species become invasive using life history traits, interactions with the novel community and phylogenetic relationships between native and invaded communities based on field and laboratory experimental setting. Results of this study will contribute to the understanding factors underlying the variations in invasion potential of ambrosia beetles under
different environmental settings and species interactions. It will envision future trends of invasive behaviour of these beetles with climate change.

Imrit, Arshad, York University; Brock Harpur; Kathleen Dogantzis; Amro Zayed

Eusociality and purging selection

Eusociality, characterized in part by cooperative brood care, and reproductive division of labour, evolved independently several times in insects. The evolution of eusociality has been hypothesized to lead to differences in the extent of both positive and negative selection. While population genomics studies of eusocial insects have so far focused on positive selection, there has been no study of the extent of negative selection in social insects, and its relationship to the evolution of caste-biased genes. To address this knowledge gap, my research will estimate the extent of negative selection in honey bees, bumble bees, and wasps, through analysis of published population genomic datasets. My study will compare the relationship between the strength of negative selection and caste-specific patterns of gene expression, and examine if the strength of negative selection correlates with the level of social complexity in this species triad.

Irazuzta, Sebastian, McMaster University

Functional diversity of wild bees varies more than species diversity among oldfield and prairie sites

Worldwide, flying insect diversity and abundance are declining. Native bees could be particularly sensitive to increases in exotic and invasive plant species because they may not provide food and nesting material for many species. I hypothesized that communities with higher native plant composition should support more native bees and exhibit higher functional trait diversity. I tested this hypothesis in southern Ontario, simultaneously sampling bees over three years at a remnant prairie site, a newly-created tallgrass prairie site, 2 oldfield sites, and a wet meadow site. Though bee species diversity is the most common metric for assessing bee communities, I also used food specialization, nesting, size, and sociality traits to assess how functionally diverse the bee communities were. Bee species diversity and evenness did not differ among the sites. However, functional trait diversity was higher in the remnant prairie and newly created prairie sites than in the two oldfield sites. Surprisingly, the wet meadow site, despite having high graminoid abundance, had high functional trait diversity. This study supports the idea that native plant restoration does increase bee community health, and that functional guild diversity is a more informative measure of bee community functioning and habitat restoration success then species diversity alone.

Isitt, Rylee, Department of Biology, University of New Brunswick; Steve Heard; Jon Sweeney; Paal Krokene; Bjørn Økland, Deepa Pureswaran

Trans-continental invasion risk of spruce bark beetles

The concept of a tri-trophic niche – the trophic interactions between a herbivore, its host, and predators can be a useful framework for discussing the invasion potential of bark beetles. We have used this concept to guide field experiments investigating novel host utilization and predator avoidance by the spruce bark beetles Dendroctonus rufipennis and Ips typographus under hypothetical invasion scenarios. Host utilization experiments taking advantage of prior introductions of exotic spruce species allow us to determine if the bark beetles will feed on and reproduce within host species available in a potentially invasive range. By using synthetic pheromone lures, we can also test for attraction of predatory insects to the aggregation pheromones of bark beetles within a potentially invasive range. Our results to date suggest that both of our study species pose some risks of invasion: Ips typographus will utilize and reproduce within North American spruce, while Dendroctonus rufipennis avoids direct detection (via semiochemicals) by predatory insects in Europe.
Islam, Shahinur, Memorial University of Newfoundland; Brendan F. Wringe, Department of Fisheries and Oceans Canada, Bedford Institute of Oceanography; Ian R. Bradbury, Fisheries and Oceans Canada; Ian A. Fleming, Ocean Sciences Center, Department of Ocean Sciences, Memorial University of Newfoundland

Early-life fitness trait variation among divergent North American and European farmed and wild Atlantic Salmon (Salmo salar) populations

The escape of farmed fish and their potential ecological and genetic interaction with wild fish, is a major concern for aquaculture. Understanding the potential for and magnitude of interbreeding among wild and escaped farm salmon thus requires measures of both potential and realized reproductive success. In Newfoundland, there are plans underway to farm European origin (EO) salmon in addition to the current North American origin (NA) Saint John River strain. We thus undertook a common-garden experiment using controlled laboratory crosses of different combinations of NA and EO origin wild and farmed salmon and measured the survival and eight other fitness-related traits (e.g., fertility, development, growth) expressed during early life. Preliminary findings indicate that there were clear maternal effects on alevin size at hatch and emergence. We detected significant development and growth differences among the different cross-types. Generally, both NA and EO farm fish exhibited a higher growth and faster development than their related hybrids and wild conspecifics. However, there was no significant difference in fertilization success or survival at different early-life stages examined (i.e., eyed-up, hatch and emergence) among the different cross-types. Overall, this work suggests genetically based differences in traits with known fitness implications between cross-types in a common-environment setting at early-life stages. Keywords: Development, maternal and paternal effects, early life-history, fitness, hybridization.

Jackson, Don, University of Toronto; Lauren Lawson, Department of Ecology and Evolutionary Biology, University of Toronto

Are we transforming freshwater ecosystems to brackish/saline ones?

Freshwater ecosystems are being increasingly modified through a variety of stressors, including their salinization resulting from various anthropogenic activities such as mine runoff and agriculture. Within southern Canada, the use of de-icing salt in winter is the primary factor contributing to the salinization of aquatic ecosystems. The prolonged use of de-icing salt on our roadways and increasing application on private parking lots and sidewalks, is contributing to our freshwater ecosystems becoming modified into systems that may be stressful or lethal to native taxa. We examine winter and summer conditions of rivers and streams across southern Ontario, particularly within the Greater Toronto Area, to assess how these ecosystems are being altered; determine whether conditions pose threats for acute and chronic exposure of freshwater organisms; and characterize spatial and temporal trends in these relationships.

Jacobs, Shoshanah, University of Guelph

Jarvis, Lauren, University of Toronto; Cindy Chu, Ontario Ministry of Natural Resources and Forestry; Bailey McMeans, University of Toronto

Considering the cumulative effects of abiotic, biotic and human factors on fish productivity

Fisheries' health is vulnerable to the persistent threat of global change. In response to climatic or developmental changes fish alter their behaviour to maximize resource consumption or minimize energetic costs. These behavioural changes depend on the temperature preferences of individual species of fish, which can be broadly categorized as a cold-, cool- or warm-water species. However, additional biotic (e.g. competition), abiotic (e.g. water clarity), or human (e.g. angling pressure) factors interact to heighten or dampen temperature effects on these uniquely responding groups. My research seeks to determine how the relative influences of various biotic, abiotic, and human factors on fish productivity differs among key predatory species: cold-water lake trout, cool-water walleye, and warm-water smallmouth bass. By demonstrating that different species become more or less productive under different conditions will help inform predictive models and anticipate fisheries health under continued global change.
Jayarajan, Praveen, University of Toronto; Scott MacIvor; Marc Cadotte

Invertebrate diversity in deadwood at early stages of decay along an urban gradient

Deadwood decomposition is a driver of nutrient cycling and biodiversity, which significantly impacts forest health. Invertebrates are important contributors to this decomposition process, but their diversity in relation to urbanization is poorly studied. We investigated how urbanization and plant invasion affect invertebrate diversity associated with early-stage decay in different tree species and wood volumes. Cut branches of white pine (*Pinus strobus*) and sugar maple (*Acer saccharum*) were left to decompose at 18 urban parks across Toronto, Ontario in pairs of understory forest plots, invaded or not by dog-strangling vine (*Vincetoxicum rossicum*). After one year, branches were collected, placed in emergence traps and invertebrates were identified. From more than 30,000 individuals, we found abundance was significantly higher in pine, richness and evenness higher in maple, and abundance positively correlated with wood volume. With increasing urbanization, beetle (Coleoptera) abundance and diversity increased in pine but decreased in maple. Fly (Diptera) diversity and abundance increased with wood volume, but evenness decreased with invasion. Invertebrate associated with early-stage decay were distinct between wood types, but neither strongly affected by urbanization or invasion. Invertebrates associated with later-stage decay require attention to ultimately evaluate how urbanization threatens deadwood decomposition and ecosystem processes in cities.

Jean, Mélanie, Université du Québec; Abitibi-Témiscamingue; Nicole Fenton; Université du Québec en Abitibi-Témiscamingue

Spatial footprint of particulate pollutants around active and restored mines: Bryophyte growth and bioaccumulation

Mining impacts include their indirect footprint, such as particulate pollution produced around open pits, dry tailings ponds and access roads. Surprisingly, these indirect impacts are little known, particularly in the boreal forest, and may vary according to the mine life cycle and surrounding ecosystem. We aim to determine the spatial footprint of mines by 1) assessing baseline concentrations of metals in north-western Quebec, 2) evaluating how interactions between the mine life cycle and ecosystem type (coniferous forests, hardwood forests and wetlands) influence the spatial extent of pollution, and 3) measuring impacts on bryophyte growth. We used mosses (*Pleurozium schreberi*) as indicators because of their bioaccumulation capacity. We sampled around four mines in exploration, exploitation, closure or restoration phases place in Abitibi-Témiscamingue along 6-8 transects perpendicular to the mine perimeter (plots at increasing distance up to 1000 m). Six control transects were established in undisturbed areas. Metal and metalloid concentrations were measured in moss samples from each plot and we monitored annual moss growth in situ. Preliminary results from control plots suggest high metal concentration, high variability and a difference between coniferous and hardwood forests. Our results will help to reduce the environmental impacts of mining activities in the boreal forest.

Jennings, Alexandra, McMaster University; Susan Dudley, McMaster University

Kin recognition, biomass allocation and fitness in Blue-stemmed Goldenrod (*Solidago caesia*)

Plants often compete for limiting resources. Kin recognition can allow plants to direct competitive behaviours towards strangers (non-relatives of the same species) or helping behaviours towards relatives. Plants growing with relatives should thus have higher fitness than plants growing with strangers. Plant kin recognition has been seen in more than twenty-five studies with plants demonstrating differing responses to growing with kin. Using the perennial understory species Blue-stemmed Goldenrod (*Solidago caesia var. caesia*), I examined the kin recognition responses of juvenile (4-5 week old) seedlings as part of a multi-year research program looking at allocation and life history trade-offs at different developmental stages. Seedlings were planted either alone in a pot, in kin pairs (same maternal sibship) or stranger pairs (different families) and fertilized with high or low nutrients. I found that kin pairs bolted sooner and were significantly larger compared to strangers, consistent with the hypothesis that kin pairs were not experiencing the same costs of competition as strangers. I explore how the functional traits root allocation, stem allocation, stem elongation and specific leaf area contribute to the fitness differences between kin and stranger pairs.
Jensen, Evelyn, Yale University; Stephen C. Lougheed, Queens University; Peter van Coeverden de Groot, Queens University; Christina Tollett, Queens University; Kristen Hayward, Queens University; Sean Vanderluit, Queens University, Markus Dyck, Department of Environment, Government of Nunavut; Marsha Branigan, Environment and Natural Resources, Government of Northwest Territories

Genomic approaches for non-invasive, scat-based monitoring of polar bears across the Canadian Arctic

The polar bear is an apex arctic predator that depends on sea-ice. It will be profoundly impacted by climate change. Canada is home to ~15,000 polar bears or approximately two-thirds of the global population, with Nunavut and Northwest Territories having management jurisdiction over most. Of 19 defined polar bear managements, 13 fall within Canada, with many monitored infrequently with insufficient data to access population trends. Polar bears play a pivotal role in Inuit culture and traditional knowledge systems, and provide economic value to areas with high unemployment. Inuit communities desire monitoring methods that do not require handling bears, and that directly incorporate them and their perspectives in management. In response to these needs, we are developing a novel non-invasive monitoring approach that marries genomics, other bioassays, and northern peoples. We used SNPs derived from ddRAD genotyping to map population structure across the Canadian Arctic using archived samples. From these we selected approximately 400 SNPs for a Genotyping-in-Thousands assay that is the basis of a toolkit that includes molecular diet, contaminants, and stable isotope analyses. We are working with communities to embed use of this toolkit within a community-based monitoring program that includes community viewpoints and provides remuneration for samples.

Rob C. Johns1*, R. Drew Carleton2, Emily Owens1, Holly Blaquière3, Stéphane Bourassa4, J. Bowden5, Jean-Noël Candau4, Ian DeMerchant1, S. Edwards5, Allyson Heustis3, Patrick M. A. James7, Alison M. Kanoti8, Chris J. K. MacQuarrie6, Véronique Martel4, E. Moise5, Deepa Pureswaran4, Evan Shanks1. 1New Brunswick Department of Energy and Resource Development; 2Natural Resources Canada, Canadian Forest Service - Atlantic Forestry Centre; 3Forest Protection Limited; 4Natural Resources Canada, Canadian Forest Service - Laurentian Forestry Centre; 5Natural Resources Canada, Canadian Forest Service - Atlantic Forestry Centre; 6Natural Resources Canada, Canadian Forest Service - Great Lakes Forestry Centre; 7Université de Montréal, Département des Sciences Biologiques; 8Maine Forestry Service, Department of Agriculture

Tracking insect outbreaks: a case study of community-assisted moth monitoring using sex pheromone traps

Insect outbreaks can cover vast geographic areas, making it onerous to cost effectively monitor populations to address management and ecological research questions at a landscape scale. Community science (aka citizen science) has been serving as a useful approach to address this challenge for the spruce budworm (Choristoneura fumiferana Clemens), a major pest of spruce and fir throughout Canada and the northeastern United States. In this talk, I will discuss “Budworm Tracker”, which is a contributory community science program that that helps to monitor and collect budworm moths throughout its northeastern range. The program outsources pheromone trap ‘kits’ to volunteers who periodically check and collect moths from their traps throughout the budworm flight period, then return the data and moths to us by mail (all free-of-charge to the volunteer). The data collected through this program are being used to address a variety of ecological, sociological, and management research questions.

Johnson, Genevieve, University Of Guelph; Mehrdad Hajibabaei, University of Guelph

Evaluating the state of transcriptomic resources for freshwater stream bioindicators

With the growing human population and increased urbanization, agriculture and natural resource development activities, it is critical to monitor the health and stability of the surrounding environments. Freshwater insect biodiversity is among key indicators of overall ecosystem health because species demonstrate differing levels of resilience to contaminants or
disturbances, and shifts in their assemblages can impact local food webs. Thus, there is interest in studying species-specific reactions to environmental conditions at a molecular level to assess how organisms are impacted and why some species are more resilient to contaminants than others. High throughput DNA sequencing is consistently becoming more affordable and accessible to researchers of non-model organisms, but assembly accuracy is impacted by the amount of phylogenetic divergence between the sequenced organism and existing reference data. We are compiling genomic and transcriptomic annotations of aquatic insects to highlight which branches of the phylogeny are well studied and which have limited or no existing resources. We focus on the orders Ephemeroptera, Trichoptera and Odonata because they are readily abundant during their larval life stages in the freshwater systems across North America.

Johnston, Jason, University of Maine at Presque Isle; Elise Gudde, University of Maine at Presque Isle; Larry Feinstein, University of Maine at Presque Isle; Judith Roe, University of Maine at Presque Isle; Krista Delahunty, University of Maine at Presque Isle

Arthropod food use by forest birds at the boreal-deciduous ecotone of northern Maine

The effect of climate change on species distributions has been studied over the past two decades through empirical, theoretical, and modeling approaches. From these studies, we know that range shifts or declines in abundance near range margins have been documented for insects, boreal and temperate birds, and trees. Using DNA metabarcoding to identify arthropod species, researchers at the University of Maine at Presque Isle have sampled food use (n>300 samples) in a suite of forest insectivorous birds (n=24 species) in Acadian forest habitats of northern Maine, including bog, spruce-fir forest, and northern hardwood forest. Diets of leading edge, trailing edge, and habitat-generalist bird species were used to test food use as a mechanism of bird species range expansion and contraction. Boreal species are expected to have a higher proportion of boreal arthropods in their diet, while the converse is predicted for deciduous-dwelling leading edge species e.g. Northern Cardinal. Habitat generalists are predicted to have a more species rich diet. Data analyses are in progress. Analysis of life history characteristics of arthropod species in relation to bird species groupings will provide insight into community composition at ecotones, especially when life history characteristics of both predators and prey vary significantly between biomes.

Kaur, Mandeep, Department of Zoology, Guru Nanak Dev University; Pooja Chadha, Department of Zoology, Guru Nanak Dev University

Genotoxic and Cytotoxic Effects of an Endophytic Fungus Schizophyllum commune in Spodoptera litura A Possible Mechanism for its Insecticidal Activity

Fungal endophytes are ubiquitously found in plants and are being increasingly explored as biocontrol agents due to their ability to protect plant from various diseases and insect pests and to support plant health. They are most promising alternative to chemical pesticides. Previously in endophytes, ascomycetes were much explored as biocontrol agents, however other genera were not yet explored. Schizophyllum commune is basidiomycetes belonging to the schizophyllaceae family. The present study was conducted, to assess the insecticidal potential of an endophytic fungus Schizophyllum commune and its mechanism of toxicity by studying genotoxic effects as well as repair potential using Spodoptera litura (Fabricius) as model. Different endophytic fungi were isolated from medicinal plants and tested for their insecticidal potential against Spodoptera litura (Fabricius). S.commune isolated from Aloe vera showed maximum mortality. DNA damage and repair studies were carried out. With increase in exposure time of insect larvae to fungal extract, DNA damage was found to be enhanced. The extent of recovery of damage caused by fungus was found to be very low indicating long term effect of treatment (Mandeep Kaur et. al., Scientific reports, 2018, 8(1), 4693). This is first report showing insecticidal potential of S. commune and associated genotoxic effects. Overall the study highlights endophytes (basidiomycetes) as a biocontrol agent.

Kelly, Clint

Sexual selection on shape and size of morphological traits in Japanese beetles
Kernaghan, Gavin; Amanda Griffin; Ayesha Hussain, Mount Saint Vincent University

Resistance and tolerance to tannins in dark septate root endophytes

Tannins are plant defense compounds found in bark, leaves and roots that can inhibit fungal growth by a variety of mechanisms. As roots are colonized by a diverse array of fungi, it is likely that at least some groups are tolerant to tannins. We compared the effect of both tannic acid (hydrolysable) and spruce root tannins (condensed) on the growth of a range of root associated fungi, including ectomycorrhizal, saprobic, pathogenic and root endophytic species. Levels of tannin tolerance were mapped onto a 28S tree to determine which phylogenetic groups contained tannin tolerant species. Ectomycorrhizal fungi were very sensitive to tannins, while some other groups were slightly more tolerant. However, species of dark septate root endophytes (DSEs), e.g. Phialocephala spp., were notably less susceptible than others. This pattern was similar for condensed and hydrolysable tannins. The DSEs can resist tannins by producing polyphenol oxidases, which can detoxify tannins, as well as tannase, to utilize tannin as a carbon source. However, DSEs may also tolerate tannins through their ability to grow under nitrogen limitation, which may occur when tannins disrupt cell normal membrane function. We also hypothesize that tannin tolerant DSEs facilitate the colonization of roots by other decomposer organisms.

Keyghobadi, Nusha, University of Western Ontario; Maryam Jangjoo, Sick Kids Hospital; Nikita Frizzelle, University of Western Ontario; Jens Roland, University of Alberta; Stephen Matter, University of Cincinnati

Morphological and genetic correlates of dispersal in a butterfly

Dispersal is a key ecological process that determines the dynamics and evolution of spatially structured populations. Individuals of a given species can vary in the propensity or ability to disperse, and in some species suites of co-varying traits are associated with dispersal and define dispersal syndromes. We used mark-recapture data from a metapopulation of the Rocky Mountain apollo butterfly to distinguish dispersers (i.e., individuals that had moved between different habitat patches) from non-dispersers. We then compared dispersers and non-dispersers at a suite of morphological and genetic characteristics. Dispersers did not from non-dispersers in flight-associated morphometry. However, dispersers had lighter wing colour and lower flight thoracic temperatures than non-dispersers. Dispersers showed significantly different patterns of gene expression, including higher expression of a number of genes involved in energy metabolism and heat stress. Dispersal was also significantly associated with non-synonymous variation at the phosphoglucose isomerase (Pgi) gene, the product of which catalyzes an early step in glycolysis. Our results suggest that dispersal in this species is consistently associated with a suite of traits related to energy metabolism, body temperature, and their interaction.

Kielstra, Brian, University of British Columbia; Bernadette Charpentier; Lenka Kuglerová; Les Stanfield; Antoine Morin; John Richardson

Improving stream network cumulative effects models by incorporating multiscale processes

Biomonitoring programs assess how communities deviate from reference conditions for guiding protection and restoration. Lacking suitable reference sites and incorporating spatial context (e.g., network connectivity) remain important challenges for cumulative effects models. Using a spatiotemporally extensive benthic macroinvertebrate (BMI) dataset, we assessed regional-scale variability in site deviations from predicted/hindcasted reference conditions (i.e., in the absence of a set of stressors). We assessed importance of environmental (e.g., geology) and land cover (e.g., % urban) factors to BMI community metrics. We hindcasted metrics to assess regional variability in deviations from reference. For a spatial subset, we incorporated spatial factors (e.g., headwater conditions and network connectivity) to assess predictive capacity improvements. Both environmental and landscape factors had a median importance of 18% (% increase in mean squared error when factor is randomly permuted) across metrics but varied in their importance range (environmental: 643%; land cover: 453%). A median of 76% of sites fell within ±1 SD of reference conditions, 17% fell between ±1 and ±2 SD, and 5% were >±2 SD across all metrics. Spatial components resulted in varying changes to predictive capacity depending on component type. Using regionally-informed models can provide expected community conditions before getting any boots wet.
Modelling the influence of linear feature proximity on gray wolf (*Canis lupus*) habitat selection and movement

Anthropogenic linear features represent one of the most profound human impacts on landscapes, often leading to alterations in wildlife behaviour and predator-prey dynamics. For apex predators, including gray wolves (*Canis lupus*), linear features may represent a trade-off between elevated human interactions and increased ease of movement or prey encounters. This trade-off between risk and reward likely varies, however, between different types of linear features depending on their use. This study tests the effects of landscape variation, namely anthropogenic linear features, on the movement and space-use of GPS-collared wolves in eastern Manitoba. We simultaneously model wolf movement and selection by comparing used to available steps (linear connections between relocations). Models that include both linear feature proximity and habitat type best describe individual selection and movement responses. Wolves avoid linear features associated with high rates of human activity and select for features with reduced activity. They increase selection for low-use linear features when in dense habitat, indicating wolves may use these features to increase ease of travel. Monitoring the combined effects of linear features and habitat proximity can help elucidate anthropogenic influences on wolf movement and thus provide critical insight into the complex interplay between disturbance, wildlife movement, and predator-prey dynamics.

Physical and biological dimensions of urbanization lead to novel landscape variation in mosquitofish phenotypes

Urbanization dramatically alters the physical and biological dimensions of landscapes, potentially leading to novel selection pressures and novel phenotypes. Here we seek to understand how both physical and biological dimensions of urbanization interact to drive phenotypic evolution of mosquitofish morphology and behavior. We examine the magnitude and direction of urbanization-driven phenotypic evolution due to shoreline development and invasive species introductions (predators and competitors), as well as trait variation associated with innate landscape attributes, including lake size and eco-region (desert or coast). We examine morphology and behavior of wild-caught western mosquitofish (*Gambusia affinis*) from 21 lakes in California, USA. We find that both physical and biological dimensions of urbanizationshoreline development and introduced invasive predators and competitorslead to suites of traits associated with feeding and survival in complex, sheltered fringe habitats. Furthermore, morphological trait responses to urbanization were similar to increasing lake size and a shift toward a less temperate eco-region (desert), whereas behavioral responses were similar to those from reduced lake size and a more temperate climate (coastal). As such, urbanization may lead to novel trait combinations not found on natural landscapes.

The structural and socioeconomic features of cities predict the traits of Passerine species likely to breed in them

Given the current pace and extent of environmental change it is important to attempt to develop a predictive understanding of the community reorganization that follows environmental turnover. Here we focus on the consequences of urbanization. Species level life-history traits predict a species ability to colonize cities. While cities tend to be more similar to each other than nearby natural environments, features of cities also vary. Despite this, most analyses of urban biodiversity treat cities as equivalent habitats. We hypothesized that variations in city characteristics predict the traits of species that live there. To test this we combined georeferenced records of Passerines likely to breed in American cities from iNaturalist and eBird databases (31190 records; 167 species; 853 urban areas). The best predictor of life-history trait variation was the median income of the urban area; other work suggests that this is correlated with the amount of green space in a city. As median income increased, cities tended to support species that were less likely to be migratory and that...
had relatively large clutches, smaller body sizes, and shorter lifespans. Features of cities and the traits of species are important predictors of the new group of species that can persist following urbanization.

Kits, Joel, Agriculture and Agri-Food Canada; Tim Dumonceaux, Agriculture and Agri-Food Canada; Charles Vincent, Agriculture and Agri-Food Canada; Saint-Jean-sur-Richelieu

Biodiversity of Auchenorrhyncha on blueberry in Quebec

Blueberries are one of Canada's highest value fruit crop, and a major agricultural commodity in Quebec. Phytoplasmas, plant diseases primarily vectored by leafhoppers, are a serious threat to blueberry production. Recent discoveries of phytoplasma-infected blueberry plants in Quebec prompted us to study the leafhoppers and their relatives (Auchenorrhyncha) feeding on blueberry in order to identify potential vectors. We collected specimens on blueberry plants on 25 farms located in Southern Quebec during the summers of 2017-2018. Specimens were identified based on morphology and COI barcodes. We have identified 41 taxa from the samples, mostly Cicadellidae but also including Aphrophoridae, Clastopteridae, Derbidae, and Membracidae. Dominant species include *Empoasca fabae*, *Graphocephala hieroglyphica*, *Limotettix instabilis*. Several taxa were identified as both nymphs and adults, suggesting a particularly close association with blueberry. Tests using LAMP showed specimens of several species were carrying phytoplasmas. Results are compared with previous studies of leafhoppers on blueberry.

Klemet-N'Guessan, Sandra, Trent University; Raeya Jackiw; Christopher G. Eckert; Anna L. Hargreaves

Edgy conservation: Canadian at-risk plants are overwhelmingly range-edge populations and under-studied

As biodiversity declines toward the poles, high-latitude countries will contain the poleward range edge of many species, potentially biasing national conservation efforts toward range-edge populations whose global conservation value remains contentious. Using all 215 vascular plants assessed for protection in Canada as a case study, we ask whether national species-conservation rankings are biased toward range-edge populations and justified by adequate research. Of 193 plant taxa deemed at-risk in Canada, 76% were only found in Canada at the northernmost 20% or less of their range. Higher threat categories had more peripheral taxa, peaking at 85% for endangered plants, and the mismatch between national and global threat rankings was significantly greater for peripheral vs. non-peripheral taxa. Of the research effort on plant species deemed at-risk in Canada, peripheral taxa received about half the conservation research effort as non-peripheral taxa, and only 1% of studies assessed at-risk populations in the context of their wider geographic range information that is critical to establishing their relative conservation value. Thus, flora conservation in Canada is largely the conservation of edge populations, yet edge populations themselves and the geographic context that makes them unique are understudied, a research gap we must close to improve evidence-based conservation.

Kohn, Michael H., Rice University, BioSciences

Possible conservation genomic lessons on adaptive evolution learned from the study of warfarin resistance in rodents

The role of adaptation and introgression in multilocus adaptation perhaps still is best characterized in natural populations of model organisms experiencing defined selective regimes. This is because drift plays a less prominent role than selection, but as I will discuss, is surprisingly effective. We observe that in house mice and Norway rats, which evolved resistance to the anticoagulant poison warfarin and related compounds. Despite immense genetically effective population sizes Ne at the global scale these species have surprisingly small Ne at the regional and local scales. In addition, migration, independent evolution, and population structure strongly affect the distribution of the main alleles conferring resistance at the vitamin K epoxide reductase gene (Vkorc1) and newly identified loci involved in this adaptation. Population structure at standing genetic variation under selection may strongly affect the observed alleles, but these may not be detected (replicated) in another population; a pattern that may be commonly observed in endangered species. I discuss the term Pan-adaptive genomeweb showing that even at global, regional, and local scales resistant populations differ in the loci and alleles, even at the main resistance gene Vkorc1. Annotation of adaptive candidate variants reveals that many would be interpreted as deleterious if it was not suspected that these are adaptive in a specific context.
Koiter, Lauren, University of Waterloo; Laura Beecraft, University of Waterloo; Michael Lynch, Metagenom Bio Inc.; Trevor Charles, University of Waterloo; Rebecca Rooney, University of Waterloo

Effect of Glyphosate Exposure on Periphyton Community Structure

Glyphosate is one of the most commonly used herbicides in the world as it inhibits the 5-enolpyruvylshikimic acid-3-phosphate synthase (EPSPS) pathway in photosynthetic organisms. This may impact the community composition of aquatic surface attached microorganisms, collectively called periphyton. Periphyton are complex communities that play a key role in aquatic nutrient cycling and as the base of many aquatic food chains. We hypothesize that glyphosate exposed communities will have a decrease in abundance of eukaryotic organisms such as diatoms and green algae due to inhibition of the EPSPS pathway, an increase in the abundance of cyanobacteria because some have a glyphosate resistant class of the EPSPS pathway, and a change in bacteria community composition as species able to metabolize glyphosate benefit. We conducted a three-week dosing experiment with field-collected periphyton in microcosms. Early results indicate that the change in periphytic community structure depends on the originating community, with samples from different locations responding distinctly to glyphosate additions. Generally, cyanobacteria abundance declined relative to control microcosms, but bacterial and eukaryote responses were mixed.

Konopka, Joanna, Western University; Danny Poinapen, Schulich School of Medicine and Dentistry, Western University; Tara Gariepy, London Research and Development Centre, Agriculture and Agri-Food Canada; David W. Holdsworth, Schulich School of Medicine and Dentistry, Western University; Jeremy N. McNeil, Department of Biology, Western University

Timing of failed parasitoid development in Halyomorpha halys eggs

Invasive species can destabilize ecological communities by becoming novel hosts, pray, predators or competitors for native species, with lasting effects on population dynamics of native individuals. The establishment and spread of invasive Halyomorpha halys have presented native natural enemies in the introduced areas with such a challenge. The native parasitoids readily parasitize eggs of H. halys, but their progeny rarely develops in fresh eggs of this host. The barriers to successful development of native parasitoids in H. halys eggs remain unidentified. To determine the timing of failed development of native parasitoids in fresh H. halys eggs, we examined the temporal development of the Trissolcus euschisti parasitoid within suitable and unsuitable host eggs using a DNA barcode-based approach, and in situ 3D visualization by X-ray micro-computed tomography (micro-CT). Parasitoid development in fresh H. halys eggs fails soon after parasitization (egg or early larval stage) as limited or no larval development was observed 24 h after initial parasitization. We propose that host cellular immune response and/or disrupted parasitoid teratocyte growth pattern might cause arrested parasitoid development in H. halys eggs. We also provide a time window for further investigation of these potential mechanisms that result in failed parasitoid development in H. halys.

Korfanty, Greg, Masters Student; Lisa Teng; Nicole Pum; Jianping Xu

Contemporary gene flow is a major force shaping the Aspergillus fumigatus population in Auckland, New Zealand

Aspergillus fumigatus is a globally distributed opportunistic fungal pathogen capable of causing highly lethal invasive aspergillosis in immunocompromised individuals. Recent studies have indicated that the global population consists of multiple, divergent genetic clusters that are geographically broadly distributed. However, most of the analyzed samples have come from continental Eurasia and the Americas where the effects of ancient vs. recent factors are difficult to distinguish. Here we investigated environmental A. fumigatus isolates from Auckland, New Zealand, a geographically isolated population, and compared them with those from other parts of the world to determine the relative roles of historical differentiation and recent gene flow in shaping A. fumigatus populations. Our data suggest that the Auckland A. fumigatus population contains both unique indigenous genetic elements as well as genetic elements that are similar to those from other regions such as Europe, Africa, and North America. Additionally, susceptibility testing identified two triazole-resistant strains, one of which contained the globally distributed mutation TR34/L98H in the cyp51A gene. Our
results suggest that contemporary gene flow, likely due to anthropogenic factors, is a major force shaping the New Zealand A. fumigatus population.

Kou-Giesbrecht, Sian, Columbia University; Jennifer L. Funk, Chapman University; Steven S. Perakis, U.S. Geological Survey; Amelia A. Wolf, University of Texas at Austin; Duncan N. L. Menge, Columbia University

Should nitrogen-fixing trees be planted during assisted forest restoration?

Forests are a significant CO2 sink, sequestering a quarter of anthropogenic CO2 emissions. However, the negative radiative forcing of forest CO2 sequestration is offset by the positive radiative forcing of soil emissions of nitrous oxide (N2O), a potent greenhouse gas. Forest restoration has predominantly focused on maximizing CO2 sequestration, without considering soil N2O emissions. As such, nitrogen-fixing trees have been recommended for planting during forest restoration: they are proposed to relieve nitrogen limitation of neighbouring plant growth by enriching soil nitrogen. However, by enriching soil nitrogen, they can stimulate significant soil N2O emissions. We show preliminary results that a nitrogen-fixing tree species promotes net CO2 sequestration relative to a non-fixing tree species under low nitrogen supply but net soil N2O emissions under high nitrogen supply. These results are replicated with a modelling approach suggesting that they are generalizable. Using the model, we projected CO2 sequestration and soil N2O emissions stimulated by nitrogen-fixing trees over time, and estimate the time intervals over which planting nitrogen-fixing trees is effective for climate change mitigation. Due to projected intensifying nitrogen deposition these results suggest that planting nitrogen-fixing trees will be less effective than planting non-fixing trees in assisted forest restoration for climate change mitigation.

Kraus, Dan, Nature Conservancy of Canada

Ours to save: The distribution, status and conservation needs of Canada’s nationally endemic species

Endemic species are restricted to a particular geographical region, such as an ecoregion or country. This restricted range can increase their vulnerability to extinction and they are often the focus of conservation. NatureServe Canada and the Nature Conservancy of Canada, in consultation with experts from across the country, have developed the first comprehensive list of Canadian endemic species. We identified over 310 species, sub-species and varieties that have only been documented from Canada. Most Canadian endemic species are vascular plants and arthropods. Nationally endemic species occur across Canada with the highest numbers in BC, Quebec and Yukon. BC, Yukon and Nova Scotia have the most endemic species that only occur within their jurisdiction. The analysis also identified concentrations of endemic species, many of which are associated with glacial refugia or unique habitats. Only 10% of Canada’s endemic species are globally secure and less than 20% have been assessed by the Committee on the Status of Endangered Wildlife in Canada. The results of this analysis can be used to prioritize conservation actions and to inspire public support for species and habitat protection in Canada.

Krause, Samantha, University of Lethbridge; Samantha Booth, University of Lethbridge; Peter Mower, University of Lethbridge; Marcus Dostie, University of Lethbridge; David Logue, University of Lethbridge

Tracking communication: a spatially explicit approach to duet function

Vocal duets occur in many bird species. Duet participation serves various functions, including cooperative resource defence, mate-guarding, and mate localization. We are using an observational dataset to study the functions of duet participation in the Adelaide’s warbler (Setophaga adelaidae). In this species, duets occur when a male sings and his mate emits call notes. We continuously recorded behaviour, vocalizations, and locations from eight radio-tagged mated pairs. We use these data to test two predictions of the resource defense hypothesis: that duets are associated with border conflicts and tend to occur near shared borders. We will also test whether mates tend to move closer to each other after a duet, as predicted by the mate localization hypothesis. This is the first study to combine detailed tracking data and GIS software to study duet function, and the first to analyse duet function in a warbler (family Parulidae). More broadly, this
project emphasizes the value of integrating modern geographical techniques in the study of animal communication, and furthers our understanding of vocal duetting as a model of cooperative behaviour and conversation-like communication.

Kreiner, Julia, University of Toronto; John Stichcombe; Stephen Wright

Population genomics of herbicide resistance and agricultural adaptation

The evolution of herbicide resistance in weed populations is a highly-replicated example of adaptation surmounting the race against extinction, but the factors determining its rate and nature remain poorly understood. We have taken both comparative and population genomic approaches to address how population genetic factors may influence the rate and nature of adaptation. In a meta-analysis framework, we took advantage of the extensive literature on the molecular basis of herbicide resistance; across 118 studies and 79 species, our findings are consistent with theoretical predictions that self-fertilization reduces resistance adaptation from standing variation within populations, but increases independent adaptation across population. At the within-species level, and to understand the evolutionary mechanisms driving the spread of herbicide resistance, we sequenced and assembled the genome of a predominant agricultural weed, Amaranthus tuberculatus, and investigated the population genomics of 163 glyphosate-resistant and susceptible individuals in Canada and the USA. We found multiple origins and modes of resistance adaptation across the range, from new mutation, preexisting variation, and gene flow, and found that the mode of adaptation depended on the timescale that selection had been taking place. Lastly, I will introduce an approach for assessing the extent of contemporary evolution and adaptation to agriculture in A. tuberculatus through a paired natural-agricultural population sampling scheme, coupled with sequencing of herbarium specimens that date back to the 1800s. Overall, this work contributes key insights into the mechanisms, prevalence, and timescale of evolution to anthropogenic environments, and informs on the scale of management strategies needed to prevent the further spread of resistance and agricultural weeds.

Kulkarni, Manisha, University of Ottawa

Exploring socioecological determinants of vector-borne disease emergence and risk in eastern Ontario

Tick-borne Lyme disease and mosquito-borne West Nile virus constitute present and increasing public health risks in Canada. Ongoing climate and environmental changes are driving tick population expansion into new areas, placing more Canadians at risk, with Lyme disease considered an emerging threat in many major population centres. At the same time, the risk of sporadic West Nile virus epidemics remains high. Populations at risk for Lyme disease and West Nile virus are principally defined by the geographic occurrence of their respective arthropod vectors, highlighting the importance of identifying high risk areas to target interventions and mitigate disease risk. By linking entomological and epidemiological disease surveillance data using spatial analytic approaches we have identified potential hotspots of vector-borne disease transmission and human vector-borne disease incidence at the regional and landscape scales in eastern Ontario. Our research has revealed different geographic patterns and disease profiles for West Nile virus and Lyme disease with environmental risk concentrated in urban and suburban areas, respectively, largely owing to their different ecologies. Interestingly, however, hotspots of environmental risk do not necessarily translate to high disease incidence in humans, implying that both social and ecological factors are important to consider when identifying populations at risk.

Kunegel-Lion, Melodie, University of Alberta, Biological Sciences; Mark A Lewis

Factors governing outbreak dynamics in a forest managed for mountain pine beetle

Mountain pine beetle (MPB) outbreaks have caused major economic losses and ecological damages in North American pine forests. Using ecological and environmental factors impacting MPB life-history and stands susceptibility can help with the detection of MPB infested trees and thereby, improve control. Temperatures, water stress, host characteristics, and beetle pressure are among those ecological and environmental factors. They have different roles on MPB population dynamics at various stages of an outbreak. However, a deeper quantitative analysis on a local scale is required to make detailed connections between ecological and environmental variables and MPB outbreak phases. We studied the current isolated MPB outbreak in Cypress Hills. We used logistic regressions on a highly-detailed and georeferenced data set to
determine the factors driving MPB infestations for the different phases of an outbreak. We showed that incoming flights from outside the park are driving MPB population increase during the outbreak onset more than a change in stand susceptibility. At its peak, the MPB outbreak depends mainly on nearby beetle pressure, low summer temperatures, and the presence of tall trees. A decrease in the number of vigorous susceptible pines, as suggested by lower relative humidity levels and a decrease in pine cover, drives the MPB population collapse. This can help managers make appropriate decisions on where to focus their effort depending on which phase the outbreak is in.

Kwok, Allison, Trent University; Marcel E. Dorken

Measuring sexual selection in natural plant populations using the index of mate monopolization

Measuring sexual selection in plant populations is challenging. Because plants require third party vectors for pollination, it can be difficult to observe mating events and track successful pollination. For this reason, an indirect measure of sexual selection in plants - the index of mate monopolization (m) - has been developed but its ability to reveal patterns of sexual selection in natural populations has not been tested. This indirect measure of sexual selection is much more easily obtained than more direct measures, such as the selection differential, s. To test the effectiveness of m as a proxy of s, we quantified daily values of m from patterns of correlated paternity in two populations of Sagittaria latifolia. We measured floral traits known to affect pollinator visitations, and genotyped flowering shoots and a subset of the seeds with seven SSR loci. We used paternity analysis to estimate the magnitude of s on the floral traits and compared our estimates of s to our calculations of m.

Laberge, Frederic, University of Guelph; Caleb Axelrod, Integrative Biology, Guelph; Timothy Fernandes Biology, Toronto-Mississauga; Bailey McMeans, Biology, Toronto-Mississauga; Kevin S. McCann, Integrative Biology, Guelph

Ecophysiology of the nearshore-offshore axis in freshwater fishes

The factors contributing to efficient resource use by predators are not well known. We investigated if fish predators enhance their ability to forage in space to broaden the pool of available resources and/or their ability to make better decisions about where and when to find available resources. To tackle these questions, we used an ecophysiology approach looking for associations between use of the nearshore and offshore energy channels within lakes, assessed by carbon stable isotope analysis, and biochemical/anatomical proxies of fish swimming (muscle glycolytic potential, heart ventricle size) and cognitive (brain size) performance. Results from a Georgian Bay food web suggest that pelagic foraging requires enhanced swimming capacity and that flexible exploitation of the nearshore-offshore axis requires enhanced cognitive capacity. Thus, the ability to make good foraging decisions appears more important than swimming capacity for efficient resource use by fish predators. However, results from additional lake systems where the same fish species use the nearshore and offshore habitats differentially suggest that life in the more complex nearshore habitat also requires enhanced cognitive capacity. More work is needed to understand what features of nearshore habitat use or foraging contribute to fish cognitive demands, and if those demands vary with trophic levels.

Labrie, Genevieve, CRAM; François Dumont, CRAM; Caroline Provost, CRAM

Fruit production and climate change: does genetic and species diversity improve resilience for Quebec agroecosystems?

Climate change could have negative consequences on agroecosystems and crop diversification has been shown to improve resilience in these production systems. In Quebec, fruit production (orchards, vineyards, small fruits) are economically important and are not immune to future climate changes. The principal objective of this project is to evaluate how genetic and species diversity influence productivity in Quebec orchards, vineyards and raspberry farms. For all production types, three levels of crop diversification have been selected: monoculture, low diversity and high diversity. A total of 27 farm fields have been selected and will be monitored between 2019 and 2022. Each diversification type will be represented by three farms. Arthropod diversity will be monitored every two weeks from May to September by pitfall traps, yellow sticky traps and yellow pan traps. Soil microorganism biodiversity will be monitored by soil sampling once a year and identified
by DNA barcoding. Farm production yield from the five years preceding the project and during the four years of the project will be compared between diversification levels and with respect to soil microorganisms and arthropod biodiversity. Arthropod diversity from pitfall traps in 2019 are presented here and compared between diversification levels.

Lachance, Simon, University of Guelph; Melanie Charbonneau, University of Guelph; Ian Scott, London Research and Development Centre, AAFC; Rob Nicol, Fanshawe College

Tarnished plant bug responses to saponins and hop essential oil: potential bioinsecticides to manage greenhouse tomato and cucumber crop pests

The bioactive phytochemicals from tomato and hop, saponins and essential oils respectively, are value-added products that can be extracted from crop residues. Both phytochemicals have repellent activity, cause molting interference and have a cytotoxic effect through increased permeation of cell membranes. Various doses of saponins and hop essential oils, ranging from 5 to 400 mg/ml, applied to tomato and cucumber leaves were tested to evaluate the repellent potential to the tarnished plant bug (TPB), as well as effects on behavior and development. Saponins had low repellent properties and low acute toxicity to the TPB, but caused a slight prolongation of the nymphal stage. Hop essential oil exerted a strong repellent effect to the TPB. However, higher doses of saponins and hop proved to be phytotoxic to both plants. Next steps are to determine appropriate formulations to improve repellent efficiency and residual activity, and the potential impacts of these broad-spectrum bioinsecticides on natural enemies of TPB.

Lachance Linklater, Emma, Queen's University; Sarah A. Sonsthagen, United States Geological Survey; Gregory J. Robertson, Environment and Climate Change Canada; Vicki L. Friesen, Queen's University

An exploration of population genomic structure of Glaucous Gull (Larus hyperboreus) in the Canadian Arctic

Climate change poses a significant threat to the future of arctic ecosystems. To effectively conserve arctic species, genetically differentiated populations must be defined for adaptive and neutral genetic variation to be appropriately managed. The aim of this study is to compare genetic differentiation within and among populations of Glaucous Gull (Larus hyperboreus), a circumpolar arctic species. Although currently listed as Least Concern, Glaucous Gull declines have been reported across their range in Arctic Canada. Glaucous Gulls also hybridize with some white-headed gull species which may lead to introgression and outbreeding depression. As apex predators, Glaucous Gulls develop toxins in their tissue and are excellent bioindicators of the long-range transport of contaminants in the Arctic. Currently no population genetic information exists for this species, and management units have not been delineated. We are using next-generation sequencing to compare DNA from tissue samples collected from across the breeding range. We will assess sequences for genetic diversity, evaluate the frequency of hybrids, and determine the extent of population differentiation. Detailed information on population genetic structure and hybridization will help conservation practitioners manage the persistence of Glaucous Gull populations. A proactive management strategy will benefit both Glaucous Gull and the entire arctic ecosystem.

Laforest-Lapointe, Isabelle, University of Calgary; Christian Messier, Université du Québec en Outaouais; Steven W. Kembel, Université du Québec à Montréal

Dynamics of the tree leaf microbiome along a gradient of increasing anthropogenic stresses

Tree leaves harbor a great variety of microorganisms including fungi, bacteria, and viruses. Tree leaf microbial communities have been studied in natural ecosystems but less so in urban settings, where anthropogenic pressures on trees could impact microbial communities and modify their interaction with their host. Studies of urban leaf microorganisms have mostly focused on fungal pathogens (e.g. powdery mildew or tar spot) but recent research has shown that leaf bacterial communities can positively influence plant health through the production of secondary metabolites and protection from pathogens. Additionally, trees act as vectors spreading bacterial cells in the air in urban environments due the high density of microbial cells on aerial plant surfaces, with possible effects on human health. Characterizing urban
tree leaf bacterial communities is thus key to understand their impact on urban tree health and on the overall urban microbiome. In this study, we aimed (1) to describe the bacterial communities present on five urban tree species leaves along a gradient of increasing anthropogenic pressures on the island of Montreal, and (2) to compare them to natural forest communities. Our results show that there is a gradual shift in leaf bacterial community composition from natural to urban environments. As anthropogenic pressures increase, urban leaf communities show a reduction in the abundance of Rhizobiales and Rhodospiralles, two taxa that are known to perform nitrogen-fixing and photosynthesis mechanisms respectively therefore contributing to nitrogen and carbon cycles in natural forest. In contrasts, taxa including Sphingomonales, commonly associated with the human microbiome, were more abundant in urban settings. Individually-planted street trees exhibit a higher variation in their leaf bacterial structure than trees planted together in parks. In conclusion, we find that urban trees possess characteristic microbial communities compared to rural trees, and our results provide a starting for future research to understand the mechanisms of interactions between urban trees, microbes, and humans.

Laforge, Michel, Memorial University; Eric Vander Wal, Department of Biology and Cognitive and Behavioural Ecology Program, Memorial University

Green-up or snow-off? Spring drivers of herbivore migration

Spring is energetically costly for female herbivores, as they face heightened energy demands from migration, gestation, and lactation. Spring in northern climates is a time of rapid environmental change: melting snow facilitates foraging and travel, and newly-emergent vegetation provides a valuable nutritional resource. These processes are spatio-temporally variable; thus, habitat selection for herbivores in spring is a process that requires individuals to be plastic in response to environmental change. Individuals must optimize the timing of important life-history events such as migration and parturition and adopt habitat selection strategies that maximise use of profitable resources. We used remotely-sensed data to examine the timing of female caribou (*Rangifer tarandus*) migration and parturition as a function of two measures of environmental changes—snow-melt and vegetation green-up. We generated resource selection functions to test whether caribou selected for areas associated with these environmental changes during migration and parturition. Our results show that caribou migration typically occurs shortly after snow melt, with parturition and the subsequent energetic costs associated with lactation occurring during the peak of green-up. Our results have implications for understanding how herbivores adjust their migratory behaviour in the face of climate change to ensure access to resources when energetic needs are highest.

Lalonde, Robert, Department of Biology, Barber School, UBC Okanagan; J. Bannerman, Department of Entomology, University of Manitoba; J. MacEwen, Deparment of Biology, UBC Okanagan; N. Earley, Department of Biology, UBC Okanagan

The Eurytoma complex attacking Diplolepis rose gall formers in the British Columbia interior

Gall wasps in the genus Diplolepis parasitize various species of native and introduced Rose in Canada, exploiting host tissues in buds, stems, leaves and flowers at different times during the growing season. Although there is a diversity of gall forms, gall wasps are parasitized by highly concordant complexes of parasitoids and inquilines and at least one member of the genus Eurytoma is typically part of a galls complex of parasitoids. Since many of these gall wasp species parasitize the same host plant and develop over the same time in the season, it is possible that an opportunistic parasitoid will exploit a range of hosts rather than specialize on a single host. We sampled Eurytoma larvae from galls of two Diplolepis species: *D. variabilis* and *D. rosaefolii* at various sites up and down the Okanagan valley. These gall formers develop more-or-less synchronously on leaves of *Rosa woodsii* and often occur together on the same individual host plant. We extracted DNA from sampled Eurytoma larvae and amplified the Cytochrome b locus. Later on, we reared adult Eurytoma from a large series of samples of *D. variabilis* galls, extracted DNA and amplified both the Cytochrome b, and CO1 loci. This latter procedure was used to allow us to associate our earlier samples with published CO1 barcodes for Eurytoma species. We found that two species of Eurytoma were present in galls of both host species: *E. longavena* and *E. spongiosa* (Zhang et al., 2014). There was no apparent differentiation with respect to host, but one species, *E. longavena*, seems to be restricted to the south part of the Okanagan valley.
Lamb, Robert J., University of Manitoba, Department of Entomology; Terry D. Galloway, University of Manitoba, Department of Entomology

Dynamics of chewing louse (Insecta: Phthiraptera) populations on pigeons, nighthawks, woodpeckers and owls

In 1022-year studies of 22 species of Phthiraptera on 15 species of avian hosts, samples of 12 species of lice on six hosts were sufficient to assess temporal variation of population size (measured as PV). PV for abundance was usually species-specific for the community of lice on a given host, and populations of common species tended to be more stable than rare ones. Louse prevalence was more stable than mean intensity. For woodpeckers, louse abundance increased with mass of the host, but this relationship was less clear for owls. Few trends in louse abundance or temporal variability were detected, except for a louse on nighthawks, which declined in abundance and showed increased temporal variability, associated with a reported decline in host abundance. Although the numbers of hosts sampled were large in comparison with nearly all other studies of chewing lice, sample size was the greatest challenge in estimating temporal population variability precisely. As an example, PV for great horned owls (n = 262) declined as annual sample size increased, and although year to year abundance seemed unstable, this variability was due largely to sampling error. Populations of chewing lice were relatively stable in comparison with those of other insects.

Lamothe, Karl, Fisheries and Oceans Canada; D. Andrew R. Drake, Great Lakes Laboratory for Fisheries and Aquatic Sciences, Fisheries and Oceans Canada; and Trevor E. Pitcher, Great Lakes Institute for Environmental Research, University of Windsor

Genomic considerations for the reintroduction of SARA-listed freshwater fishes

Fishes are among the most threatened taxa in Canada with over 70 species, subspecies, and/or designatable units presently listed for protection under the Species at Risk Act (SARA). Protecting these species requires a diverse set of strategies based on the best-available data and information. One approach identified under SARA and in Canadian federal recovery strategies for improving the status of SARA-listed fishes is species reintroduction, which involves the release of individuals into areas from which they have been extirpated with the goal of re-establishing self-sustaining populations. The success of reintroduction relies on a comprehensive understanding of species life history and ecology, with considerations around population genetics and genomics. However, SARA-listed species are some of the most poorly known species in Canada due to their rarity and relative lack of research investment prior to the enactment of SARA. In this presentation, I will review genomic considerations around past reintroduction efforts of SARA-listed fishes and discuss the challenges around developing a robust reintroduction program for future fish reintroductions. I will conclude by offering some questions for future research that would benefit SARA-listed fish species.

LaPointe, Alisha-Lynn

A comparison of thermal tolerance in brook charr (Salvelinus fontinalis) at the intra-catchment scale

Increasing temperature trends in rivers, resulting from climate change, will undoubtedly have population-scale impacts on the spatial distribution of cold-water species. In this study we tested the hypothesis that brook charr residing in brooks with low temperatures, will also have a lower thermal tolerance; furthermore, brook charr exposed to habitual heat stress would consequently have a strengthened thermal tolerance. Brook charr were retrieved from two brooks along the Cains River in Miramichi, New Brunswick; the studied sites were Salmon Brook, and Estey Brook with respective maximum temperatures of 17.9°C and 16.6°C reached prior to the study. Critical Thermal Maximum (CTMax) tests were conducted and indicated that brook charr from Salmon Brook (warm) have a higher thermal tolerance (p < 0.001) than those in Estey Brook (cool). It is well established that temperature acclimation has an influence on the thermal tolerance of brook charr. Our results suggest that pre-conditioning of thermal tolerance due to environmental controls, may also act at intra-catchment scales and that groundwater dominance, rather than geographic location, best explains this variability. Further tests to be conducted include, cardiac and gill histology, stable isotope analysis, haematology, and ageing by otolith. Preliminary results indicate that brook charr exposed to repeated thermal stress may be able to withstand elevated thermal
stress relative to those in groundwater insulated water bodies; evidently, the study has the potential to have implications toward conservation of salmonid species.

Laporte, Martin, Laval University; Jeremy Le Luyer; Maeva Leitwein; Clément Rougeux; Louis Bernatchez

On the importance of epigenomic in conservation

Epigenetics is the study of gene expression changes that do not involve alterations in the DNA sequence. Here, we present evidence from three salmonids models: i) the Coho salmon (Oncorhynchus kisutch), ii) the Lake whitefish (Coregonus clupeaformis) and iii) the European whitefish (Coregonus lavaretus) to show how epigenomics can improve our ability to conserve and manage aquatic resources. The topics addressed to answer this question include developmental plasticity, transmissibility of epimarks, speciation, and adaptation. Next generation sequencing at three molecular levels (genome, epigenome and transcriptome) have been produced to investigate on the importance of epigenomic in evolution. Overall, our results point out the necessity of including epigenomic approaches in future conservation and management efforts, particularly when organisms are kept in captivity.

le Roux, Courtney, University of New Brunswick; Dr. Joseph J. Nocera, University of New Brunswick,

Roost connectivity networks of an urban aerial insectivore

Chimney swifts (Chaetura pelagica) are synanthropic aerial insectivores that spend the entire day in flight when not roosting or nesting. Their communal roost sites are generally limited to very large masonry chimneys, which are uncommon and dispersed across the landscape. It is unknown whether swifts will use multiple roosting sites during the breeding season; if they did, then roost sites may function as a connective network. Preliminary data from Nova Scotia in 2018 showed movement between roosts > 100 km in some instances, with tagged individuals changing roost sites on several occasions. We sought to then quantify the connectivity among roost sites on the breeding grounds of chimney swifts from June to August 2019 throughout Nova Scotia. We fit 38 swifts with nanotags coded for a system of automated radio telemetry (MOTUS) receivers to provide fine scale location and movement data. Preliminary data analyses from 2019 will be presented in terms of better quantifying our 2018 radio-tracking observations. This roost connectivity at a large landscape level has never been documented in chimney swifts and has implications for the conservation of important roosts and in defining critical habitat. We will address the influence of an individuals sex and breeding status on movement between roost sites, and the role of central place foraging theory on the frequency of movements between roosts. We will also use these movement data to identify sites that are the most central to maintaining the overall connectivity of the roost network and thus most in need of conservation.

Le squin, Amael, University of Sherbrooke; Dominique Gravel, University of Sherbrooke; Isabelle Boulangate, IRSTEA

Does the local demography integrate within the Hutchinsonian niche theory, or is it just turmoil appearing at conflicting spatial scales?

Niche theory has been applied to project species distribution in response to environmental factors. It is commonly defined as the set of environmental conditions that allows a species to maintain a positive intrinsic growth rate, r. Measuring this growth rate is not straightforward, particularly for size-structured populations such as trees. Often the niche, and therefore the associated species distribution, is projected using the correlation between current distribution and abiotic variables only. Our goal is to test the climatic niche theory along a gradient for Northern America tree species. First, we developed a formula relating individual performance to the populations performance, namely r. Second, we investigated how the probability of occurrence (Pocc), predicted by a species distribution model, is correlated to the population growth rate r previously derived. We found no correspondence between Pocc and r, suggesting that either local demographic processes play a minor role on tree spatial distribution at large spatial scale, or that subtleties in the demographic rates, out of the scope of coarse environmental data, play a major role and prevent us to deduce speciesrange.
LeBlanc, Nathalie, University of New Brunswick; Scott A. Pavey

Genomic Population Structure of Striped Bass (*Morone saxatilis*) from the Gulf of St. Lawrence to Cape Fear River

Striped Bass are a facultative anadromous fish with a native range that extends along the Atlantic coast of North America from the Gulf of St. Lawrence to Florida. Many populations conduct long migrations resulting in mixed stock fisheries. Previous genetic investigations have encountered difficulty reliably distinguishing between all populations. This study examined the genetic structure of Striped Bass populations from the Gulf of St. Lawrence to Cape Fear River in North Carolina, including several poorly understood populations in Kennebec River, Saint John River, and Mira River. A panel of 1200 SNPs found highly divergent (FST = 0.1-0.22; p-value < 0.0001) populations in Canada (Miramichi River, Shubenacadie River, Saint John River), moderate divergence (FST = 0.03-0.04; p-value < 0.0001) of southern resident populations in Roanoke River and Cape Fear River, and low but significant divergence (FST = 0.01-0.02; p-value < 0.0001) among Hudson River, Delaware River, and Chesapeake Bay populations. We evaluated SNP markers for their ability to assign individual Striped Bass to their origin population and were able to assign individuals back to most populations with 99% accuracy. These SNPs will form the basis of a Rapture panel that can be used for future mixed stock analysis as well as ongoing investigations into possibly new Striped Bass populations in Canadian rivers.

Lecomte, Nicolas, Canada Research Chair in Polar and Boreal Ecology; Sylvain Christin; Éric Hervet

Automatic monitoring of biodiversity

1. A lot of hype has recently been generated around deep learning, a novel group of artificial intelligence approaches able to break accuracy records in pattern recognition. Over the course of just a few years, deep learning has revolutionized several research fields such as bioinformatics and medicine with their flexibility and ability to process large and complex datasets. As ecological datasets are becoming larger and more complex, we believe these methods can be useful to ecologists as well. 2. Here we review existing implementations and show that deep learning has been successfully applied to identify species, classify animal behavior, and estimate biodiversity in large datasets, such as camera-trap images, audio recordings, and videos. We demonstrate that deep learning can be beneficial to most ecological disciplines, including applied contexts, such as management and conservation. 3. We also identify common questions about how and when to use deep learning, such as what are the steps required to create a deep learning network, the tools available to help and what are the requirements in terms of data and computer power. We provide guidelines, recommendations and useful resources such as a reference flowchart to help ecologists get started with deep learning. 4. We argue that at a time when automatic monitoring of populations and ecosystems generates a vast amount of data that cannot be effectively processed by humans anymore, deep learning could become a powerful reference tool for ecologists.

Leeper, Abigail; DePaul University; Jalene M. LaMontagne, DePaul University

Mast seeding and a spruce budworm outbreak: is there a benefit to trees being asynchronous?

Mast seeding is defined as the spatially synchronous and temporally variable production of seed crops by populations of perennial plants. The primary ultimate hypotheses for this reproductive phenomenon are described as benefits that synchrony provides through seed predator satiation or increased pollination efficiency. Based on these hypotheses, asynchronous individuals should have reduced fitness. Despite mast seeding being described as synchronous within populations, considerable variation in the reproductive patterns of individuals has been recorded in tree populations, leading to the question of the possible benefits of asynchrony. In the event a predator prefers reproductive buds of plants, such as eastern spruce budworm (SBW), mast seeding synchrony may not be beneficial. We test the hypothesis that levels of reproductive synchrony in white spruce are related to the defoliation level by SBW. Since 2012, 308 trees have been monitored for cone production at six sites in northern Wisconsin, with 2013 being a mast year. In 2014, we detected a SBW outbreak, impacting three sites containing 176 trees. As of 2018, 20% of study trees have died from SBW defoliation. Implications of population-level synchrony in mast seeding events and SBW defoliation will be discussed in terms of both its ecosystem and evolutionary significance.
LeFait, Alexis, Saint Mary's University

Lei, Calvin, University of Waterloo; Rebecca C. Rooney, University of Waterloo

Vegetation diversity along an elevation gradient in mountain peatlands

Rocky mountain peatlands in the Upper Bow River Basin are poorly understood systems, uncharacterized and unmapped by the government in Alberta, Canada. This study characterizes vegetation biodiversity of mountain peatlands and identifies the changes in vascular plant and bryophyte composition within communities associated with elevation. To investigate changes in plant community composition, eleven sites were selected along an elevation gradient ranging from 1415 to 2102 meters above sea level. Sampled vascular plant and bryophyte species identities and abundance data were collected at each site using three 50-meter transects and five 1m² quadrats along each transect. Preliminary results, using a Mantel Test, suggest that site elevations are significantly related to the differences in vegetation species composition among the sites (r = 0.5223, p = 0.001). Additional sites along the elevation gradient are required to improve resolution of the observed changes in plant community composition with elevation. Data collected in this study, such as species lists, contributes to a broader understanding of these peatlands by providing valuable information to hydrologists, and landscape ecologists. Biodiversity information can also be used by stakeholders to determine the health of these mountain peatlands and can have conservation applications by potentially identifying rare species.

Leitwein, Maeva, postdoc at Laval university Bernatchez's Lab; Hugo Cayuela; Anne-Laure Ferchaud; Eric Normandeau; Patrick Berrebi; Bruno Guinand; Pierre-Alexandre Gagnaire; Louis Bernatchez; Département de biologie et Institut de Biologie intégrative et des Systèmes, Université Laval 2ISEM (Institut des Sciences de l’Évolution de Montpellier)

Genome-wide consequences of human mediated hybridization assessed with haplotypes

Human-mediated introductions of individuals from distinct origins into natural recipient populations provide unique opportunities to understand the genomic footprints of recent hybridization. The induced gene flow following hybridization often results in heterogeneous pattern of local ancestry, with genomic regions showing high or low frequencies of introgressed foreign ancestry. Such patterns might be modulated either by neutral, positive or negative selective evolutionary mechanisms. To understand which mechanisms are involved, it is important to take in consideration local variation in recombination rate that will modulate the genome-wide ancestry profiles through time. Indeed both the time since hybridization events and the local variation of the recombination rate might result in different evolutionary outcomes. In this study, we will present two cases studies involving two salmonids species, the Brown Trout (Salmo trutta) and the Brook Charr (Salvelinus fontinalis), for which decades of stocking practices have resulted in admixture between wild populations and introduced domestic strains. In both cases, we provide a detailed picture of the domestic ancestry patterns across the genome by using large genome-wide dataset (>75,000 and >33,000 mapped SNPs). Taking advantage of the ancestry tracts length distribution among wild individuals, we were able to retrieve the time since hybridization events. Then, we assessed the evolutionary consequences of the domestic introgression at different scales: (i) the whole genome, (ii) the chromosomes and (iii) along 2Mb sliding windows. This approach allowed identifying genomic regions susceptible to confer adaptive introgression or on the contrary prevent the introgression of maladaptive alleles. Our results highlight the necessity of taking in consideration both the time since hybridization events and the local variation of the recombination rate and introgression rate pattern to under the evolutionary outcomes following hybridization.

Levenstein, Brianna, Dept of Biology & Canadian Rivers Institute, UNB; Emma Bowser, (Dept of Biology & Canadian Rivers Institute, UNB); Tim Cox (UNB); Madisyn Harper (AAFC); Jack Nason (UNB); Bonnie Robertson; Alexa Alexander-Trusiak (ECCC, Dept of Biology & Canadian Rivers Institute, UNB)

Integrated biomonitoring in the Havelock watershed: an interdepartmental project
In 2007, Agriculture and Agri-Foods Canada (AAFC) funded a project to restore approximately 200 m of Ridge Brook (Havelock, NB), a trout- and salmon-bearing stream which runs through a cattle pasture, in an effort to improve stream habitat quality. Using Canadian Aquatic Biomonitoring (CABIN) protocols, benthic macroinvertebrates (BMI) were studied to monitor water quality changes in the restored section of the stream, a reference site upstream, and a test site downstream. Samples were taken by AAFC in 2010, 2011, 2012 and 2016, but no clear patterns were seen in BMI community structure between sites or years. In 2018, the three Ridge Brook sites were resampled, along with other established CABIN sites in nearby watercourses, to get a better understanding of whether the restoration project was successful in improving habitat quality in Ridge Brook. We found that there were strong regional patterns in BMI community structure and that all Ridge Brook sites exhibited high BMI abundance and algal biomass compared to the other watercourses. The results of our study suggest that a more comprehensive (as opposed to localized) approach to rehabilitation may be necessary when trying to restore and improve stream habitat.

Lewthwaite, Jayme, Simon Fraser University; Arne Mooers;
Community, trait-level and phylogenetic homogenization of Canadian butterfly communities over the past century

Are communities shifting towards more generalist species assemblages in response to climate change? If species are non-randomly filtered out of habitats as a result of climate change, trait diversity may follow in a similar fashion. Generalist traits may be crucial in allowing species to expand their range margin or remain resilient in situ, whereas environmental filtering may remove habitat specialists. As such, we would expect to see a functional homogenization where there is a gradual replacement of specialist species by generalist species. Additionally, if climatic niche space shows phylogenetic signal, we should expect that closely related species will be affected similarly by climate change. However, sister taxa may occupy ecologically similar habitats or alternatively, sister taxa in this group may be specialized for different niches. Thus, it is unknown whether communities will become more or less phylogenetically clustered as a response to environmental stress. Using a curated distribution dataset of over 300 Canadian butterfly species and 500,000 records that span the past century, I measure potential homogenization over time using 3 axes: community, trait-level and phylogenetic change. This work will allow us to prioritize individual species at a heightened risk of extinction as well as investigate fundamental questions in ecology and evolution, such as the relative role of climate in community assembly processes.

Li, Peiwen, Queens University; Peter V.C. de Groot Queen's University; Stephen C. Lougheed, Queen's University
Fine-scale genetic structure in anadromous Arctic char in Lower Northwest Passage: Genomic insights for a sustainable fishery

Arctic char (Salvelinus alpinus) is the northernmost salmonid species in the world, distributed abundantly across the Canadian Arctic. Char exhibit anadromy where individuals will return to their natal rivers for breeding. Various studies have examined the genetic population structure in char, but typically used limited numbers of markers and geographically disparate sampling locales. Documenting fine-scale population structure could provide insights into the factors that shape genetic diversity in char and guide the establishment of regional sustainable fisheries of char, an economically- and culturally-important species for northern peoples. We use genome-wide panels of single nucleotide polymorphism markers obtained from double-digest restriction site-associated DNA sequencing to evaluate population structure in char from the Lower Northwest Passage, Nunavut. We find marked genetic structure at two scales: (i) Between King William Island sites and Chantrey Inlet locales, (ii) Among rivers at scales less than 120 kilometers. Our results suggest that natal philopatry causes differentiation among even adjacent rivers, that other factors (e.g. colonization history, marine foraging patterns) cause deeper population divisions, and that individuals may over-winter in non-natal rivers. Our study illustrates the power of genomics to study cryptic population structure in non-model organisms, which will help guide management strategies for sustainable char fisheries.

Light, Michael, MSc Biology Acadia University; Dr. Dave Shutler; Dr. Christopher Cutler; Dr. N. Kirk Hillier
Chemical ecology and biology of *Varroa destructor* (Anderson and Trueman), a primary pest of western honey bees (*Apis mellifera* L.)

Honey bees (*Apis mellifera* L.) are the most agriculturally beneficial eusocial insects for crop pollination. Chemical communication is critical in maintaining colony structure and activity, which may be exploited by parasites. *Varroa destructor* (Anderson and Trueman; Acari: Varroidae) is regarded as one of the biggest threats to apiculture, blamed for annual colony mortalities of over 30% in some regions. The objectives of this thesis were to identify odorants important to *V. destructor* for further development of techniques to disrupt its lifecycles through in-colony treatment. Honey bee colony volatile collections involving ex-situ techniques were used to identify individual compounds and odor detection sensitivity of *V. destructor* to these compounds through gas chromatography-mass spectrometry and gas chromatography-linked electrotarsal detection, respectively. Volatile components identified in this and previous research were then tested for concentration-dependent responses using electrophysiology. Electrotarsogram responses indicated significant difference among odorants in eliciting responses, suggesting the potential application of this procedure in screening putative repellents or odors that disrupt host detection (disruptants) to live *V. destructor*. Results from this research can be applied to colony-wide testing of active odorants in developing effective alternative methods for *V. destructor* control as well as developing methods for future research exploring chemical ecology of social insects.

Light, Marilyn, Orchid Specialist Group/SSC/IUCN; Michael MacConaill, University of Ottawa, retired

Tracking Ghosts: Paralobesia (Tortricidae) and the Showy Lady's Slipper Orchid

The showy lady's slipper, *Cypripedium reginae*, is a host of two tortricids, *Paralobesia cypripediana* (Forbes), and *P. marilynae* (Royals & Gilligan). The preferred oviposition sites are floral bracts. The respective ranges of these two moths remains unclear as few adults have been collected or reared. Paralobesia marilynae has only been confirmed from Gatineau Park QC and the Purdon CA in Lanark C., ON, (Royals, Landry & Gilligan (2018). Herbarium specimens and online images were examined for adherent egg shells: egg shells were observed on 17 specimens at CAN, DAO, and MT, and 19 online images at GBIF and SERNEC of collections from ME, MN, MB, ND, ON, QC, and VT. Distribution was disjunct: MB, ND, and MN to the west, and four other clusters: eastern Ontario /southwestern Quebec, north of the St. Lawrence River, southern Gaspe Peninsula, and northeastern USA. Apart from a western cluster (MB), and recent collections in eastern Ontario/southwestern Quebec, it is not known whether other moth populations are extant. Herbarium specimens and online images can be useful for tracking insects with adherent eggs but site visits are needed to further investigate with due regard to the potential vulnerability of both host and moths.

Lindsay, Kate, University of Guelph

Scipopus: Finding a satisfying generic concept

Scipopus Enderlein is a large group of Neotropical flies often recognized by their orange heads and black bodies. Despite their seemingly conspicuously appearance, the genus lacks a proper generic definition and diagnosis. The goal of my research is to identify synapomorphies to define the genus and to differentiate Scipopus from the other three closely related genera in the Scipopus group: Pseudeurybata Hennig, Phaeopterina Frey and one undescribed genus. Preliminary DNA barcode data shows these four genera as distinct clades. The Scipopus group, along with several other Micropezid genera are relatively easily separated on the species level but on the generic level show high occurrences of homoplasy and character overlap, making them an evolutionarily interesting group to study.

Little, Chelsea J. University of Zurich, UBC; Florian Altermatt, University of Zurich/Eawag


A central problem for understanding the relationship between biodiversity and ecosystem functioning is how to scale up the results of plot-scale or laboratory experiments to real ecosystems. While much work has focused on biomass production in terrestrial ecosystems, other functions are also essential. For example, in freshwater ecosystems, the brown
food web is as important as the green one because of low primary production, and it relies on inputs from adjacent terrestrial ecosystems. We investigated the roles of terrestrial landscape configuration and density of dominant shredding macroinvertebrates in headwater streams in controlling organic matter processing. We show that delivery of detritus to streams can be predicted based on the spatial arrangement of land use types in a catchment. In these forested headwater streams, leaf litter supply does not limit detritus processing. Rather, based on field surveys with a high level of spatiotemporal replication and on laboratory mesocosm experiments, we show that nonlinear density dependence of leaf shredding by macroinvertebrates determines patterns in total leaf litter processing within and between catchments. Due to this nonlinearity, maximizing a given species-abundance may not provide high return on investment in terms of ecosystem function: per-capita contribution to decomposition declines with increasing density, likely due to interference competition. Thus, incorporating heterogeneous density distributions throughout a catchment into estimates of total leaf litter processing drastically changes our understanding of ecosystem function. We show how to assess the contributions of different trophic levels in an empirical meta-ecosystem to its overall functioning.

Liu, Suqi Department of Agriculture and Land; Christine Noronha Agriculture and Agri-Food Canada

A biological study of Agriotes sputator, (coleoptera:elateridae) the dominant wireworm species in PEI

The larvae of Agriotes Sputator are a major pest of agricultural crops in Prince Edward Island. However, not much was known about this pest except that it has a 5 year life cycle. We conducted an in

Liu, Weihan, University of Toronto; Marc Cadotte

Unearthing invasion mechanisms: do plant-soil feedbacks promote the growth of one of Canada's most invasive plants?

Human welfare, through the loss of ecosystem processes, is gravely threatened by invasive species. One of Canada's most invasive plant species, the Dog-Strangling Vine (also known as Vincetoxicum rossicum or DSV), extirpates native species to a point of creating virtual monocultures. Below-ground interactions are important in shaping plant communities and in determining the success and impact of plant invasions. For example, invasive plants can leave soil legacies that promote their own growth or reduce the growth of native species. I hypothesized that DSV benefits from positive plant-soil feedbacks; that is, DSV will grow more abundant in soils which it has already invaded. A growth chamber experiment with four factors (viz., soil invasion level, sterilization, activated carbon, and species) and a randomized complete block design was used to disentangle potential plant-soil feedbacks. The effects of soil treatments on plant biomass were species-specific. Soil sterilization reduced DSV biomass, with its effects being stronger on uninvaded soil than invaded soil. These results suggest that the net effect of the soil microbiome on DSV is positive, with the microbiome being more important for DSV in uninvaded soil. In the future, molecular data will be used to acquire further insight into these plant-microbe interactions.

Lloyd, Vett, Mount Allison University; Anna M. Duncan; Kelsey C. McIntyre

Genetic hybridization between Ixodes scapularis and Ixodes cookei

Ixodes scapularis Say, 1821 (the black-legged tick) is becoming established in Canada. The northwards expansion of I. scapularis leads to contact between I. scapularis and Ixodes cookei Packard, 1869, a well-established tick species in Eastern Canada. Examination of I. cookei and I. scapularis collected from New Brunswick revealed ticks with ambiguous morphologies, with either a mixture or intermediate traits typical of I. scapularis and I. cookei, including in characteristics typically used as species identifiers. Genetic analysis to determine if these ticks represent hybrids revealed that four had I. cookei derived mitochondrial DNA but I. scapularis nuclear DNA. In one case, the nuclear sequence showed evidence of heterozygosity for I. scapularis and I. cookei sequences, whereas in the others, the nuclear DNA appeared to be entirely derived from I. scapularis. These data strongly suggest genetic hybridization between these two species. Ixodes cookei and hybrid ticks were readily collected from humans and companion animals and specimens infected with Borrelia burgdorferi Johnson et al., 1984, the causative agent of Lyme disease, were identified. These findings raise the issue of
genetic introgression of *I. scapularis* genes into *I. cookei* and warrant reassessment of the capacity of *I. cookei* and *I. cookei × I. scapularis* hybrids to vector *Borrelia* infection.

Loboda, Sarah, McGill University; Jade Savage; Toke Hoye; Chris Buddle

Earlier and shorter activity periods of Arctic fly species linked to declining abundances

Recent climate change has advanced spring species activity. However, less is known about the effects of warming on species phenology through the entire active season. Focusing on muscid flies, the most important pollinators in the Arctic, we explored temporal trends of phenology of twelve species in Greenland over the whole flight period between 1996 and 2014. We also tested if phenological shifts were associated with species traits or abundance declines, documented for these flies over the last two decades. We found that despite a warmer and prolonged summer season in the Arctic, the duration of the flight period of some important pollinator species was reduced, especially for small-bodied species. The shrinkage of the activity period of these flower visitors coincided with their drastic decline in abundance. Our results highlight the need to better understand the link between phenology, demography and species traits.

Loewen, Charlie, University of Toronto; Benjamin Gilbert; Donald Jackson, University of Toronto, Department of Ecology and Evolutionary Biology

Exotic predatory fish and their effects on prey diversity in mountain lakes

Sportfish have been introduced to create or sustain angling opportunities in freshwater ecosystems worldwide; however, consequences for native biota have often varied, making it difficult to predict where future introductions might have the greatest impacts. In western North America, the legacy of historical salmonid introductions offers a unique venue for evaluating the effects of exotic predatory fish on prey communities across major gradients in climate, morphometry, lithology, and land-cover. Here, we synthesize fish stocking and zooplankton community composition data for a broad set of mountain lakes and ponds to understand how introductions have altered multiple taxonomic, functional, and phylogenetic dimensions of native biodiversity. We then consider several relevant environmental factors that moderate (i.e. dampen or amplify) the impacts of introduction and help explain observed heterogeneity in community responses. Finally, we apply space-for-time substitution to assess interactions between exotic sportfish and climate change, whereby the varying impacts of stocking along elevational and latitudinal gradients are used to infer the probable consequences of introductions under future warming. In the face of current threats to global biodiversity, our work provides novel insights concerning the cumulative effects of invasive predators and climate change on limnetic invertebrate communities.

Lopez, Moroni, Student

Identifying the genetic basis of within-species diversity: a study of the genetic loci responsible for pelvic polymorphism in *Culaea inconstans* (brook stickleback)

Stickleback populations around the world are great subjects for the study of parallel evolution. Brook stickleback individuals are known to exhibit different pelvic phenotypes, with some stickleback having pelvic spines (ancestral trait), and other lacking pelvic spine development at all (derived trait). Alberta is home to the highest prevalence of unspined individuals among brook stickleback populations. The purpose of my research is to find the genetic loci responsible for pelvic polymorphism in brook stickleback. To do this, I am using brook stickleback DNA samples collected from Muir Lake (Alberta). By analyzing the DNA sequences of spined and unspined individuals and aligning them to the threespine stickleback genome (which has been widely research) and the tubesnout genome, I am seeking to identify the genetic loci responsible for pelvic polymorphism in brook stickleback from Lake Muir. Based on these genetic analyses, I will also determine whether spined and unspined individuals mate at random or if assortative mating is taking place.
Lorenzo, Antonio, University of Toronto; Nicole Mideo (University of Toronto)

Deep sequencing allows for detection of drug-resistant *Plasmodium falciparum* strains in malaria infections

Human malaria infections typically consist of multiple co-infecting *Plasmodium falciparum* genotypes that can have distinct phenotypic traits for drug resistance and sensitivity. Traditional techniques used to quantify and characterize the parasites within hosts do not offer enough resolution to distinguish between different genotypes. High-throughput sequencing (HTS) remedies this lack of resolution, allows for the detection of drug resistant phenotypes and characterization of parasite community structures within infections. HTS data shows significant variation in clearance rates of haplotypes within patients and can be used as a tool to monitor the emergence of drug resistant strains. Lastly, our analysis shows that the evenness of parasite communities within infections may predict the presence of drug resistant strains and affect treatment outcomes.

Louca, Stilianos, University of British Columbia

Microbial ecology and evolution, a field's coming of age

Microorganisms, notably bacteria and archaea, are the most ancient and the most widespread form of life on Earth, strongly shaping Earth's surface chemistry over billions of years. Understanding how microorganisms evolve over these time scales, and how microbial communities assemble and function in modern ecosystems, is a major missing piece in our understanding of life. The nearly complete absence of microbial fossils, the incredible diversity of extant microorganisms, and technical challenges involved in characterizing microorganisms in nature, have long limited our understanding of microbial ecology and macroevolution compared to larger organisms. In this talk, I will describe my work towards resolving these issues using field surveys, experiments, mathematical modeling and analyses of massive global sequencing datasets. My talk will demonstrate how modern microbial ecology and evolution theory converges at the intersection of thermodynamics, Earth-system science (including geology) and traditional ecological and evolutionary theory."

Lougeed, Stephen, Queen's University; Ivana Schoepf (Queen's University)

The evolving roles of field stations in science, society, and the environment

Field stations are engines of leading-edge research and student experiential learning. There is increasing need for public outreach, political engagement, research networks, and partnerships with governments and ENGOs. We will speak on the value of field stations in facilitating partnerships that have local, regional, and national impacts through the lens of the Queen's University Biological Station (QUBS). Founded in 1945, QUBS has grown from a parochial 20-hectare facility, to one comprising 3400 hectares and two campuses, that welcomes users from all over the world. QUBS lies within the Frontenac Arch World Biosphere Reserve, and has a seat on its advisory council. QUBS contributed to the creation of an Important Bird Area, motivated by high density of cerulean warblers, a songbird that has lost ¾ of its global population over 50 years. A partnership with the Nature Conservancy of Canada led to the creation of our education centre. QUBS is a case study on how field stations might help Canada meet its UN Aichi Target 11 obligation to conserve e 17% of its terrestrial lands. These and other examples showcase how field stations can have far-reaching positive impacts on science

Lumley, Lisa; Esther Pouliot, Natural Resources Canada; Jérôme Laroche, Université Laval; Brian Boyle, Université Laval; Bryan Brunet, University of Alberta; Roger Levesque, Université Laval; Felix Sperling, University of Alberta; Michel Cusson, Natural Resources Canada

Continent-wide population genetic and genomic structure of the spruce budworm, *Choristoneura fumiferana*, North Americas most destructive conifer defoliator.

Defoliation by the spruce budworm, *Choristoneura fumiferana*, has shaped boreal forest structure across North America, apparently resulting in panmixia across vast regions. We tested this hypothesis by
Lumsden, Genevieve, University of Guelph; Evgeny V. Zakharov - Canadian Centre for DNA Barcoding, University of Guelph; J. Scott Weese - Pathobiology, University of Guelph; Robbin L. Lindsay - National Microbiology Laboratory, Public Health Agency of Canada; Claire M. Jardine - Pathobiology, University of Guelph

I know what you ate last summer DNA metabarcoding for tick blood-meals.

Eastern North America, the vector-host assemblages for Borrelia burgdorferi, the causative agent of Lyme disease, are likely changing due the northward range expansion of both the pathogen and its vector, Ixodes scapularis. Vector blood-meal analysis (BMA) can identify the origin of blood-meals consumed by ticks thus providing valuable insights into host-vector interactions. DNA metabarcoding may be an effective way to assess vector BMA; however, studies on questing, unengorged ticks are lacking. Here we aimed to: 1) assess the ability of DNA metabarcoding to identify blood-meals in engorged adult ticks fed on known hosts, and 2) test the technique on unengorged nymphs that fed on unknown hosts as larvae. To infer host species identification, vertebrate DNA was amplified and sequenced for comparison against known COI barcode references. Preliminary results yielded a putative species identification for 68.8% of engorged adults (n=16) and 18.2% of unengorged nymphs (n=55). Further optimization of the technique will be conducted to improve detection of remnant blood-meals in unengorged nymphs. Validating this approach as a convenient tool for tick BMA will permit comprehensive investigations into the role of vertebrate hosts in the transmission of B. burgdorferi and other tick-borne pathogens.

Lundholm, Jeremy, Biology, Saint Mary's University; Hughstin Grimshaw-Surette, Biology, Saint Mary's University

Green roof ecology: what we know, where it is headed, and how it can expand fundamental ecology.

Green roofs have become a common feature in cities worldwide and provide valuable ecosystem services (ES). Ecologically novel aspects of green roof systems can thwart the direct application of research findings from ground-level ecosystems, so we need rooftop studies to understand green roof functioning. Since the early 2000s, green roof ecologists have found strong links between the choice of planted species and ES, trade-offs between plant type and optimization of different ES, and evidence for the value of green roofs as urban faunal habitat. More recent biodiversity-ecosystem functioning research in many regions has shown that more diverse plant species mixtures tend to improve ES over monocultures. Pollinator use of green roofs is substantial but often depends on building height and floral resource availability. Belowground research on green roofs shows a diversity of mutualistic fungi that likely make important contributions to ES. Functional and phylogenetic approaches to green roof plant communities already show promise in improving predictions of ES, and we are beginning to understand rooftop vegetation dynamics. The diverse functions of green roofs have driven ecologists to ask novel ecological questions. Consequently, green roof ecology has also produced surprising insights that can inform fundamental ecology and natural history.

Luo, Ruiping, University of Toronto; Dr. Benjamin Gilbert, University of Toronto

Effect of temperature and water availability on trophic interactions

Global changes in climate, including shifting temperature and changes in drought, can impact the strength and consequences of trophic interactions. Some variables impact dynamics at all trophic levels, as with temperature-induced shifts in plant growth, herbivore feeding rates and herbivore-predator encounter rates. Other variables directly influence a single trophic level, as commonly occurs with drought affecting primary productivity. The interacting effects of these variables, and how they differentially alter trophic dynamics, is poorly understood. We tested the impact of temperature and water availability in a simple three-level food chain, consisting of common milkweed (Asclepias syriaca), oleander and milkweed aphids (Aphis nerii and Aphis asclepiadis), and aphid midges (Aphidoletes aphidimyza). We considered separately the plant alone, the plant with its specialist herbivores, and plant-herbivore-predator communities. We found that changes in temperature and water availability led to different dynamical outcomes, with temperature showing a stronger initial impact through changes in herbivore population growth rates, and water availability largely altering the final herbivore carrying capacity. These changes reflected shifts in plant growth and, to a lesser degree, in predator
impact. Our results suggest that global climate changes may have distinct consequences for initial insect outbreak and long-term population persistence.

Lyons, Caitlyn, University of Western; Dr. Zoë Lindo, University of Western Ontario

Making connections: Above- and belowground communities in boreal peatlands

The aboveground plant community and the belowground microbial community are intrinsically connected; plants provide resources to the microbial community through litter inputs, which, in turn, releases nutrients for plant uptake through decomposition processes. In boreal peatlands the above- and belowground communities are acutely linked, because the whole soil profile is partially decomposed plant matter (peat), and dictates the nutrients available to the belowground microbial communities. We characterized the aboveground plant community and the belowground microbial community in two boreal peatland types; a Sphagnum dominated and a Carex dominated fen. The Sphagnum fen with its poor quality plant litter inputs (high C) had a corresponding higher fungi:bacteria and higher Gram positive:Gram negative bacteria microbial community compared to the Carex dominated fen. Differences in these microbial functional groups are indicators that the two fens undergo different rates of carbon and nutrient cycling that can, in turn, affect plant composition. As plant community composition in peatlands are predicted to shift and decomposition rates are expected to increase under climate change, our work highlights the importance of understanding plant-soil microbial interactions.

MacDonald, Maggie, University of Alberta; Maya Evenden, University of Alberta

Identification of ground beetles (Coleoptera: Carabidae) captured in semiochemical-baited traps targeting the pea leaf weevil, *Sitona lineatus* L. (Coleoptera: Curculionidae) in pulse crops on the Canadian Prairies

The pea leaf weevil (PLW), *Sitona lineatus* L. (Coleoptera: Curculionidae), is a significant pest of field pea, *Pisum sativum* L. (Fabaceae), and faba bean, *Vicia faba* L. (Fabaceae), that has recently invaded the Canadian Prairie Provinces. Pea leaf weevil adults feed on foliage of young plants in the spring and larva feed on nitrogen-fixing root nodules and can damage up to 90% of root nodules in high densities. Current PLW management strategies consist of adult population monitoring, insecticide application, and insecticidal seed treatments. Semiochemical-based monitoring can detect population spread of PLW in the Prairie Provinces but results in significant carabid bycatch. Ground beetles (Coleoptera: Carabidae) are natural enemies of pest populations in arable land systems. Although their contribution is not fully understood, their predatory behaviour is crucial for pest management in sustainable agricultural systems. The research objectives of this study are to survey carabid species captured as bycatch in monitoring traps that target PLW, compare carabid assemblages by trap treatment and crop type, and to assess landscape-level environmental factors that influence abundance and diversity of carabids using landcover data from Alberta Biodiversity Monitoring Institute (ABMI). Results from this research project will expand knowledge of the carabid community structure in Alberta pulse crops, assess which species of carabids are associated with PLW, and determine which habitat factors promote carabid diversity in agroecosystems.

Mackay, Patricia A., University of Manitoba, Department of Entomology; Robert J. Lamb University of Manitoba, Department of Entomology

Predation stabilizes mean intensity (colony size) but not prevalence in a wild population of a native aphid

Aphid populations tend to be highly unstable. Predation is thought to reduce aphid abundance, but little is known about the contribution of predators to the stability of aphid populations. Here, aphid abundance was broken down into two separate parameters, prevalence and mean intensity, following the format used by parasitologists, where prevalence is the proportion of stems infested and mean intensity is the mean number of aphids per infested stem. All three parameters were then assessed for degree of stability or temporal population variability using the statistic PV (population variability). A 20-year study of *Uroleucon rudbeckiae* on *Rudbeckia laciniata* (tall coneflower) reveals that for abundance PV= 0.72, for prevalence PV=0.63 and for mean intensity PV=0.38. The substantially lower PV of mean intensity, indicating greater stability, is due to the rapid influx of a variety of predators into individual colonies with the subsequent high level of
predation reducing the range in colony size and colony longevity. The stability of prevalence, on the other hand, is less influenced by predation: why has yet to be determined.

Mackellar, Hannah, Trent University; Dr Erica Nol (Trent University); Dr Glen Brown (Ontario Ministry of Natural Resources and Forestry)

Nest Timing and Reproductive Output of Whimbrel (Numenius phaeopus) Breeding at Two Sites in the Hudson Bay Lowlands, Canada

We monitored 371 Whimbrel nests in the Hudson Bay Lowlands at Burntpoint, Ontario (55.2°N, -84.3°W) and Churchill, Manitoba (58.8°N, 94.2°W). Daily nest survival rates (DSRs) recorded in this study were the lowest ever recorded, and the majority of nest failure was due to depredation. DSR was consistent across sites, but was subject to a strong annual effect. Our findings suggest this may be related to annual temperature conditions experienced at the final stopover site prior to breeding. This previously unexplored link between annual nest DSR and weather in the final stopover site highlights the importance of continued research to understand migration routes and carryover effects in this declining shorebird. Our results also shed light on the relationship between initiation date and reproductive output, weather, and site in the hudsonicus Whimbrel. We found that hatched nests had significantly earlier average initiation dates than failed, though there was wide variability in nest timing across sites and years. Nests were initiated significantly earlier in Burntpoint than in Churchill, likely due to long-term trends in local weather. Meanwhile, annual variation in initiation date was, contrary to predictions, not explained by yearly snowmelt timing or weather conditions in the breeding and stopover grounds.

Mackie, Connor, Department of Biology (Dalhousie University); Julie LaRoche, Department of Biology (Dalhousie University); Jennifer Tolman, Department of Biology (Dalhousie University); André Comeau, IMR (Dalhousie University)

Studying microorganisms in sediment, water column, and Salmo salar guts at an aquaculture farm in Nova Scotia (Canada)

The increase in production intensity of finfish aquaculture facilities has caused concern over the resulting environmental effects from organic loading. Traditional environmental monitoring methods have involved macroscopic observations and taxonomic identification of benthic macrobiota. However, these traditional methods are often expensive and time consuming. DNA sequencing of microorganisms offers a cheaper and faster monitoring method, not only for the benthos, but also the gut microbiome of the fish themselves. The purpose of this research is to study the microbial communities in the environment and aquacultured fish over the production cycle of a Salmo salar (salmon) farm in Atlantic Canada. DNA from water and sediment samples was analyzed through amplicon sequencing of 18S ribosomal RNA (targeting the V4 region) and 16S ribosomal RNA (by targeting both V4V5 & V6V8 regions). In addition, samples will be analyzed via metagenomic sequencing. Preliminary data indicate that our results will: (i) contribute to the characterization of benthic and pelagic microbiomes associated with finfish aquaculture sites, and (ii) assist in building a database of indicator species for harmful conditions to make future monitoring faster and easier.

MacNeil, Liam, Dalhousie University; Dr. Julie LaRoche; Brent Robicheau; Connor Mackie

In-situ Monitoring of Surface Nano-Microplankton Using Convolutional Neural Networks for Submersible Holographic Microscopy

Marine phytoplankton are foundational to aquatic food webs and act as a primary node for processes such as nutrient cycling and carbon sequestration in the global ocean; further still, the rapid generation time of microbial communities implies a capacity to respond quickly to environmental conditions. Currently, temporal data for marine microbial communities remains relatively scarce, but by expanding our understanding of microbial diversity and seasonal succession, we can improve predictions of future changes and ultimately the fate of ecosystem processes (e.g. biogeochemical cycling) under a changing climate. From 2016 to present, we employed a submersible holographic
microscope to collect weekly surface-water samples (1m) within a temperate coastal inlet (Bedford Basin, NS). Holographic microscopy generated holograms from which convolutional neural networks (CNNs) classified Nano-microplankton using broad morphological features (e.g. chains, pinnate/centric diatoms, etc.) to produce high-throughput community data. Here we provide insights into the succession of phytoplankton community composition and abundance for 2016-2017. These weekly observations provide a time series that demonstrate CNNs are both a powerful monitoring tool for marine microbial communities, and a complement to genomic sequencing and flow cytometry that respectively produce information about community composition and abundance for limited size classes (i.e. Pico-nanoplankton).

MacPhail, Victoria, York University; Rich Hatfield, The Xerces Society for Invertebrate Conservation; Leif L. Richardson, Gund Institute for Ecological Economics, Rubenstein School of Environment & Natural Resources, University of Vermont; Sheila R. Colla, Faculty of Environmental Studies, York University

All it takes is a photo: how citizen scientists can enhance researcher-collected data to fill knowledge gaps and inform conservation efforts for bumble bees (Bombus spp.) in Canada

A common roadblock to species conservation efforts is a lack of awareness and data. Citizen science is a growing field that can help as volunteers can collect data over a broader spatial and temporal coverage than a research team could often cover alone, while increasing their own knowledge. The Bumble Bee Watch program has users take and submit photos of bumble bees that are then identified by regional experts. Results will be presented that show the power of combining both researcher and citizen science data to answer ecological questions and increase conservation actions for bumble bees. Over 36,000 records representing 40 different species, including >1,000 records of four at-risk species, have been submitted. This data is helping to fill knowledge gaps related to basic biology (e.g. phenologies) and distribution (e.g. range expansions). Data is used in species status assessments, property management decisions, and research into topics from habitat suitability to conservation breeding, further leveraging the impact of a single observation. Bumble Bee Watch has increased awareness of the diversity of bumble bees and improved identification skills in its participants. Many participate because they want to learn about the species in their area, contribute to science, and help save the bees.

Madi, Naima, Université de Montreal; Jesse Shapiro (Université de Montréal); Michiel Vos (European Centre for Environment and Human Health, University of Exeter; Pierre Legendre (université de Montréal)

Diversity begets diversity in microbiomes

Microbes are embedded in complex microbiomes where they engage in a wide array of interspecific interactions. However, how these interactions shape diversification, and ultimately biodiversity, is not well understood. Two competing hypotheses have been put forward to explain how species interactions could influence diversification rates. Ecological Controls (EC) predicts a negative diversity-diversification relationship, as with increasing diversity niches are increasingly filled, preventing the evolution of novel types. Diversity Begets Diversity (DBD) predicts a positive relationship, with diversity promoting diversification via niche construction and other species interactions. Using the Earth Microbiome Project, the largest standardized survey of global biodiversity to date, we demonstrate DBD to be the dominant driver of microbiome diversity. Only in the most diverse microbiomes does EC play a role, presumably because of increasingly saturated niche space. Genera that are strongly associated with particular biomes show a stronger DBD relationship than non-residents, consistent with prolonged evolutionary interactions driving diversification. Genera with larger genomes also experience a stronger DBD response, which could be due to a higher potential for extracellular metabolic interactions and niche construction. Our results demonstrate that microbiome diversity and its potential for future diversification is crucially shaped by species interactions.

Maglione, Rémi, Université du Quebéc; Mélanie Cadieux (AAC); Marie Ciotola (AAC); Vicky Toussaint (AAC); Martin Laforest (AAC); Steven Kembel (UQAM)

Shifts in phyllosphere microbiota mediated by cover cropping protect squash against pathogens
Cover cropping is a sustainable agriculture approach whereby a plant species such as cereal rye is used to cover the ground prior to planting the crop of interest. Cover cropping potentially provides many ecosystem services including weed control and reduction of bacterial diseases, a major economic threat for producers. We have recently demonstrated that leaf surface (phyllosphere) bacterial community structure changed when squash is grown with a rye cover crop treatment, follow by a decrease of Pseudomonas syringae symptoms, compared with bare soil and plastic cover treatments. Our current hypothesis is that rye material is the main source of beneficial bacteria colonizing squash leaves. To test this hypothesis, we sampled several potential sources of bacteria in our agricultural system: rye material, soil, air, rain water, leaves and seeds of our squash. To model the contribution of each environment to the bacterial community structure of the squash phyllosphere, we used a path analysis approach. Path coefficients suggest that rye cover crops are the main driver of shifts in squash phyllosphere microbial communities. This work provides new insights into the potential for cover cropping approaches to drive bacterial dynamics in agriculture along with the ecological and economical services these microbes provide.

Malloch, Bruce, University of Toronto; Dr. Scott MacIvor

Litter mesofauna of dog-strangling vine (*Vincetoxicum rossicum* (Kleopow) Barbar.) invaded urban forests

Urban landscapes host unique ecological systems, often with introduced or invasive species playing a large role in structuring communities. Dog-strangling vine (*Toxicodendron rossicum*) is extremely successful in its introduced range in Eastern North America, particularly in urban settings, but relatively little is known about how it affects the diversity of adjacent communities. This study assesses litter-inhabiting microarthropods along an urbanization gradient, at sites either invaded by dog-strangling vine or not, and inorganic soil analyses were calculated to further characterize the sample sites. Leaf litter samples were collected at 16 locations across the Greater Toronto Area, Canada, and arthropods were extracted by heat and identified to genus using morphology. Dog-strangling vine was not found to significantly affect litter microarthropod diversity however diversity was negatively correlated with urbanization. In particular, fungivorous taxa were sensitive to urbanization while predatory and phytophagous taxa appeared more resilient. Litter microarthropods are a critical part of decomposition-based food webs and this study offers insights into how this community responds to anthropogenic pressures.

Maloney, Jamie, Faculty of Forestry, University of Toronto; Dr. Jay Malcolm

Use of beetle (Coleoptera) communities from window-pane traps to test the sustainability of forest management in northern temperate hardwood forests

In the 1950s, single tree selection (STS) became the dominant silvicultural system used in hardwood stands in Ontario. Although intended to be sustainable, evidence suggests that this system may be altering forest structure and composition over time, with potentially important implications for biodiversity. We compared family-level beetle (Coleoptera) community composition sampled via window-pane traps between mature STS managed and unmanaged stands in the temperate forests of south-central Ontario. The effect of trap placement within stands were also investigated; specifically, (i) traps placed in sugar maple and eastern hemlock trees, both in the lower canopy and nearby understory, and (ii) traps placed on early- and late-decay snags and downed woody debris. A total of 28,826 beetles were collected from 30 sites. No statistical difference was observed between beetle abundances in unmanaged and managed sites. However, strong effects were observed due to wood posture, trap height, tree species, and decay class (listed in order of significance). Results provide insights into micro-habitat partitioning and the responses of beetle communities to human landscape transformations as well as the sustainability of STS in south-central Ontario. Efforts to evaluate this silvicultural system are critical due to its widespread and continuing use.

Manning, Faye, University of British Columbia; Curtis, Walker, Pither

An experimental assessment of freshwater diatom dispersal via waterfowl feathers
Dispersal is a fundamental ecological process that can profoundly influence the diversity and functioning of ecosystems. Yet, for microorganisms, dispersal remains a black box. Among freshwater diatoms, waterfowl have long been considered potential dispersal vectors, but experimental assessments of this possibility are lacking. We conducted a novel experiment designed to emulate diatom transport by waterfowl feathers, and to test the individual and interactive effects of humidity and transport time on dispersal success (factorial design, N = 8 replicates per treatment combination). Each replicate involved dipping a mallard breast feather in a solution inoculated with a single strain of diatoms (genus Nitzschia), then subjecting the feather to one of 4 humidity levels and one of 4 transport durations within a chamber through which air was passed. Finally, the feather was dipped into sterile media. We equated dispersal success with evidence of growth after 2 weeks. Our experiment indicated strong potential for successful dispersal via feathers overall, and revealed a significant interaction between humidity and transport time: dispersal success declined with transport time, but less so under high relative humidity. We place our findings in the context of waterfowl dispersal distances and inter-lake distances within the major migratory flyways of North America.

Manning, Paul, Dalhousie University

Ivermectin residues in cattle dung impair insect-mediated dung removal but not organic matter decomposition

Veterinary parasiticide residues in livestock dung have been widely shown to negatively affect the abundance and diversity of dung-associated insects. While these losses are concerning from a conservation perspective, they may also translate to impairment of decomposition-related ecosystem functions in agricultural landscapes (e.g. nutrient cycling). Most research focusing on decomposition-related ecosystem functioning has focused on dung beetles (Coleoptera: Scarabaeoidea) while other insects, particularly flies, have received comparatively less attention. Using a field experiment, we selectively modified which insect groups were able to colonize cow dung (beetles only, flies only, beetles and flies together, and an insect-free control). In semi-field mesocosms half of the insects were exposed to 1 ppm ivermectin in dung, while the other half was exposed to ivermectin-free dung. Comparison of beetles and flies in ivermectin-free dung showed that beetles removed nearly twice as much dung than flies. Comparison of dung removal across all treatments showed that ivermectin residues significantly reduced dung removal provided by beetles by 47%, and dung removal provided by beetles and flies together by 32%. Organic matter decomposition was not significantly affected by insect colonists or by the presence of ivermectin indicating that in some cases decomposition occurs independently of insect activity and chemical perturbations.

Marchand, Philippe, Université du Québec en Abitibi-Témiscamingue; Mathieu Bouchard, Direction de la recherche forestière, Ministère des Forêts, de la Faune et des Parcs du Québec

Improving quantitative reconstructions of forest insect outbreaks by combining dendrological and aerial survey data

Insect outbreaks are among the main disturbances shaping the dynamics of the Canadian boreal forests, and precise estimates of past defoliation across different host species, forest compositions and climatic conditions are essential in order to predict future changes in the geographic range and intensity of these outbreaks. In this study, we produce quantitative maps of defoliation intensity for the 1967-1992 spruce budworm outbreak in Quebec by combining two complementary data sources: aerial surveys, which partition the study region into discrete defoliation classes, and tree-ring data from forest inventory plots, which provide a quantitative record of cumulative defoliation via its impact on tree growth. We use a hierarchical Bayesian model that relates the underlying outbreak intensity (latent variable) to both the defoliation classes in aerial surveys (ordinal logistic regression) and the standardized tree-ring widths (autoregressive moving average model). We discuss the utility of these results for calibrating the reconstruction of past outbreaks from tree-ring data only.

Mariño, Joany, Memorial University of Newfoundland; Amy Hurford; Suzanne Dufour

A stage-structured model reveals emerging population dynamics in chemosymbiotic bivalves.
Thyasirid bivalves are particulate feeders, obtaining nutrients from free-living chemosynthetic bacteria. However, some species are symbiotic and harbour bacteria extracellularly in enlarged gills. Symbiotic thyasirids are mixotrophs, digesting symbiotic bacteria as an additional resource. I investigate trophic symbiosis in the thyasirids by comparing two closely related species: Thyasira cf. gouldi, which is symbiotic, and Parathyasira sp., which is asymbiotic. I have used allometric and life history data to parameterize a Dynamic Energy Budget (DEB) model for each species. The main finding was that the symbiotic species has lower energy reserves relative to the asymbiotic, which leads to different energy allocation patterns despite similarities in the species' life histories. I hypothesize that smaller energy reserves together with harbouring symbionts are adaptations to a fluctuating environment. To test this hypothesis requires relating the individual energy budget to the population-level, because the consequences of a smaller energy reserve (e.g. producing fewer and larger eggs, having slower growth and maturation) are likely to be reflected in the population demography. Thus, I will present a stage-structured model that accounts for the species' physiological differences according to the DEB model. My findings provide a potential mechanistic explanation of the dynamics of the thyasirid populations, which are be difficult to obtain from either direct field measurements or laboratory experiments. My results will highlight how the symbiotic association is likely to change the energy budget of a mixotrophic bivalve and thereby determine the population dynamics, which is of interest in a wide range of trophic symbioses.

Marleau, Justin, McGill University; Andrew Gonzalez, McGill University

A meta-ecosystem approach to community rescue in aquatic food webs

Ecological communities commonly experience abiotic stresses such as severe temperature fluctuations and acidification. These stresses can reduce the abundances of community members and alter community composition, which in turn impact ecosystem processes. Spatial processes such as dispersal and the diffusion of nutrients could modify the trajectories of communities evolving in response to environmental stress. At the Large Experimental Array of Ponds (LEAP) in the Gault Nature Reserve, 96 experimental ponds were exposed to a planned acidification treatment in order to investigate whether plankton communities could recover from the stress. In this talk, we present a phosphorus-multiple algae-multiple zooplankton meta-ecosystem model that explicitly considers ecophysiology and temperature sensitivity to help understand the biotic and abiotic processes at play in LEAP. Our results suggest that a few zooplankton speciestraits coupled with phosphorus limitation of phytoplankton and temperature-dependent growth can give rise to qualitatively reasonable predictions of the dynamics of biomass and the species assemblages seen in LEAP. However, the addition of dispersal and diffusion did not result in the predicted effects of connectivity, which was matched by the empirical results. We conclude that spatial effects were limited in this experiment and we use the model to identify conditions where the movement of materials and organisms could matter. These results suggest that adding abiotic processes through a meta-ecosystem approach will improve our understanding of community recovery to human-imposed stressors.

Martchenko, Daria, Trent University; Aaron B. A. Shafer

Exploring the evolution and ecology of the North American mountain goat (Oreamnos americanus) using genomic data

The North American mountain goat (Oreamnos americanus) is an iconic alpine species that faces pressures from climate change, industrial development, and recreational activities. Genomic data, i.e. genetic data across all chromosomes of a species, can provide additional insights for management and conservation initiatives. We have assembled the first draft genome for the mountain goat. Using this genome and RADseq data from across the range we explored the contemporary population demography. Across the species range there is variability in the habitat, altitude, temperature and precipitation, forest cover, and slope. We also used the RADseq data to model the associations between genetic factors and environmental variables.

Martin, Rosemary, University of Toronto; Shannon McCauley

Winter ecology of aquatic insects in a changing climate
The overwintering of aquatic insects has received relatively little attention. My research explores how winter conditions such as ice coverage duration and oxygen levels influence the activity levels, survival, and body condition in aquatic insects such as dragonflies, caddisflies, and backswimmers, as well as impacts on later life history events and cross-seasonal food webs.

Martin, Kathy, Environment and Climate Change Canada; Kristina Cockle; Kurt Trzcinski; Karen Wiebe

Woodpecker Legacies: effects of tree cavity production and longevity on cavity-using vertebrates

About 20% of birds globally use tree cavities for nesting and roosting, but about 75% of these species depend on other species or processes to provide their cavities (non-excavators). Most woodpeckers produce cavities that they only once for breeding, but these cavities can remain useable by many other species for one to several decades. Across all zoogeographic regions, we find strong positive correlations between species richness of excavators and non-excavating cavity nesters. We investigate the functional role of woodpeckers in terms of regulating the abundance and diversity of non-excavators in cavity nesting vertebrate communities. Over a two decade study (1995 to 2016) in interior British Columbia, we monitored the dynamics of cavity production, survival and use by more than 30 species of birds and mammals. We determined that excavating woodpeckers contributed a strong positive influence on the standing stock of cavities (cavity production) and the extent of their use (species richness, abundance) at the site and landscape levels. We conclude that woodpeckers generate considerable legacies in supplying a critical habitat attribute that maintains the abundance and diversity of tree cavity-using communities in temperate forests.

Peter Mason

The State of Biological Control in Canada

Biological control provides an ecosystem service for reducing impacts of problem species. Among the four types natural and conservation biological control are underdeveloped while inundative biological control and importation biological control, driven by industry and government, respectively, have provided successful reductions of species causing negative impacts. Importation biological control focuses on non-native species and generates significant scientific outputs. Biological Control in Canada has an optimistic future.

McCann, Kevin, University of Guelph; John Fryxell; Andrew MacDougall; Andrew Gonzalez; Gabriel Gellner; Gregor Fussmann; Brian LaPointe

Ecological Entanglement: Spooky Actions at a Distance

Here, we look at the role of connected ecosystems through the lens of stability. Specifically, we use a simple set of models to elucidate the fact that ecosystem imbalance -- fundamental changes in stability that generally drive changes in community composition and ecosystem function -- may not be expressed at the local scale where human impacts often originate (e.g. agriculture) but rather, due to cross-ecosystem connectivity, imbalance from local impacts can occur 100s even 1000s of km away. Here, we argue that our theoretical results resonate with our empirical understanding of the current global increases in ecosystem imbalance, and that the theoretical framework outlined here emphasizes numerous potential spatial solutions (and research directions) that may be employed to mitigate these growing global environmental problems. Curiously, our theoretical framework also suggest that thinking local can in deed lead to regional and even global consequences due to natures high connectivity.
McCann, Sean, Simon Fraser University; Catherine Scott, University of Toronto, Department of Biological Sciences; David Bradbeer; Christina Frey, Vancouver International Airport; Jennifer Cory, Simon Fraser University, Department of Biological Sciences

Invertebrate foraging by water birds at Vancouver International Airport: can a bottom-up approach be used to mitigate bird strike risk?

Vancouver international Airport (YVR) is situated in a tidal estuary, hence the majority of bird-aircraft collisions involve ducks, gulls, and shorebirds. Omnivorous and adaptable species such as Mallards, Northern Pintail, Green-winged Teal, and Dunlin use the runway-adjacent grassy infields for foraging in the fall and winter. Dietary analyses these birds indicate that terrestrial invertebrates such as earthworms, crane fly larvae, caterpillars of noctuid moths and click beetle larvae are fed upon most often. We are studying whether reduction of these prey groups can be accomplished using chemical and non-chemical interventions, with the hopes of reducing bird presence adjacent to the runways at YVR. Application of a broad-spectrum insecticide (Acelepryn) to the soil in early fall of 2018 reduced earthworm numbers by 55%, tipulid numbers by 92%, noctuid abundance by 99% and elaterid abundance by 36%. Reductions of this scale represent a substantial decrease in invertebrate biomass available to foraging birds over the fall and winter, and may well result in lowered bird presence on insecticide-treated areas of the airfield. With these results in hand, we will continue to study the effectiveness of such chemical controls as well as cultural and biological control of the invertebrates favoured by waterfowl at YVR.

McCulloch, Baily, University of Alberta; Stan Boutin University of Alberta


As apex predators disappear worldwide, their absence can have complex ecological consequences, and their role in structuring systems facing rapid anthropogenic change is a critical avenue of study. The loss of apex predators can cause a trophic cascade known as mesopredator release, an increase in the numbers of smaller predators a potential conservation concern on a global scale. This effect is well documented, but varies in magnitude and is not consistently observed; the influence of anthropogenic disturbance, which is known to affect mesopredator abundance, is rarely considered. We investigate the relative strength of predator removal and human disturbance on mesopredator abundance. The Alberta governments wolf control program provides a natural experiment to study mesopredator release on a landscape scale, while neighbouring Saskatchewan offers a less human-modified baseline. Using an expansive network of camera traps and an emerging method for estimating density of unmarked species, we compare population densities of wolves and mesopredators across one region in Alberta undergoing active wolf control, one region with no wolf control, and a reference region in Saskatchewan. We demonstrate that anthropogenic landscape change is associated with a larger increase in mesopredator density than the top-down effect of apex predator loss.

McGlynn, Terry, California State University; Dominguez Hills

How colonies of tropical ants adapt to thermal challenges

The capacity of organisms to adapt to novel thermal challenges is foundational for adapting and evolving in response to rapid climate change. Ectothermic animals require heat from the environment to function, but they cannot operate once it gets too hot. I present a series of experiments conducted on the colonies of the Ectatomma ruidum in Costa Rica, designed to understand how colonies organize labor within colonies to respond to thermal challenges. Animals were marked in the field performing work in different thermal regimes, and brought into the lab, subjected to thermal treatments, and persistence in a thermally challenging environment was assayed. I found evidence that the expression of thermal tolerance varies among workers based on their task, and that this expression is governed by a circadian rhythm. These results suggest that colonies are actively governing the expression of heat shock proteins, and this expression may be labile.
McGregor, Rob, Institute of Urban Ecology, Douglas College; Nathan Pennykid; Joanna Teng; Matthew Watkins; All from Institute of Urban Ecology, Douglas College

Down by the bay: *Omus audouini* (Coleoptera: Carabidae) populations at Boundary Bay, British Columbia

Canadian populations of *Omus audouini* (Coleoptera: Carabidae) are limited to coastal lowlands near Boundary Bay in Delta, British Columbia and on Southern Vancouver Island. This species is considered vulnerable to habitat loss and human disturbance and has been designated threatened under the Committee on the Status of Endangered Wildlife in Canada (COSEWIC). Surveys in 2018 at Boundary Bay established that *O. audouini* populations were associated with a plant community dominated by Douglas Aster (*Aster subspicatus*). Results of 2019 surveys for *O. audouini* from multiple locations across Boundary Bay will be presented along with associated plant community information.

McLeod, Anne, Memorial University of Newfoundland, Shawn J. Leroux Memorial University of Newfoundland,

*It's the journey not the destination: how different dispersal mechanisms influence food web stability,*

There is considerable empirical and theoretical evidence showing that diverse ecological communities may not be inherently unstable contrary to suggestions by May’s seminal study. One plausible mechanism which may reconcile theory and observation is the incorporation of connectivity between communities. Most research examining the movement of species between communities focuses on simple hierarchical movement, or the ability of species at progressively higher trophic levels to link resources within space. While examples of megafauna acting as ecosystem integrators linking spatially distinct habitats are replete, there are similar examples of resources linking communities. Here, we build on recent mathematical frameworks to distill the stability analysis of these complex, spatially segregated food webs into local food webs connected by organism specific dispersal rates between communities. Traditionally, this approach considers dispersal to be a species-specific value leading to a symmetric diffusive-like spreading of organisms. Organisms, however, respond to local environmental cues to move directionally depending on a trade-off between the known local and the unknown regional conditions. In our analysis we contrast the influence of different dispersal mechanisms and non-hierarchical dispersal on food web stability. These insights are critical for anticipating species responses to local to landscape level anthropogenic changes and habitat alterations.

McMeans, Bailey, University of Toronto; Matthew M. Guzzo; Timothy Bartley; Timothy Fernandes; Paul J. Blanchfield; Henrique Giacomini; Kevin S. McCann; Trevor Middel; Michael D. Rennie; Mark Ridgway; Brian Shuter

Winter in water: differential responses and the maintenance of biodiversity

The ecological consequences of winter in freshwater systems are an understudied but rapidly emerging research area. Here, we argue that the historical oversight of winter has led researchers to underestimate the importance of time in the coexistence of species. This may be especially true for thermal and reasonably well-mixed aquatic ecosystems, where seasonal changes in the spatial thermal environment might fundamentally structure species dynamics and mediate coexistence. With climate change shortening winter periods, a conceptual framework for the ecological implications of winter, and altered winter conditions, is urgently needed. Using data for freshwater fishes, we demonstrate that physiological traits (e.g. thermal preference) combined with local factors (e.g. lake size) drive differential behavioral responses to winter among species (e.g. pelagic vs. benthic foraging). Behavioral differences translate into growth differences, meaning that winter, and inter-annual variation in winter duration, could provide opportunities for spatiotemporal niche partitioning that favor different species under different conditions. Our perspective is that: 1) winter behavior, and capacity for winter growth, should be heavily context dependent, and 2) such variation in ecological responses to winter could be important for biodiversity maintenance in a wide range of ecosystems.
McNeil, Jeremy, The University of Western Ontario; Isabel Ramirez, Centro de Investigaciones en Geografía Ambiental Universidad Nacional Autónoma de México; Zoe Lindo, Department of Biology The University of Western Ontario

Differences in soil microarthropod communities within and outside a monarch overwintering colony.

We tested the hypothesis that following decomposition of dead monarch butterflies, Danaus plexippus, the release of cardenolides and pyrrolizidine alkaloids, sequestered as protection against natural enemies, would affect the soil microarthropods within monarch overwintering sites. Data obtained from soil samples collected in February and May, 2018, showed that the overall density of microarthropods, oribatid mites and collembola were significantly lower within the roosting colonies that in the controls. The species diversity of oribatid mites was also lower within the colony, but the differences were only significant in the February. These observations lend support to our hypothesis but additional research is required to demonstrate that the differences observed are actually the result of direct or indirect effects of the compounds released from decomposing monarchs. The possible role of chemical cues resulting from changes in soil flora and fauna within the context of locating the overwintering roosting sites is discussed.

McNickle, Gordon, Purdue University

Evolutionary game theory, functional traits, and community ecology

Ecologists have long used functional traits to quantify differences among species that are thought to be important for defining the ecological niche, and interpreting patterns in community ecology. Yet, the approaches are largely inference based and a fully predictive framework for community ecology has remained elusive. Evolutionary game theory (EGT) is a mathematical framework where species experience frequency dependent interactions that are mediated through traits. (Game theorists usually say strategy not trait, but these are synonyms in this context.) Most ecologists are familiar with classic matrix games like the hawk-dove game, or the prisoner’s dilemma. These classic games gave important insights into ecology and evolution, but they were limited to just a few categorical traits. EGT has developed into a rich set of mathematical tools for any number of continuous traits, and includes continuous population dynamics. Indeed, modern continuous EGT allows for the explicit representation of biological fitness as a function of: (i) species interactions mediated through traits; (ii) multi-species frequency dependent population dynamics; (iii) density dependence within a species, and; (iv) limitations of the abiotic environment. I will argue that EGT is a powerful, but vastly underappreciated predictive framework for community ecology.

Meehan, Matthew, Western University; Kurtis Turnbull; Zoë Lindo

Metabolic demands on soil predators and prey selection under warm conditions

Predator-prey dynamics are controlled by many factors, including movement rates, nutrient demands, and body sizes of both predators and prey. Climate warming is expected to affect predator-prey interactions through greater metabolic demands for ectotherms. We use a combined physiological and behavioural approach to model predator behavior under warm conditions (20°C) using a predatory mite (Stratiolaelaps scimitus (Womersley)) species and three prey species: a collembolan (Folsomia candida Willem) and two mites (Oppia nitens Koch and Carpoglyphus lactis (Linnaeus)) that differ in movement, nutritional quality and body size. We measured CO2 production, as a proxy of metabolism for S. scimitus, and measured soluble protein, lipids, carbohydrate content and movement rates for each taxon. We subsequently performed no choice and choice feeding experiments. Predator mites consumed C. lactis quickest in our no choice feeding experiment, followed by F. candida and O. nitens. In our choice feeding experiment, prey preference remained the same but feeding rates were lower due to prey interference, highlighting the complexity of these dynamics, irrespective of temperature.

Meng, Eric

A Genetic Assessment of New Brunswick’s Endangered Canada Lynx (Lynx canadensis)
Understanding the impact of a population bottleneck on genetic diversity is essential for the conservation of a recovering species. Because genetic diversity is linked to an increased ability for adaptation at both functional and phenotypic levels, it provides the most direct measure of a population’s capacity to cope with environmental change. In New Brunswick, Canada lynx (Lynx canadensis) are listed as ‘Endangered’ due to their near extirpation in the 1900s, and the population has only recently begun to recover. Here, we use single nucleotide polymorphisms (SNPs) obtained from GBS sequencing data as well as two mitochondrial loci – D-loop and Cyt b – to assess the genetic structure and variability of Canada lynx in New Brunswick. Also, we assess the data for evidence of a recent genetic bottleneck event using coalescent-based estimates of Ne over time. Bayesian clustering analysis indicated the presence of a single genetic cluster, which was further supported by F-statistics. Highly negative inbreeding coefficients and a low estimated Ne also suggest that a behavioural inbreeding avoidance mechanism may be operating in New Brunswick’s lynx. While we were unable to detect evidence of a genetic bottleneck, marker type and insufficient time post-bottleneck are likely obscuring direct detection.

Merot, Claire, Université Laval - IBIS; Claire Mérot; Eric Normandeau; Emma Berdan; Haig Djambazian; Loannis Ragoussis; Violaine Llaurens; Maren Wellenreuther; Louis Bernatchez

Genomics of an adaptive balanced inversion polymorphism in a seaweed fly

Chromosomal inversions are frequently involved in balanced polymorphisms. By limiting recombination, inversions tighten several genes underlying complex phenotypes and different rearrangements may represent distinct strategies. To fully understand the evolution and maintenance of an inversion polymorphism, it is essential to link the genomic architecture with the selective mechanisms. Here, we combine ecological-experimental studies with population genetics and genomics to address both the adaptive and genomic landscapes of a chromosomal inversion in the seaweed fly Coelopa frigida. The inversion comprises 10% of the genome, and determines three male morphotypes that vary in population frequency. To understand the selective mechanisms, we genotyped 1,500 flies in 16 natural populations along a 1,000 km latitudinal gradient in North America, and raised 5 generations of experimental evolution in four controlled treatments. Results show that the polymorphism is maintained by a combination of spatially-varying selection, antagonistic natural/sexual selection and heterozygote advantage. To characterize the genomic features, we combined genome assemblies based on PacBio and 10xGenomics technologies, population re-sequencing and linkage mapping. The long reads allowed dissecting the inversion contents and breakpoints, and to detect deleterious or repetitive elements possibly underlying the heterozygote advantage. Finally, genomic and ecological information were linked in a large-scale population genomics analysis. We optimized a low-cost protocol to generate high-quality libraries for each fly collected along the environmental gradient. Low-coverage whole-genome sequencing yielded 100X population coverage and 1-2X individual coverage, producing robust population allele frequencies and individual genotype likelihoods. This allowed to investigate the population structure and connectivity, signatures of selection and environmental associations. By contrasting loci within and outside the inversion, we also address the adaptive and evolutionary significance of the inversion relatively to collinear genome.

Messier, Julie, University of Waterloo; Antoine Becker-Scarpitta; Cyrille Violle; Mark Vellend

Root and allocation traits inform the response of plant species and communities to climate change

Global warming is affecting the distribution and performance of all animal and plant species on the planet. While we have identified general trends in species response to changing climates, we still do not know how individual species will respond and functional composition of communities will change. Here we test whether, and which, phenotypic traits describing plant adaptive strategies can predict species response to a 2°C warming that occurred between the 1970s and 2010s in a temperate forest. We assessed the relationship between the change in average elevation and abundance of the 50 most abundant temperate understory plant species on Mont Mégantic and 8 functional traits. At the community level, we examined how the functional composition of understory plant communities has changed at this site over that time. At the species level, we find that Mycorrhizal Fraction, Rooting Depth and Leaf Mass Fraction are associated with species elevation and abundance response to warming. At the community level, the functional composition of communities has changed, but largely in terms of root traits, especially Mycorrhizal Fraction and Rooting Depth. Our findings indicate that
allocation traits and root traits are associated with species ability to respond to climate change and urge future research to pay attention to the belowground niche.

Metaxas, Anna, Department of Oceanography, Dalhousie University

Dispersal, connectivity and making a difference

Marine benthic populations, communities and ecosystems are mostly comprised of sessile or near-sessile organisms which rely on larval dispersal to maintain connectivity. In turn, connectivity can play a significant role in ensure persistence and recovery after perturbations. Conservation efforts often focus on persistence and recovery, both internationally and on multiple national stages. For example, countries, including Canada, are racing to meet their obligation to conserve at least 10% of their coastal and marine areas by 2020 through the establishment of marine protected areas and similar efforts are mounted on the international stage, to conserve regions of the seabed and the high seas using area-based management tools (ABMT) to do so. The design of effective ABMTs requires, in part, scientific evidence to establish representative and well-connected systems that protect biodiversity and ecosystem services. While many ABMTs have considered representation, the inclusion of connectedness among habitats, populations or ecosystems remains more elusive. I will use examples from our own work to illustrate the current state of including ecological connectivity as a design element in ABMTs. Based on those, I will discuss the evidence on the relative importance of connectivity in designing marine protected areas.

Miller, Joshua, University of Alberta; Chandra McAllister (University of Alberta); Rhiannon Peery (University of Alberta); Marion Mayerhofer (University of Alberta); Tod Ramsfield (Northern Forestry Center, Natural Resources Canada); Andy Benowicz (Alberta Environment and Sustainability Resource Development); Deogratias Rweyongeza (Alberta Agriculture and Forestry); Janice Cooke (University of Alberta)

Genomics of resistance to western gall rust in lodgepole pines

Over their long life spans, forest trees are continually exposed to a variety of pests and pathogens which they are required to defend against. One such pathogen is Cronartium harknessii, the causative agent of western gall rust (WGR) in pine trees (Pinus spp.). WGR can cause mortality among juvenile trees, and reduce the yield of merchantable timber from mature trees. To examine the genetic basis of WGR resistance in lodgepole pine (Pinus contorta spp. latifolia), we combined high resolution phenotyping of a seedling resistance screen with genotyping of the same individuals using high density single nucleotide polymorphism (SNP) data. A total of 1,752 seedlings representing 62 families, were inoculated with C. harknessii in a controlled environment growth room. Following inoculation, disease symptoms were tracked for 26 weeks, with detailed phenotypes assessed every two weeks. SNP genotyping was performed on a custom lodgepole pine expressed sequence tag-derived SNP chip, yielding 19,186 loci for analyses. We then conducted survival analysis to investigate inter-family differences in disease progression, and genome-wide association analyses to see if differences in disease progression and overall resistance could be attributed to specific loci. These results will help elucidate the trait architecture for resistance to C. harknessii, and form the basis for genomic selection of resistant plants, which can be integrated into breeding programs.

Miryeganeh, Matin; Hidetoshi Saze,

Transcriptomic and Epigenomic Responses of Mangrove Trees to Different Stressful Environments

Mangroves are salt tolerant trees that grow in coastal saline water in tropics and subtropics and are adapted to harsh conditions with high salinity, extreme tides, strong winds, high temperatures, and anaerobic wetlands. They have developed specific morphological and physiological characteristics, such as breathing and support roots, salt-excreting leaves, and viviparous seedlings. Mangrove communities show gradual phenotypic changes in forest structure such as tree height and biomass that usually decrease due to increasing stress factors along the tidal gradients. We have set the study site in a mangrove forest located along the estuary of a river and coastal area of Pacific Ocean in Okinawa-Japan. This forest is consisted mainly of three mangrove species from the family Rhizophoraceae, and show highly developed
morphological adaptations to extreme conditions. We are investigating how methylation variation is distributed among individuals from different habitats in different level of stress, and how this variation is correlated with their morphological differences and gene expression. To produce a high-quality reference genome, we generated a de novo assembly of representative mangrove species. We have done a complementary detailed de novo annotation of genes based on RNA sequencing data. Gene expression analysis identified remarkable genomic characteristics that are conserved within each group but differ among them and annotations of Gene Ontology, revealed differences in the transcriptome profiles among the two populations. We are constructing genome-wide DNA methylation maps comparing phenotypically different individuals of each species that are growing in different distances from the coastal area. This study may help to evaluate the risk of plant species in fluctuations of the environmental conditions and can make a good model system for studying epigenetic mechanisms related to abiotic stress adaptation in tropical forest trees.

Mittelstaedt, Hannah, University of Maine; Elliot Johnston; Hannah Webber; Amy Baron; Jessica Muhlin; Brian Olsen; Amanda Klemmer

Bottom-up effects of seaweed harvest on intertidal food webs

The rocky intertidal shores in the Gulf of Maine are dominated by the brown alga, Ascophyllum nodosum, commonly known as rockweed. Rockweeds complex structure alters abiotic conditions in the nearshore environment and provides habitat for a productive and diverse community of sessile and motile, benthic and epiphytic invertebrates that support top-predators, such as birds. Rockweed is commercially harvested, allowing us to test bottom-up, food-web effects of anthropogenic removal of a foundation species on invertebrates and birds. To assess the impacts of harvest on invertebrate community structure and food-webs, we designed a commercial-scale before after control impact (BACI) experiment with 52 sites across the coast of Maine. Invertebrate, bird, and rockweed biomass surveys were conducted at both control (unharvested) and impact (harvested) sites in 2018 and 2019. Short-term changes in rockweed biomass, due to harvest, altered invertebrate community composition and biomass between control and impact sites. Our preliminary findings suggest that shifts in community structure may cascade up the food web, with rockweed biomass predicting shorebird presence and abundance. Understanding how anthropogenic removal of a foundation species not only influences primary consumers such as intertidal invertebrates but top-predators such as birds, can inform sustainable ecosystems-based management and conservation strategies.

Mlynarek, Julia; Andrew Laflair; Kai Zhang; Paula Vilcu; Kathrin Sim; Rebecca Rizzato; Dana Gagnier; Roselyne M. Labbe

Predatory capacity and life histories of two native North American nabids

Cultivated tomato, Solanum lycopersicon is an important crop grown in greenhouses and fields throughout Canada. Yet, managing pests on this crop continues to represent a major challenge, particularly in light of new invasive pests species for which few to no native natural enemies have been well investigated. The objective of this study was to better understand the biological control potential of Nabis americoferus and Nabis roseipennis through conducting life history and predatory functional response trials. Our study shows that N. americoferus develops faster than N. roseipennis and they consume a lot prey but they eat more aphids than whiteflies. These findings contribute to improving our overall understanding of damsel bug natural history. This research can directly assist in the development of best practices for the application of nabids for the biological control of pests in greenhouse and field crops in Canada.

Moffat, Chandra, Agriculture and Agri-Food Canada; Paul Abram

Rethinking biological control programs as planned invasions

Despite notable successes, the majority of biological control programs fail, often due to a poor match between the traits of a biocontrol agent and the recipient environment; that is, a lack of agent
Mogensen, Steph, University of Calgary; J.R. Post, University of Calgary; P.M. Schulte, University of British Colombia

Impact of size on foraging related behavioural consistency in rainbow trout

Behavioural consistency of individuals has been observed in a variety of organisms. For example a particularly important suite of behavioural traits mediate risk acceptance during foraging, due to trade-offs between resource acquisition and risk of predation mortality. We might expect larger individuals to exhibit more risk accepting behaviours. In this study we test that hypothesis by exploring the effect of individual size on the behavioural consistency of young of the year rainbow trout.

Moise, Eric, Natural Resources Canada - Canadian Forest Service; Joseph Bowden, Natural Resources Canada - Canadian Forest Service; Michael Stastny, Natural Resources Canada - Canadian Forest Service; Heather Spicer, Memorial University; Jenna McDermott, Natural Resources Canada - Canadian Forest Service

Incorporating overwintering success as a component of spruce budworm management

Winter diapause is a critical life stage for many insect species. From an applied perspective, understanding environmental factors that influence overwintering success (i.e. survival + sublethal, downstream performance metrics) may benefit forest insect pest management. For instance, management of spruce budworm outbreaks relies on pre-winter insect collection to predict post-winter densities. However, overwintering mortality is assumed to be equal across all environments. For this study, we quantified insect overwinter success by deploying prediapause budworm across field sites that varied in structure (tree composition, age) and elevation. Spruce budworm survival was approximately 73%, but was not influenced by forest stand composition, age or elevation. In contrast, larval development time was shortest for budworm from high elevation sites and longest for low elevation sites. Lastly, pupa mass was highest for the lowest and highest elevation sites, although the overall effect of elevation was only marginally significant. In sum, pre-winter pest monitoring may overestimate the density of insects that emerge the following spring, although this is not influenced by forest structure or elevation. However, downstream insect performance is influenced by elevation, with the most positive impact on individuals from high elevation sites.

Monk, Wendy, Environment and Climate Change Canada @ CRI; Trevor T Bringloe Environment and Climate Change Canada; Zacchaeus G Compson Centre for Environmental Genomics Applications; Catherine B Choung Environment and Climate Change Canada @ Canadian Rivers Institute, University of New Brunswick; Kathryn L Korbel, Department of Biological Sciences, Macquarie University; Natalie K Rideout, Canadian Rivers Institute, Department of Biology, University of New Brunswick; Donald J Baird, Environment and Climate Change Canada @ Canadian Rivers Institute, University of New Brunswick

Disentangling multiple stressor pathways in floodplain ecosystems using weight-of-evidence and network meta-analysis approaches

Freshwater systems are dynamic, diverse ecosystems connecting terrestrial, riparian, subsurface and aquatic habitats. We present an evidence-based framework to explore direct and indirect effects of multiple stressors and test this structure with a detailed example of urbanisation in floodplain ecosystems. Using evidence obtained from peer-reviewed scientific literature, the strength of direct and indirect effects of individual and multiple components was quantified using an evidence-weighted analysis and a quantitative network meta-analysis. Results demonstrated the power of adopting a systematic framework to advance quantitative assessment of ecosystems affected by multiple stressors. Direct pathways were generally stronger providing the core network skeleton but there were many more significant indirect pathways indicating clear evidence gaps in our mechanistic understanding of these processes. A second framework example in the Peace-Athabasca Delta (Alberta, Canada) combines environmental and social-cultural components using data from peer-reviewed literature, observed field data, and expert knowledge. Both networks illustrated novel disturbance pathways that could be used for hypothesis generation for further scientific inquiries and development of strategic management and monitoring strategies. Our results highlight the broader applicability of adopting the proposed framework for assessing complex environments.
Conserving evolutionary history does not result in greater diversity over geological timescales

Alternative prioritization strategies have been proposed to safeguard biodiversity over macro-evolutionary timescales. The first prioritizes the most distantly related species (maximizing phylogenetic diversity) in the hopes of capturing at least some lineages that will successfully diversify into the future. The second prioritizes lineages that are currently speciating, in the hopes that successful lineages will continue to generate species into the future. These contrasting schemes also map onto contrasting predictions about the role of slow diversifiers in the production of biodiversity over paleontological time scales. We consider the performance of the two schemes across ten dated species-level paleo-phylogenetic trees ranging from foraminifera to dinosaurs. We find that prioritizing phylogenetic diversity for conservation generally led to fewer subsequent lineages, while prioritizing diversifiers led to modestly more subsequent diversity, compared to random sets of lineages. Importantly for conservation, the tree shape when decisions are made cannot predict which scheme will be most successful. These patterns are inconsistent with the notion that long-lived lineages are the source of new species. While there may be sound reasons for prioritizing phylogenetic diversity for conservation, long-term species production might not be one of them.

Moore, Jean-Sébastien, Université Laval; Eric Normandeau, Université Laval; Terry Beacham, Fisheries and Oceans Canada; Ruth Whitler, Fisheries and Oceans Canada; Thibault Leroy, Université de Montpellier, Eric B. Rondeau, University of Victoria; Jong S. Leong, University of Victoria; Ben F. Koop, University of Victoria; Louis Bernatchez, Université Laval

The demographic and selective history of Coho Salmon

Pacific salmonids are widespread fishes that constitute natural resources of economic, ecological, social and historical value and are currently undergoing massive declines due to a host of human related perturbations. Despite billions of dollars being spent in population supplementation programs, the evolutionary history and spatial distribution of genetic diversity within most of these fish remains poorly documented. Here we present genome-wide data that represent the extant diversity of the Coho Salmon (*Onchorhyncus kisutch*) in North America to address three goals. First, we decipher the demographic history of the species. We inferred a complex history involving secondary contact between small isolated glacial refugia. However, we also demonstrated that the majority of present-day genetic diversity has been reshaped by survival in a single refugia during the latest glacial maxima, and proposed a scenario out-of Cascadia whereby ancestral populations located in the south of the distribution range have expanded in postglacial time ~ 12,000 years ago swamping out most of the diversity from other putative refugia. Following this expansion, we identified particular populations having undergone continuous declines in population size (Ne). Second, we demonstrated that this demographic history was not sufficient to generate strong differences in the load of deleterious mutations among populations. Last, we combined multiple evidence from our demographic modelling, analysis of recombination landscape and genome-wide landscape of diversity suggesting that linked selection and biased gene conversion has played and is playing a major role in shaping genetic diversity across the Coho Salmon genome.

Morbey, Yolanda, Western University

Identifying behavioural state transitions from activity traces of song birds using changepoint analysis

In automated data collection systems (e.g., automated radio telemetry, video analysis), the analyst is faced with the task of sorting through and extracting meaningful information from high-resolution time series, often containing millions of detections across multiple birds. Changepoint analysis allows an analyst to detect the occurrence of single or multiple changepoints in the distribution of time series data. Drawing from multiple examples of differing complexity, I will show how this statistical method can be be used to identify precise transition times between inactive and active periods in diel
and seasonal contexts in song birds. I will also discuss best practices for automating changepoint analysis in order to maintain objectivity.

Moreau, Deb, Agriculture and Agri-Food Canada, Kentville Research and Development Centre; Sudarsana Poojari, Cool Climate Oenology and Viticulture Institute, Brock University; José Ramón Úrbez-Torres, Agriculture and Agri-Food Canada, Summerland Research and Development Centre; Mark Ritchie, Agriculture and Agri-Food Canada, Kentville Research and Development Centre; Susan Carbyn, Agriculture and Agri-Food Canada, Kentville Research and Development Centre; Debra Oxby, Agriculture and Agri-Food Canada, Kentville Research and Development Centre

Incidence of grapevine viruses and insect vectors under cool-climate conditions of Nova Scotia

Commercial wine-grape are impacted by a number of virus diseases that are considered to be economically important because of impacts to grapevine health and fruit quality. Once a grapevine is infected then insect vectors can further spread the virus within the vineyard. Nova Scotia’s (NS) industry is predominantly based on the production of hybrid cultivars with an expansion of V. vinifera plantings in recent years. Little is known about the incidence and impact of virus diseases and vectors on hybrids, particularly under cool-climate growing conditions. Approximately 965 samples (from 24 hybrids and 14 V. vinifera blocks) were tested for Grapevine leafroll-associated virus-1 and -3 (GLRaV-1 and -3), Grapevine fan leaf virus, Grapevine red blotch virus (GRBV) and Grapevine Pinot gris virus (GPGV) by PCR/RT-PCR using virus-specific primers. Presence of all five viruses was confirmed. Findings of GRBV and GPGV are considered first records for NS. In 2017, a survey was conducted to establish presence of insect vectors. Grape mealybug (Pseudococcus maritimus), Fruit Lecanium Scale (Parthenolecanium corni) and Cottony Maple Scale (Pulvinaria innumerabilis), known vectors of GLRaV-1 and -3, were observed. Results highlight the need to develop best management practices to minimize the impact and spread of grapevine viruses in NS vineyards.

Moreau, Gaétan, Université de Moncton; Jean-Philippe Michaud; Hélène N. LeBlanc

Exhuming Mégnins hypothesis as a mechanism for insect succession on remains

Although patterns of insect succession on vertebrate remains have been clearly documented, actual mechanisms of succession have yet to be empirically supported. Two main mechanisms have been proposed in the literature but the applicability in carrion ecology of one of them, facilitation by pioneer species, was recently put into disrepute. Sequential emanation of decomposition-related gases as a causal mechanism of succession was advanced in the late-1800s by the French entomologist Pierre Mégnin and was never empirically tested. Because the sequence of decomposition-related gases in carrion isn’t known, we tested the hypothesis indirectly by delaying the exposure of carcasses to insects from 0 to 5 days. As expected, the decomposition process was slowed down by longer delays in exposure. Increasing delays in exposure caused increasing shifts in the occurrence of pioneer colonizers (i.e., Calliphoridae) but small or insignificant shifts in late successional species. Certain insect taxa were associated to some successional stages of decomposition more than others, despite the confounding effect of exposure delays. Considering the totality of the evidence, we conclude that Mégnin’s hypothesis is a valid mechanism to explain the succession patterns observed on vertebrate remains.

Morin, Hubert, UQAC

Using paleoecology to understand the dynamics of spruce budworm outbreaks and their impact on the landscape.

A major challenge that we face due to climate change is ensuring that we can reliably predict the future dynamics of spruce budworm (SBW) outbreaks, the impact of these perturbations on the landscape and, consequently, how these events will affect forest management. One approach for improving our understanding is to look at the dynamics of past outbreaks, in particular how these dynamics varied under different climatic contexts. Dendrochronology has successfully reconstructed chronologies of SBW outbreaks by relying on living trees and samples collected from old wooden buildings, but chronologies are relatively short. Other techniques must be developed to extend chronologies further back through the Holocene, i.e., for several centuries and even millennia. Our preliminary results, using sunken fossil trees
collected from the shoreline deposits of boreal lakes, indicate that we can reconstruct > 700 years of SBW outbreaks. To extend this record back even further, we developed a paleoecological technique based on a new proxy of past SBW populations: lepidopteran wing scales. These highly resistant structures are well preserved in lake sediments and are produced in phenomenal quantities during SBW outbreaks. Their abundance can be assessed in conjunction with charcoal and pollen records. Here, we present a reconstructed chronology of SBW outbreaks over the entire Holocene, and we compare this SBW record with fire chronologies of different climatic conditions.

Morris, Douglas, Department of Biology, Lakehead University

Habitat selection, conservation, and the future of evolutionary game theory.

Most of the processes that interest us as ecologists and evolutionary biologists share a codependence on the density of individuals and the frequency of strategies. And yet, when we confront the most important challenges facing humans, biodiversity, and the future of our planet, we often fail to include that codependence. Implicitly, we imagine systems resting at their eco-evolutionary equilibrium. The dynamics of populations seldom coincide with that assumption, and are even less likely to do so in a future dominated by further anthropogenic disturbance. The implication is that we need to pay more attention to eco-evolutionary trajectories, and dynamic strategy states, than we do to eco-evolutionary equilibria. Theories and applications of density-dependent habitat selection illustrate one way to achieve that objective. Neighbour invasion landscapes of habitat selectors reveal the full suite of density and frequency-dependent strategies of habitat use, and thus the density-dependent costs of invoking strategies other than that which attains eco-evolutionary stability. Wild and experimental populations confirm the theory, and provide new insights into the importance of understanding games of habitat selection.

Mossman, Vanessa; Jess Vickruck; Louis-Pierre Comeau

Atlantic Soil Carbon & Biodiversity Project

Agriculture and Agri-Food Canada (AAFC) is about to take its deepest look yet into the chemistry, structure, and life of soils across Atlantic Canada. During the summers 2019-2021, researchers will take one-square metre samples of soil from farmland, wetland and forested areas in Newfoundland and Labrador, Prince Edward Island, New Brunswick, and Nova Scotia. The ~500 samples collected will then be subjected to further analysis of microfaunal diversity and abundance (nematodes, springtails, and others), hosted mycorrhiza, fungi, and bacterial communities, while also examining extracellular enzymes, soil organic matter fractions, and SOM 13C turnover rate determination over the next three years. The latest technologies will be used to achieve such understandings, with involvement from AAFC soil researchers and university-based scientists, PhD students, and undergraduates from across the country. The goal is to pull all of the results together to attain a profound understanding of the dynamics of the various organisms between different ecosystems throughout the growing season, with intention to develop biodiversity maps. The assorted ecoregions within the sampled provinces are expected to be highly influential in the biodiversity output, with latitudinal and longitudinal variation in soil composition and changes in pedoclimate amongst ecosystems and ecoregions hypothesized to trigger an observable gradient in the species and abundance of the microorganisms in focus. In testing the correlation of taxa with respect to said pedoclimates, a tighter grasp on the biodiversity across both fine and larger scales will be achieved, increasing the accuracy of the maps to come.

Mourant, Alexandre, Université de Moncton; Gaétan Moreau, Université de Moncton; Nicolas Lecomte, Université de Moncton

Indirect effects of an ecosystem engineer: How the canadian beaver affects wood-boring beetle demographics.

Ecosystem engineers rearrange resource accessibility to consumers through their activities. While this concept is largely accepted in theory, empirical studies that actively quantify the spatiotemporal magnitude of this effect remains scarce in the scientific literature, thus hindering the integration of the concept in food web theory. Here, we studied the case of the Canadian beaver (Castor canadensis), who modifies deadwood accessibility to wood-boring beetles through flooding and
foraging. In the Kouchibouguac national park, 16 beaver ponds were paired to control sites (beaver- unaltered watercourses) around which we quantified primary wood-boring beetle colonization and activity. Following transects perpendicular to the shoreline of ponds and streams, we assessed beetle colonization by counting emergence holes on snags, while beetle activity was monitored by capturing insects in flight-intercept traps. Our results show that beavers positively affected Scolytinae and Cerambycidae colonization and modified host selection relative to snag diameter for Scolytinae. We also found beetle activity to be positively affected by beavers, where larger ponds harbored more beetle abundance than smaller ones and control sites. Altogether, this study demonstrates the positive and indirect association between the Canadian beaver and wood-boring beetles. From a conservation perspective, this could represent that viable beaver populations can help maintain key wood-boring beetle habitats.

Mozzon, Christina, Department of Biology, Laurentian University; Jeffrey Gagnon, Department of Biology, Laurentian University; Albrecht I. Schulte Hostedde, Department of Biology, Laurentian University

The consequences of eating like a human: how eco-physiology of raccoons (*Procyon lotor*) is impacted by anthropogenic food waste across natural to urban gradients

Global expansion of cities has led to multiple challenges for wildlife as they strive to adapt to drastic changes in their landscape. However, the ease of access to anthropogenic food waste has allowed some species to prosper in urban habitats. While there is high resource accessibility in cities, there are also physiological consequences associated with anthropogenic food consumption that are rarely studied. We examined the impact of an urban diet on raccoon (*Procyon lotor*) body condition, fat metabolism, and glucose metabolism. Blood samples, hair, and morphometric measurements were collected from individuals throughout Southern Ontario, across a natural-urban gradient. Stable isotope analysis was used to quantify access to, or consumption of, human food by the raccoon. Preliminary results demonstrate that increased access to anthropogenic food waste leads to higher blood glucose levels and greater body mass. This research provides us with a preliminary model on the impacts of urbanity on wildlife populations. Ultimately, evolutionary changes may be occurring to raccoons as they adapt to a new food resource.

Mullin, Melanie, University of Alberta; Jonathan Cale, University of Alberta; Jennifer Klutsch, University of Alberta; Shiyang Zhao, University of Alberta; Caroline Whitehouse, Alberta agriculture and forestry; Nadir Erbilgin, University of Alberta

Reaching new heights: Chemical signatures of lodgepole pine trees change with elevation, but not with latitude

Assisted tree migration is used in forestry as a climate change adaptation strategy. However, few studies have reported how climate change affects tree vulnerability to invasive herbivores. In western Canada, mountain pine beetle is expanding its range facilitated, in part, by climate-change, and has invaded areas that were historically climatically unsuitable to their survival. As a result, novel lodgepole pine stands in Alberta are being attacked. Thus, it is timely to determine if the vulnerability of lodgepole pine trees varies across the provinces-elevational and latitudinal gradients. Tree vulnerability to beetles is usually assessed via tree defenses. Thus, we investigated the concentration of tree defense chemicals along elevation and latitude gradient. We focused on monoterpenes and diterpenes as they are the primary pine defenses against bark beetles. We also quantified the concentration of soluble sugars and starch as these support the production of defense chemicals. Concentrations of terpenes increased with elevation while soluble sugars decreased. Latitude had no effect. Furthermore, environmental influence on pine chemistry was stronger along the elevation gradient. We suspect tree genetics were influential along latitude gradient. These findings stress the importance of considering plant defenses against range expanding insect herbivores in assisted tree migration.

Murray, Brent, UNBC; Brent Murray; Austin Bartell, UNBC; Helen Davis, Artemis Wildlife Consultants; Ildiko Szabo, UBC Beaty Biodiversity Museum

Spatial Genetic Analysis of Threatened Western Screech Owl subspecies in British Columbia: Megascops *kennicottii kennicottii* (Coastal) and Megascops *kennicottii macfarlanei* (Inland).
Western Screech-Owls (*Megascops kennicottii*) subspecies in Canada are currently listed as threatened (COSEWIC 2012). Two subspecies are recognized, both residing in British Columbia, the coastal *Megascops kennicottii kennicottii* (N=1500-3000) and interior *Megascops kennicottii macfarlanei* (N=350-500). The two subspecies are generally identified by plumage differences, although in British Columbia suspected contact zones exist. In order to understand the genetic relationships among the populations, a number of genetic markers system have been employed on samples collected through a range of collaborators including provincial biologist, private consultants and wildlife rescue centres. Although previous studies of US populations showed distinct haplotype differences between the two subspecies, analysis of the BC populations shows a more complicated evolutionary history. We find haplotype sharing between the two subspecies with the significant genetic structure observed (AMOVA, Fst=0.551, p=0.001) being driving by both haplotype frequency differences and the presence of regional haplotypes. Microsatellite analysis confirms subspecies differences with both DAPC and STRUCTURE analyses showing genetic structure by subspecies and geographic location. DAPC analysis best supports K=2 with 25/27 owls collected on the coast clustering as M. *k. kennicottii* and 37/40 interior birds clustering as M. *k. macfarlanei*. STRUCTURE analysis best supports K=3 or 4 with clustering noted between subspecies and regional populations. Analysis of RADSeq derived SNP variation is ongoing. In sum, the results show genetic structure that supports the current subspecies designations, but also shows differences among regional populations and evidence for introgression.

Murray, Rosalind, University of Toronto, Shannon McCauley, UTM; Locke Rowe, U Toronto

Multiple environmental stressors influence dragonfly performance, immunity and survival

Organisms are frequently bombarded with multiple biotic (e.g. predators, cannibals, parasites) and abiotic (e.g. temperature, salinity, oxygen) stressors throughout their lives. Understanding how animals cope with multiple, often novel, stressors is important for predicting population persistence in the face of rapidly changing environments. Here, I present data on the effect of salinity pollution and cannibal stress on dragonfly performance, survival and immunity.

Neilson, Eric, Canada Forest Service, NR-Can; Elyse Mathieu, Canada Forest Service, NR-Can; Claudia Ayala Castilla, Canada Forest Service, NR-Can; Ellen Whitman, Canada Forest Service, NR-Can

Assessing the risk of wildland fire to caribou habitat

The frequency and intensity of wildland fires are projected to increase in Canada s boreal forest due to climate change, increasing risk to forest values such as species habitat and timber supply. Effective risk management requires comparing disturbance (frequency and intensity) to its impact on a value of interest. Woodland caribou (*Rangifer tarandus caribou*) are a forest-dwelling species whose populations are in decline in Canada due, in part, to habitat disturbance. Fire removes woodland caribou habitat by reducing forage and facilitating population growth of competitors and predators. We assessed the risk posed by wildfire to the habitat of central mountain caribou in a managed forest in west-central Alberta. We compared caribou habitat quality, defined as the distribution of caribou habitat selection, to the impact of wildfires across the study area. We simulated fires across the study area using current fuel and weather conditions and defined their impact as fire frequency and the probability a fire is stand-replacing. Fires in high quality caribou habitat were not more frequent but were more likely to be stand-replacing. We discuss strategies for managing current and future trade-offs between caribou habitat quality and timber supply in a changing climate.

Newar, Sasha; Jeff Bowman (Ontario Ministry of Natural Resources and Forestry)

Ultrasound Use in Rodents

A broad range of mammals, from bats to whales to shrews, use ultrasound (calls exceeding the range of human hearing) for a wide variety of benefits. In general, ultrasound serves two purposes for mammals: social communication (the sharing of information between individuals) and individual communication (specialized and primitive echolocation). Many rodents can produce ultrasound, including ground squirrels, flying squirrels, mice, and guinea pigs. However, there is a substantial gap in our understanding of how these non-echolocating mammals are using ultrasound and the pressures that
select for ultrasound use in some rodents. I present linear models to study the traits associated with ultrasound use across all rodents while controlling for phylogeny and investigating vocal range and limits. It has been speculated that the three drivers of vocal traits are size, predator avoidance, and the acoustic environment. Additionally, I explore trends in time partitioning, methods of locomotion, sociality, and phylogenetic proximity across a broad range of rodents. The models presented are intended to expand our current understanding of bioacoustics evolution and can be applied by predicting the vocal ranges of cryptic and rare species that would benefit from passive acoustic monitoring.

Newediuk, Levi, Biology Dept. Memorial University; Christina M. Prokopenko, Biology Dept. Memorial University; Eric Vander Wal, Biology Dept. Memorial University; Tal Avgar, Ecology/Wildland Resources, Utah State University

Animal movement behaviour reveals fine-scale relationships between resources and conspecific density in complex landscapes

Optimal foraging theory predicts that animals should maximize their exploitation of resources for the lowest energetic cost. Because of this, animals should allocate foraging effort among patches in proportion to resource availability. However, optimal foraging is an oversimplification of the reality animals experience, because they must move through complex landscapes to reach the highest-resource foraging patches where profitability also varies according to resource depletion by conspecifics. Resource selection functions provide coarse empirical evidence for density-dependent resource selection, manifesting as decreased preference for high-resource patches when conspecific density is high. However, RSFs do not incorporate the fine-scaled responses to resource availability and density that are needed to understand how selection patterns emerge from individual movement. Using integrated step selection analysis, we illustrate the fine-scaled movement processes of individual female elk (Cervus canadensis) in Riding Mountain National Park in response to density estimated from annual surveys. We predict that elk will spend less time foraging and move more quickly through high-resource areas as conspecific density increases. Our approach synthesizes the foundational ideas in foraging ecology with contemporary methods to provide new insight into how foraging animals move through complex landscapes.

Nicolas, Angie, University of British Columbia; Zelie Gahon, Agro Paris Tech; John Richardson. University of British Columbia

Effects of groundwater flows on communities of terrestrial invertebrates in riparian areas.

In forested landscapes the presence of discrete groundwater inflow is typically associated with higher soil moisture levels, pH and organic matter content. Previous research in boreal riparian areas has linked these conditions to higher diversity of riparian plants where discrete riparian inflow points (DRIPs) occur. For other moisture-associated taxa, such as some riparian insects, DRIPs may also represent an attractive source of nutrients and act as cool, moist refuge during drought periods. Based on hydrological models of groundwater flows, we evaluated the effects of DRIPs on the distribution and composition of terrestrial macroinvertebrate communities. We used pitfall traps to compare ground-dwelling taxa from riparian areas with and without DRIP occurrence along three headwater streams in coastal British Columbia. During spring and summer months DRIPs were consistently associated with higher groundwater tables, higher soil moisture and elevated groundwater pH but no differences in temperature and organic matter content compared to non-DRIPs. Against our predictions, preliminary results show decreased abundance and species richness of arthropod communities at DRIPs compared to the drier counterparts. These results suggest that the influx of groundwater may not increase resource value of riparian areas for mobile invertebrates likely to be captured in pitfall traps.

Nielson, Kayleigh; Rosemarie De Clerck-Floate; Jason Pither

Soil moisture and nutrient impacts on biological control of spotted knapweed by seed-feeding weevils Larinus spp.

Spotted knapweed (Centaurea stoebe ssp. micranthos) is a widespread invasive plant found throughout western North America that has caused significant negative ecological and economic impacts. Releases of insect biocontrol agents have resulted in inconsistent control, and it is unclear how biocontrol will be influenced by climate change. In the Southern
Interior of British Columbia, which is forecast to experience increased drought and wildfires, the responses of both biocontrol insects and their host plant to shifts in moisture and nutrient regimes are unknown and may impact the future efficacy of spotted knapweed biocontrol. To assess current and predict future efficacy of spotted knapweed biocontrol in the context of changing climate, I will undertake a three-part study using the seed-feeding weevils Larinus minutus and L. obtusus (Coleoptera: Curculionidae) including: (1) a systematic literature review of spotted knapweed biocontrol response to environmental heterogeneity, (2) morphomolecular analysis of Larinus spp. to compare species’ distributions to their purported climatic niches, and (3) greenhouse and common garden experiments comparing Larinus sp. and spotted knapweed development under different moisture and nutrient treatments. The results will inform management strategies and further our understanding of climate change impacts on plant-insect interactions.

Nisole, Audrey, Ressources Naturelles Canada; Don Stewart, Ressources naturelles, Canada; Véronique Martel, Ressources naturelles Canada; George Kyei-Poku, Ressources naturelles Canada; Michel Cusson Ressources naturelles Canada

An innovative molecular diagnostic tool for monitoring and identifying spruce budworm s natural enemies.

We have developed a DNA-based tool for the identification of spruce budworm natural enemies. The existing method for detection and identification of the latter relies on laboratory rearing of field-collected larvae, followed by morphology-based identification of emerging parasitoids and/or microscopic analysis of fungal pathogens in larval carcasses. Although valuable, this approach remains labour-intensive, costly, and can show limited accuracy. In order to overcome these limitations, we set out to use real-time quantitative PCR and TaqManÔô technologies to design a suite of molecular assays. Species-specific single nucleotide polymorphisms (SNPs) can be found in mitochondrial (COI) and nuclear (28S rDNA) genes. We targeted these regions to develop a set of specific primers and probes that can amplify targeted sequences directly from a crude spruce budworm DNA extract. The final product is a molecular identification key that works like a standard insect identification key where answers to questions at each step of the key depend on whether certain molecular signatures are detected. This approach has so far generated very encouraging outcomes. Here, we compare the results generated by our molecular assay, run on spruce budworm 4th-instar larvae collected in New Brunswick, with those obtained using the traditional, morphology-based identification procedure.

Noble, Daniel, University of Guelph

Nutrient retention of tallgrass prairies on marginal lands of conventional farms

Humans have made significant alterations to the Earth’s natural systems. One major change has been the conversion of Earth’s native vegetation to intensive agricultural production systems in order to yield various commodities and services. Removal of permanent vegetation cover has significantly reduced water quality since nutrients not retained by crops and soil are transported to aquatic systems. One potential management technique in Ontario to decrease excess nutrient and water transport is to install permanent cover of diverse native tallgrasses within agricultural systems. The purpose of this study is to address whether prairie filter strips mitigate nutrient transport along the vadose zone and groundwater flow path in both clay and sand textured agricultural systems. I will investigate the hypothesis that prairie tallgrasses will reduce nutrient transport along the vadose zone and groundwater flow path since their greater rooting depths and dense rooting network, especially in the upper parts of the soil column, will facilitate nutrient uptake and water retention. To test this hypothesis, plant tissue quality, soil nutrient, soil pore water, and shallow groundwater samples will be collected (April 2019 November 2019) from corn fields and adjacent prairie fields and analyzed for nitrogen and phosphorus. This research will provide greater understanding of the ecosystem services prairie vegetation provides by stabilizing nutrient and hydrological cycling in these agroecosystems, thereby offsetting the environmental footprint intensive farming systems create on terrestrial and aquatic ecosystems.

Noonan, Meghan, Memorial University of Newfoundland; Shawn J. Leroux, Memorial University of Newfoundland; Luise Hermanutz, Memorial University of Newfoundland

Modelling scenarios for forest restoration after moose (Alces alces) overbrowsing
Within degraded landscapes, forests are failing to naturally regenerate, resulting in a loss of key species and producing persistent open canopied patches within previously closed canopied systems. Hyper-abundant ungulates can act as a disturbance and hinder natural forest regeneration when they severely overbrowse vegetation. In Newfoundland (Canada), hyper-abundant moose have suppressed balsam fir advanced regeneration producing alternate stable states. We integrated data from field observations and experiments, aerial photographs and drone imagery to parameterize mathematical models of boreal understory and canopy regeneration in Newfoundland. We used simulations to evaluate several restoration scenarios for moose impacted forests, including reduced browsing pressure and seedling planting. Model outcomes suggest active restoration via planting birch and balsam fir seedlings is required to restore the understory and canopy vegetation to its natural state in large canopy gaps, and any planting should be done under low moose browsing pressure or within moose exclosures. In small canopy gaps, passive restoration via moose reduction is sufficient to restore balsam fir, however, birch seedling planting is still required to reach historic birch targets. The study found that Markov models parameterized by aggregate data with simulated herbivory can be used to support experimental studies and strengthen evidence for restoration planning.

Noronha, Christine, Agriculture & Agri-Food Canada; Md Bahar; Suqi Liu; Natasha Mosher-Gallant

Buckwheat: A promising IPM tool for wireworm management

Buckwheat (*Fagopyrum esculentum*) is not only a crop with high nutritional and medicinal value but is also used in agricultural practices to suppress weeds and build soil quality. Wireworm damage to

Novotny, Nolan, University of Manitoba: Biological Sciences; James F. Hare, University of Manitoba: Biological Sciences

Slave-making ants and the slave workforce: Optimization of a multiple-species slave workforce relative to host microhabitat optima

Slave-making ants raid host-species colonies, abscond with brood, and raise host workers that perform the colonies domestic tasks. In Canada, *Temnothorax americanus* enslaves *T. ambiguus* and *T. longispinosus*, which can co-occur within slave-maker colonies. Workers of these host species may specialize in certain tasks, akin to sub castes in other ant species, or perform optimally in different contexts. Unenslaved *T. ambiguus* colonies occur in warm microhabitats while *T. longispinosus* colonies occupy cooler microhabitats while *T. longispinosus* colonies occupy cooler microhabitats, presumably achieving optimal performance at different temperatures. We tested whether slave-makers capitalize on host-specific temperature optima by matching their slave workforce to their environmental conditions. We acclimatized *T. americanus* colonies to 25°C or 15°C in controlled environment chambers, and offered simultaneous choices of pupae of the two host species to assess any effect of temperature on pupal retrieval preference. *T. americanus* at 25°C preferred *T. longispinosus*, but at 15°C, preferred *T. ambiguus*. This reversal relative to our prediction may reflect a preference to retrieve the least efficiently defended host species. GLMs testing for effects of slave-maker colony composition on retrieval preference revealed that *T. ambiguus* pupae and male abundance in the retrieving colony enhanced the preference for *T. longispinosus* pupae, possibly reflecting a mechanism promoting slave workforce diversification.

O’Brien, John

Modelling Northwest Atlantic demersal fish and benthic invertebrate assemblages in support of marine protected area network planning

Marine classification schemes based on physical surrogates often inform marine conservation planning in lieu of detailed biological data, but may poorly represent ecologically relevant biological patterns required for effective MPA network design. We used a community distribution modelling approach to identify and delineate unique mesoscale (10s to 1000s km) assemblages of groundfish and benthic invertebrates in four regions of eastern Canada: the northern and southern Gulf of St. Lawrence, Scotian Shelf & Bay of Fundy, and Newfoundland & Labrador. Hierarchical clustering of species
occurrence data from annual multispecies trawl surveys revealed 3 to 6 groupings (predominant assemblage types) in each region. We used random forest modelling to identify environmental covariates with assemblage distributions. Spatial distributions of assemblages in all regions were associated largely with gradients in minimum annual bottom temperature and large geomorphic features (e.g. troughs, banks, continental slope). Indicator analyses identified 3 to 34 emblematic species of each assemblage type. Biological classifications such as ours will inform the design of ecologically coherent MPA networks by ensuring representative communities are captured in the design, identifying candidate species for development of genetic tools to assess connectivity, and highlighting areas that will be sensitive to climate change.

O'Brien, Paul, University of Manitoba; Jeff Bowman, Trent University, Ontario Ministry of Natural Resources and Forestry; Colin Garroway, University of Manitoba

Examining reinforcement of reproductive barriers between North American flying squirrels in a recent area of sympatry

There is now a globally detectable pattern of climate change caused species range movements. Southern flying squirrels (*Glaucomys volans*) have expanded their range northward into central Ontario due to warming climate and have subsequently come into secondary contact with closely related northern flying squirrels (*G. sabrinus*). Within this recent zone of sympatry, the two species have produced fertile hybrids, but the ultimate consequences of hybridization remain unknown. If hybrids are less fit than parental types, then reproductive barriers are expected to evolve and complete speciation. We examined whether the two species have diverged in their habitat use by analyzing 17 years (2002-2018) of capture data across both sympatric and allopatric sites. We analyzed the capture data using nonmetric multidimensional scaling (NMDS). We collected vegetation data around each trap location within sites and fit ordinations with the habitat factors we predicted would influence squirrel occurrence. In general, we observed temporal fluctuations in abundance of both flying squirrel species, and intermediate patterns of fine-scale habitat selection by the two species at sympatric sites. We expect continued observation to demonstrate whether these two species will become ecologically isolated in areas of sympatry through divergence in habitat use or whether climate-change will lead to a loss of biodiversity.

Oh, Sang; A Jares; Kyung Cheol Ma; Duck Soo Choi; Hyo Jeong Kim; Jin Hee Lee

Occurrence pattern and damage of thrips species in persimmon orchards in Jeollanamdo Province

The striped pattern or corking damage of fruit skin caused by thrips have occurred on persimmon, especially an astringent persimmon. An investigation on the occurrence pattern and damage of thrips species in persimmon orchards was conducted in 9 fields in Jeollanamdo Province. According to the survey every 10 to 15 days using sticky traps, seven thrips species were captured, including *Frankliniella intonsa* (Trybom), *F. occidentalis* (Pergande), *Scirtothrips dorsalis* (Hood), *Ponticulothrips diospyrosi* Haga et Okajima, *Thrips tabaci* (Lindeman), *T. palmi* (Karny), *T. hawaiiensis* (Morgan), *F. intonsa, F. occidentalis* dominated in the thrips species, and increased steadily from late April and peaked in late June, 2018. *S. dorsalis* occurred four generations from April to October and the highest density were in early August. The percent of damaged fruits were 32.1% in organic orchards and no damage were observed in sweet persimmon.

Oke, Michael; Michael Adedotun Oke Foundation

Overview of Marketing of tomatoes in Baskets in Gwagwalada area Council of the Federal Capital Territory Abuja Nigeria: The Implication and profitability

Tomatoes business is a lucrative business in Gwagwalada area council of the Federal Capital Territory, The markets women are involved in the selling of tomatoes for the teeming population and this serves as business opportunity, food security and employment generations. This paper look at the various methods involve such as the transportation of tomatoes, selection of the bad ones from the good one. The observation made is that the ripe tomatoes that are undergoing at the bottom of the basket do spoil, but separation are made from the ripe and spoils. There are market for the good ripe ones, but the damages ones thus not have value, but sales at a lower rate to some of the buyers. Therefore more researches are needed to look at the best methods of conveying the tomatoes, suggestions were made for the best Technology for...
preservation and transportation. Pictures were taken to ascertain the findings and questionnaires were distributed and analyzed, group discussion were also made to receive various input for the stakeholders of tomatoes business in Gwagwalada. Keywords: Marketing, tomatoes, market women, Gwagwalada.

Oke, Krista, University of Alaska Fairbanks; Cunningham, C.J., Fisheries, Aquatic Science, & Technology (FAST) Lab, Alaska Pacific University; Baskett, M.L., Department of Environmental Science and Policy, University of California Davis; Carlson, S.M., Environmental Science, Policy, and Management, University of California Berkeley; Clark, J., National Center for Ecological Analysis and Synthesis (NCEAS); Hendry, A.P., Department of Biology and Redpath Museum, McGill University; Karatayev, V., Department of Environmental Science and Policy, University of California Davis; Kendall, N., Washington Department of Fish & Wildlife; Kibele, J., National Center for Ecological Analysis and Synthesis (NCEAS); Kindsvater, H.K., Department of Ecology, Evolution, and Natural Resources of Rutgers University and Department of Fish and Wildlife Conservation, Virginia Polytechnic Institute and State University; Kobayashi, K.M., Department of Ecology and Evolutionary Biology, University of California Santa Cruz; Munch, S., Southwest Fisheries Science Center, National Oceanic and Atmospheric Administration; Reynolds, J.D., Earth to Ocean Research Group, Department of Biological Sciences, Simon Fraser University; Vick, G., GKV & Sons; Lewis, B., Division of Commercial Fisheries, Alaska Department of Fish and Game; Westley, P.A.H., College of Fisheries and Ocean Sciences, University of Alaska; and E.P. Palkovacs, Department of Ecology and Evolutionary Biology, University of California Santa Cruz.

Patterns and consequences of widespread declines in Alaska salmon body size

Truncated age structure and shifts towards smaller individuals at maturity are widely observed in a range of exploited taxa, yet the ecological and societal consequences of changing body size are largely unknown. In Alaska, declines in salmon body size among certain species and regions have long been reported, but despite the immense value of salmon to Alaska, a broad scale synthesis of body size trends is lacking. We examine 60 years of phenotypic measurements of 10.4 million individual salmon from four species in Alaska to quantify the extent of the size declines, their local and regional scale drivers, and the associated socio-cultural, economic, and ecological consequences. Our multi-species approach revealed that body size has declined across four salmon species throughout Alaska, a trend largely attributable to individuals returning to spawn at a younger age on average than in the past. Pacific salmon (Oncorhynchus spp.) and people along the North Pacific Rim have been entwined for millennia, and observed shifts in body size over the past 30 years have already come at a cost to Alaskas salmon-dependent people and ecosystems. Results suggest that widespread size declines have negative impacts on egg production, marine-derived nutrient subsidies, human food security in rural communities, and commercial fisheries revenue. The factors contributing to decreasing size and age of salmon are likely impacting other harvested fish species, with potentially widespread effects for ecosystems and people worldwide.

Olivier, Chrystel Y.; Tyler Wist; Ruwandi Andrahennadi; Adam Jones; Alyssa Parker

Feeding, movement and oviposition behavior of flea beetles and diamond back moths on hairy canola.

Flea beetles and diamond back moths (DBM) are major insect pests that threaten canola production in the Canadian prairies each year. Flea beetles feed on canola seedlings and later on pods, and DBM larvae feed on canola leaves and have several generations per growing season. For both insect pests, insecticides are the only control options. Recently, natural lines of Brassica napus exhibiting high numbers of trichomes on their leaves and stems were identified. Feeding, oviposition and movement behavior of flea beetle and DBM were observed on these hairy canola plants and on plants of a commercial, glabrous canola cultivar. Relationship between the hairiness of the plant and the insect pest behaviors and the effect of plant growth stages, temperatures and soil moisture conditions on insect pest behavior will be discussed.

Oomen, Rebekah, University of Oslo; Anna Kuparinen, University of Jyväskylä; Jeffrey A. Hutchings, Dalhousie University

Consequences of linked genomic architectures for population responses to environmental change.
Recent advances in both next-generation sequencing technologies and eco-evolutionary modelling are unlocking the potential for integrating genomic information into predictions of population responses to environmental change. One key aspect in this regard is genomic architecture: the structural characteristics and associated inheritance models of genes underlying adaptive traits. For example, whether a trait is controlled primarily by a single locus or multiple loci will greatly influence its evolution in response to environmental stressors. As single-locus control of complex traits is thought to be rare, eco-evolutionary models typically assume many unlinked loci are involved in adaptation. Yet, blocks of physically linked genes that undergo little or no recombination, such as those associated with some chromosomal rearrangements, have emerged as taxonomically widespread phenomena that can facilitate rapid adaptation, especially in the face of gene flow. Inheritance of linked genomic architectures resembles that of single loci, thus enabling single-locus-like modeling of polygenic adaptation. We develop single-locus evolutionary theory for adaptive traits largely controlled by multiple linked loci for the purpose of predicting responses of natural populations to directional environmental stressors, such as climate change and harvesting. We review known systems for which such an approach might be useful and discuss barriers to implementation.

Oram, Ryan, Royal Saskatchewan Museum; Cory S. Sheffield

Unveiling the Masquerade: The Role of DNA Barcoding in North American Hylaeus Taxonomy

Species conservation is dependent on accurate identification of taxa involved. Thus, taxonomy, the science of naming and describing species, is important for taxa facing declines and possible extinction, including bees. Hylaeus are a group of small black, relatively hairless bees that usually have yellow markings (maculations) present on their face, thorax and legs, with ~50 species recorded from North America. However, the identification of Hylaeus is often quite difficult due to variation in the body maculations, resulting in some species being grouped (e.g. Hylaeus affinis/modestus) in many published studies instead of being treated separately; this is especially true for females. Using molecular data (a 658-bp COI gene sequence—the DNA barcode) we now have a better understanding of the relationships among and between species, a clearer picture of the species diversity in North America, and a method to accurately identify aberrant species. DNA barcoding has also shed light on taxonomically difficult taxa, including H. mesillae and H. modestus, which historically have been treated as morphologically variable and widely distributed; DNA barcoding is suggesting that these two species are actually assemblages of six and four species, respectively, each with smaller, overlapping distributions.

Orobko, Melissa, Simon Fraser University; Isabelle M Côté (Simon Fraser University); Thomas W Therriault

Multiple stressors, nonlinearities, and cumulative effects: Why and how should we better integrate these three solitudes?

Escalating cumulative human impacts are considered one of the most serious challenges for marine ecosystems. Assessing and managing cumulative effects from multiple human activities is difficult for a number of reasons, including the facts that multiple stressors can interact in different ways (i.e., antagonistically, additively, or synergistically), and stressors can have nonlinear effects on ecosystems. Although stressor interaction types, nonlinear ecosystem effects, and cumulative effects have been well studied in isolation, few studies integrate across these issues. Here, we synthesize the primary literature dealing with various combinations of these issues to identify trends in how they have been integrated. We also identify generalities in how multiple stressors interact to create nonlinear effects on ecosystems, and how stressor interaction types and nonlinearities are incorporated into cumulative effects assessment. Finally, we highlight gaps in these trends and generalities, and recommend improvements for future integrated research that improves the assessment and management of cumulative effects, particularly for marine ecosystems.

O'Sullivan, Antoin, Canadian Rivers Institute - UNB; R. Allen Curry, Canadian Rivers Institute, Department of Biology and Faculty of Forestry and Environmental Management, University of New Brunswick; Tommi Linnansaari Canadian Rivers Institute, Department of Biology and Faculty of Forestry and Environmental Management, University of New Brunswick

Ice Cover Exists (ICE): A quick method to delineate groundwater inputs in running waters for cold and temperate regions
Groundwater can be important in regulating stream thermal regimes in cold, temperate regions and as such, it can be a significant factor for aquatic biota habits and habitats. Groundwater typically remains at a constant temperature through time, i.e., it is warmer than surface water in the winter and cooler in the summer. Further, small tributaries are often dominated by groundwater during low flows of winter and summer. We exploit these thermal patterns to identify and delineate tributary/groundwater inputs along a frozen river (ice-on) using publically available satellite data, and we tested the findings against airborne, thermal infrared (TIR) data. We utilise a supervised maximum likelihood classification (sMLC) to identify possible groundwater inputs while the river is in a frozen state (kappa coefficient 96.77 when compared to visually delineated possible groundwater inputs). We then compare sMLC identified possible groundwater inputs to TIR classified groundwater inputs which confirmed there was no statistical difference (C=0.78), i.e., confirming groundwater inputs can be delineated in north temperate river systems using available satellite imagery of the system's frozen state. Our results also established the spatial extent and influence of possible groundwater inputs in two seasons. The thermal plumes were longer and narrower in winter; this is likely related to seasonal differences in dispersion regimes. We hypothesize that differences between summer and winter is related to either (1) tributaries which are modulated by shading in the summer, or (2) aquifer disconnection from the river in the winter owing to frozen ground conditions and lack of aquifer recharge. This method of establishing tributary/groundwater inputs and contributions to surface water thermal regimes is relatively simple, and can be useful for science and management as long as ice cover exists (ICE), that is, the system can achieve a frozen state.

Ouellet-Fagg, Christine, University of Guelph; Kevin J. Parsons, University of Glasgow; Cameron M. Nugent, University of Guelph; Kris Christensen, University of Victoria; Anne E. Easton, University of Guelph; Roy G. Danzmann, University of Guelph; Moira M. Ferguson, University of Guelph

A comparative analysis of genetic linkage maps: characterizing the evolution of genomic architecture through chromosomal rearrangements in Arctic charr (Salvelinus alpinus)

The relative roles of genetic divergence and chromosomal rearrangements in adaptive diversification remain unclear, particularly in the early stages of reproductive isolation. Genomic incompatibilities evolving as a result of chromosomal rearrangements could promote reproductive isolation. Salmonid genomes are characterized by diverse chromosomal architectures due to fusions and fissions after whole-genome duplication, and may have been influenced by recent geographical isolation in multiple glacial refugia from which northern freshwater habitats were recolonized within the last 10,000-20,000 years. Chromosomal changes could help to reinforce the genetic isolation generated primarily by ecological mechanisms following post-glacial recolonization, such as resource polymorphism. We compared the genetic linkage maps of Arctic charr (Salvelinus alpinus) derived from two glacial lineages (Atlantic and Arctic) to describe intraspecific diversity in genome architecture. We discovered that the scale of variation in chromosomal rearrangements was no greater between the glacial lineages than within them. Inter- and intra-population linkage map polymorphisms were detected not only on autosomal chromosomes, but also on the sex chromosome. Rearrangements involving metacentric chromosomes were the most extensive, suggesting that chromosomal polymorphism may not be a crucial factor in population divergence. However, the various sex chromosome rearrangements detected could have implications for the development of reproductive isolation.

Owens, Emily, Canadian Forest Service; E. Owens; R. Johns, D.; Pureswaran, C.; MacQuarrie, J.; Fidgen, J.; Allison, J-N.; Candeau, P.; James, V.; Martel, S.; Bourassa, J.; Bowden, H.; Spicer, I.; DeMerchant, E. Shanks; A. Kanoti

Using Community Science as a Tool to Engage the Public and Collect Important Data Over Large Geographical Areas: A Case Study Using the Budworm Tracker Program

The Budworm Tracker Program is a community scientist led by a group of experts committed to engaging and involving the public in the spruce budworm research. Our goal is to keep all interested parties informed of ongoing research and results, and provide the public with the opportunity to speak to and hear from our scientists and experts and about early intervention strategy. One of the ways we communicate and engage with the public is through is through this community science program: The Budworm Tracker Program. In this program, hundreds of citizens help researchers monitor spruce
budworm populations and detect moving moths, which may be contributing to the spread and rise of the current outbreak. This talk will highlight its communications strategies, how we inform the public, and our efforts to share our research."

C.M. Pearce, S. Williams, L. Keddy, and J. Blackburn, Pacific Biological Station, Fisheries and Oceans Canada

Use of plastic tubes for predator protection of geoduck clams: do tube diameter, length, and cover mesh size affect growth and survivorship?

Intertidal culture of the Pacific geoduck clam (*Panopea generosa*) involves planting juveniles in sediment in tubes covered with mesh for predator protection. We examined the interactive effects of tube diameter (10.2 and 15.2 cm), length (25.4 and 30.5 cm), and mesh size (6 and 12 mm) on percent shell-length increase, percent wet-weight increase, and percent survivorship of cultured juvenile geoducks (mean shell length ± SD = 29.6 ± 4.8 mm) over 12 months. Percent increase in shell length and weight were both significantly affected by the main effects of tube diameter and mesh size, as well as the interaction between the two factors. Shell length was also significantly affected by the main effect of tube length. Geoducks were significantly shorter and lighter in the 10-cm/6-mm (diameter/mesh) treatment than in the 10-cm/12-mm, 15-cm/6-mm, and 15-cm/12-mm treatments. The 25-cm long tubes were associated with significantly longer (but not heavier) individuals than the 30-cm ones. Average survivorship (±SE) ranged from 38.3±7.1% to 55.0±6.5% (mean ± SD: 47.7 ± 2.5%) in the eight treatments and was not significantly affected by any main effects or interaction terms. The results have implications for commercial geoduck culture where clams are protected with solid plastic tubes.

Paisker, Mitchell, University of Maine; Hamish Greig, University of Maine; Amanda Klemmer, University of Maine; Robert Northington, Husson University; Kathleen Brown, University of Maine; Ethan Cantin, University of Maine

Legacy effects of riparian timber harvest on Maine streams

While numerous studies have documented the acute effects of riparian forest disturbance on aquatic communities, little work has examined the legacy effects of such disturbances. Here we revisit fifteen streams in the western mountains of Maine that were sampled prior to a series of replicated riparian timber harvest treatments that were applied in the 2000-2001 winter. We examine the long-term (17-year) effects of riparian forest harvest on stream physical characteristics, macroinvertebrate communities, fish assemblages, and reciprocal subsidies between the forest and stream. Preliminary results show differences in macroinvertebrate communities linked to timber harvest regime, with clear-cut and streamside harvesting leading to macroinvertebrate communities different in both functional feeding guild and diversity than unharvested control streams. This work demonstrates that stream systems integrate land use changes over large temporal and spatial scales. Furthermore, legacy effects of anthropogenic disturbance are unlikely to be reversed immediately after disturbance cessation.

Palmier, Kirsten, University of Regina, Royal Saskatchewan Museum; Andrew D. S.; Cameron Cory; S. Sheffield Biology, University of Regina

Another piece to the pathogen puzzle: male *Bombus* spp. at risk with yeast infections

Native bumble bees (*Bombus* spp.) are proficient pollinators in most agricultural and natural landscapes. However, in recent years bumble bee populations have experienced dramatic declines globally, including in Canada. The closely related *Bombus terricola* (Yellow-banded Bumble Bee) and *B. occidentalis* (Western Bumble Bee) have both experienced dramatic population declines and reductions in their respective ranges and are considered species at risk in Canada. The exact causes of these declines are still unknown, but they are likely due to a combination of stressors that includes pathogens. Our current knowledge of bee pathogens is limited as evidenced by the fact that newly recognized pathogens are still being identified. Field caught bumble bees were euthanized, dissected and screened for various pathogens, parasites and additional abnormalities within the gut. During the initial dissections, it was noted that male specimens of *B. terricola* and *B. occidentalis* exhibited enlarged proventriculi. Microscopy and polymerase chain reactions have confirmed
that these structures contained an unknown fungal proliferation. Here, we present the first observations of this mystery yeast in both bumble bee species. Whether the presence and/or imbalance of this yeast is a contributing factor to their declines is still unknown, but it is one more piece of the pathogen puzzle that needs consideration.

Paquette, Chelsey, Université de Sherbrooke; Jade Savage, Bishop's University; Patrick Bergeron, Bishop's University; Dany Garant, Université de Sherbrooke

Investigating individual and environmental determinants of parasitism in a wild eastern chipmunk (Tamias striatus) population

Understanding the interactions between parasites, hosts, and their shared environment is central to ecology and evolution. Variation in parasite prevalence may be the result of varying environmental and population characteristics; however, variation in levels of parasitism may also depend on individual factors that influence both exposure and susceptibility to parasites. Using 12 years of data from a population of wild eastern chipmunks, we investigated the effects of host space use, sex, age, body mass and food abundance on the number of bot fly parasites found on chipmunks. We found that adult males had more parasites than females and that the effect of activity and exploration on parasitism varied according to sex. More active/explorative males had more parasites. This suggests that the benefits associated with high levels of activity and exploration (food/mate acquisition) may come at the cost of acquiring parasites. For juveniles, levels of parasitism were greater when juveniles emerged in the spring as opposed to the fall, possibly because spring emergence is synchronized with the peak of bot fly eggs in the environment, low food availability and a longer activity period. Our results suggest an important effect of both individual and environmental characteristics on levels of parasitism.

Parachnowitsch, Amy, UNB; Jonas Kuppler, Ulm University

Do plants listen to their flowering neighbours?

Plant-plant communication through leaf volatiles has been shown for diverse plant species, but floral volatiles could also provide important information about the surrounding plant community. Given that plants respond to leaf volatiles, and that floral volatiles are generally emitted in greater amounts and higher diversity, it seems likely that plants could also respond to floral volatiles to change their reproductive behaviour. Plants could use information about their mating environment to synchronize flowering with conspecifics and/or alter display signals and rewards to improve pollination and ultimately reproductive success and fitness when in competition with coflowering heterospecifics. Here we test the idea that plants change their flowering behaviour in response to flowering conspecifics and discuss the implications for the ecology and evolution of flowering plants.

Paradis, Anouk

Landscape and habitat drivers of trait and species diversity in butterfly communities

Species respond to environmental changes and contribute to ecosystem services according to their intrinsic characteristics, i.e. functional traits. Anthropogenic land use at both the local (habitat patch) and landscape scales can lead to biotic homogenization and species loss. Floral resource composition and structural configuration of vegetation (e.g. vegetation height) provide resources to species and shape biological communities. Butterfly species (Lepidoptera: Papilionoidea) are common indicators of environmental change, because of the range of traits and sensitivities they display. Understanding the relationship between various environmental drivers and trait composition can inform us whether landscape filters species on the basis of their traits or if population extinctions are random. At the local scale, we found that vegetation structure configuration was better than floral composition at explaining variation in functional diversity. Using a multiple regression model, we found that most (70%) of the variance in functional diversity can be explained by the diversity of vegetation structure, the proportion of vegetation between 0.5 to 2 meters, between 2 to 5 meters, and over 5 meters, along with butterfly richness. At the landscape scale, we tested for effects of land cover on community weighted mean trait
values. We found a high positive correlation between vegetation structure diversity and wingspan, suggesting that landscape simplification might filter out small-winged butterfly species. Understanding the drivers of trait and species composition in pollinators like butterflies is important to designing effective conservation and policy actions.

Parent, Jean-Philippe, Agriculture et Agroalimentaire Canada; Paul. K. Abram, Agriculture and Agri-Food Canada

Combination of physical and biological control: Aphid parasitoids on shaky ground?

Alternatives to chemical control using physical control methods to kill or disrupt insect pests have recently seen a resurgence. Physical pest control methods based on vibration have been developed as a general disruptor of physiology and behaviour. Recently, it has been shown that some aphid species are negatively impacted by these methods. However, little information is available on the impact of vibrations on aphid natural enemies. In this study, we investigated the potential for combining physical and biological control by measuring the impact of non-specific vibrations (substrate-borne white noise) on parasitism model using the aphid parasitoid Aphidius ervi and its host the pea aphid Acyrthosiphon pisum. We predicted that exposure of aphids to vibrations prior to parasitoid exposure, could compromise their ability to subsequently defend themselves against parasitoids (resulting in increased parasitism rate) by inducing costly generalized stress responses. If vibrations are continuously applied while parasitoids are present, it might disrupt their behaviour (decreasing parasitism levels). Twenty aphids colonizing whole plants were subjected to different combinations of vibration incidence and timing (no vibration, vibration for the first 24h, no vibration) and parasitoid exposure (parasitoids introduced after 24h, no parasitoids). We then measured: (i) aphid survival; (ii) aphid reproduction (number of nymphs produced), (iii) aphid location on the plant and (iv) parasitism rate. The impact of substrate-borne vibrations as a disruptive physical control method on higher trophic levels and its compatibility with biological control will be discussed using our experiments as a case study, as well as the potential applicability in agricultural settings and the challenges to overcome.

Parizadeh, Mona; Benjamin Mimee; Steven W. Kembel

Monitoring the effects of neonicotinoid pesticides on the phyllosphere and soil bacterial communities in a three-year soybean and corn rotation

The phyllosphere and soil are habitats to beneficial bacterial communities which play a vital role in plant growth and health and ecosystem regulation. In sustainable agriculture, it is crucial to comprehend the composition of these communities, their changes in response to disturbances, and their resilience to agricultural practices. Many years of widespread pesticide application against pests may have had non-target impacts on these beneficial microorganisms. Neonicotinoids are a family of systemic insecticides being vastly used to control early-season and foliar-feeding pests in recent decades. There are a few studies on their long-term and non-target effects on agroecosystem microbiota. In this study, we intended (i) to characterize soybean and corn soil and leaf bacterial community composition and (ii) to identify bacterial variation and temporal changes in a three-year soybean/corn rotation and in response to neonicotinoid seed treatment. Using 16S rRNA gene amplicon sequencing, we found out that host species, growth stages and time are stronger drivers of variation in bacterial composition than neonicotinoid application. However, neonicotinoids did have an impact on microbial community composition, especially in the taxonomic composition of soil communities. We discuss the implications of our study in predicting agroecosystem responses to pesticide application and crop rotations.
Paterson, James, Trent University; James Baxter-Gilbert, Centre for Invasion Biology, Stellenbosch University; Frederic Beaudry, Environmental Studies and Geology Division, Alfred University; Patricia Chow-Fraser, Department of Biology, McMaster University; Christopher B. Edge, Canadian Forest Service, Natural Resources Canada; Andrew M. Lentini, Toronto Zoo; Jacqueline D. Litzgus, Department of Biology, Laurentian University, Sudbury, ON, Canada Chantel E. Markle, School of Geography and Earth Sciences, McMaster University; Kassie McKeown, Toronto Zoo; Jennifer A. Moore, Biology Department, Grand Valley State University; Jeanine M. Refsnider, Department of Environmental Sciences, University of Toledo; Julia L. Riley, Department of Botany and Zoology, Stellenbosch University; Jeremy D. Rouse, Parry Sound District Office, Ontario Ministry of Natural Resources; David C. Seburn, Seburn Ecological Services; J. Ryan Zimmerling, Canadian Wildlife Service, Environment and Climate Change Canada; Christina M. Davy, Environmental and Life Sciences Program, Trent University

Road avoidance and its energetic consequences for reptiles

Roads are one of the most widespread human-caused modifications to habitats that can increase wildlife mortality rates and alter behaviour. For animals living near roads, how do roads affect movement patterns and fitness? Roads can act as barriers with variable permeability to movement and can increase distances wildlife travel to access habitats. Movement is energetically costly, and avoidance of roads could impact an animal's energy budget. We tested whether reptiles avoid roads or road crossings, and explored whether the energetic consequences of road avoidance may decrease individual fitness. Using telemetry data from Blanding's turtles (Emydoidea blandingii; 286 turtles, 15 sites) and eastern massasaugas (Sistrurus catenatus; 49 snakes, 3 sites), we compared frequency of observed road crossings and use of road-adjacent habitat by reptiles to simulations. Turtles and snakes did not avoid habitats near roads, but both species avoided road crossings. Compared to simulations, turtles made fewer crossings of paved roads with low speed limits, and snakes made fewer crossings of all road types. Turtles travelled longer daily distances when their home range contained roads, but the predicted energetic cost was negligible: substantially less than the cost of producing one egg.

Pedersen, Eric, Concordia University - Department of Biology

How can we go from movement models to metapopulations?

Both movement ecology, which focuses on modelling patterns of organismal movement across landscapes, and metapopulation and metacommunity ecology, which focuses on how patterns of dispersal across landscapes shape communities, have been the focus of growing ecological research in the last decade. However, there has, to date, been very little research into how to derive the structure of a metapopulation model (the patches and connections between them) from modern movement models. In this talk, I will lay out the ambiguities in metapopulation ecology about what a patch is that make this task difficult, and will discuss a promising approach to solve this: defining what a patch is based on residency time, and using modern graph-based statistical clustering methods applied to a given movement model to divide a landscape into patches.

Peery, Rhiannon, University of Alberta; Catherine I. Cullingham; Joshua M. Miller; Bianca M. Sacchi; Janice E.K. Cooke; David W. Coltman

The effect of host genotype on susceptibility to pests and pathogens: examples from the lodgepole pine/mountain pine beetle system

Mountain pine beetle (MPB) outbreaks are an episodic process in western North America. In this current outbreak, which has impacted millions of hectares of lodgepole pine, MPB has undergone an unprecedented range expansion from its historic range into novel habitats where lodgepole pine hosts are putatively naïve. The aim of this study is to determine the influence of tree genotype on MPB attack success. To address this aim, we have generated high-density SNP genotypes for three lodgepole pine sampling strategies: 1) intensive sampling from four stands within MPBs historic range during and after peak MPB outbreak, 2) paired attacked and un-attacked trees from 16 stands sampled within MPBs historic range and leading edge of the outbreak, and 3) 39 stands throughout the lodgepole pines Canadian range. Ongoing analyses of these data sets are identifying (1) loci linked to survival during an epidemic within MPBs historic range; (2)
loci associated with attack status in the historic and expanded MPB ranges; and (3) relationships among loci in historic and naïve stands regardless of attack status. Candidate loci identified through outlier analyses and genome wide associations will be further studied to determine how these genes potentially influence host susceptibility to MPB attack.

Peller, Tianna, McGill University; Samantha Andrews, Memorial University; Shawn Leroux, Memorial University; Frédéric Guichard, McGill University

Extending marine metapopulations to marine meta-ecosystems: examining the nature, scale and significance of marine resource flows

Extending the marine metapopulation framework to incorporate the non-living compartments of ecosystems, and their potential to flow across space, is an important next step for spatial marine ecology. To facilitate this extension to marine meta-ecosystems, we synthesize and analyze empirical evidence of marine resource flows to characterize the benthic ecosystems they have been observed to couple and to assess their directionality, scale, and significance for ecosystem functioning. We find that resource flows commonly couple different types of benthic ecosystems and can occur bidirectionally. Our synthesis yields a general movement kernel, which suggests that the probability of resource flows coupling benthic ecosystems decreases with increasing distance between ecosystems. In accordance, we find a significant negative relationship between the magnitude of subsidization of recipient organisms and the distance from the resource origin. Compared with evidence of larval dispersal distances, our findings indicate that resource flows may frequently couple benthic ecosystems across smaller spatial scales. Overall, our findings suggest that considering differences in functioning across coupled ecosystems, and the respective scales of different types of spatial flows, will be important components of a marine meta-ecosystem framework. Additionally, they highlight the importance of accounting for resource flows when establishing marine conservation strategies.

Penney, Matthew Steven, Acadia University; Donald Stewart, Acadia University; Timothy Rawlings, Cape Breton University

The population genetic structure of a commercial sea cucumber (Cucumaria frondosa) using RADseq

Invertebrate fisheries have been emerging as important economic components of nations in tropical and temperate regions. Since the early 1980s, fisheries for the Atlantic Sea Cucumber Cucumaria frondosa have been developing along the Atlantic coastline of North America. Fishing now occurs in Maine, New Brunswick, Quebec, St. Pierre and Miquelon (Newfoundland), and the Scotian Shelf. Long-term management of sea cucumber fisheries in Canada is precautionary with the intent of avoiding the emergence-and-collapse trends seen in other fisheries, particularly in Asia and Oceania. While studies have shown the benefit of incorporating genetic analysis and rotational harvesting into management plans in terms of yield, many plans to not examine genetic structure and are thus underinformed. The Scotian Shelf currently has 14 COI sequences from area 4Vs, which is insufficient for examining population structure of the Shelf. Restriction Site-Associated DNA Sequencing (RADseq) is a Next Generation Sequencing technology capable of generating large datasets of Single Nucleotide Polymorphisms (SNPs) from a subset of the total genome for high-resolution genetic analysis. This makes it useful for examining genetic patterns in marine invertebrates with dispersive larval stages. A variant of this technique, Double-Digestion RADseq (ddRAD), is applicable to non-model organisms, which makes it broadly applicable to emerging fisheries. For this study, ddRAD will be used to generate a large SNP dataset for C. frondosa specimens from the Scotian Shelf in fishing areas 4Vs, 4W, and 4X. Specimens will also be sampled from area 3Ps in St. Pierre and Miquelon (Newfoundland) and from Iceland. These data will then be used to analyze population genetic structure specific to the Scotian Shelf and compared to other populations. This will include calculations of Wrights F-statistics, Analysis of Molecular Variance (AMOVA), Isolation by Distance (IBD) and Resistance (IBR), and heterozygosity. Ancestry and migration will also be examined using ADMIXTURE and the assign package in R. This study will provide information about genetic structuring, such as source-sink dynamics, to better inform future management plans for this emerging fishery.
Patterns of gene flow, morphological variation, and environmental associations in southern Newfoundland Atlantic Salmon (*Salmo salar*)

The interaction between selection and gene flow is central to the formation of discrete populations, as selection against migrants can serve as a barrier to gene flow, or continuous migration may prevent or limit local adaptation. Atlantic salmon (*Salmo salar*) are generally characterized by discrete locally adapted populations at the scale of individual rivers, but the relative importance of natural selection and gene flow from nearby rivers remain poorly understood. The objective of this study is to explore this association between gene flow, phenotype (i.e., morphological variation), and the environment in salmon populations distributed across southern Newfoundland. Specifically, we examine morphological variation using geometric morphometrics, and genetic differentiation using 77 sequenced microsatellites genotyped in 2043 juvenile salmon caught from across southern Newfoundland (2016-2017). Migration rate estimates and genetic distance were used as predicted variables in a Bayesian multiple regression with river watershed characteristics, juvenile salmon morphology, and geographic distance between rivers as predictors. The results suggest that morphological variation had the greatest effect on genetic distance and gene flow, although temperature, precipitation and geographic distance were also significant. This work highlights the potential importance of selection and local adaptation in characterizing patterns of gene flow among wild Atlantic salmon populations.

Biotic interactions affect fitness but don't drive local adaptation: a meta-analysis

Local adaptation is fundamental to the diversification and distribution of species yet the importance of its various ecological drivers, particularly biotic interactions, remains unclear. Biotic interactions can drive local adaptation if they impose consistent and divergent selection on the interacting species. If local adaptation to biotic interactions is common, we expect experiments to detect greater local adaptation when the biotic environment is left intact. We tested this hypothesis with a meta-analysis of > 100 common-garden experiments including > 100 taxa. We found local adaptation was neither more common nor stronger when biotic interactions were left intact. The lack of widespread local adaptation to biotic interactions was not because interactions did not affect fitness nor was it due to general constraints on local adaptation. Our results suggest that biotic interactions often fail to drive local adaptation even though they affect fitness, perhaps because the biotic environment is less predictable at the spatial and temporal scales required for local adaptation.

Effect of clear-cutting created ecotones on macromoth assemblage structure in western Newfoundland

Macromoths provide numerous important ecosystem services including pollination, herbivory and as food for many migratory birds and mammals. Ecotones form the transition between contrasting habitats, and are important for biodiversity, often supporting distinct and higher species diversity than the adjacent habitats. To evaluate edge effects across clearcut-forest transitions in western Newfoundland, nocturnal macromoths were light-trapped within remaining forests, along forest edges, and within clearcuts, using traps hung at ~2.5 meters high. We established four replicate sites in the region, where the clearcuts were all created within the past five years. At each site, we placed a light trap within the ecotone and 30 meters into the adjacent habitats (3 traps per site), for a total of 12 traps. We collected moths during June, July, and August 2018, for 3 nights each month during the new moon, for a total of 108 trap-nights. We identified all macromoths to the species level to test for edge effects on community structure (i.e., diversity, abundance, composition). The collection consists of >2500 specimens representing >100 species. We hypothesized that abundance would be highest in clear-cuts due to greatest visibility, and diversity would be highest at the edges due to the edge effects. To verify these relationships, several data analyses were completed using R, including analysis of covariance, non-metric
multidimensional scaling, permutational multivariate analysis of variance and species diversity estimation. This work is important in the context of sustainable forest management, and for understanding biodiversity in the region.

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Pither, Jason, UBC, Okanagan Campus; Brian J. Pickles; University of Reading

Predicting broad-scale diversity patterns among ectomycorrhizal fungi based on new and old hypotheses

Understanding the processes that influence diversity patterns across spatial and temporal scales is central to ecology and biogeography, but is challenging when studying belowground organisms. Hence, diversity patterns among ectomycorrhizal fungi (EMF) despite their ecological and economic importance remain poorly quantified and understood. Researchers have begun to explore EMF diversity at larger spatial scales, but a coherent assessment of the potential factors moderating diversity across scales is lacking. Here we review the literature and place our findings in the context of Vellends framework for community ecology, which helps clarify: i) putative drivers of diversity patterns, ii) inconsistencies in the literature, iii) remaining knowledge gaps, and (iv) key geographic regions lacking data. We also propose new hypotheses emphasizing the influences of historical-biogeographical processes on EMF diversity patterns, and combine these with the predictors identified in the literature to produce a qualitative model of EMF diversity patterns across Canada and the United States of America. This provides a visual representation of all of the factors hypothesized, explicitly or implicitly, to influence the broad-scale diversity patterns of EMF. Additionally, the model identifies geographic regions that are predicted to harbour high EMF diversity, which may help to improve the sampling efficiency of future projects.

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Poissant, Jocelyn, University of Calgary; Stefan Gavriliuc, University of Calgary; Matthew Workentine, University of Calgary; Emily Jenkins, University of Saskatchewan; Philip McLoughlin, University of Saskatchewan; John Gilleard, University of Calgary

 ITS2 metabarcoding of mixed parasitic infections in Sable Island horses

Free-living vertebrates are commonly infected by a large diversity of gastro-intestinal parasitic nematodes. However, research on the ecology and evolution of mixed parasitic nematode infections in natural populations has so far been limited by our inability to differentiate parasite species non-invasively using traditional coprological techniques. In 2014, we established a long-term individual-based population study of host-parasite interactions in the wild using the Sable Island feral horse population as a model system, and have since monitored strongyle infections yearly in >600 pedigreed individuals. In this presentation, we will describe the recent development and application of an ITS2 DNA metabarcoding assay providing highly repeatable qualitative and quantitative assessments of mixed strongyle infections in our study population. Preliminary results indicate that Sable Island horses are infected by > 10 strongyle species and that mixed infections vary extensively among individuals. These findings suggest that early research in this system which focused on aggregate strongyle fecal egg counts may have overlooked important aspects of host-parasite interactions, including variation in host resistance to different parasites and species-specific pathogenicity. Limitations of the metabarcoding approach, applicability in other wildlife systems, and future research directions will be discussed.

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Prager, Sean, University of Saskatchewan; Tyler Wist, Sabine Banniza

Detection and identification of a fastidious bacteria species from ash tree infesting psyllids

Candidatus Liberibacter species are best known for causing severe economically important diseases of Citrus and Potato. These pathogens are transmitted by hemipteran sucking insects, specifically psyllids. Detection of these pathogens is complicated and difficult because of uneven distribution in host plants combined with a largely unculturable nature. The death of black (Fraxinus nigra) and mancana (Fraxinus mandshurica) ash trees in parts of western Canada, including the provinces of Alberta and Saskatchewan, has been associated with infestation with the cottony ash psyllid (Psyllopsis discrepans). This insect is native to southern Europe and in recent times has spread to most of Europe and the UK, Canada and the US. It is listed as an invasive species by the Saskatchewan Invasive Species Council. The psyllids cause dieback over time due to stunted growth of branches and a thinning canopy. Eventually, the plant dies because there is not enough
foliage to support the tree. However, how the insect actually kills the trees remained a mystery. We hypothesized that the death could be due to a psyllid-transmitted Liberibacter. In this study, we used a combination of conventional and quantitative TaqMan PCR using 16S rDNA-based TaqMan primerprobe specific for Liberibacter and Sanger sequencing to determine the presence of Liberibacter from psyllids collected from Ash trees in Saskatoon. Species identification of the psyllids was made using a universal primer for the Cytochrome oxidase 1 (CO1) gene. Combined PCR and Sanger sequencing results generated two sequences that were 1058 and 1085 bp long. BLAST search for homology showed 99-100% sequence similarity to a Candidatus Liberibacter solanacearum sequence (Genbank accession number: KX197200) isolated from the Nearctic psyllid (Bactericera maculipennis) of US provenance.

Priadka, Pauline, PhD Candidate, Laurentian University; Dr. Glen S. Brown, Wildlife Research and Monitoring Section, Ministry of Natural Resources and Forestry; Dr. Frank F. Mallory, Biology Department, Laurentian University

Climatic effects on long term population trends of moose (*Alces alces*).

Species spanning wide bioclimatic gradients are likely to experience varying effects of climate across their population range. Assessing temporal and spatial variability in climate effects on populations, and in relation to endogenous factors such as density dependence, may therefore reveal variation in the importance of drivers of population dynamics. We used long-term time-series (years 1970-2015) to identify 45+ year effects of climate on moose (*Alces alces*) population size across a bioclimatic gradient in Ontario, Canada. We used Gompertz state-space models in a Bayesian framework to estimate the effects of year-round climatic variability on moose populations in 21 management units. We predicted that temporal population variability of moose will reflect winter severity (snow depth), maximum summer and winter temperature (heat stress indices) and the start and length of the growing season when calving occurs. We also predicted that climate effects will vary in importance for north and south populations, reflecting the present latitudinal bioclimatic gradient in the study area. We demonstrate that understanding how climate is affecting temporal and spatial variability of widely distributed species can help clarify mechanisms of population change and is an important consideration for species conservation and management.

Prokopenko, Christina, Memorial University of Newfoundland; Tal Avgar, Department of Wildland Resources, Utah State University; Adam Ford, Department of Biology, University of British Columbia; Eric Vander Wal, Department of Biology, Memorial University of Newfoundland

Trait-mediated functional response: antipredator traits drive prey switching in multi-prey systems

The density of prey is one the most important drivers of consumption rates by predators and has long been used to explain mechanisms of prey preferences in nature. In addition to density, prey vary widely in the expression of traits that reduce their vulnerability to consumption by predators. In multi-prey systems, how antipredator traits vary among prey (i.e., their dissimilarity) ought to affect consumption rates if predators switch among prey that are most abundant, most vulnerable, or both. We infuse classical theories in ecology with a quantitative modelling framework to test how antipredator traits accelerate or hinder prey switching - the trait-mediated functional response. We demonstrate our models utility using a theoretical example of one predator and two prey, where antipredator traits (e.g., crypsis, defense, or flight response) increase the predation costs during searching, chasing, and handling stages of the predation. We reveal a novel concept that links behavioural and community ecology - trait-density equivalency - demonstrating that consumption rates can produce prey switching behaviour that cannot be predicted by prey density alone. We combine foundational and contemporary predator-prey theory with trait-based ecology, providing a useful framework to guide future research through the reality of diverse predator-prey systems.

Proulx, Alex, Brock University; Miriam Richards

Demographic polymorphism of the solitary sweat bee Lasioglossum zonulum

Eusociality evolved from a solitary ancestor through a demographic shift from one to two broods per season and a social shift from solitary bivoltine to eusocial behaviour. Studying socially polymorphic bees that exhibit both solitary and
eusocial behaviours allows for a better understanding of this evolutionary transition. However, demographically polymorphic bees have not been reported or studied, leaving a knowledge gap concerning the first steps in the evolutionary transition to eusociality. The sweat bee Lasioglossum zonulum is a Holarctic species that is reported to be solitary univoltine but appears to be bivoltine in the Niagara region. We aimed to determine the social organization of L. zonulum and examine possible social or demographic polymorphisms by studying populations from both Calgary and Niagara. Specimens collected using pan traps and blue vane traps were used to create flight phonologies, confirming that L. zonulum is univoltine in the more Northern Calgary population and bivoltine in Niagara. Measurements of size, wear and ovarian development were used to determine that the Niagara population is solitary bivoltine and not eusocial. L. zonulum is therefore a demographically polymorphic species, expressing both univoltinism and bivoltinism. This species is uniquely representative of the evolutionary transition from solitary to eusocial behaviour.

Proulx, Raphaël, Université du Québec à Trois-Rivières; Watson, C.; Dubois, R.; Pépino, M.; Loiselle A.; Giacomazzo, M.; Rainville, V.; Martin CA.; Desrochers, L.; Rheault, G.; Deschamps, L.; DeGrandpré, A.; Paquette, C.

Predicting the species richness of ecological communities using minimal information: A first assessment of 12,750 communities.

One way of representing the structure of ecological communities is to rank species according to their relative abundance (Rank abundance distributions; RADs). The geometric series is a RAD model that can be inverted to predict the species richness of a given community using only two parameters: abundance of the most common species and total number of individuals sampled in the community. The objective of this work was to compare geometric series predictions with the species richness observed in 21,750 plant or animal communities across the globe. The number of taxa represented in the datasets spanned two orders of magnitude. Across the 27 datasets analyzed, mean major axis slope and intercept between predicted and observed species richness were 0.94 (0.82-1.07) and 0.001 (0.331-0.268), respectively. Additional analyses showed that prediction is not affected by survey type, sampling effort, or taxonomic group. Our findings indicate that it is possible to estimate the species richness of ecological communities by parameterizing RAD models with a minimal amount of information. Our results suggest that species dominance is key in determining the structure of ecological communities.

Purvis, Emily, Western University; Matthew Meehan Zoe Lindo

Agricultural field margins provide food and nesting resources to bumblebees (Bombus spp., Hymenoptera: Apidae) in Southwestern Ontario, Canada

Bumblebees are declining globally, largely due to habitat loss driven by agricultural intensification. Within agriculturally dominated landscapes, natural habitat patches (e.g. meadows, wetland edges) are fragmented, increasing the value of uncropped agricultural field margins for providing a source of food and nesting resources to bumblebees. We compared bumblebee communities sampled in agricultural field margins and natural habitats across Southwestern Ontario, Canada in order to assess differences in habitat quality. We then examined the effect of floral resources and soil/nesting characteristics on the bumblebee communities present in each habitat, independent of classification. Our data revealed that bumblebee abundance, diversity, and community composition did not differ between habitat types. However, when examined independently of habitat type, bumblebee abundance, diversity, and composition increased with floral abundance, floral diversity, the number of rodent holes, and sandy soil texture. These results suggest that agricultural field margins are not inherently degraded bumblebee habitat and can provide food and nesting resources comparable to natural habitats in a fragmented agricultural landscape. Ensuring field margins contain the necessary resources for bumblebees has implications for mitigating habitat loss caused by the agricultural fields themselves.

Quanz, Meaghan, Dalhousie University; Dr. Tony Walker, Dalhousie University - School for Resource and Environmental Studies; Dr. Ken Oakes, Cape Breton University; Rob Willis; Dillon Consulting Limited

Effects of waterborne effluent on wetlands surrounding an industrial wastewater treatment facility
A former tidal estuary (Boat Harbour) in Pictou County, Nova Scotia has been used to treat industrial effluent from a chlor-alkali plant and a bleached kraft pulp mill since 1967. This effluent created large volumes of unconsolidated sediment impacted by inorganic and organic contaminants. Boat Harbour will no longer be used to treat effluent after January 2020 under the Boat Harbour Act (2015), with remediation efforts commencing thereafter. To inform remedial decisions, baseline assessments of the area have begun, and include assessments of surrounding wetlands, which were both directly and indirectly contaminated by untreated industrial effluent. This study builds on prior chemical assessments by evaluating potential effects on wetland biological communities through completion of contaminant and invertebrate community analyses. Sediment, surface water and sediment-based biota samples were analyzed for polychlorinated dibenzo-p-dioxins/polychlorinated dibenzofurans, metals and total mercury. Comparison of this data to provincial and federal guidelines revealed several contaminant exceedances in wetland media. Benthic invertebrate community analysis was based on Environment and Climate Change Canada’s Wetland CABIN protocol. Wetlands surrounding Boat Harbour exhibited varying amounts of abundance and diversity. Passive samplers were deployed for analysis of methylmercury to determine concentrations of bioavailable mercury, as previous studies have documented high concentrations of total mercury in Boat Harbour sediments.

Quintero Galvi Julian Fernando, PhD student Universidad Austral de Chile; Julian F. Quintero-Galvis 1; Pablo Saenz-Agudelo 1; Esteban Oda 1; Marcela Franco 2; Juan L. Celis-Diez 3; Guillermo C Amico 4; Soledad Vazquez 4; Aaron B.A Shafer 5; Roberto F. Nespolo 1; Affiliations for numbers: 1.Instituto de Ciencias Ambientales y Evolutivas, Universidad Austral de Chile, Valdivia. Chile. 2.Facultad de Ciencias Naturales y Matemáticas, Universidad de Ibagué. Ibagué, Colombia. 3.Pontificia Universidad Católica de Valparaíso Escuela de Agronomía Quillota, Chile. 4.INIBIOMA, CONICET-Universidad Nacional del Comahue, Bariloche, Argentina 5.Forensic Science & Environmental Life Sciences, Trent University, Peterborough, ON, Canada.

Genetic structure and demographic history in Dromiciops (Microbiotheria), an endemic marsupial from Chile and Argentina

Dromiciops gliroides is an endemic marsupial from the temperate rain forests of Chile and Argentina (Valdivian forest), and is the only living representative of the order Microbiotheria, the ancestors of Australian marsupials. This emblematic species is also known for its ecological role as disperser of at least 16 plant species, but there is debate regarding its phylogeographic origin. Only one study, more than a decade ago, analyzed this aspect and proposed the existence of three latitudinally segregated clades. Yet it still remains unclear if these can be considered as different species limits and what are the complete genetic relationships among these, and what is the demographic history of these clades. Here, we use a genomic approach (RADseq) to analyze the evolutionary history, historical demography and population structure of D. gliroides across most of its geographic range. Our preliminary results indicate a marked genetic structure of two geographic clusters (northern and southern), and further substructure within these groups that appears to be linked with some landscape features. Further analyses of the geographic distribution of genetic diversity will be discussed and will shed light on the role of the landscape and historical events such as last maximum glacial period in shaping the evolutionary history of this emblematic animal.

Raghu, Shravan, Carleton University; Myron Smith; Andrew Simons

The maintenance of mediocrity: Using experimental evolution to understand the persistence of bet-hedging traits

Environmental fluctuations account for the evolution of much of the diversity of life. However, these fluctuations can also threaten extinction especially when they are severe and unpredictable. A strategy to maximize long-term fitness under such conditions is bet hedging where fitness in average or expected environments is sacrificed for increased fitness in rare but calamitous environments. A bet-hedging strategy is suboptimal over short timescales, but optimal over long timescales because it buffers temporal variance in fitness. Although empirical evidence for bet hedging exists, it is unclear how such strategies can persist when selection is expected to improve suboptimal traits in the short-term. It has been proposed that the maintenance of bet hedging is possible only if the ability to adaptively track environments is constrained in the short-term. In this study, we test this hypothesis by evolving bet hedging under fluctuating selection and asking whether it has evolved as a constraint on adaptive tracking. We take an experimental evolution approach to evolve Saccharomyces cerevisiae in a regime consisting of repeated heat-shocks separated by incrementally extended benign conditions. The
evolved constraint is expected to contribute to the persistence of heat-shock tolerance, a costly trait, despite prolonged intervening periods of benign conditions

Ramirez, Samantha, University of Guelph; Ellen Esch; Andrew MacDougall

Ontario Crop Productivity: Variation in yield with varying land suitability for agriculture

Agricultural yields are susceptible to losses during extreme weather events related to climate change, jeopardizing food security. Yield losses may be mediated by underlying quality or variation in soil fertility, topography, drainage and growing degree days of agricultural land. For instance, crops grown on poor quality land may be more susceptible to the negative consequences of climate change as compared to crops grown on high quality land. This study investigates yield response of corn, soybeans and pasture to different land qualities in Ontario from 2011 to 2017. Yield is quantified using the Normalized Difference Vegetation Index (NDVI), which measures vegetation productivity. Google Earth Engine was used to obtain NDVI and the coefficient of variance (CV) of NDVI at a provincial and county scale. Relatively stable CV values were evident across all land qualities, yet certain counties showed greater variation in productivity on poor quality land suggesting greater susceptibility to extreme weather. Evidence of small but significant declines in NDVI in response to poor quality land suggests that producers cannot overcome the biophysical limitations of poor quality land on yield. Understanding crop response to land quality can help producers mitigate yield losses during extreme weather, thus equally stabilizing food availability.

Ramsay, Scott, Wilfrid Laurier University

Using Computer Simulations to Explore the Influence of Tutoring on a Range-wide Change in the Structure of White-throated Sparrow Song

Since the late 1990s white-throated sparrows have experienced a cultural shift in their songs with the familiar triplet ending replaced by doublets. This shift has spread eastward across the breeding range at over 200 km per year. Song-learning may have facilitated this rapid change, specifically via the tutors young males hear during their first year. Field experiments that broadcast novel songs have shown that tutoring can be manipulated in free-living birds; however, this approach is only effective in small populations with restricted post-natal dispersal. In this study we took an alternative approach, using computer simulations to examine how tutoring affects patterns of song variation across a landscape. We modeled four different tutor sources: improvisation; father and his neighbours; winter flocks; and territorial neighbours at the start of the first breeding season. We measured the rate of change of proportion of doublets, loss or fixation of doublets, and clustering of songs by type. When males have only a single tutoring opportunity, exposure on the wintering grounds provides the best match to field observations. Overall, the simulations will allow us to more effectively target field studies to better understand the role of song learning in a rare, decades-long process.

Rathnayake, Manoj Kaushalya, University of NewBrunswick; Paul Marino, Memorial University of Newfoundland

Year to year variation in the spore-dispersing fly assemblages of brood site mimicking Splachnaceae mosses

Splachnum ampullaceum (herbivore dung scent mimic) and S. pensylvanicum ( omnivore dung scent mimic) grow either alone or intermixed on summer moose (Alces alces L.) dung in bogs and, via olfactory and visual deception, have their spores dispersed to fresh dung by flies. Over three consecutive summers, their deceptive fly-moss spore dispersal networks were examined. Results suggest that both mosses attract a generalized fly fauna with a low network specialization (H2 average = 0.171) and low average connectance (0.799). Most of the flies were also associated with summer moose dung. The fly fauna of S. ampullaceum was more similar to that of summer moose dung than was that of S. pensylvanicum, suggesting a dispersal advantage for S. ampullaceum. The network structure varied among years but the assemblage of spore-dispersing flies was loosely arranged and highly generalized all three summers and is similar to that of seed dispersal networks. The yearly faunal variation is likely a consequence of the local abundance of summer moose dung and of brood sites for carrion flies, which are primarily attracted to S. pensylvanicum. The local presence of carrion fly brood sites may be a factor promoting the coexistence of the two mosses.
Rauen Firkowski, Carina, University of Toronto; Marc Cadotte; Marie-Josée Fortin

Not all disturbances are created equal: A trophic metacommunity perspective on how disturbance and environmental fluctuation interact

Natural environmental fluctuations play an important role in structuring biodiversity. Yet, anthropogenic disturbances are increasing at unprecedented rates, disrupting natural processes and threatening biodiversity. Understanding how ecological systems will respond to anthropogenic disturbances is one of the largest societal challenges. Although ecologists have a good comprehension of how different sources of disturbances can impact ecological communities, the current understanding has not been fully incorporated into the theories predicting how spatial heterogeneity structures ecological systems. We seek to understand the interactive effects of anthropogenic disturbances and environmental fluctuations using a mathematical modelling approach based on a trophic metacommunity. Particularly, we assess how trophic metacommunities assembled under contrasting patterns of environmental fluctuations respond to different sources and degrees of anthropogenic disturbance. We contrasted four different disturbance types: connectivity loss, habitat destruction, patch depletion and metacommunity depletion. Our results highlight that the overall patterns of trophic metacommunity responses differs between sources of disturbance. Additionally, we show that the severity of disturbance impacts can be mediated by environmental fluctuation. Our modelling framework allows us to identify the key mechanisms contributing to trophic metacommunity recovery from different types of disturbance and environmental conditions, providing important insights that can inform best management practices under different scenarios.

Reale, Denis, UQAM; Anne Charmantier, Centre d’Écologie Fonctionnelle et Evolutive, CNRS; Christophe de Franceschi, Centre d’Écologie Fonctionnelle et Evolutive, CNRS

Genetic differentiation in behaviour traits between neighbouring avian populations living in contrasted habitat

Understanding the causes of population divergence is a central goal in evolutionary biology. An efficient way to disentangle the relative importance of plastic versus genetic sources of population divergence is to conduct reciprocal transplant experiments. This type of experiment has rarely been conducted for animal populations separated by small spatial scale and for behavioural traits. Here, we evaluated the sources of divergence between three Corsican blue tit populations (Cyanistes caeruleus) inhabiting contrasted habitats and separated by distances of 6 to 25 km. First, in a common garden experiment between two distant populations (25 km), we showed that genetic divergence explained phenotypic differences for several morphological and behavioural traits. Second, using a reciprocal transplant cross-fostering experiment between the two neighbouring populations (6 km), we showed that genetic divergence (i.e. population of origin effect) explained phenotypic differences in handling aggression. Significant brood-of-origin effects suggest that the behavioural traits were heritable. Furthermore, Qst-Fst comparison revealed that the trait divergences likely result from dissimilar selection patterns rather than from genetic drift. Our results indicate that, despite gene flow, neighbouring populations can show genetic divergence for ecologically relevant traits. They highlight the need for more studies on the processes generating biodiversity at small spatial scales.

Regan, Charlotte, University of Saskatchewan; Philip McLoughlin, University of Saskatchewan

Causes and consequences of adult sex ratio bias in Sable Island horses,

A populations adult sex ratio (ASR) has substantial impacts on individual behaviour and life-history and thus on population dynamics. Despite this, little is known about the causes and consequences of variation in the ASR because the majority of research has focused on pre-adult sex ratios. We used data from the long-term individual-based study of Sable Island horses to shed light on the causes and consequences of ASR bias in wild animal populations. We found that the sex-ratio was even in foals, yearlings, and sub-adults, but was significantly male-biased in adults (3 years +), with the degree of bias varying across the island. Survival analyses indicated that the sex-ratio bias was driven by higher survival of male sub-adults and adults. The survival difference of adult males versus adult females is driven by the reproductive costs experienced by females, but the survival difference of sub-adult males and females is mediated by differences in
dispersal timing and distance. We also found that male-biased ASR was associated with reduced female fecundity and foal survival, and smaller band sizes. These relationships between ASR bias and female reproduction may mean that the increasing male bias in this population will have knock-on effects on population dynamics.

Regel, Colby, University of Calgary; Lawrence D. Harder, University of Calgary,

Ecological and Functional Correlates of Mate Number in Seed Plants

Multiple paternity within fruits is common (Mitchell et al. 2013). For seed plants, reliance on pollen-transport vectors and mixed pollinations, resulting from pollen carryover among flowers and the visitation of multiple pollen vectors to an individual flower, generates inevitable polygamy and diverse paternity within fruits (Richards et al. 2009). An enduring question remains whether mate diversity is simply an emergent property of pollination or is a beneficial feature of plant mating systems subject to selection (Pannell and Labouche 2013, Barrett and Harder 2017). We conducted a meta-analysis of morphological and ecological traits on variation in effective male mate number, Ep (inverse of correlated outcrossing, rp; Ritland 1989) for 281 populations of 108 species of seed plants. Most species exhibited an Ep of less than ten mates but varied with outcrossing rate, inbreeding, pollinator, growth habit, sexual system, ovule number and pollen type, herkogamy and self-incompatibility, with associations differing for mate number among versus within fruits. Larger body size and separation of sexual functions were found to promote Ep. These associations occurred independently of phylogenetic relatedness, consistent with indirect selection on mate diversity that promotes outcrossing success. Furthermore, the implications of mate similarity for parameter estimation will be discussed.

Rehan, Sandra, York University

Maternal manipulation and the formation of social hierarchies in the subsocial bee, *Ceratina calcarata* (Hymenoptera: Apidae)

By manipulating resources or dispersal opportunities, mothers can force offspring to remain at the nest to help raise siblings creating a division of labour. In the subsocial bee, *C. calcarata* mothers manipulate the quantity and quality of pollen provided to the first female offspring producing a dwarf eldest daughter. The dwarf eldest daughter forages for her siblings and forgoes her own reproduction. To begin to understand how the mothers manipulation of pollen affects the physiology and behaviour of offspring, we measured the effects of pollen quantity and pollen type on offspring development, adult body size and behaviour. We found that by experimentally manipulating pollen quantities or pollen types we could recreate the dwarf eldest daughter phenotype. This behavioural phenotype begins to explain how maternal manipulation of resources could lead to the development of the social organization and reproductive hierarchies, a major step in the transition to highly social behaviours.

Reich, Miranda H., University of Alberta; Jack Hogg (Montana Conservation Science Institute); Dave Coltman, University of Alberta

The relationship between inbreeding coefficients, heterozygosity, and horn growth in bighorn sheep

Horns are a sexually selected trait that are used by bighorn sheep (*Ovis canadensis*) rams in yearly intraspecific fights to determine status and for access to mates. Since horns are a sexually selected trait, they could be a signal of a rams genetic variation measured by heterozygosity and directly affected by inbreeding. The goal of this study was to test the hypothesis that horn growth is negatively affected by inbreeding and positively related to heterozygosity at National Bison Range (NBR). NBR is a National Wildlife Refuge located in northwestern Montana, USA that has supported a bighorn sheep population since 1922 with individual monitoring beginning in 1979. The current NBR pedigree goes back ten generations to 1980 and includes approximately 500 sheep. This study first updated the NBR pedigree by doing microsatellite genotyping using blood and tissue samples from 160 sheep and a parentage analysis in Cervus. Then inbreeding coefficients were calculated directly from the pedigree. Finally, linear regressions and heterozygosity-fitness correlations were done to determine whether a rams inbreeding coefficient or heterozygosity had an effect on his horn growth.
Reid, Christopher, University of Toronto; Ina Anreiter, University of Toronto; Megan Frederickson, University of Toronto

Investigating the molecular basis of cooperation in an ant-plant mutualism,

Superficially, the evolution of inter-species cooperation, or 'mutualism', seems counter-intuitive. Cooperation is costly, and we might expect natural selection to filter out genotypes that confer benefits to others at an immediate cost to oneself. However, in theory, natural selection should favour mutualism as long as cooperation is reliably reciprocated and confers net fitness benefits to all parties. Despite a sound theoretical understanding of how natural selection might favour the evolution of cooperative genes, we still know little about the genes themselves. This is especially true in animal mutualisms, where the costs and benefits of cooperation are often cashed out in the form of complex behaviours. In defensive ant-plant mutualisms, ants act as bodyguards for their plant hosts, behaving aggressively toward herbivores that attempt to feed on them. Working in the Peruvian Amazon, we took behavioural measures of bodyguard behaviour on 60 colonies of the plant-ant Allomerus octoarticulatus, and collected workers engaged in bodyguard and brood care behaviours. Correlating gene expression with variation in ant behaviour is improving our understanding of the molecular basis of mutualism.

Renkema, Justin, Agriculture and Agri-Food Canada

Interactive effects of entomopathogenic nematodes and mulches on white grubs (Coleoptera: Scarabaeidae),

Reyes, Elijah, Simon Fraser University, Leithen M'Gonigle

Evolution of dispersal traits in continuous, heterogeneous landscapes

Dispersal is a ubiquitous process that has the potential to affect important spatial interactions such as competition for resources. If individuals disperse passively (i.e. without a determined direction), we can expect dispersal to be costly when resources are not evenly distributed because individuals may not be locally adapted to their new location. Therefore, how resources are distributed in the landscape influences dispersal, specifically the probability and width of dispersal. However, how dispersal evolves when individuals use multiple resources is not well understood. We present an individual based model in which individuals compete over two continuously distributed resources. We show that resource specialization can evolve and, when the different resource types are distributed differently across the landscape (e.g., different autocorrelations), specialists on these different resources evolve different dispersal strategies. Additionally, we show that when resource competition depends on ecological traits, such that individuals adapted to different resources do not compete as strongly as those adapted to the same resource, a third generalist strategy can emerge with its own dispersal strategy. This suggests that the mode of competition can directly affect the evolution of dispersal-related traits.

Reynolds, Jordan, University of Waterloo; Dr. Rebecca Rooney from the University of Waterloo,

Avian species richness in Rocky Mountain peatlands

Species richness is a component of predicting how biodiversity will change in future climate scenarios and to understand this change we must figure out what variables influence species richness. In Rocky Mountain peatlands, we lack a basic ecological understanding of bird communities, such as how many species inhabit mountain peatlands and what influences their presence. This study aims to describe bird species richness along an elevation gradient in the Alberta Rocky Mountain peatlands and understand what variables, such as Natural Subregion and peatland size, influence species richness. The two-day bird surveys were conducted in 23 mountain peatlands in the Upper Bow River Basin, Alberta distributed evenly across Natural Subregions. I found that bird species richness decreased with increasing elevation and Natural Subregions were a stronger predictor of species richness compared to elevation. These findings indicate that differences among Natural Subregions other than elevation, such as soil type, temperature, precipitation, and vegetation communities, are more important for predicting species richness than elevation alone. These results suggest that bird
species richness in Rocky Mountain peatlands differ among Natural Subregions; future research can help to clarify which components of Natural Subregion are the strongest drivers of bird diversity.

Rezendes, Victoria, UNBC MSc student; Victoria Rezendes; Katherine Bleiker; Jeanne Robert; Dezene Huber

Hot stuff. The temperature dependent life cycle of spruce beetles.

We investigated temperature conditions that yield prepupal diapause, a developmental delay, in spruce beetles (Dendroctonus rufipennis Kirby). We compared development indexes at constant temperatures (21°C, 15°C, and 12°C) between three geographically distinct beetle populations of Duffey Lake and Prince George, British Columbia and Whitecourt, Alberta. Development rates ultimately decreased with temperature across all populations. Mortality was inversely associated with temperature, meaning that more beetles died at cooler temperatures. Additionally, spruce beetle pupation phenology varies by population with Whitecourt insects being the least likely to pupate at each experimentally tested temperature. Prince George beetle pupation was not significantly different than Duffey Lake beetles at 21°C, but was less likely at both 15°C and 12°C. Degree day accumulation is the most important predictor in spruce beetle pupation. Host tree also impacts pupation probability at each experimental temperature. Information from this research provides insight into spruce beetle population dynamics in the context of a changing climate.

Richards, Miriam; Dept. Biological Sciences, Brock University

Social trait definitions influence evolutionary inferences: A phylogenetic approach to improving social terminology

The comparative method relies not only on a good understanding of the phylogenetic relationships among taxa, but also on consistent terminology for describing phenotypes. Clear and consistent terminology allows similar phenotypes to be described and phylogenetically analysed in different organisms, whereas inconsistent terminology is a major impediment to comparisons, even for taxonomically restricted groups such as bees. Here I propose that the usefulness of social terminology can be judged by its value in phylogenetic trait-mapping aimed at uncovering evolutionary transitions between solitary and social behaviour. I propose a three-step approach to evaluate and update social terminology, in which definitions are first updated based on recent behavioural studies (step 1), mapped onto a phylogeny (step 2), and then re-evaluated for their utility in the trait-mapping exercise (step 3). To demonstrate the approach, I define four terms important for understanding social evolution in bees (solitary, social, eusocial, and hypersocial) and map them onto a very recent phylogeny of Apidae. This not only illustrates an objective method for evaluating social terminology, but also provides novel inferences about social evolution in Apidae, including support for a parasocial origin of eusociality and 2 to 4 Major Evolutionary Transitions to hypersociality.

Richardson, Paul,University of Waterloo; Stephen D. Murphy, University of Waterloo; Lars Jonas Hamberg, University of Waterloo

Fountain of Old? Accelerating forest succession through living mulch relocation

Ecosystems may maintain biodiversity and functioning best after developing spontaneously through succession, but extractive industries engaged in rehabilitation and offsetting face pressure to achieve results more rapidly than nature provides. We hypothesized that aspects of succession may be fast-tracked by relocating slow-growing ecological structures from mature ecosystems to younger ones, provided that supportive habitat features are also reproduced. We tested this idea in collaboration with an aggregate producer engaged in expanding and offsetting a Niagara Escarpment limestone quarry. Excavating topsoil, propagule banks and overlying litter from mature sugar maple forest, we experimentally relocated bulk volumes of this living mulch to nearby sites spanning a successional gradient typical of anthropogenic landscapes (a sand-gravel pit; recently afforested fields; older conifer plantations; mature maple stand). We deposited woody debris, planted shrub clusters and installed artificial shade shelters in subplots to replicate different conditions of the donor site. After 1.5 years, treated plots everywhere supported plant communities which were significantly more similar to the donor forest than were adjacent untreated areas. Similarity was remarkably high in conifer plantations, and habitat mimicry treatments produced variable positive impacts. Theoretical and practical
implications for accelerating succession are promising, but longer-term assessment of multiple ecosystem attributes is required.

Richardson, John, University of British Columbia

Moving the boundaries on ecosystems: energy flows across metaecosystems

Over the course of almost a century, ecology has gone from tightly bounded views of ecosystems, such as those of Lindeman and Clements, to appreciating that connections across ecosystem boundaries have large influence. Flows of energy and nutrients between ecosystems can be one of the main contributors to recipient ecosystems productivity and composition. These processes are becoming better described, and many experiments have demonstrated the magnitudes of these system-wide effects. From our work we have explored the effects of experimental additions or exclusions of cross-ecosystem resource subsidies, which yield large effect sizes, but unevenly distributed among recipients in timing and amount. Our studies show that the recipients of these spatial flows are specific, and the dynamical consequences accrue to particular consumers and not always an overall system stimulation. To date, most experiments have been addition-reference comparisons, and we need more treatment levels. Experimental manipulations of timing and magnitude will be useful for determining when a subsidy resource contributes or not. We need to be more predictive about the flows to specific recipients, and how the subsidy to their productivity moves through their communities.

Rideout, Natalie, Canadian Rivers Institute @ UNB Fredericton; Zacchaeus Compson (Centre for Environmental Genomics Applications); Wendy A Monk (Environment and Climate Change Canada @ Canadian Rivers Institute, University of New Brunswick & Faculty of Forestry and Environmental Management, University of New Brunswick); Mehrdad Hajibabaei (Centre for Biodiversity Genomics & Department of Integrative Biology, University of Guelph); Donald J Baird (Environment and Climate Change Canada @ Canadian Rivers Institute, University of New Brunswick)

The floodplain wetland puzzle: How DNA-metabarcoding plays an integral role in elucidating relationships between environmental drivers, invertebrate traits and ecosystem function

Floodplains are disturbance-driven ecosystems with high spatial and temporal habitat diversity, making them both highly productive and hosts to high biodiversity. The unpredictable timing of flood and drought years creates a mosaic of habitat patches at different stages of succession, while water level fluctuation directly influences macrophyte community dynamics, and thus habitat structure. This habitat complexity and diversity of disturbance regimes makes floodplains an ideal ecosystem in which to examine the links between biodiversity, traits and ecosystem function. Despite the rise in trait-based science, taxonomic resolution has imposed limitations, particularly in wetland and floodplain ecosystems where communities are vastly understudied compared to their riverine counterparts. Compared to traditional biomonitoring, DNA-based biomonitoring from high-throughput genomics sequencing methods is powerful in that it can reliably characterize community composition in unprecedented detail, allowing us to assess how disturbance and environmental variables interact with invertebrate traits and ecosystem function. Using structural equation modelling, we take a whole ecosystem approach to examine ecosystem health across a floodplain disturbance gradient. We focus particularly on how wetland habitats shape communities and, further, how those communities influence ecosystem function through trait diversity metrics. We also examine and compare which traits are associated with crucial ecosystem gradients.

Rinas, Christina, Université de Sherbrooke; Mark Vellend, Université de Sherbrooke,

Species diversity of arboreal lichen and bryophyte communities along a temperate-to-boreal elevation gradient

Understanding how and why biodiversity varies along environmental gradients has important implications for predicting future ecological responses to environmental change. Many studies address diversity along gradients for taxa such as vascular plants and vertebrates, however, arboreal lichens and bryophytes remain understudied. In this study we examined patterns of species diversity of arboreal lichens and bryophytes growing on sugar maple and balsam fir trees along an
elevation gradient at Parc national du Mont Mégantic in Québec. Our questions were: (i) Are arboreal lichens more responsive to elevation gradients than bryophytes? and (ii) Do arboreal lichens and bryophytes follow the common pattern of a decline in species diversity with elevation? We found that elevation was a significant predictor of species diversity for lichens on fir trees, but not for bryophytes or lichens on maple trees. Furthermore, diversity for lichens on fir trees increased with elevation, contrary to most published diversity-elevation patterns for other groups. We speculate that bryophytes on maples may be more response to fine scale moisture gradients, whereas lichens on maples may be responding to competition from bryophytes. Further studies of other environmental gradients may be important in explaining patterns of diversity for arboreal communities.

Riva, Federico, University of Alberta

Using hierarchical models to assess butterfly abundance, behavior and phenology

Much of contemporary ecology and conservation biology focuses on understanding species responses to environmental change. However, because we rarely know the true state of a population, we commonly base our inference on samples. In other words, the state of an unknown latent ecological process is assessed through the lens of a detection process, which conditions our observations if detection probability is less than one - the rule rather than the exception in ecological data. Hierarchical models, i.e., sequences of probability models that describe conditionally dependent random variables, have been increasingly used by ecologists in the last 20 years to estimate the abundance (or occurrence) of a species accounting for detection probability. Here, I describe the hierarchical model framework using butterflies as model organisms. I discuss how this approach is valuable not only for estimating the abundance of a species, but also to investigate its biology through the lens of the detection process.

Rix, Rachel, Dalhousie University; G. Christopher Cutler, Dalhousie University

Stress, Stimulation, and Tradeoffs: Hormesis in the Beneficial Insect Predator, *Podisus maculiventris* (Hemiptera: Pentatomidae)

Hormesis refers to the stimulatory effects or increased tolerance to challenge that occur following exposure to low doses of chemical, physical, or biological stress. Hormesis is ubiquitous.

Robicheau, Brent, Dept. of Biology, Dalhousie University; Co-authors: Jennifer Tolman; Ian Luddington; Dhwani Desai; Julie LaRoche Affiliations: Dalhousie University

Marine microbial diversity and UCYN-A within the eastern Arctic Ocean

In the ocean, microbes called diazotrophs fix atmospheric nitrogen. One of these diazotrophs, UCYN-A, is a fascinating symbiotic unicellular cyanobacterium. Having lost its photosystem II, UCYN-A has adapted to directly exchange algal-host carbon for fixed-nitrogen. In 2018, UCYN-A was documented in the western Arctic Ocean from the Beaufort and Chukchi Seas, thus increasing its known global distribution beyond the tropical latitudes where nitrogen fixation is usually studied. Here we focus on marine eDNA samples collected from Baffin Bay and the Canadian Arctic Archipelago. We show that UCYN-A is indeed present in the eastern Arctic Ocean through the use of highly multiplexed amplicon sequencing (16S & 18S rDNA and nifH targets), phylogenetic analysis, and quantitative-PCRs. Microbial community structure, particularly where UCYN-A is present, is further examined in relation to oceanographic data collected during sampling. Not only does this work confirm UCYN-A’s larger presence within the Arctic marine environment, but also provides a comprehensive look at the marine microbial community structure for this region.

Robinson, Samuel, University of Calgary; Lincoln Best, University of Calgary; Ralph Cartar, University of Calgary Paul Galpern; University of Calgary

Lagged and current effects of canola bloom on wild bee abundance in southern Alberta,
Populations of wild insects exhibit a wild range of temporal population dynamics, which makes predicting how they respond to shifts in food resources difficult. Pollinating insects are even more complex, as their abundance in a given area is constrained by both distance from their nest to their food plants. Foragers might take advantage of temporary increases in canola flowers, but estimating this effect is difficult because changes in abundance may only be obvious in the next year (lagged effect). We surveyed bee abundance of 20 common quasi-social (non-Bombus) bee species during 2015 and 2016 across an agricultural region of southern Alberta, Canada, and modelled how adjacent semi-natural land (SNL), current canola crops, and last year's canola crops affected abundance. Overall, the most important predictor of bee abundance in 2016 was their abundance in 2015. SNL increased abundance in 2016, but abundance in 2015 was unaffected by SNL. However, these generalities dissolved for individual species, with the effect of SNL being positive for some species, nonexistent for most, and negative for others. There was no current or lagged effect of canola on bee abundance, either generalist or specialist, implying that having nearby canola crops do not increase solitary bee abundance during the following year. Our results suggest that: a) bee populations are relatively consistent year-to-year among sites, b) canola bloom does not affect solitary bee fitness, and c) the relationship between SNL and bee abundance is highly species-specific. Perhaps both mass-flowering crops and SNL are less relevant to wild bees in agroecosystems than currently thought.

Rochon, Kateryn, University of Manitoba

Roe, Amanda, Natural Resources Canada - GLFC; Mingming Cui, Université Laval; Marion Javal, Stellenbosch University Melody; Keena, USDA Forest Service; Juan Shi, Beijing Forestry University; Isabelle Giguère, Université Laval; Gwylim Blackburn, Université Laval/Natural Resources Canada; Richard Hamelin, University of British Columbia; Ilga Porth, Université Laval

Surprising population structure in the native range of the invasive Asian Longhorned beetle (Cerambycidae: Anoplophora glabripennis Motschulsky)

Asian longhorned beetle (Anoplophora glabripennis ALB), is a native forest pest in China and the Korean peninsula. This species has successfully invaded and spread to hardwood forests in North America and Europe. ALB mines the heartwood of a range of tree species and poses a significant threat to invaded forest ecosystems. Tracking the ALB invasion requires knowledge of its native population structure. In this study, we generated genome-wide markers using high throughput sequencing technology (Genotyping-by-Sequencing) to characterize genetic variation within and among native ALB populations. Our results showed clear population differences between ALB populations in China and South Korea, as well as pronounced population structure within China. These results provide much greater clarity to the native population structure than earlier work using mitochondrial DNA and microsatellites. The results provide insights into the history of human-mediated dispersal of ALB and potential for local adaptation within the native range. These data provide a foundation for future work on the global invasive history of ALB.

Roehl, Larissa, University of New Brunswick; Scott Pavey Department of Biological Sciences, University of New Brunswick, Saint John

Using environmental DNA to determine wood turtle (Glyptemys insculpta) presence in New Brunswick, Canada rivers

Worldwide turtle and tortoise populations are declining, including the semi-aquatic wood turtle (Glyptemys insculpta) of eastern North America. With a limited survey season a more efficient method of detection was needed to monitor this cryptic species. DNA barcoding with environmental DNA has been shown to be an effective method of monitoring cryptic species. Water samples were collected in October 2017 and 2018 from an upstream and downstream site on fourteen rivers in New Brunswick, Canada. In our eDNA lab, the samples were filtered, extracted and with the use of species-specific primers and probe amplified using quantitative polymerase chain reaction (qPCR). With the use of qPCR, wood turtle eDNA was detected in five of six rivers known to inhabit the species. This method is a promising tool that can be used for the conservation and monitoring of G. insculpta.
Rogers, Sean, Bamfield Marine Sciences Centre

Field stations as sentinels for environmental change

The CSEE meeting represents an important opportunity to highlight the legacy of research stations for testing critical questions in association with field-based ecological and evolutionary research in Canada and abroad. Our field stations continue to support collaborative science on these front lines of environmental change to better understand shifting climate and ecosystems and to generate robust projections of future conditions and biodiversity. Field stations are a critical part of the scientific infrastructure that brings the basic tools of science into the field and connect scientists to these environments. Yet, to fulfill this vital role for these research objectives, field stations must continue to evolve and provide improved opportunities for collaboration and access to the environment. All of this is against the backdrop of the increasing challenges we face to fund these important resources.

Roland, Jens, University of Alberta; Steve Matter, University of Cincinnati

Hot winters, and the dynamics of alpine Parnassius smintheus butterflies

Butterflies serve as one the best examples of bio-geographical range-shifts due to climate change. The mechanisms by which weather and climate alter butterfly dynamics are, however, often lacking. We use 23 years of population data from 21 sites in the Rocky Mountains of Alberta to identify weather variables (means and/or extremes) that best explain annual rates of population change (Rt) of alpine Apollo butterfly, Parnassius smintheus. Extreme cold, and extreme warm temperatures in early winter are associated with dramatic population declines, particularly in years with little or no snow. Weather at any other time of year bears little relation to annual population change. By planting eggs in fall, and recovering eggs through the winter, we identify warm events during winter as being particularly detrimental to egg survival, and hence to population growth. Results imply that over-wintering eggs are particularly susceptible to warm temperature extremes in early winter, and that snow cover at this time of year is critical for ameliorating the effects of such extremes.

Rollinson, Njál, University of Toronto

How (not) to inherit a long-term research program: a perspective from an early career researcher

Long-term studies have the potential to experience a greater longevity than the research programs of their founders. Transfer of long-term research across generations can ensure a study’s persistence, and can be immensely beneficial to the careers of young researchers. But adopting a long-term research study can come with considerable difficulty. Some of these difficulties are simple and obvious, such as appropriate training and financing, but there can be other issues that lurk beneath. My talk will focus on my first-hand experience over the last three years, having started a tenure track faculty position while simultaneously taking the reigns on my former advisor’s long-term study. I will speak to the enormous benefits of adopting some else’s long-term research program, as well as some unanticipated costs. By underlining where I went wrong and the future problems I anticipate, I hope to provide some advice on what (not) to do as an early career field researcher.

Romero, Nora, Brock University; Miriam Richards, Brock University

Phenology and changing species composition of bee communities in restored landfill sites

For many species of bees, we lack basic natural history information about the timing of important life history events (phenology), social behaviour, and even the length of flight seasons. Furthermore
Romero, Berenice, University of Saskatchewan; Sean Prager, University of Saskatchewan

Host-preference and performance in a plant pathosystem

Aster leafhoppers (Macrosteles quadrilineatus Forbes) are carried into the Canadian Prairies by wind currents originating in the US. Crops’ quality and yield can be severely affected by Aster Yellows disease, which is caused the Aster Yellows Phytoplasma, a fastidious bacteria primarily transmitted by Aster leafhoppers. Aster Yellows symptoms vary among plant species, but include excessive branching, abnormal development of floral parts, and misshapen seeds. In many cases, however, plants will be asymptomatic, making it difficult to visually identify infected plants, or they will be similar to those produced by other pathogens. Even though this disease has a low incidence in canola (<0.01%), outbreaks have been documented in recent years, resulting in devastating losses for local growers. Little is known about the host choice and performance of this insect species on field crops and weeds and if the infection with Aster Yellows can impact on their behavior and/or physiology. In order to address some of these concerns and to provide a better understanding of AY epidemiology, no-choice and two-choice bioassays will be conducted with Aster leafhoppers under various experimental conditions.

Rose, Sonja, Dalhousie University; Jennifer Tolman; Julie LaRoche; Erin Bertrand, Dalhousie University

Using BIOLOG Technologies To Access Carbon and Nitrogen Substrate Preferences In A Novel Heterotrophic Marine Diazotroph

Traditionally, cyanobacterial lineages have been viewed to be the main group responsible for biological nitrogen (N2) fixation in the ocean. This has been brought into question however as we realize heterotrophic diazotrophs are more diverse and distributed than previously believed. The recently cultured Candidatus Thalassolituus haligoni, was isolated from Bedford Basin and belongs to the widely distributed and important family: Oceanospirillaceae. It was shown that the isolate fixes N using 15-N2 stable isotope injections under a carbon mixture. Its fully annotated genome demonstrated the potential for various carbon metabolic pathways while experiments have shown growth curves on simple hydrocarbons and a long carbon chain polymer. To aid in exploring the carbon metabolism of the isolate, phenotypic BIOLOG plates will be used to identify two substrates which promote growth, leading to high biomass yield and cellular N2 fixation rates. Overall this work presents the isolate as a potential model organism for heterotrophic diazotrophs and aims to provide insight into biological N2 fixation at the physiological level and the impact this understudied group has on the nitrogen cycle.

Roth, James, University of Manitoba; ChloeWarret Rodrigues; Megan Dudenhoeffer, University of Manitoba, Department of Biological Sciences

Use of sea ice by foxes at the Arctics edge

Many northern predators are limited by resource availability, especially in winter, but marine resources become more accessible when the Arctic ocean freezes. Arctic foxes may use sea ice to access seals when densities of lemmings, their primary terrestrial prey, are low. Red foxes have increased use of historic Arctic fox dens on coastal tundra where lemming cycles are damped, potentially to facilitate a similar marine-based foraging strategy. We examined sea-ice use by Arctic foxes and red foxes on the west coast of Hudson Bay in northern Manitoba using satellite collars (2017-2019) and fecal DNA analysis of scats collected from coastal dens (2012-2018). Half of 14 collared Arctic foxes used sea ice, but only one of 10 red fox ventured onto the ice, and then only minimally. Long-distance movements were common in both species, but Arctic foxes primarily dispersed onto sea ice whereas red foxes moved inland into forest. We found marine prey in 17% of Arctic fox fecal samples, on average, and this frequency increased when lemming densities were lowest, but none in red fox samples. Access to marine resources does not appear to explain red fox incursion onto the tundra.

Roy, Denis, Natural Resource Sciences McGill University; Sarah Lehnert, Great Lakes Institute for Environmental Research, University of Windsor; Clare J. Venney, Great Lakes Institute for Environmental Research, University of Windsor
NGS-µsat: Bioinformatics framework supporting high throughput microsatellite genotyping from next generation sequencing platforms

Although genetic techniques are moving toward collecting massive amounts of genome-wide data through genome-scans, microsatellite markers (µsats) still trump genome-wide surveys in some key applications such as parentage analyses, pedigree tracking, assessing likelihoods of disease conditions and DNA fingerprinting, among others. A long-standing issue with the continued use of µsats has been the time-consuming processes for developing, optimizing and scoring markers and to make produced data easily reproducible. Generating µsats data has traditionally relied on assessing fragment lengths by electrophoretic methods which can be highly variable. Newer, high-throughput sequencing protocols have made the development and production of µsats data more efficient, but few bioinformatics support the generation of such raw sequenced µsat data. We introduce NGS-µsat 1.0, an R-based pipeline for converting raw sequenced µsat data capitalizing on the breadth of information from raw sequence reads. This platform-independent framework scores µsats by focusing on actual repeat motifs rather than assessing fragment lengths. We describe the algorithms and use them to scores two known captive-bred Chinook salmon families. In comparative analyses with software screening fragment lengths, we show the relative quality and reliability of our novel technique which produces cleaner more accurate data translating into more reliable inferences using downstream applications. The development of this framework and its continued refinements through future releases, may spawn a resurgence in µsat use for population, conservation and forensic genetic applications.

Evaluating the accuracy of the Alberta Wetland Rapid Evaluation Tool in determining relative wetland value.

To successfully conserve a wetland ecosystem, conservation practitioners rely on assessments of its ecological value. It is vital that these assessments be accurate in determining relative wetland value so that the most ecologically important wetlands are protected or restored appropriately. The Alberta Wetland Rapid Evaluation Tool-Actual (ABWRET-A) has been created to estimate the functional performance of wetlands in the settled area of Alberta, Canada, and give them categorical relative value scores. However, the extent to which ABWRET-A can accurately estimate relative value across wetlands in the area is not clear, and there has been no review of this tool since implementation in 2015. Here, we test for biases made in site selection for ABWRET-A calibration, and how those biases affect the relative value scores that those wetlands receive. We found that wetlands chosen for ABWRET-A calibration were significantly larger than both natural wetlands in that area, and wetlands targeted for loss since ABWRET-A implementation. This is concerning since there is an apparent positive relationship between the size of a wetland, and the relative value score it receives. This suggests that ABWRET-A may be inaccurately estimating relative wetland value for wetlands in the applied area. Our findings suggest that ABWRET-A calibration sites need greater representativeness to the natural variability of wetlands in the applied area for the tool to accurately estimate the relative value of wetlands in that area. A recalibration of this tool will improve its ability to accurately determine the relative value of a wetland so that the most valuable wetlands are indeed protected or restored appropriately.

LANDMARK: A novel approach to the selection of biomarkers in high-throughput sequencing data

High-throughput sequencing (HTS) datasets are notoriously noisy. Furthermore, current biomarker selection methods, such as Linear Discriminant Analysis Effect Size (LEfSe), can fail to account for specific distributional properties and feature interactions that are present in these complex datasets. These issues can impact the replicability of various models while also obfuscating the discovery of potential biomonitoring biomarkers due to elevated false-discovery rates. Contemporary machine learning approaches can be leveraged in order to address these issues. Non-parametric ensemble methods, such as the Extremely Randomized Tree Classifier, have been shown to be particularly effective with the types of datasets commonly generated in HTS studies. While commonly used to classify samples, methods such as these can also aid in the discovery of potential biomarkers. We show that feature importance metrics extracted from modern
classification tools, in combination with distributional information about the features themselves, are sufficient to isolate biomarkers of interest while controlling the false-discovery rate. In synthetic tests, the sets of biomarker discovered - while small - contain enough information to successfully classify samples.

Rush, Jessica, AAFC/AAC; Bob Vernon; Lindsey Goudis; Wayne Barton; Jessica Rush

Broflanilide, an effective new insecticide for managing wireworms (Coleoptera: Elateridae) in cereals

Field and lab insecticide efficacy studies conducted with broflanilide, a novel insecticide (IRAC Group 30) developed for chewing insect pests, indicate the insecticide is highly effective in providing both crop stand protection and wireworm population reduction when applied as a wheat seed treatment. We present results of studies conducted in 2012-2018, and discuss implications for managing wireworms in cereal and other crops.

Russell, Ty, University of Alberta, Biological Sciences; Catherine Cullingham, U of Alberta dept of biological sciences; David Coltman, U of Alberta dept of biological sciences

Development and implementation of a species-discriminating genetic resource for identifying hybridization in mule and white-tailed deer

Hybridization, the genetic admixture of two diverged lineages, is a phenomenon with a huge variety of potential outcomes. Some may be net benefits for a population, such as the sharing of adaptive alleles between species, but often the integration of genetic incompatibilities causes an overall detrimental effect. Mule deer (Odocoileus hemionus) and white-tailed deer (O. virginianus) form a large hybrid zone with sympatric areas throughout western Canada and the United States that presents an opportunity to observe the persistence of two divergent lineages despite gene flow. The extent of this interspecific gene flow has been estimated in different parts of the hybrid zone using various genetic markers expected to be insensitive to deeper introgression levels. Because hybrids are sometimes fertile, we sought to create a genetic resource capable of identifying cryptic backcross hybrid generations. In this talk, I will discuss the development of a species-discriminating SNP assay composed of loci fixed between species and its use in interrogating the Alberta portion of the Odocoileus spp. hybrid zone. We then used this panel to investigate whether hybridization may be facilitating the spread of chronic wasting disease (CWD), a neurodegenerative prion disease endemic in Alberta that affects both species.

Ruzzante, Daniel, Dalhousie University; Greg McCracken; Brage Forland; John MacMillan; Colin Buhariwalla; Joanna Mills-Flemming; Hans Skaug

Validation of close-kin mark-recapture (CKMR) methods for estimating population abundance

Knowing how many individuals there are in a population is a fundamental problem in the management and conservation of freshwater and marine fish. We compare abundance estimates (census size, Nc) in seven brook trout (Salvelinus fontinalis) populations using standard mark-recapture (MR) and the close-kin mark-recapture (CKMR) method. Our purpose is to validate CKMR as a method for estimating population size. CKMR is based on the principle that an individual's genotype can be considered a recapture of the genotypes of each of its parents. Assuming offspring and parents are sampled independently, the number of parent-offspring pairs (POPs) genetically identified in these samples can be used to estimate abundance. We genotyped (33 microsatellites) and aged ~2400 brook trout individuals collected over 5 consecutive years (2014-2018). We provide an alternative interpretation of CKMR in terms of the Lincoln-Petersen estimator in which the parents are considered as tagging the offspring rather than the offspring recapturing the parents. Despite various sources of uncertainty, we find close agreement between standard MR abundance estimates obtained through double-pass electrofishing and CKMR estimates, which require information on age-specific fecundity, and population- and age-specific survival rates. Population sizes (50AÜ) are estimated to range between 300 and 6000 adult individuals. Our study constitutes the first in situ validation of CKMR and establishes it as a useful method for estimating population size in some marine systems.
Saddler, Alycia, University Of Ontario Institute of Technology; Helene N. LeBlanc

Response of *Stomoxys calcitrans* (Diptera, Muscidae) to VOC profiles from Ontario, Canada dairy farms

*Stomoxys calcitrans* are significant pests of dairy and beef cattle livestock. Their seasonal abundance is known to cause billions of dollars in damage to the industry in the United States. While similar damage has been documented in Canada, the majority of the research explores population dynamics of stable flies with respect to seasonal and temporal conditions. Fewer pest management approaches target the extremely sensitive olfactory system of *S. calcitrans*, which is used for the detection of semiochemicals related to host-seeking and oviposition activity. Exploring potential semiochemical targets that impact host-parasite interactions, at livestock facilities, can give insight in creating novel integrated pest management (IPM) approaches. Volatile organic compounds (VOCs) were sampled at dairy farms in Southern Ontario to determine important components of volatile profiles at such sites. Further, we used coupled gas-chromatography-electroantennography (GC-EAG) to identify VOCs presenting electrophysiological activity in *S. calcitrans*, for further exploration of their significance in behavioural modification. The data collected illustrates that VOC profiles taken at livestock facilities are subject to change over the summer months, and novel targets have been identified for IPM programs. This study supports a body of research in the US which suggests plant essential oils may become useful pest repellents.

Salisbury, Sarah, Dalhousie University; McCracken, G.R. - Dalhousie University; Perry, R.; Keefe, D. - Department of Fisheries and Land Resources, Government of Newfoundland and Labrador; Kess, T. - Bedford Institute of Oceanography, Department of Fisheries and Oceans; Koop, B.F. - University of Victoria; Nugent, C.; Ferguson M.M.; Danzmann; R.G. - University of Guelph

Genetic divergence among sympatric resident and anadromous Arctic char (*Salvelinus alpinus*) in Labrador

The sympatric polymorphisms often observed in salmonids, generally thought to have a relatively recent (Quaternary) origin, offer a unique opportunity to study the genetic causes and consequences of incipient speciation. In contrast to the hypothesis that resident and anadromous Arctic char are solely a product of plasticity, we observed significant neutral genetic differences among sympatric resident and anadromous Arctic char (*Salvelinus alpinus*) forms in a single lake in Labrador using microsatellite markers (Salisbury et al. 2018, CJFAS). Building upon this work, we employed an 86 K SNP chip to investigate the character and consistency of the genomic differences among resident and anadromous morphs from three lakes in Labrador. Our results reveal variable, but high levels of genetic differentiation among sympatric morphs across all lakes. The SNPs and genes under divergent selection among morphs differ widely among lakes. However, parallel divergent selection across lakes is apparent upon a subset of homologous and paralogous genes, including one gene which is potentially responsible for the body size dimorphism among morphs. Our results suggest that the genetic differentiation among sympatric resident and anadromous Arctic char is largely non-parallel apart from a few critical genes potentially fundamental to the manifestation of these morphs.

Samad-zada, Farida, University of British Columbia Okanagan; Brett van Poorten(2); Shannon Harris(2); Lyse Godbout(3); and Michael Russello(1);  1. Department of Biology, University of British Columbia, 2. Applied Freshwater Ecology Research Unit, BC Ministry of Environment and Climate Change Strategy, 3. Pacific Biological Station, Fisheries and Oceans Canada

Genome-wide analysis of black kokanee to investigate life-history evolution and inform fisheries management

Black kokanee represent a unique ecotype of sockeye salmon (*Oncorhynchus nerka*) that spend their entire lives in freshwater ecosystems and differ from other kokanee ecotypes genetically, morphologically and behaviorally. Specifically, the ecotype can be distinguished based on its black olive colouration upon maturity, and spawning habitat preferences, typically ~50 m below the lake surface. Black kokanee stocks are endemic to Lake Tazawa in Japan; however, they have recently been described in a number of lakes in southwestern British Columbia, including Seton, Anderson and Alouette lakes. Given the recent efforts to re-introduce anadromous sockeye back into the Alouette Reservoir, there is a need for rapid genetic identification between resident and anadromous *O. nerka* within the system, as
well as for assessment of genetic diversity of newly established anadromous sockeye populations. Here, we conduct a genome-wide analysis of black kokanee populations across the lakes in British Columbia to investigate the genetic distinctiveness of Lake Alouette kokanee and anadromous sockeye relative to each other as well as to anadromous sockeye and resident kokanee from neighboring watersheds. Additionally, genomic data will be used to address questions related to the evolution of life-history traits of black kokanee and reconstruct the origin of the ecotype across its pan Pacific distribution. Understanding the genetic structure of the resident and re-introduced populations will have important implications for management questions related to re-establishment of anadromous sockeye populations in Lake Alouette.

Samarasinghe, Himeshi, McMaster University; Renad Aljohani; Carlene Jimenez; Jianping Xu

Fantastic Yeasts and Where to Find Them: Discovery of the Opportunistic Yeast Pathogen Cryptococcus deneoformans in Saudi Arabian soils

The environmental yeast Cryptococcus deneoformans is the causative agent of fatal meningoencephalitis responsible for over 180,000 annual deaths worldwide. It is commonly found in the soil in temperate climates. Although infectious cryptococcal spores originate exclusively from the environment, environmental reservoirs are relatively unexplored compared to clinical populations. Here, we discovered 76 C. deneoformans isolates in a survey of 562 soil samples collected from six Saudi Arabian cities. Multilocus sequence typing (MLST) revealed the isolates to be predominantly clonal with some evidence of sexual recombination. Three MLST genotypes present in this population have been previously reported from North America, South America and Europe while the remaining three genotypes are unique to Saudi Arabia. Our results indicate recent introductory events facilitated by human movement as the origin of the Saudi Arabian C. deneoformans population. Saudi Arabia is a top travel destination due to its thriving oil industry and religious significance. Introduction was likely followed by expansion via asexual and sexual reproduction. Our study is the first to report the presence of C. deneoformans in a desert climate, representing a novel expansion to its ecological niche, while highlighting the significant role played by human migration in the spread of microbial pathogens.

Sandor, Sarah, McMaster University; Jianping Xu, McMaster University

The Tale of Mushrooms and Insects: Living Together, Changing Together

Mushroom-insect species interactions are fascinating systems to study due to the transient nature of mushroom fruiting bodies, which form for only one short stage of the mushroom lifecycle to allow for spore dispersal. Despite the unpredictability of fruiting body formation, mushrooms are a common food source and egg-laying site for insects. This project involved conducting a broad ecological survey of wild mushrooms in Southern Ontario and their associated insects. Over 300 mushrooms encompassing 141 species were collected and identified through DNA barcoding using sequences of the ITS region. Insects and larvae were removed from the mushrooms and identified through barcoding using the CO1 gene: 31 insect species from thirteen families and four orders were identified. Interestingly, sixteen of these likely represent previously undocumented insect species. Flies (order Diptera) were the most abundant and many species were found associating with a range mushroom species and families. Phylogenies of the mushrooms and their associated insects were compared to assess the distribution of association and look for evidence of coevolution between these two interacting groups of organisms. This study is the first to our knowledge to examine mushroom-insect interactions using molecular techniques on both a broad scale and from an evolutionary perspective.

Sauk, Alexandra, University of Waterloo

Exploring microbial diversity across a municipal waste site

Landfills are disposal sites for household and municipal wastes. Although microorganisms are the primary decomposers in landfills, we know very little about their diversity or what controls these community compositions. To explore the microbial diversity across a Southern Ontario landfill, six samples were collected from three leachate wells, a composite leachate cistern (two temporal samples), and one impacted groundwater well. Six metagenomic datasets were created from total community DNA. In parallel, the DNA for these six samples and an unimpacted groundwater well sample
underwent 16S rRNA gene amplicon sequencing. Based on a comparison between metagenome-derived 16S rRNA genes, scaffolds with a biomarker set of 16 syntenic ribosomal proteins, high quality metagenome assembled genomes, and the 16S rRNA gene amplicon data, 24 bacterial and archaeal phyla were present at >1% relative abundance within the landfill. The Patescibacteria, Bacteroidetes, and Proteobacteria had the highest abundances, while most other phyla were present at low abundance, with some fluctuations between sites. Below the phylum level, very few organisms were identified across multiple sites, indicating that while phylum-level signatures are conserved, individual populations vary widely across the landfill. Correlation to geochemical conditions and contaminant concentrations identified factors controlling microbial diversity patterns across the landfill.

Savage Jade, Bishop's University

A swarm of Canadian flies: almost 10,000 species and still counting.

Biodiversity can be measured and estimated using a wide range of methods and metrics but checklists and raw species numbers remain essential tools for monitoring changes in local and regional biotas. In Canada, total species numbers are well-known and regularly updated for most terrestrial vertebrates but comparable data for hyper-diverse taxa such as insects is usually outdated by many decades. The Biota of Canada initiative was created to fill this gap and the first volume (terrestrial arthropods) was published in 2019. Highlights from the Diptera chapter are presented and priorities are outlined to further improve our understanding of the most species rich order in the country.

Schamp, Brandon, Algoma University; Ashley Jensen, Algoma University

Evidence of limiting similarity revealed using a conservative assessment of coexistence

The concept of limiting similarity is important in ecology because it encapsulates the expectation under niche theory that differences among species are fundamental to coexistence. A growing body of research has tested for evidence of limiting similarity, but only a small number have produced support. Here, we use an example data set to highlight one explanation for the paucity of support for limiting similarity. We test whether coexisting plant species that share bees as pollinators flower asynchronously, a form of temporal niche separation consistent with limiting similarity. We demonstrate that a more conservative assessment of coexistence that includes only individual plants that have achieved reproduction, is consequential in whether we find evidence of significant flowering asynchrony. Our results add to the modest collection of null model studies that have produced evidence of limiting similarity. We conclude that the conservative approach to assessing coexistence that we describe here can reduce noise in coexistence data, improving our power to test for evidence consistent with limiting similarity. Using this approach may or may not result in an increase in evidence supporting limiting similarity; however, it will certainly give researchers more confidence that they have not missed existing evidence of limiting similarity.

Schang, Kyle, University of Waterloo; Andrew Trant, University of Waterloo

Quantifying Ecological Legacies: Understanding how ancient human settlement has modified forest structure and diversity in the Great Bear Rainforest

Understanding how past-human actions have influenced their environment is becoming increasingly important in understanding how current ecosystems function. Heavy intertidal resource use from Coastal First Nations communities has led to habitation sites containing vast shell-midden deposits within their soils. Here we examine various forest stand metrics, such as species diversity, physiology, and seedling regeneration to determine if forest stands on habitation sites differ from those in surrounding areas. We show that species richness for both adults and seedlings on habitation sites is significantly less than that of non-habitation sites, but species evenness is higher on non-habitation sites. We also found that trees, particularly western redcedar (Thuja plicata) and sitka spruce (Picea sitchensis) were significantly taller and wider on habitation sites than compared to those on non-habitation sites. Here, we demonstrate the influence shell-middens have had on surrounding forest stands and the importance of understanding past-human influences to better understand current ecosystem functionality.
Schmidt, Allison, Dalhousie University; Kate E Arpin, Dalhousie University, Department of Biology; Heike K Lotze, Dalhousie University, Department of Biology

Blue carbon revisited: the case for standing stock

Marine macrophyte ecosystems, including mangroves, salt marshes, seagrass meadows and macroalgal beds (e.g., kelp, rockweed), fringe continents around the globe. Despite only occupying 0.7% of the ocean area marine macrophytes rival or exceed the standing carbon stock of many terrestrial biomes thereby playing a major role in global carbon storage. Using published literature from 1950-2019, we collated data on the extent, % tissue carbon and biomass of each macrophyte ecosystem to estimate standing biomass-based carbon stock. Macroalgae covered 60-98% more area than any other marine macrophyte but had 22 and 35% less carbon in their tissues relative to salt marshes and mangroves, respectively. Biomass was highest in salt marshes where it was also the most variable. Overall, the highest standing carbon stock was in salt marshes, followed by mangroves, macroalgae and finally seagrasses. Due to the long-term persistence of these coastal habitats, the carbon can be locked in their standing biomass for decades to millennia depending on the type of vegetation. As such, the standing carbon stock of marine macrophytes should be considered in the global carbon budget because only then will we fully understand their contribution to and the impact of their loss on climate regulation.

Schmidt, Chloé, University of Manitoba; Colin J Garroway, University of Manitoba

Productivity biodiversity relationships at genetic and species levels and an exploration of causes,

Spatial patterns in both species and genetic biodiversity are thought to be shaped by similar processes. Primary productivity predicts biodiversity at the species level well, but it is unclear whether it also predicts biodiversity at the genetic level. If true, we should detect a positive correlation between patterns of species and genetic diversity that are produced by common causal mechanisms. To explore this hypothesis, we used publicly archived raw genetic data to quantify genetic diversity at >1000 sites sampled across North and South American mammals, birds, reptiles, and amphibians. We summarized spatial patterns in species and genetic diversity to test for correlations between the two levels of biodiversity, and used multi-level structural equation modeling to identify causal pathways governing productivity biodiversity relationships. In addition to productivity, we accounted for effects of environmental heterogeneity and human disturbance. Most spatial variation in genetic diversity was shared with species level patterns. While species and genetic diversity generally increased with productivity, specific factors mediating these relationships differed. Identifying the factors which cause correlations between genetic and species level diversity is important for our basic understanding of the drivers of biodiversity, and for managing the ecological and evolutionary consequences of environmental change.

Schoepf, Ivana, Queen's University; Adriana Lopez Villalobos, Queen's University

Beyond Borders: Augmenting access and profile of research and data generated at field stations,

Field stations provide ideal venues for leading-edge ecological, evolutionary and environmental research. Data generated from resources at field stations may lead to peer-reviewed publications. However, typically, only some of the research data collected at field stations is published fully and is readily available as a resource to the entire research community. Many field stations also have data generated from their own resources, as well as, legacy data that is unavailable to researcher beyond those who have collected it. This data is waiting to be rescued, curated and re-used. At the Queens University Biological Station (QUBS) we are seeking to enhance the resources available to researchers worldwide. We have created a searchable portal that includes all peer-reviewed publications produced from research conducted at our field station (http://research.qubs.ca). We are also digitizing specimens from our Fowler Herbarium vascular plant collection and will make it available through Canadensys and GBIF. Moreover, we are digitally transcribing historical data from researchers, who have worked at QUBS over the years, and we are uploading records generated from our
climate stations. We will discuss the various strategies that we are developing to increase accessibility of field station data resources and augment the profiles of such facilities.

Schonberger, Zach, University of Guelph; Kevin McCann

Structural asymmetry and cascading autochthonous subsidies in the coupling of grazing and detrital energetic pathways

Recent empirical work has shown that autotroph and detritus-based food webs are connected through nutrient cycling, autochthonous subsidies, and generalist consumers. Theoretical frameworks have historically incorporated nutrient cycling and subsidies, while ignoring the role of generalist consumers. To understand how the structure of these connections between seemingly distinct energetic pathways influences system stability, they must be integrated into theory. Here, we adopted a four dimensional nutrient cycling model that allows a consumer to feed on both the resource and detritus, and analyzed a gradient of consumer attack rate ratios. Our results suggest that feeding structures with higher attack rates on detritus are stabilizing, but become destabilizing with complete specialization on detritus. We also considered the abundance of each compartment across the same gradient of attack rate ratios, finding that a trophic cascade occurs with the same feeding structure that stabilizes the system. We end by arguing that the cascading autochthonous subsidies to detritus stabilize the consumer-detritus subsystem, and thus confer stability to the overall system.

Schüller, Katharina, Maastricht University; KateYina StaHková; Joel S. Brown

Surplus Ovules Permit Female Choice in Oak Trees

Many plants produce surplus ovules that never become fruits. Oak trees produce six ovules per flower. Just one of them matures to an acorn. In stands of oak trees, long-distance fertilization is unusually common. Furthermore, nearby oak trees are often absent as pollen donors. For a wind-pollinated species such as oak, these observations cannot be explained by leptokurtic pollen flow that declines with distance between plants. Here, we extend a two-step lottery model of Craft et al. (2009) to test the hypothesis that oak trees pursue a form of within-flower female choice to increase the diversity of fathers. With our simulations, we show that producing multiple ovules per flower may allow selection for the rare father, thus increasing the chances that distant trees will be successful fathers. As the number of potential father trees increases the number of ovules maximizing the diversity of fathers increases as well. However, when considering a certain cost function for ovule production, six ovules per flower achieves a balance between the benefit of diversifying fathers and the costs of producing multiple ovules per flower. We simulate the consequences of a trees position within a stand and found a positive association between distance to an edge of the stand and the diversity of fathers. Finally, we analyze data from three different field studies to validate the hypothesis that oaks exhibit female choice. In all three cases, the female choice hypothesis explains the real observations significantly better than a random choice from the six available ovules.

Schwarzfeld, Marla, Agriculture and Agri-Food Canada; Victoria Nowell

Of pointy palps and glowing cheeks: Sorting out the phylogeny of the predatory mite family Cunaxidae using molecules and morphology,

Cunaxidae is a cosmopolitan family of predatory mites, including both active and ambush predators of small arthropods and nematodes. The family currently includes six subfamilies and 27 genera; however, no molecular studies have been conducted to test subfamily or generic monophyly. We are constructing a phylogeny based on COI and 18S, which mostly supports the existing subfamily arrangement with one surprise. However the generic limits are less clear, and within one subfamily in particular (the Cunaxinae), the genera are clearly in need of revision. This has led to a search for novel morphological characters to help delimit and redefine these genera.
Schweiger, Anna, Université de Montréal; Etienne Laliberté

CABO - The Canadian Airborne Biodiversity Observatory,

The Canadian Airborne Biodiversity Observatory CABO uses spectroscopy to study the four most important global drivers of biodiversity change affecting terrestrial ecosystems: land-use change, climate change, nitrogen deposition, and biotic invasions. Linking spectra of plants to plant form and function enables to study the effects of changes in plant community composition and plant diversity on ecosystem function remotely. CABO uses an integrative, cross-scale approach linking plant functional traits to leaf-level spectra and spectral images collected by unmanned aerial vehicles (UAVs), airplanes and satellite sensors across Canadian biomes, from the Arctic tundra to Northeastern forests. In addition, CABO is building an extensive spectral library providing the foundation for all future applications of high-resolution biodiversity censuses based on multi- and hyperspectral imagery. Here we give an overview of CABO and present some of our first results, including the detection of invasive plant species and species differentiation with spectra, and a spectral diversity metric enabling to map spectrally unique plant communities at the landscape scale.

Scott, Brittni, Acadia University; Dr. Don Stewart; Dr Soren Bondrup-Neilsen

Investigation into Connectivity and its Consequences for the Black Bears (Ursus americanus) of Nova Scotia,

The largest threat facing black bear populations is loss of continuous forests due to habitat fragmentation. Habitat fragmentation encourages small, isolated populations that suffer from decreased genetic diversity and population-level instability. To avoid local extirpation, it is important to study connectivity patterns, identify at-risk populations, and employ conservation measures. The level of connectivity among black bears within the province of Nova Scotia has never been studied. Additionally, it has not been investigated if the peninsular geography of the province limits connectivity to black bears outside the province. Using microsatellite analysis on hunter sourced black bear samples from across Nova Scotia and New Brunswick, genetic substructuring was analysed to investigate connectivity patterns. This analysis found evidence of three subpopulations in the Maritimes, with one in New Brunswick and two dividing Nova Scotia northeast to southwest. Additionally, genetic diversity was estimated to be consistently lower in Nova Scotian subpopulations compared to the New Brunswick subpopulation. This indicates a level of impediment of black bear movement between Nova Scotia and New Brunswick, as well as between northeast and southwest Nova Scotia. Additionally, this inhibited connectivity may be adversely affecting black bear genetic diversity in regions of the Maritimes.

Scott, Laura, Trent University; Jeff Bowman, Ontario Ministry of Natural Resources and Forestry and Trent University; Christina Davy, Ontario Ministry of Natural Resources and Forestry and Trent University

Fiddler on the roost: behavioural variation between the eastern small-footed bat (Myotis leibii) and the little brown bat (Myotis lucifugus).

Personality is defined as behaviours that are repeatable across circumstances and time. The study of personality and behavioural variation in mammals has been a significant field of research; however, the ecological evolution of personality in bats has been relatively understudied. The eastern small-footed bat (Myotis leibii) and the little brown bat, (Myotis lucifugus) are two closely related North American species that display different roosting behaviours. M. leibii are often found roosting on the ground, whereas, M. lucifugus do not frequently roost on the ground. These differences cause them to encounter different ecological and evolutionary conditions. To further knowledge about these speciesbehaviour, we asked: what are the ecological and evolutionary consequences of habitat selection? We hypothesized that M. leibii will display adapted behaviour due to the evolutionary ecology of ground roosting. To determine this, we examined inter- and intra-specific variation in behaviour using an open-field test. We created a 3-dimensional modified open-field test to examine behaviours, such as flying, landing, and crawling. Bats were tested in ~1hr nighttime and daytime trials while being video recorded. This experiment allowed observed behaviours to be correlated to personality traits such as activity, boldness/shyness and exploration/avoidance in different experimental locations.
Scott, Catherine, University of Toronto Scarborough; Sean McCann, Simon Fraser University; Maydianne Andrade, University of Toronto Scarborough

Scrambling male widow spiders find females faster by following silk trails of rivals

Social information can allow individuals to bypass the costs and risks of exploration, but may also intensify competition. Here we show that mate-searching males can exploit inadvertent social information produced by rivals to find females faster, increasing their mating success even in spite of heightened competition. In western black widows (*Latrodectus hesperus*), first-male sperm precedence leads to intense scramble competition for access to sedentary females. Unmated females signal to males via silk-bound pheromones, but cease signaling shortly after copulation. Through field- and lab-based studies we demonstrate that females mature asynchronously in nature, creating brief windows of detectability. Larger males are more successful at localizing females, but smaller males achieve higher average search speeds. Critically, all males improve their mate-searching success by following silk draglines (byproducts of locomotion in spiders) produced by rivals to arrive at receptive females webs faster. Silk-following males arrive at webs in which rivals are already courting, but pre-copulatory courtship lasts several hours, so the first male to arrive is not necessarily first to mate. Moreover, we show that mate-searching males vastly outnumber signaling females on any given night. We conclude that social information use by males increases their fitness because patterns of female receptivity necessitate competition.

Scott, Andrew, McMaster University; Ian Dworkin, McMaster University; Reuven Dukas; McMaster University

Sociability in fruit flies: Genomics, behaviour, plasticity and fitness

Sociability, defined as the tendency of animals to engage in non-aggressive interactions with each other, is a highly ecologically relevant trait for which natural variation is observed throughout the animal kingdom, across populations within a species, and also among individuals within a population. This natural variation within populations, which is observed as sociability phenotypes in animals (including humans) ranging from solitary introverted behaviour to highly social extroverted behaviour, may have an important impact on potential fitness outcomes, however the genetic basis of this variation is not well understood. Using fruit flies as a genetic and behavioural model system, I have quantified natural genetic variation in sociability using inbred line screening, revealing that sociability has low-moderate heritability, has a minimal genetic correlation between the sexes, and exhibits genetic variation in phenotypic plasticity. In addition, I have undertaken a large-scale artificial selection project to uncover potential trade-offs with other behavioural and morphological traits, and to better understand the genetic architecture of sociability using evolve-and-resequence (E&R) techniques.

Scrafford, Matthew, Wildlife Conservation Society Canada; Justina Ray, Wildlife Conservation Society Canada

A comparison of wolverine conservation challenges across their North American range

Wolverines are considered by many biologists and conservationists to be an umbrella species that resides in wilderness areas free of human disturbance. We argue that this is a simplistic description of wolverine ecology that requires nuance for proper management of wolverines and other wildlife species. Wolverines exist across three major biomes in North America: mountain, tundra, and boreal forest. These biomes cover a gradient of latitudes with dynamic climates, habitats, and human disturbances. Wolverines have shown a unique ability to withstand substantial human development pressures in some portions of these biomes but are declining in others. We discuss the distinctions associated with understanding these patterns and unique management actions that are required to enable the persistence of wolverines across their range.

Shafer Aaron,

Genomic estimates of effective population size predict conservation status
Shafiq, Muhammad, University of the Punjab

Evolution and diversity of cotton leaf curl disease complex and associated whitefly biotype complex species in Pakistan

Cotton leaf curl disease (CLuCD) is an important limiting factor for cotton, tomato, vegetable and ornamental crops in the Pakistan. Symptoms of CLuCD include severe upward and downward leaf curl with cup-shape, yellowing and stunted plant growth. This disease is caused by begomoviruses (single-stranded DNA viruses (family Geminiviridae) that are transmitted by whiteflies). The begomoviruses are either bipartite (with two genomic components known as DNA A and DNA B), monopartite (with a genome homolog of DNA A component of bipartite begomoviruses) or monopartite associated with DNA satellites (mainly betasatellites). All three types of begomoviruses are main player in CLuCD complex. These viruses are transmitted by the whitefly. An overview presenting the emergence and evolution of CLuCD and associated whitefly biotypes in Pakistan and its effect on future food security and their control is discussed.

Shanmukha Swamy Saggere; Rani Monica, 2nd year Ph.D student; Dr. Aurora M Nedelcu (Supervisor) Department of Biology, Loring bailey hall, UNB

From life-history trade-offs to somatic cell differentiation

Rani M. Saggere and Aurora M. Nedelcu The evolution of complex multicellularity from single-celled ancestors required cooperation among cells, with some cells specialising in survival (somatic cells) and others in reproduction (germ cells). We have proposed that the evolution of somatic cells involved the co-option of life-history trade-off genes that are expressed when temporary repression of reproduction is beneficial in terms of long-term survival. To address this, we used the volvocine green algal group that encompasses both unicellular (e.g., Chlamydomonas) and complex multicellular organisms with somatic and germ cells (e.g., Volvox). In Volvox carteri, somatic cell differentiation is controlled by regA a master regulatory gene that induces a permanent repression of cell division. The closest homolog of regA in its single-cell relative, Chlamydomonas reinhardtii, is RLS1. To gain insight into the adaptive and mechanistic role of RLS1 we assessed the fitness and gene expression pattern of an RLS1 mutant grown in normal and nutrient-limited conditions. As predicted, relative to its wild-type strain, the mutant gained a benefit in reproduction but incurred a cost in long-term viability. This study provides direct evidence for the co-option of life history trade-offs during the evolution of somatic cells.

Sharkey, Janean, University of Guelph; Nigel E. Raine

Assessing the population health of Common Eastern Bumble Bee (Bombus impatiens) in tallgrass prairie and oak savanna in southern Ontario using molecular techniques

There are increasing concerns about bumble bee (Bombus spp.) population declines. Although the causes of declines are not fully understood, a primary driver is thought to be land use change. Here we investigate the factors influencing the success of native bumble bees under different levels of restoration and management in tallgrass prairie and oak savanna. Formerly widespread and common, these habitats types are now rare and fragmented in southern Ontario. Harnessing molecular techniques we can determine the relatedness of individuals sampled in the field, and estimate the number of bumble bee colonies at each site through analysis of microsatellite markers and sibship analysis. Using these approaches, we have assessed nest densities of Bombus impatiens populations in restored and remnant tallgrass prairie and oak savanna by determining worker relatedness through non-lethal DNA sampling of tarsal claws. This is a first step towards assessing the health of bumble bee populations in these habitat types. Mapping nests may provide further insight into their foraging range and the relative value of different habitats necessary for population persistence. Our results will inform habitat management strategies to support and enhance bumble bee populations, and contribute to a better understanding of bumble bee ecology and life history.

Shaw-McDonald, Samantha, University of Guelph; John M. Fryxell, University of Guelph

Responses to harvest selectivity and temperature in an exploited population
Harvesting strategies rarely accommodate the effect of changing environmental conditions, such as water temperature, which can have their own limiting effects on aquatic population dynamics. I investigated the relationships among harvest selectivity, harvest intensity and water temperature to test how these anthropogenic and environmental factors interacted in influencing the population dynamics of Daphnia magna, as an experimentally tractable model for other size-structured populations. Selective harvesting of reproductive-sized individuals caused a reduction in population density compared to non-selective harvesting at the same level of harvest intensity. Increased water temperature provided a relief effect for harvested populations, where the depressive effect of size-selective harvesting was less pronounced at 25 deg C than at 15 deg C; presumably due to the more rapid rate of maturation allowing for more individuals to be recruited between each harvest event. Other population metrics of biomass, population growth rate and population density showed similar trends. The interactions between harvest strategies and temperature altered the ability for populations to recover from population loss between harvest events, illustrating important relationships between anthropogenic stressors and climate conditions for aquatic species that are regularly exploited.

Shimizu, Mei

Studying Speciation and Adaptation with Microfluidic Devices,

Shovon, Tanvir, University of Regina; Mark Vanderwel

How do above- and below-ground competition affect performances of white spruce seedlings?

Recruitment of white spruce (Picea glauca), one of the most widely distributed conifer species in the boreal forest, is reportedly declining in areas of western Canada where there is limited water availability. The adverse effects of moisture, nitrogen and light limitation on performance of white spruce seedlings may be compounded by above- and below-ground competition from neighbouring understory plants and trees. To test this hypothesis, we conducted a competition-removal experiment on white spruce seedlings in a water-limited island forest landscape within the Canadian Prairies. In 2016, we measured the height and diameter at root collar of 572 natural seedlings. In 2017, we excavated a 20-30 cm deep, 75-cm radius trench around 55 of these seedlings to remove belowground competition, and manually cleared all vegetation within a 75-cm radius of another 105 seedlings to remove aboveground competition. We took hemispherical photographs above each seedling to calculate canopy openness, and re-measured the height and diameter of all seedlings in 2017 and 2018 to calculate pre- and post-treatment growth. There was a pronounced difference in precipitation between years, with spring-summer precipitation 58% higher in 2016 and 62% lower in 2017 than average levels. A greater decrease in diameter growth of seedlings growing under competition in the dry year than seedlings growing without competition. Seedling growth was limited by canopy trees by shading and below-ground competition from neighbouring plants in open areas. Neither competition treatment affected the growth of seedlings under shade compared to control seedlings. Removal of below-ground competition had a positive effect on seedlings located under an open canopy, but removal of above-ground competition did not. These results indicate that local competition compound the stress caused by low-moisture and below-ground competition did reduce seedling performance in high-light areas in a dry year. The interactions between light, moisture, and competition that we report have implications for white spruce regeneration in water-limited areas, especially as inter-annual variation in precipitation increases in a changing climate.

Shutler, Dave, Acadia University; Thomas Davis Moore; Nicoletta Faraone, Acadia; N. Kirk Hillier, Acadia

Blind to what counts: nest odours

A critically important aspect of avian reproduction is avoiding nest predation; one of the riskiest times in a birds life is when they are at a nest, whether it be as an egg, a nestling, or a parent. One strategy is to conceal nests, which is often quantified based on human assessments of visual cues. However, many biting arthropods, most reptilian and mammalian predators, and probably some avian predators of nests, likely rely more on olfaction than vision to find nests. This means that there has almost certainly been strong selection for birds to conceal nest odors, but there has been virtually no research devoted to this. As a beginning to addressing this lacuna, we collected samples of nesting material from tree
swallow nests during nest-building, egg stages, nestling stages, and following fledging. We are using a combination of solid-phase microextraction of nest materials, and in-nest static odor collection using polydimethylsiloxane tubes to trap nest odors. Odors associated with each of these nest stages will subsequently be analyzed with gas chromatography-mass spectrometry, with a long-term intent to understand how biting arthropods and predators may make use of the olfactory cues we identify.

Slatculescu, Andreea, University of Ottawa; Manisha Kulkarni, University of Ottawa

Lyme disease risk areas in Southern and Eastern Ontario predicted by species distribution models for the tick vector.

Lyme disease is a vector-borne illness caused by Borrelia burgdorferi, transmitted to humans through the bite of Ixodes scapularis ticks in eastern North America. Populations at risk for Lyme disease are defined by the geographic distribution of the tick vector, which is driven by global environmental and climate changes. Species distribution modelling uses computer algorithms to predict the geographic distribution of a species using environmental data. We aimed to develop a maximum entropy (MaxEnt) model for I. scapularis in Ontario. METHODS We generated tick presence/absence points by field sampling at 124 sites across southern and eastern Ontario between 2015 and 2018. We obtained satellite remote sensing data on land cover and vegetation from the Ontario Land Cover Compilation v.2.0 and climate normals for 1981/2010 from Natural Resources Canada to develop 33 grid files for distance and proportion of land cover features, climate and precipitation averages, growing season variables, and degree days > 0!. We used ticks submitted from the public via the passive tick surveillance system as test data for model validation. RESULTS The preliminary MaxEnt model for I. scapularis, trained on active tick surveillance data across the province and tested on an external dataset, predicts a high to moderate habitat suitability for I. scapularis ticks across southeastern Ontario with good discrimination capacity (AUC=0.876 on test data). Variables with the highest contribution to the model are proportion of agriculture and water, elevation, distance to forest, and degree days above > 0!. CONCLUSION We developed a species distribution model that predicts the geographic distribution of I. scapularis ticks in southern and eastern Ontario as an estimate of environmental risk for Lyme disease.

Sleep, Darren, SFI

Umbrellas, Indicators, and Flagships: woodland caribou as a management tool of the boreal forest

Given the environmental challenges facing managers with limited budgets, shortcuts to successful biodiversity conservation have become increasingly appealing and necessary. The indicator species concept has been in existence for almost 4 decades and has been met with successful use in the detection of contaminants, changes to water or air quality, agricultural range condition, or to classify biotic communities. The umbrella species, a sub-category of the indicator species concept, was proposed over 20 years ago as a means of conserving biodiversity through the management of a single species, thus simplifying the demands for data on habitat requirements and populations for a vast array of species. While the plea for a quantitative evaluation of the concept has gone mostly unheeded, many species have been proposed as umbrella species based on a suite of criteria thought to make them suitable surrogates. In Canadas boreal forest, the woodland caribou (Rangifer tarandus) has been suggested to be an indicator of both boreal forest health and an umbrella for the conservation of boreal biodiversity as early as 2002, shortly after the umbrella concept was proposed. The use of caribou as an umbrella has been reinforced by governments, non-government agencies, ENGOs and the media ever since. However, an exhaustive review of the literature reveals that only 3 recent attempts (2016, 2018, 2019) have been made to test the effectiveness of caribou as an umbrella species, and results have been variable. This presentation will summarize those results, discuss the relative strengths and weakness of each, and discuss what is missing in the evaluation of caribou as a potential tool in the conservation of boreal diversity.

Small, Christopher, University of New Brunswick; Dr. Tillmann Benfey, University of New Brunswick; Dr. Bryan Crawford, University of New Brunswick

Developmental and morphological consequences of polyploidy in teleost fish
Many whole genome duplication (WGD) events have occurred during evolutionary history and because these WGDs can relax selection on copies of conserved genes, WGDs are often linked to the evolution of novel traits. Increased cell size is another consequence of increased genome size, but research has focused primarily on how duplicated genes evolve after WGD, rather than how changes in cell size affect development of tissue architecture. WGDs in plants result in increased cell size and a commensurate increase in the size of the organism. This pattern holds true in some animals such as mollusks and arthropods, however ploidy transitions are embryonic lethal in birds and mammals. Teleosts and amphibians represent a middle ground; polyploids are often viable, but the correlation between cell size and body size has been decoupled although their cells are larger, polyploid individuals are no larger than their diploid counterparts. Using transgenic zebrafish with fluorescent histones, ploidy can be measured non-lethally very early in development to identify individuals for comparison. Comparing size and organization of developing myotomes and the surrounding vasculature at the cellular level highlights how teleosts compensate for increases in ploidy and cell size at the tissue level to maintain body size.

Smith, Nicola, Simon Fraser University; Isabelle Côté, Simon Fraser University

Fear of native predators promotes biotic resistance on Caribbean coral reefs

Biotic resistance is the ability of a community to prevent or limit the success of non-indigenous species in novel environments. Typically, native species confer resistance by outcompeting or preying on non-indigenous species. In this study, we investigated whether depredation by native predators promotes biotic resistance on coral reefs.

Smith, Todd, Acadia University; Laura Ferguson (Acadia University); Caoimhe McParland (Acadia University); Amy Prescott (Acadia University); Emma Costello (Acadia University)

Fitness, pathogenesis, and immunity in mosquitoes infected with Hepatozoon blood parasites from frogs and snakes

Hepatozoon species are cosmopolitan protozoan parasites that infect erythrocytes of terrestrial vertebrates, including snakes and frogs in eastern Canada. Species of Hepatozoon infecting ranid frogs and natricine snakes are vectored by mosquitoes of the genus Culex. These parasites are ubiquitous, yet we know little about their interactions with their mosquito hosts. To explore the impact of infection on mosquito physiology, we investigated the effects of Hepatozoon species on the fecundity of Culex mosquitoes, the cause of death in mosquitoes that ingest heavily-infected blood meals, and the role of insect immunity in this pathogenesis. Increases in infection intensity of H. sipedon decreased the number of eggs produced by infected C. pipiens, and heavy infections of Hepatozoon species in C. territans resulted in death of mosquitoes, caused at least partly by perforation of the gut wall. Further, increased infection intensity raised oxidative stress in C. territans but also suppressed other components of the immune system, which likely facilitates invasion but may promote host mortality. Overall, we find that Hepatozoon species decrease mosquito fitness and may modify mosquito physiology to enhance their own infectivity. This host-parasite system provides opportunities to further understand the dynamics of blood parasite infection in arthropod vectors.

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Functional and genetic diversity of hyperdiverse neotropical insects across an elevational gradient

We are interested in understanding who lives where, how they do so and how that is changing across multiple elevation gradients in northwestern Costa Rica. In the tropics, a metric mile of vertical distance is associated with large changes in biodiversity. Less variable, cold and wet high elevation cloud forests ought to have species characterised by narrow
physiological tolerance. Conversely, highly variable, hot and dry low elevation forests ought to have species with wider tolerances and structural adaptations. After more than a decade of work in these Costa Rican forests, we know that diversity changes with elevation, but how coupled are the genetic patterns with functional change? How exactly does the abiotic environment change across this gradient? We will present new findings in rove beetles (Staphylinidae) regarding changes in physiology (CTmax) and structure (cuticular nanostructure measured using scanning electron microscopy) that vary across this neotropical elevational gradient.

Solà, Mireia, UQAM, CRAM; François Dumont, CRAM; Caroline Provost, CRAM; Eric Lucas, UQAM

From phytophagy to zoophagy: Evaluation of Lygus lineolaris (Palisot de Beauvois) (Hemiptera: Miridae) trophic behavior under different IPM strategies in strawberry fields,

The Tarnished plant bug (TPB), Lygus lineolaris (Palisot de Beauvois) (Hemiptera: Miridae), entails one of the most actual phytosanitary problems in North America because no efficient control strategy is available. This omnivorous species shifts from phytophagy to zoophagy susceptibility changing its population dynamics and distribution in the field while exerting variable crop damage. Here we present a project to reveal TPB trophic choices under different integrated pest management strategies (IPM) in strawberry fields: i) the use of mustard (Sinapis Alba) (L.) and buckwheat (Fagopyrum esculentum) (Moench) as trap crops, ii) the use of the predator Nabis americoferus (Carayon) (Hemiptera: Nabidae) and, iii) the use of the parasitoid Peristenus digoneutis (Loan) (Hymenoptera: Braconidae). Then, by different and complementary experiences in the field and in the laboratory (behavioral, molecular & olfactometer tests, modelling, etc.), TPB feeding choices under simple & combined IPM strategies and in the presence of alternative crop pests, will be assessed. Overall, the design of a complex IPM strategy in relation to TPB behavior is a new perspective of pest study that can completely change the way of managing TPB and may finally succeed controlling it.

Solís Sosa, Rodrigo, Simon Fraser University; Arne Mooers; Maxim Larrivee; Christina Semeniuk; Sean Cox

Understanding the Monarch Butterfly Migration: A Systems Dynamics Approach

The monarch butterfly, iconic species that migrates annually across North America, has steeply declined in numbers over the past decade. Currently, the most studied and supported cause of the monarchs plight is the milkweed-limiting hypothesis. This hypothesis states that milkweed loss across the monarchs breeding range due to the use of GM-specific herbicides has been the bottleneck of its migratory and biological cycle. Recently, evidence has accumulated suggesting that this might not be the only factor affecting the monarch, and perhaps not the most important. Here, we built a population model of the monarch butterfly through a System Dynamics approach to assessing the leverage that different alternative factors (anthropogenic and non-anthropogenic) may have in the overall trends seen in the overwintering colonies. Namely, we wanted to explore if the monarch was affected by patch configuration (depensatory effects), by parasitism (change in sex ratio over time), and climate change (increase on extreme weather events during the fall migration), and compared them with the effect of the primary current hypothesis, the milkweed-limiting hypothesis. This research is on its final stages and preliminary results and insights will be shared.

Solmundson, Kirsten; Jeff Bowman; Rebekah Horn; Rebecca Taylor; Micheline Manseau; Paul Wilson

Evolutionary Genomics of Ontario’s Boreal Caribou

Caribou (Rangifer tarandus) is an iconic North American species currently experiencing declines in range and population size. In Canada, caribou are divided into 12 evolutionarily significant units; all are currently at risk of extinction. These lineages can broadly be divided by their location during the Pleistocene glaciation- barren-ground, north of the Laurentide ice sheet, and boreal, south. Despite a northward contraction over the past century, a few herds of boreal caribou (R. t. caribou) have persisted >150km south of the continuous range, on the Lake Superior coast and near-shore islands. These herds have recently experienced dramatic declines, raising conservation concerns. A study indicated most boreal caribou in Ontario have introgressed with barren-ground caribou (R. t. groenlandicus) following the retreat of the ice sheet (~10 kya). We are examining the evolutionary history of boreal caribou using admixture tests, phylogenomic trees, and
Principle Component Analysis (PCA) with whole genome data collected from herds throughout Ontario, Manitoba, and Quebec. Our preliminary results indicate that the Lake Superior herds may represent an ancestral lineage of boreal caribou that, due to isolation, has not introgressed with barren-ground caribou. This research aims to reveal the evolutionary origins of Ontarios caribou to encourage scientifically-informed management.

Soroye, Peter, University of Ottawa; Deirdre Leowinata, University of Ottawa; Maxim Larrivée, Insectarium de Montréal; Charles-A. Darveau, University of Ottawa; Jeremy T. Kerr, University of Ottawa

Absence of latitudinal and temperature clines in dispersal traits in *Lycaena epixanthe* highlights importance of contiguous habitat for climate change-related range expansion

Warming temperatures cause poleward range expansion for many species, including butterflies. While relaxation of speciesphysiological constraints is likely to facilitate range expansion, genetic variation and phenotypic plasticity can also drive these shifts. In the Hudson Bay Lowlands and James Bay area of Canada, climate warming accelerated sharply in the late 1990s, which could have created a strong impetus for geographical range expansions in species found there. We collected 478 specimens of Bog Copper butterflies (*Lycaena epixanthe*) over the summers of 2011 and 2012, from a transect which passed from the center to the poleward limit of the Bog Coppers known distribution in Eastern Canada. We investigated variation in morphological and physiological traits across this gradient and for evidence of selection for increased dispersal capacity at these poleward range limits. Unexpectedly, wing surface area did not vary across the transect, and mass and wing loading increased nearer to the speciesnorthern range boundary. Wing surface area increased by ~17% compared to historical records, suggesting warming drove uniform phenotypic or evolutionary responses favoring increased dispersal capacity. Metabolic enzyme activity (phosphoglucose isomerase, PGI; hexokinase, HK; and citrate synthase, CS) did not vary with proximity to the range edge. While there was no evidence that frontier populations compensated physiologically for lower flight performance in colder environments through selection on enzyme activity levels, we cannot rule out selection on polymorphic enzymes and other properties associated with polymorphism, such as thermal sensitivity. While speciesmorphology and physiological traits may play important roles in poleward range expansion with climate change, patterns in these traits need not follow simple geographical gradients to facilitate dispersal beyond historical range limits. We highlight the importance of maintaining contiguous habitat for speciesadaptation to rapid climate change.

Sperling, Felix, University of Alberta; Julian Dupuis, University of Kentucky; John Acorn, University of Alberta; Scott Nielsen, University of Alberta; Felix Sperling, University of Alberta

Gene flow within a butterfly (*Papilio machaon dodi*) metapopulation persisting in a dendritic ecological network of riverine corridors

Southern Canadian populations of the swallowtail butterfly, Papilio machaon dodi, are restricted to eroding habitat along banks of major rivers where their larval host plant, Artemisia dracunculus, occurs. This presents an opportunity to infer how habitat connectivity relates to gene flow and population structure in a vagile species. Habitat suitability models indicate that eroding banks of the Red Deer, South Saskatchewan, Old Man, and Milk River comprise a dendritic ecological network of habitat corridors in a matrix of unsuitable prairie and agricultural habitat. However, while butterfly larvae may be limited to specific habitats, gene flow among disjunct populations may be structured by long-range dispersal of vagile adults with less specific habitat requirements. To assess gene flow and population structure, we used dRAD sequencing to map thousands of SNPs across the nuclear genome of 161 individuals collected in southern Alberta. Hierarchical population structure was assessed using model-based clustering analyses, and pairwise genetic distances were estimated between all individuals. Landscape genomic analyses did not accord with connectivity predictions based on habitat suitability, suggesting that habitat suitability and landscape permeability are distinct conceptual constructs. Other factors, such as environmental variation throughout the species range, may determine spatially divergent population structure.
Sperling, Janet, University of Alberta; Jacalyn Normandeau, Department of Biological Sciences, University of Alberta; Zachary MacDonald, Department of Renewable Resources, University of Alberta; Evelyn Merrill, Department of Biological Sciences, University of Alberta; Felix Sperling, Department of Biological Sciences, University of Alberta; Katharine Magor, Department of Biological Sciences, University of Alberta

Is the variability of bacterial microbiomes of ticks a methodological artifact or biologically real?

Ticks are associated with hundreds of bacteria, but recent research has argued that this diversity is an artefact due to overamplification of surface bacteria or contaminants from the DNA extraction process. We used 16S rRNA sequences to survey variability in the bacterial communities associated with the one-host winter tick, Dermacentor albipictus, on elk, Cervus canadensis, in the Ya Ha Tinda area of Alberta. By restricting our focus to one tick species with a simplified life cycle on a single host species and a single location, we expected that if overall bacterial diversity is due primarily to external contaminants then we would find lower diversity than has been reported for ticks exposed to more diverse conditions. We examined bacterial diversity on host elk of differing ages, sexes and migratory status, as well as ticks of differing life stages and sexes. We found extensive variability in bacterial diversity, with a trend toward greater diversity in tick males and nymphs than females, but no differences among elk groups. This diversity was comparable to that reported for other ticks sampled under more heterogenous conditions. We conclude that the bacteria associated with ticks reflect genuinely diverse biological assemblages, rather than error from lab sampling processes.

Spicer, Heather, Memorial University (Grenfell Campus); Heather Spicer1,3; Joseph Bowden2,3; Eric Moise2,3; Raymond Thomas1. 1Memorial University (Grenfell Campus), Boreal Ecosystems and Agricultural Sciences program 2Memorial University (Grenfell Campus), School of Science and Environment, 3Canadian Forest Service, Atlantic Forestry Centre

Physiological consequences of climate change on the performance and metabolism of the eastern spruce budworm (Choristoneura fumiferana, Clemens)

Climate change is projected to have significant consequences for forest ecosystems, including for eruptive forest insects, such as the spruce budworm. Despite current knowledge that temperature affects insect performance (e.g., reproduction, body mass, feeding), the underpinning physiological mechanisms are not yet fully understood. Using environmental chambers, I established six temperatures (n=6) to simulate a range of historical and projected growing season temperatures for Newfoundland, Canada. I monitored growth, development, feeding and metabolic rate (using an infrared gas-exchange analyzer). My results indicate that temperature significantly decreased development times for both pupae and adults (p < 2.2 x 10^-16), but there was no consequence for pupal (p= 0.054) and adult mass (p= 0.952). At both fifth-instar and adult stages, an increase in temperature resulted in a significant increase in metabolic rate (L5: p= 0.043, and Adult: p= 0.014). Feeding assay results suggest that despite shorter maturation periods and greater metabolic losses, the lack of an effect on budworm mass can likely be attributed to the positive relationship observed between warming and compensatory feeding (p= 0.019 for net growth efficiency and p= 0.045 for growth rate). Work to analyze budworm lipids is also underway, which could provide further insight for performance under future climate scenarios.

Springer, Stevan, University of Prince Edward Island

A test of phenotypic adaptation in full genetic resolution.

Despite countless examples of non-neutral molecular evolution, we still have no statistical way to determine which traits hold the fitness differences that drive molecular adaptation. I will describe a test of adaptation which uses mutational neighborhoods to estimate the probability of a given phenotypic change. The neighbourhood of changes created by all single mutations of an allele tells us the accessibility - how common or rare a phenotypic change is by mutation alone. This space provides a null model for trait evolution. Traits that evolve by a series of accessible changes could be spandrels – they diverge as expected given their space. Deviation from this null expectation (evolution toward a phenotype rarely produced by mutation) implies selection on the measured trait. I apply this logic to the evolution of myoglobin in whales. Whales hold oxygen in their muscles, and selection to increase dive time has resulted in substitutions that increase myoglobin concentration. These mutations simultaneously increase two traits: folding stability and surface charge. Either
difference could plausibly prevent precipitation at high concentration, so which of the two traits did selection target? I used biophysical estimates on the 3D structure of myoglobin to estimate neighborhoods for both stability and charge. I found that the divergence in myoglobin stability fits the null expectation, it increased by accessible changes and thus could be a spandrel. The difference in charge appears to be an adaptation. Charge evolved in an improbable direction given the space, and so it was likely a direct target of selection.

Srivastava, Diane, Canadian Institute of ecology and Evolution (CIEE)

Preparing for the future by rescuing the past: Canada's data crisis and how we can fix it,

Good science needs good data. The preservation of ecological and evolutionary data has become critical in a rapidly changing world, as it allows the setting of historical baselines, the fitting of population models, and guides the restoration of previous ecosystems. However, there have been only localized attempts to ensure that data remains accessible, and most of these focus on current data collection. A critical need is to recover past research data, some of which stretches back decades through generations of research careers. I describe here the Living Data Project, a new initiative spearheaded by the CIEE, in which we pair graduate students trained in data management with either retiring researchers or historical datasets, and then use the rescued datasets as nuclei for new analyses.

St. Clair, Colleen Cassady, University of Alberta; Anne Forshner, Parks Canada Agency; Aditya Gangadharan, University of Alberta and IUCN; David Laskin, Parks Canada Agency; Jesse Whittington, Parks Canada Agency

Railway mortality for several mammal species increases in areas with poor sight lines and escape terrain

Railways are an important source of direct mortality for many populations of large mammals, but unlike roads in this context, have been little studied or mitigated. We evaluated temporal and spatial factors affecting mortality risk using 646 railway morality incidents collected over 24 years through Banff and Yoho National Parks where train strikes have become a leading cause of mortality for grizzly bears. The spatial analysis compared topographic and land cover attributes of mortality locations to paired random locations at three spatial scales for three guilds; bears, other carnivores, and ungulates. We ranked variables by summed model weights across guilds and scales. Mortality risk generally increased in areas with high track curvature, lower forest cover, near water, and near roads. Mortality risk was moderately correlated with maximum posted train speed and topographic complexity. Factors affecting mortality risk varied across guilds but not spatial scales within guilds. Mortality rates were highest in winter, spring, and early summer for ungulates, other carnivores, and bears, respectively. Mitigations to reduce mortality risk could focus on areas where wildlife have poor sight lines and escape terrain, especially near water.

Standen, Katherine, Wilfrid Laurier University; Jennifer L. Baltzer, Wilfrid Laurier University

Environmental Drivers of Plant Community Composition and Function Across a Boreal Productivity Gradient

Amplified climate warming in Canada’s boreal forest is leading to permafrost thaw and changes in soil nutrient availability, both of which may drive changes in plant function either through plastic responses of plants to changing environmental conditions or shifts in community composition. Changes in traits at a community scale may impact ecosystem productivity but we know little about the magnitude of these changes or the main drivers in boreal systems. To this end, we sampled plant community composition and function across an environmental gradient in a boreal permafrost peatland to determine whether species turnover or functional trait plasticity was driving changes in community function and evaluate environmental drivers of these changes. Variability in community function across this boreal peatland site seemed to be due mainly to shifts in community composition. In general, both community composition and function were predominantly driven by depth to permafrost. Specifically, deeper permafrost lead to a shift in community composition from dominance of slower-growing evergreen shrubs to that of faster-growing graminoid species with a corresponding increase in faster plant traits, which may lead to greater overall ecosystem productivity. Overall, our study provides clearer understanding of how continued climate change will shape the plant dynamics, and thus ecosystem productivity, of Canada’s boreal peatlands.
Sternan, Jillian, DePaul University; Abigail C. Leeper; Jalene M. LaMontagne, Department of Biological Sciences, DePaul University

Synchrony of Mast Seeding Patterns in a Boreal Forest Community

Mast seeding is defined as the synchronous and highly variable production of seed crops over time by a population of perennial plants. Studies of mast seeding are typically conducted on a single-species, however, it is rare for a species to exist in isolation. There are few studies on synchrony in mast-seeding patterns at a community level. While the predator-satiation hypothesis states that seed-predator populations are kept low and then satiated during a mast year, therefore community level synchrony would affect the reproductive success of multiple tree species. However, the pollination-efficiency hypothesis proposes that mast seeding events increase pollination success and therefore should be relevant for only single-species. To determine if mast seeding patterns are synchronous in a boreal-forest community, we deployed seed traps at six sites and quantified five years of seed production for both coniferous and deciduous tree species in Michigan, USA. We collected seeds in spring each year, counted seeds, and identified them to species/genus. We found moderate to low levels of synchrony in reproduction within sites. Differences in the proximate drivers of mast seeding across taxa and seed development times likely contribute to variation in community-level seed production patterns, which may also influence seed-predator population dynamics.

Stewart, Don, Acadia University; Don Stewart, Department of Biology, Acadia University; Sophie Breton, Département de Sciences Biologiques, Université de Montréal; Emily E. Chase, Institut Méditerranéen d'Océanologie y Microbes Evolution Phylégénie et Infections, Aix-Marseille University; Brent M. Robicheau, Department of Biology, Dalhousie University; Davide Guerra, Département de Sciences Biologiques, Université de Montréal; Manuel Garrido-Ramos, Departamento de Genética, Facultad de Ciencias, Universidad de Granada

Exploring the origin(s) of the unusual system of doubly uniparental inheritance of mitochondrial DNA in bivalves: How many times did it evolve?

Doubly uniparental inheritance (DUI) of mitochondrial DNA (mtDNA) in bivalves is the only known exception to the general rule of strict maternal transmission of mtDNA in metazoans. Discovered in the 1990s, DUI is characterized by the observation of two distinct sex-associated mitochondrial lineages that includes female-transmitted mtDNA inherited through eggs to all offspring, and male-transmitted mtDNA that is inherited through sperm and enters all eggs at the time of fertilization. Interestingly, this male mtDNA is only retained and subsequently transmitted through male offspring. This phenomenon is found in the orders Unionoida (families Hyriidae, Margaritiferidae, Unionidae), Mytiloida (family Mytilidae), Veneroida (families Arcticidae, Donacidae, Mactridae, Solenidae, Veneridae) and Nuculanoida (family Nuculanidae). The taxonomic breadth of these families within the Bivalvia is enormous, and there has been considerable debate since DUI was first described as to whether this phenomenon evolved only once or multiple times. Recent attempts have been made to use reading frames that have no obvious homology to previously characterized genes and no blatantly known function (called mitochondrial ORFan genes) in bivalves to provide insights into the singular origin (or multiple origins) of DUI in ancestral bivalve lineage(s). Here we review the results of various in silico analyses that have focused on both describing the potential homology of these ORFan genes with known genes and also tried to characterize their putative functions. For example, of the current hypotheses aimed at explaining the origin(s) of DUI, some propose that some of these ORFans are the product of endogenization of selfish viral genes into the mitochondrial genomes of ancestral bivalves. Conversely, others have suggested that ORFans are the product of ancient gene duplications followed by the evolution of novel gene functions. We review the current state of knowledge in this area and discuss the arguments put forward for doubly uniparental inheritance evolving once or multiple times."

Studd, Emily, McGill University; Allyson Menzies; Michael Peers; Yasmine Majchrzak; Rachael Derbyshire; Dennis Murray; Stan Boutin; and Murray Humphries

Seasonality of behaviour and species interactions in a boreal forest food web
Organisms choose what to eat, where to hide, and when to move with the general purpose of maximizing resource gains while minimizing predation risk. The outcomes of these behavioural decisions have implications on food web structure by shaping interactions between species. In seasonal environments the transition from frozen dormant winters to warm lush summers creates shifts in daily activity patterns that have downstream implications on food web structure. Here, I investigate the behavioural basis of seasonal species interactions, and activity-mediated food web structure. I use a simplified food web consisting of two consumers - a vegetative browser (snowshoe hare) and a seed-eater (red squirrel) - with a shared predator (Canada lynx) living in a highly seasonal environment where resource availability and species abundances fluctuate through time. With the help of newly developed miniature dataloggers to simultaneously record fine scale behaviour of the predator and both consumers over 4 years, I quantify individual behavioural responses to resources and environmental change. Combining the behavioural decisions by all three species to changing conditions, I determine interaction strengths, and provide empirical evidence that seasonal food web structure is driven by behavioural mechanisms.

Sullivan, Jennifer, Memorial University of Newfoundland; Carissa Brown

Come from away: Non-native plant establishment in Newfoundlands boreal forest,

The rate of non-native species introductions is rising globally. Newfoundland has one of the longest North American histories of continuous plant species introductions; one measured in centuries. Yet, we know little about the invasiveness of the 24.9% of Newfoundlands flora that is non-native, or of the ability of the islands boreal forests to resist non-native plant establishment. Chronic linear disturbances, such as recreational trails and forest roads, pervasive throughout North American boreal forests, are particularly vulnerable to the establishment of non-native plant species and may act as corridors of invasion. We examined presence of non-native plants along chronic linear disturbances within boreal forests of Newfoundland, and assessed the resistance of adjacent boreal forests to non-native plant establishment. We found that non-native plants occurred on the majority of observed linear disturbances; i.e., the forest stands we studied are surrounded by non-native species. Yet, non-native species have not yet established within adjacent forest areas. Under ongoing global change, our findings show that the stage is set for non-native plant establishment within the boreal forest of Newfoundland, as the increased pressures from climate change, globalization, and natural and anthropogenic disturbances continue to influence the distribution and establishment of these species.

Summers, Mindi, University of Calgary; Cole Walsh; NG Holmes; Michelle K Smith

EcoEvo-MAPS: An ecology and evolution assessment tool that targets student thinking across the major

An assessment tool Ecology and Evolution Measuring Achievement and Progress in Science or EcoEvo-MAPS was designed to measure student thinking in ecology and evolution at multiple time points during an undergraduate degree. EcoEvo-MAPS targets foundational concepts, and asks students to evaluate a series of predictions, conclusions, or interpretations as likely or unlikely to be true given a specific biological scenario. This assessment can be used by departments to measure changes in student thinking over time and as a data source when making curriculum decisions. Evidence of validity and reliability for EcoEvo-MAPS was collected through an iterative process of faculty review, student interviews, and analyses of assessment data from over 3000 students collected at 34 different institutions. These statements range in difficulty and aggregate results allow inference of which concepts students understand, learn, or struggle with during the major. EcoEvo-MAPS is part of a suite of freely available curricular instruments that can now be administered through a web portal where students complete the assessment online. The portal returns a report to the instructor that includes aggregated information on overall student performance organized by ecology and evolution topics, the Ecological Society of America Four-Dimensional Ecology framework, and Vision and Change core concepts.

Supple, Megan, University of California

Mountain lion genomes provide insights into the genomic consequences of inbreeding and genetic rescue
Mountain lions are the most widely distributed felid in the Western Hemisphere. However, mountain lion populations across much of North and South America have become increasingly isolated due to human persecution and habitat loss. To explore the genomic consequences of this isolation, we analyzed whole genomes from a panel of individuals from across their geographic range. Using these genomes, we found signatures of close inbreeding in the isolated North American mountain lion populations. However, tracts of homozygosity were rarely shared among mountain lion populations, suggesting that assisted gene flow would restore local genetic diversity. The genome of a Florida panther descended from translocated individuals from Central America had long tracts of homozygosity, in spite of recent outbreeding. This suggests that although translocations may introduce diversity into a population, sustaining diversity in small and isolated populations will require either repeated translocations or restoration of landscape connectivity. Mountain lions provide a rare opportunity to examine the potential to restore diversity through genetic rescue and to observe the effects of translocation. Our methods and results provide a framework for genome-wide analyses that can be applied to the management of small and isolated populations.

Sutton, Alex, University of Guelph; Dan Strickland, Retired Chief Park Naturalist, Algonquin Provincial Park; Nikole Freeman, University of Guelph; Marjorie Sorensen, University of Guelph; Ryan Norris, University of Guelph and Nature Conservancy of Canada

Climate-mediated carry-over effects drive population growth rate in a boreal passerine

Understanding how events throughout the annual cycle are linked is important for predicting variation in fitness, but whether and how carry over effects scale up to influence population dynamics is not known. Using 38 years of demographic data and a year-round integrated population model, we examined the influence of climatic conditions and density throughout the annual cycle on the population growth rate of Canada jays (*Perisoreus canadensis*), a resident boreal passerine that relies on cached food for over-winter survival and late-winter breeding. Our results demonstrate that fall climatic conditions, most notably freeze-thaw events, carried over to influence late-winter fecundity, which, in turn, was the main vital rate driving population growth. These results are consistent with the hypothesis that warmer and more variable fall conditions accelerate the degradation of stored food that is relied upon for successful reproduction. A simulated food cache experiment also supported this hypothesis: the best environmental predictor of weight loss in meat and berries, two food types commonly consumed by Canada jays, was the number of freeze-thaw events. Our study not only provides experimental evidence of a climatic mechanism linking events across the annual cycle but also demonstrates how carry-over effects can impact long-term population dynamics.

Sweeney, Jon, Natural Resources Canada, Canadian Forest Service; Simon Pawlowski; Peter Mayo; Peter Silk; Cory Hughes; N. Kirk Hillier

Influence of trap colour, trap type and trap height on detection of the invasive beech leaf-mining weevil, Orchestes fagi L.

The beech leaf mining weevil, Orchestes fagi L. (Coleoptera: Curculionidae), is a pest of beech trees in Europe that has recently become established and invasive on American Beech in Nova Scotia, Cana"

Szojka, Megan, University of British Columbia; Dr. Rachel Germain

The influence of dispersal through the seedbank on metacommunity diversity and population persistence

I aim to characterize any naturally occurring directional dispersal in a model system of annual plant communities, by determining the composition and species richness of the seed bank within and extending outside of habitat patches, into the inhospitable invaded matrix. In a metacommunity context, seed dormancy allows for the dispersal of seeds through time and space, as a buffer to persist through unsuitable environments. This approach will allow me to quantify the degree which endemic populations combat fragmentation within the natural landscape via dispersal potential through temporal space, and inversely the degree of dispersal from the matrix into patches by invasive grasses. These results will provide insight on how dispersal out of a patch could interact with the landscape to be directionally bias, as well as indicate what landscape or patch features may modify the degree or pattern of directionality."
Tafoya-Rangel, Felipe, Autonomous University of Aguascalientes 1; Ocampo-Acosta, G.A., Autonomous University of Aguascalientes 2; Escoto-Moreno, J.A., Autonomous University of Aguascalientes 3; Sigala-Rodriguez, J. J., Autonomous University of Aguascalientes 4; Silva-Briano, M. Autonomous University of Aguascalientes

Insects associated with Quercus sp. galls from Sierra Fria, State of Aguascalientes, Mexico

The galls are morphological arrangements that grow in an unusual way on the leaves of various trees. They are usually created by the parasitic effect of an arthropod. The galls in the genus Quercus sp. are considered a microenvironment because in them different groups of organisms are associated as inducers, tenants and parasitoids. In Mexico, 184 species of Cynipini have been described, however, little is known about the associated fauna (tenants and parasitoids) and their ecology. In this study, the fauna associated with galls is reported for the Sierra Fria region in the state of Aguascalientes (central Mexico). During 18 months of study, 85 specimens of 14 species of Quercus with the presence of galls were sampled. A total number of 3,400 galls were found belonging to 34 different types and a total of 833 associated insects were collected. The oak species most frequently found in the Sierra Fria were Quercus grisea (14), Q. aristata (12), Q. striatula (10) and Q. potosina (10). Most of the galls found were of the spherical type (75%), vase (49) and honeycomb (24). Of the total number of insects collected, the great majority (90.8%) are wasps of the Chalcidoidea, Sphecidae, Vespidae and Cynipidae Families among which have been identified the genus Andricus as inducer; Synergeus equihuai as tenant and Torymus aceris as parasitoid.

Tapia, Andrea, Universidad San Francisco de Quito; Xavier Zapata-Ríos, Valeria Ochoa-Herrera; Alex S. Flecker, Todd A. Walter; José Schreckinger

Ecohydrological classification of rivers in Ecuador

Classification of rivers on the base of their hydrological regimes, biodiversity patterns, and ecosystem processes is critical for water resource management at national and regional levels. We compiled and organized hydrological information of 85 stations across Ecuador, and used the resulting dataset to calculate ecohydrological indicators, cluster rivers types based on similarities (nMDS and PCA analysis) and generate a catchment classification through an inductive procedure. Data on biodiversity (invertebrates and fish) and ecosystem processes is still being processed. Preliminary results with different scenarios resulted in a maximum of 10 river types for continental Ecuador: three types from the Pacific coastal lowlands, four from the Andean cordillera, and three from the Amazonian floodplains. Coastal lowland rivers showed pronounced hydrological seasonality, with rivers flowing through dry forest and tropical rain forest. Andean cordillera rivers had one or two peaks of hydrological response and run through paramo, high montane forest and dry shrub forest. Amazonian rivers exhibited almost no seasonality with several hydrological peaks, and run through tropical rain forest, low montane forest and inundated forest. Based on the different ecohydrological regimes and ecosystem responses, here we offer information and guidelines for customized planning for better water resource management.

Taylor, Rebecca, Trent University; Paul Wilson, Trent University; Rebecca Taylor, Trent University

Long-term Non-invasive Monitoring of Caribou: Transitioning from Genetics to Genomics,

It has been 15 years since we collected the first fecal sample from caribou and were able to successfully extract high quality and quantity DNA from this material for genetic profiling. Since then and in collaboration with provincial, territorial and federal governments, Indigenous organisations, wildlife management boards and industry, we have analysed more than 40,000 samples from across Canada. We have developed a suite of field, laboratory and analytical methods, and have shown how genetic and ecological data can be used to generate information needed for management. Project collaborators have been highly proactive in recognizing the potential of this research in supporting a single web-based national database and repository through significant investments in field collections and in the development of tools and protocols. As a result, the national database and repository has allowed for greater collaboration and synergies between individual projects and provided a framework for large-scale and long-term monitoring work to support regional, provincial/territorial and national conservation programs. In particular, the data has been critical in assessing short- and
long-term changes in population distribution, movement and demographic parameters. Based on this experience, we expand on this foundation and embrace new technologies such as next generation sequencing and deep learning to further develop population and landscape genomic methods for long-term monitoring of caribou.

Rebecca S. Taylor, Rebeckah Horn, Sonesinh Keobouasone, Micheline Manseau, Paul Wilson

Whole genomes assess the roles of parallelism and introgressive hybridization in caribou ecotype evolution

We completed high coverage whole-genome sequencing of caribou (Rangifer tarandus) from across North America to investigate the evolution of subspecies and ecotypes. Genomic demographic reconstruction indicated a major expansion of caribou during the glacial interstitial stage of a largely ice-free North America 120 kya, with subsequent differential population trajectories of emerging subspecies. Ecotypic characterization does not match the evolutionary history of some populations, and potential phenotypic convergence of ecotypes was observed in a Beringian derived lineage evolving a boreal ecotype independent of woodland caribou where it is currently placed. Genomic characterization detected admixture among lineages, and introgression among lineages is consistent with the recent findings of many mammalian species in that introgression is a more important evolutionary driver than previously thought. Our genomic revision will provide a more accurate characterization of introgression and the complexity of ecotypic divergence relevant to delineating conservation units under Canada’s Species-at-Risk Act (SARA).

Tekwa, Edward, Rutgers University; Martin Krkoeak; Malin Pinsky

Statistical inference for alternative-stable-state models with application to coral-macroalgal bistability

Multiple attractors and alternative stable states are defining features of scientific theories in physics, biology, and economics. Here we describe a simple method that opens such theories to statistical inference by harnessing independent observations with low temporal resolution. The key is transforming the multiple-attractor, one-to-many model into a one-to-one model by allowing initial conditions to determine final states, which directly leads to parameter estimation procedures and statistics including goodness-of-fit, confidence intervals, and P-values. We apply the method to a simulation example based on coral-macroalgal dynamics, a system that has been implicated to exhibit bistability. The results show that incorporating history allows us to infer alternative stable states while minimizing false positives, even in the presence of disturbances.

Thompson, Kirsten, University of Northern British Columbia; Brent W. Murray

Genomic Analysis of Recent Mountain Pine Beetle Expansion in Alberta

Mountain pine beetle (MPB) is one of the most destructive forest insect pests of the Anthropocene. Extremely high numbers and weather events led to mass movement MPB into novel habitat in Alberta in 2006. In this study we assess the current population structure of post-expansion MPB infestations in western Canada. Beetles were sampled from 51 sites within BC and Alberta in 2016. SNPs were generated from using a ddRAD protocol (enzymes Msp1 and Pst1) with single-end illumina sequencing. DAPC analysis shows that population structure is less defined within the expanded outbreak range within Alberta. Populations from isolated sites in southern BC cluster independently from populations in northern BC and Alberta. Preliminary analysis of both adaptive and neutral SNPs shows ongoing outbreaks in Jasper National Park have a higher degree of admixture compared to most other sampled sites, which supports previous findings by Trevoy et. al. (2018). Our results show that areas where MPB spread retain a similar genetic structure to likely source populations in northern BC, except for the Jasper National Park outbreak. The genetic patterns identified here will aid in the formation of forest management models as government and industry work to lessen the impact of this aggressive pest
Thompson, Ken, University of British Columbia; Mackenzie J. Urquhart-Cronish; Dolph Schluter University of British Columbia

Patterns of phenotype expression in hybrids

The phenotype of hybrid individuals ultimately determines their fate, but little is known about the general patterns of phenotype expression in hybrids formed between natural populations. We compiled data from studies where phenotypic traits were measured in a common environment for two parents and first-generation (F1) hybrids and quantitatively evaluated patterns of hybrid phenotypes as compared to parents. Our central finding is that F1 hybrids often show fairly extreme 'phenotypic mismatch' for ecologically-divergent parental traits. We also quantify general patterns of phenotypic dominance, maternal vs. paternal-biased phenotype expression, and investigate whether genetic distance predicts dominance or transgressive segregation. We also test a fundamental untested prediction of Fisher's geometric model of adaptation, and find support for the hypothesis that the genes underlying interspecific differences are highly pleiotropic. In sum, our study suggests that hybrids formed between ecologically divergent natural populations are typically not phenotypically intermediate, but rather display novel trait combinations similar to individual recombinant hybrids. Our synthesis suggests that ecology-based hybrid incompatibilities might be an important determinant of F1 hybrid fitness.

Thompson, Patrick, UBC Department of Zoology; Joey Bernhardt; Coreen Forbes; Nathalie Westwood; Kaleigh Davis; Bianca Trevi
go Segovia; Keila Stark; Jane Yangel; Mary O'Connor

Temperature and dispersal jointly determine the dynamics and functioning of pond metacommunities

How do changes in temperature across time and space affect the composition and functioning of ecological communities? Metacommunity theory predicts that dispersal buffers diversity and ecosystem functioning by allowing species to track their preferred temperatures. In contrast, metabolic theory predicts that rates of ecosystem functioning should increase with temperature but does not consider community composition or diversity. Combining these theories, we hypothesized that the metabolic response of communities should be reduced when communities are connected by dispersal. We tested this hypothesis using experimental pond metacommunities, each comprised of four-1000L mesocosms spanning a 4.5°C spatial temperature gradient and connected by one of three dispersal rates. This spatial temperature gradient was maintained, while allowing the mesocosms to fluctuate temporally with seasonal temperatures changes. Following metacommunity theory, zooplankton species differed in their response to temperature and their ability to track optimal conditions depended on dispersal. Following metabolic theory, we also found that the abundance of phytoplankton and rates of primary productivity increased with temperature. But, in contrast to our expectation, dispersal increased the sensitivity of these community properties to temperature. Our findings suggest that the response of ecological communities respond to changing climate will depend jointly on metacommunity processes and metabolic responses.

Thomsen, Corrina, UBC Okanagan; Brian Pickles, University of Reading; Jason Pither, UBC Okanagan

Province-wide patterns, and between-layer associations, of mycorrhizal host type within British Columbia forests

Plant-soil feedbacks within forests can facilitate or inhibit success among neighbour seedlings depending in part on the type of mycorrhizal association formed; ectomycorrhizal (ECM) associations tend to promote positive, facilitative effects whereas arbuscular mycorrhizal (AM) associations tend to generate negative, antagonistic effects. Given these potential feedbacks, details about the fine-scale prevalence and distribution of ECM and AM hosts, particularly within each forest layer, could improve our understanding of recruitment dynamics and diversity patterns within forests. Using forest survey data from more than 25,000 plots distributed throughout British Columbia (BC), we first show how the proportion of different mycorrhizal types varies between the herbaceous layer, the sub-canopy, and the canopy, and we map these patterns across BC. We then quantify the strength of the association between the proportion of ECM-compatible host cover in the canopy with the same proportion in the sub-canopy and herbaceous layers. Our findings reveal significant positive associations, but also underscore how the probability that an ECM-compatible seedling co-occurs with another ECM-compatible understory plant varies enormously among forest types. Future field work will aim to quantify mycorrhizal colonization and type among herbaceous ground-layer plants, and their below-ground interactions with canopy progeny.
Investigating barriers to hybridization and vigour contributing to the low frequency of Typha × glauca (hybrid cattails) in Nova Scotia

Genomic compatibilities between progenitors, and subsequent hybrid fitness, can collectively lead to varying hybrid frequencies across regions of parental sympatry. In areas around the Laurentian Great Lakes, Typha × glauca is an invasive plant hybrid of native Typha latifolia and introduced Typha angustifolia. However, in other areas of parental sympatry including Atlantic Canada, T. × glauca has been reported as either rare or non-existent. We investigated whether low hybrid frequencies in Nova Scotia are influenced by either reproductive barriers that prevent hybrid formation, or environmental factors (salinity) that reduce hybrid fitness. Flowering times of progenitor species overlapped, indicating that asynchronous flowering times do not limit hybrid formation in this region. Viable progeny were created from interspecific crosses of Nova Scotia T. latifolia and T. angustifolia, indicating that there are no genomic barriers to fertilization and germination of hybrid seeds. Typha × glauca germination in high salinity was significantly lower than that of T. latifolia, but there was no difference at lower salinities. Therefore, while germination of hybrid seeds may be impeded in the coastal wetlands where salinity is high, inland sites have lower salinity and thus an environment conducive to hybrid germination. However, once established as seedlings, hybrids appear to have a fitness advantage over T. latifolia across all salinities through higher ramet production. Moreover, T. latifolia from Ontario had lower germination and survivorship in high salinities compared to T. latifolia from Nova Scotia, which could reflect local adaptation by T. latifolia to increased salinity. Collectively these findings show that interactions between environment and progenitor lineages can influence the viability and the consequent distribution and abundance of hybrids.

Males always reproduce at first opportunity, but females know better

Many forest ecosystems are characterized by intermittent and massive tree seed production, or masts, that constrain the reproduction of seed consumers. One such example is the mast of American Beech that drives the reproduction of eastern chipmunks (Tamias striatus) in southern Québec. Because masts do not occur every year, chipmunk first reproductive opportunity occurs at either 7 or 15 months old, for an average lifespan of 24 months. We used data from a long-term survey of wild chipmunk subpopulations to understand how pulsed resources influence their reproduction, key life-history traits and early-life telomere length. We found that males always reproduce at first opportunity, whereas 30% of females skip this opportunity and become sexually mature at 22 months old. We also reveal significant relationships between mothersage and life-history traits of their offspring, with juveniles from 22 months-old mothers having lower body mass and longer telomeres at weaning than offspring from younger or older mothers. In addition, we found trans-generational effects of mothersage on the lifetime reproductive success of their offspring. Together, our results suggest that postponing reproduction that late in life in a pulsed-resource system may have long-term fitness benefits by affecting the growth-reproduction-self-maintenance trade-offs of the offspring.

Understanding the genetic basis of pathogen loads in the honey bee (Apis mellifera)

The honey bee, Apis mellifera is a model organism for sociogenomics and is one of the most important managed pollinators. As such, recent threats to honey bee health are particularly alarming. The social honey bees live in highly crowded nests providing favorable conditions for the spread of infectious diseases. But honey bees have several social and individuals mechanisms for protecting themselves against disease. The BeeOMICS consortium has sequenced the genomes of approximately 1,000 honey bee colonies in Canada, which were evaluated for a number of traits, including the abundance of several pathogens within each colony. I plan to carry out genome-wide association studies (GWAS) on
colony pathogen loads to gain a deeper insight into the genetics of immunity in honey bees. This research will set the groundwork for breeding disease resistant honey bees using marker assisted selection.

Tollett, Christina, Queen's University; Evelyn L. Jensen; Christina Tollett; Markus Dyck; Marsha Branigan; Peter V.C. de Groot; Stephen C. Lougheed

Pan-Arctic population structure of the polar bear (Ursus maritimus) using genome-wide markers

Global warming is causing unprecedented change across the Arctic with drastic reductions in sea ice. Polar bears (Ursus maritimus) rely on ice for hunting, mating, and dispersal, and are predicted to be severely impacted by changing sea ice and shifting access to prey. Baseline information on population structure is critical to predicting and monitoring the impacts of climate change. Drawing on tissues from subsistence hunted bears, archived by the Nunavut and Northwest Territories governments, we have genotyped 358 individuals for >13,000 single nucleotide polymorphism (SNP) loci, spanning 12 of the 13 management units in Canada. Our population structure results are robust across various clustering methods showing three genetic clusters across the Canadian Arctic: the Arctic basin, the Arctic Archipelago and the Hudson complex. These results mirror those from analysis of DNA microsatellites, Analysis of a reduced panel of ~400 SNPs developed for a Genotyping-in-Thousands assay intended to be used to genotype DNA from degraded tissues and feces. Our work provides more detailed and reliable depiction of polar bear population structure across the Canadian Arctic and can help inform management.

Tousignant, Louka, Département de biologie, Pavillon Rémi-Rossignol; Louka Tousignant; Billie Chiasson, Gaétan Moreau Département de biologie, Pavillon Rémi-Rossignol, Université de Moncton

Same old same old? Landscape-scale management alters beetle community assembly within remnant old-growth forests

Old-growth forests exhibit unique ecological features such as structural diversity which includes canopy height, forest understory, basal area occupancy, tree debris size and associated decomposition class. They thus can provide several microhabitats and fulfill the needs of many species, particularly late successional species. However, forest management fragments the forest landscape, thereby potentially altering animal species assembly within isolated old-growth forest remnants. Here, we tested whether the animal species complex differs between old-growth forest stands surrounded by managed or conservation areas. To this end, flying Coleoptera communities were documented using flight intercept traps placed in 12 old-growth forest stands located within intensely-managed areas or conservation areas. To allow for a generalization of the results, four mixedwood, four softwood and four hardwood stands were used. 17147 beetle specimens from 213 species were collected. Results showed that flying Coleoptera communities changed in response to local resources and landscape management. Close habitat species such as Glischrochilus sanguinolentus were associated with old-growth forests within conservation areas while open habitat species such as Mordellaria serval were associated with old-growth forests within managed areas. This suggests that a buffer conservation area is required around old-growth forest remnants to allow for animal assembly to be unaffected.

Tremblay, Philippe, University of Ottawa; Heather Kharouba, University of Ottawa

The Role of Cold Hardiness at the Northern Range Edge Limit

Temperature is a well know factor driving species range shifts. Although several macro-scale studies have investigated this pattern, there are few instances in which the links between large scale climatic variables were tested at the local scale. In this study, we investigated the effect of low-temperature and timing on P.cresphontes northern range edge. To test those interactions, we looked at the northern range distribution of the Giant Swallowtail (Papilio cresphontes). Range limit was determined using MaxEnt and relevant climatic variables. The relevance of the most significant variables was tested in a laboratory setting using 117 caterpillars collected at the range limit. Caterpillars were tested for their supercooling point, chill-coma temperature and survival at different low temperatures. Interestingly there did not seem to be a matching limitation in individuals, as caterpillars cold tolerance were higher than temperatures present at the northern range edge. We were able to confirm that in October the Giant swallowtail uses a freeze avoidant strategy suggesting that their
northern range edge is defined by factors other than absolute low temperatures. Further investigation into the ecological relevance of these physiological thresholds will improve our understanding of dispersion under changing climate.

Turcotte, Audrey, University of Ottawa; Fanie Pelletier, Université de Sherbrooke; Marc Bélisle, Université de Sherbrooke; Vincent Fyson, University of Ottawa; Dany Garant, Université de Sherbrooke

Transmission patterns of haemosporidian parasites in passerine populations: Identification of risk areas

Parasites are important stressors in natural ecosystems involved in host population dynamics by influencing the survival, growth, and reproduction success of exposed individuals. Comprehension of dynamic patterns in vector-borne parasites, such as haemosporidian parasites, is generally more complex given that their transmission is dependent on the distribution and abundance of vectors in the landscape. Indeed, climate factors and landscape composition can affect vector development, activity level, and abundance. Thus, understanding how and at which scale environmental factors affect host exposition level to vector-borne disease is crucial to identify transmission patterns and risk areas in animal communities. I will compare two studies, occurring at different scales, that evaluate how landscape features influence haemosporidian parasites prevalence in passerine populations. The first research assessed the prevalence and environmental determinants of haemosporidian parasites in a Tree swallow population living in an agricultural landscape of the southern Québec, Canada during a 4-year period. The second research evaluated how landscape and climate influence avian malaria distribution in diverse passerine species populations from 1,193 prevalence records, located across the Americas. These results bring new knowledge about vector-borne parasite dynamic in avian communities that will help in the identification of areas at risk and increase links between studies.

Turner, Russell, Queen's University; Sarah Sonsthagen, USGS; Robert Wilson, USGS; Ryan Franckowiak, Queens University; Marie-Josée Fortin, University of Toronto; Vicki Friesen, Queen's University

GETTING ONES DUCKS IN A ROW: CONSERVATION UNITS OF COMMON EIDERS (SOMATERIA MOLLISIMA) THROUGHOUT NORTH AMERICA

Anthropogenic climate change is resulting in a variety of consequences for ecosystems and biodiversity. Collectively these changes are negatively impacting species survival and are increasing rates of extinction. Species can, however, adjust to environmental changes through range shifts, phenotypic plasticity, or genetic adaptation. To ensure successful species conservation in the face of climate change, it is now crucial that a species capacity for such change, as well as existing evolutionary differences among populations, are incorporated into species management plans. This is particularly important for species dependent on Arctic conditions because climate change will disproportionately affect these regions. Here, I evaluate the spatial genetic structure of a highly mobile Arctic breeding sea duck, the Common Eider (Somateria mollissima) by analyzing double-digest restriction site-associated DNA sequencing (ddRAD-seq) data from 320 ducks originating from 24 breeding populations spread across North America. I identify two evolutionarily significant units that show a clear west-east divide, which is suggestive of two distinct glacial refugia. I also identify five to six genetically distinct management units and detect five potentially adaptive units within North America. I also identify a pattern of isolation-by-distance across my entire study area and within the Eastern evolutionary significant unit. However, a similar pattern was not evident within the Western evolutionary significant unit. Taken together, my results reveal biologically important population genetic structure that must be considered for the successful long-term management of the eider. My thesis contributes to the growing body of literature aimed at better understanding the broad spectrum of genetic differentiation observed in avian populations that inhabit the Arctic, which will help better manage their conservation.

Turner, Julie, Memorial University of Newfoundland; Christina M. Prokopenko, Memorial University of Newfoundland; Katrien A. Kingdon, Memorial University of Newfoundland; Daniel Dupont, Memorial University of Newfoundland, Sustainable Development - Wildlife Branch; Sana Zabihi-Seissan, Memorial University of Newfoundland; Eric Vander Wal, Memorial University of Newfoundland

The walking dead: testing whether end-of-life behaviors can be used to predict cause-specific mortality
Cause-specific mortality is among the most sought-after measures in population and wildlife ecology, but we rarely know causes of death paired with detailed behavioural data in natural systems. Quantifying movement, habitat selection, and sociality provides fine-scaled insight into the behavioural disparity between living and dying. For instance, in many group-living species, diseased individuals move slower, select different habitats than their group, or actively avoid groupmates. Animals moving through habitats closer to human activity and isolated from their group are exposed to greater human imposed mortality risk. Finally, predators can be killed by conspecifics when moving outside or along territorial boundaries. Here, we test if spatial and social behaviours indicate the cause of mortality in a gregarious carnivore. We use GPS collar data from two populations of free-ranging grey wolves (*Canis lupus*) in Manitoba, Canada that are exposed to a variety of mortality risks. Integrated step selection analysis demonstrates fine-scale behavioural changes which vary across different causes of mortality, e.g., disease, humans, and conspecific aggression. Understanding how remotely-sensed behaviours common to carnivores relate to mortality can help give insight about rarely observed parts of life in a non-invasive manner.

Ullah, Aziz, University of Alberta, Edmonton Canada; Jennifer Klutsch; Altaf Hussain; Nadir Erbilgin

How do chemotypic variations in a tree species affect its primary insect enemies?

Plants generally show large chemotypic variations in their susceptibility to phytophagous insects. We investigated chemotypes in lodgepole pine from progeny trials in Alberta using monoterpene concentrations in pine phloem and conducted two assays to assess their impact on the performance of mountain pine beetle and one of its fungal symbionts. We identified four chemotypes and used the monoterpene profiles from three pine families from each chemotype to amend artificial diets. Beetle diet consisted of phloem and sapwood mixed with agar and water. For fungal diet, we prepared malt extract agar. In separate assays, we placed adult beetles and fungi on artificial diet amended with the monoterpene concentrations representing each pine family. We found a significant effect of chemotype and family on beetle gallery length and weight change. Three families were least suitable for beetle host acceptance. We also found different results regarding the fungal growth on different families and chemotypes, with two families being least suitable for the fungus. This study demonstrates that performance of both mountain pine beetle and its fungal symbionts can vary by host chemotypes. Pine families which showed least suitability for both beetles and its symbionts can be grown in Alberta to promote beetle-resistant forests.

Umphrey, Gary

Local Studies as Instruments of Scientific Inference

In this talk I will address the scientific value of local taxonomic studies. Beyond their contributions to the body of knowledge commonly classified as Natural History, I argue that local studies contribute to broader scientific knowledge in ways that are often underappreciated. Examples will be drawn primarily, but not exclusively, from the literature on ants.

Valenzuela, Francisca, University of Concepción and Dalhousie University; 2 McCracken, Gregory R.; 1 Manosalva, Alirio; 1 Habit, Evelyn; 2 Daniel E. Ruzzante; 1 Laboratorio de Ecología y Conservación de Pezces, Departamento de Sistemas Acuáticos, Facultad de Ciencias Ambientales y Centro EULA, Universidad de Concepción; 2 Department of Biology, Dalhousie University

Teasing apart Percilia in the face of natural and anthropogenic alterations of gene flow

The effective conservation of biodiversity requires the precise determination of the species to be conserved. This is particularly difficult when the species are little known and further hampering conservation efforts when the species are morphologically ambiguous such as *P. gillissi* and *P. irwini* of the genus Percilia in Chile. In this study we analyzed populations of these species inhabiting two contiguous basins (Itata and Biobío basins), to clarify their genetic status, and understand population genetic connectivity. We sequenced a region of mitochondrial DNA (COI) for 290 individuals. Genetic diversity and population differentiation were evaluated using 28 microsatellite markers for 927 individuals.
Preliminary results demonstrated a high diversity of haplotypes throughout the sampling range and suggest that populations are expanding. The phylogenetic analysis exposes three differentiated clades, one of them composed of Itata individuals, one with Biobío individuals, and a third clade comprising Itata individuals sharing genotypes with Biobío individuals. These results determine the possible existence of a hybridization zone between the two basins, revealing an unknown population and hybridization structure between the two species of Percilia. We emphasize the utility of population genetics as a tool for the correct delimitation and conservation of these endemic species.

Van Herk, Wim, AAFC; Gerhard Gries; Regine Gries; Haley Catton; Scott Meers; Peter Landolt; Jennifer Otani; Ian Scott

Identification of sex pheromones of Canadian pest click beetle species

To date, pheromone-based monitoring for pest click beetles in Canada has only been possible for the three introduced Agriotes species. Recent identification of the sex pheromones of several key native pest species promises to significantly increase our ability to both monitor and manage them. We present an overview of recent work and its potential applications.

Van Hezewijk, Brian, Canadian Forest Service; Lara van Akker, Canadian Forest Service; Vince R. Waring, Canadian Forest Service

Seasonal and landscape effects on the biotic resistance of forest communities to insect invasions

We tested if seasonality, host tree species, and landscape attributes affected the ability of different forest communities to resist invasion by an exotic tussock moth. At 20 sites on Vancouver Island, BC, spanning a broad range of landscapes, we introduced small populations of the rusty tussock moth, Orgyia antiqua. Introductions were repeated at three different periods in the year, on coniferous and deciduous host trees, and included both late-instar larvae and pupae. The survival of these small populations was monitored and related to four different landscape metrics measured at scales ranging from 50-980 m. Spring introductions had significantly lower mortality rates than either early summer or late summer introductions. We found there was little difference in predation rates between coniferous and deciduous host trees. The amount and type of forest cover in the landscape had important, but seasonally dependent effects on survival, likely reflecting changes in the habitat requirements of a shifting community of generalist predators. Our results predict that species like Asian gypsy moth, with early-season larvae, are more likely to establish in landscapes with intermediate forest cover, whereas late-season species are less likely to survive in these same landscapes.

Van Moorsel, Sofia, McGill University; Owen L. Petchey, University of Zurich; Andrew Gonzalez, McGill University

Freshwater community stability in stressful times

Community stability has been a focal subject of research in ecology over the last decades, but we still lack a thorough understanding of stability at the whole-community level, particularly in response to stress. We tested the interactive effects of two environmental stressors, acidification and heat, on the stability of aquatic freshwater communities. To this aim, we measured dissolved oxygen (DO) in freshwater mesocosms as a proxy for whole community functioning during five months in a set of mesocosms at the Gault Nature Reserve in Mont-St-Hilaire, QC. This so-called Large Experimental Array of Ponds (LEAP) consists of 107 mesocosms filled with 1000 liters of water from a nearby lake, thus containing natural freshwater communities. We used data from 12 sensor loggers deployed in mesocosms that differed in their water pH; four loggers were in mesocosms at pH 5.5, four loggers were at pH 6.5 and four loggers were at pH 8.5, which was the control-level that corresponded to the pH in the lake. As expected, acidification generally reduced DO. DO responded differently to increased water temperature during a record heat wave depending on the pH treatment. The relationship was more negative for communities at pH 5.5; they were thus more strongly affected by the high temperatures recorded at the field site. Initial results show that the two co-occurring stressors interacted and reduced community stability, however, the effect on community stability depended on the time scale. A (temporary) crash of diurnal variation in response to stress can be viewed as less stability, whereas a lack of monthly variation means more stability. We show
that it is important to consider stability at different time scales when assessing how environmental changes impact community stability.

Van Natto, Alyson, Queen's University; Christopher Eckert

Conservation genetics and significance of geographically disjunct populations

Whether geographically peripheral populations are worth conserving has been hotly debated and is particularly relevant to Canadian conservation where ~90% of at-risk species are at their northern range limit in southern Canada but much more common to the south. On one hand, peripheral populations may have low genetic variation, low fitness and be prone to extinction. Alternatively, they might be adapted to extreme range-edge environments and thus well-poised for range expansion during climate change. *Abronia umbellata* is endemic to coastal dunes from Baja California, Mexico to Oregon, U.S.A. but also occurs as disjunct populations in Washington, U.S.A. and on Vancouver Island in British Columbia, Canada that are designated at risk. Based on sequence variation at 10 single-copy genes assayed for 125 individuals from 24 populations across the species range, these disjunct populations are very similar to range edge populations in Oregon, and likely arose through recent, natural range expansion. However, southern-edge populations in Baja are genetically unique, in steep demographic decline but receive no conservation protection. The conservation significance of range edge populations may depend on which edge. In this case, unprotected ""trailing edge"" populations seem a higher priority than those benefiting from special status at the northern range limit.

van Vierssen Trip, Nyssa, York University, Faculty of Environmental Studies; V. MacPhail; S.R. Colla; B. Olivastri

Examining the public's awareness and perceptions of bee conservation in Canada

The loss of native insect pollinators is of global concern and the Canadian public is highly engaged with the issue of bee conservation. This paper illustrates the lack of bee knowledge among the Canadian public based on a telephone survey of 2000 respondents from across the country. It finds the level of self-reported concern for bees varied by age, federal voting intent and province. Younger people expressed a higher level of concern for bees than seniors, Green Party voters expressed a higher level of concern compared to Conservative Party voters and residents of Quebec and British Columbia expressed a higher level of concern compared to residents of Alberta. Attribution of responsibility for bee protection/conservation varied by age, federal voting intent and province. Urbanites were more likely to state a lack of resources as a perceived barrier to bee conservation compared to rural dwellers. In addition, this paper makes a methodological contribution to the conservation science literature by using multinomial and ordinal regression models, both highly applicable techniques to analyze survey data.

Vankosky, Meghan, Agriculture and Agri-Food Canada; Shane Hladun, Agriculture and Agri-Food Canada; Boyd Mori

*Contarina brassicola*: the biology, distribution, and impact of an unstudied gall midge

An undescribed and unstudied species of *Contarinia* midge attacking canola (*Brassica napus*) was discovered on the prairies in 2016. In 2017, a research project was initiated to study the biology and distribution of C. brassicola, as well as its potential impact on canola production. A damage survey was conducted in 2017-19. Damage symptoms and larvae were found in Alberta, Saskatchewan, and Manitoba. Midge biology was investigated using emergence cages and weekly dissection of canola plants harvested from fields in north eastern Saskatchewan where midge population densities are greatest. *Contarinia brassicola* is multivoltine, with two generations produced per year. There is some overlap in the generations likely resulting from prolonged adult emergence from overwintering sites. Egg laying by adult midge and subsequent larval development is limited to canola flower buds. Larval feeding on the developing flowers results in a galled flower that does not produce a pod or seeds. At present, midge population densities are variable, but generally low across the occupied range. Thus, C. brassicola is not expected to have an economic impact on canola production.
Veitch, Jasmine, Department of Biology, Laurentian University; Jeff Bowman, Environmental and Life Sciences Graduate Program, Trent University Ontario Ministry of Natural Resources and Forestry; Albrecht. I. Schulte-Hostedde, Department of Biology, Laurentian University

Ectoparasite Co-Occurrence and Determinants of Parasite Infections in Rodent Hosts of Algonquin Provincial Park, Ontario, Canada

Host-parasite systems are often highly dynamic as parasites immigrate, emigrate or perish, leaving some host individuals uninfected and others harbouring multiple parasitic infections. We studied whether ectoparasitic arthropods (fleas, mesostigmatid mites, botflies) form community structures or if they are randomly assembled on small mammal hosts (Peromyscus maniculatus, Napaeozapus insignis, Myodes gapperi, Tamias striatus, Tamiasciurus hudsonicus, Glaucomys sabrinus) located in Algonquin Park. Using a temporally comprehensive dataset including multiple sampling years across a decade, we modelled associations between different parasite species, and tested for effects of intrinsic (host age, sex, body weight, reproductive condition) and extrinsic factors (date, population abundance, habitat type) for each host species. We found that flea prevalence was significantly impacted by the prevalence of orange mites on a host, suggesting an interaction between the two parasites. Host reproductive condition, date, and habitat type significantly influenced parasite prevalence/diversity on hosts. There is a high degree of variation in whether parasite assemblages are random or structured, and it is not yet fully understood whether ectoparasite community structure is observed in small mammals. By examining multiple parasite taxa on a host, we can strengthen our knowledge on how parasite species interact with one another and on patterns of parasite diversity.

Vellend, Mark, Université de Sherbrooke; Victor Danneyrolles; Jonathan R. Thompson

Changes in landscape-scale tree biodiversity in eastern North America since European settlement

Temporal biodiversity trends exhibit large spatial variability, sparking debate over whether global biodiversity declines manifest at sub-global scales. To date, data availability has constrained the inferences that can be drawn about the generality of patterns or cause-effect relationships. For example, impacts of anthropogenic activities might go undetected if time series begin after major impacts have already been felt. Here we use extensive data sets characterizing tree species composition in pre-European settlement and modern forests of the northeastern United States and in Québec in order to quantify long-term biodiversity change at the landscape scale following massive anthropogenic environmental change. Taxonomic diversity (Gini-Simpson index) showed no tendency for temporal change, on average. In Québec functional diversity tended to increase over time. In the northeastern U.S., biodiversity increases were greatest in landscapes with higher maximum historical proportions of the landscape in agriculture. In both regions, beta diversity tended to increase over time at small spatial scales (e.g., adjacent townships) but to decrease at larger spatial scales. Our interpretation is that human land use in these regions increases environmental heterogeneity within landscapes (increasing or stabilizing alpha diversity and small-scale beta diversity), while simultaneously decreasing environmental contrasts between distant landscapes (decreased large-scale beta diversity).

Vickruck, Jess

Development of Regional Management Strategies and Decision Making Tools for Control of Colorado Potato Beetle (CPB)

CPB are the most economically important insect pest of Canadian potato. Control of CPB relies heavily on applications of systemic and foliar insecticides, predominately neonicotinoids and spinosyns, respectively. Growers are at high risk of local CPB populations developing resistance to insecticides and require both up-to-date knowledge of local development of resistance and new management tools. The project objectives are to: (1) determine local susceptibility of CPB populations to different classes of insecticides through a national resistance-monitoring network; (2) better characterize molecular basis of developing resistance; and (3) develop novel extension tools to improve resistance management practices. In 2018, a total of 37 populations of CPB were obtained from 6 provinces for resistance screening. Many showed either resistance or reduced susceptibility to neonicotinoids and spinosyns in comparison to the anthranilic diamide products being tested. Insecticide use surveys accompanied most populations submitted and indicated that in the
last five years, 69% of respondents applied neonicotinoids, 40% applied spinosyns and 21% had applied diamides and/or pyrethroids. Samples will continue to be collected for the next four growing seasons (2019-2022) to determine susceptibility to registered insecticides and contribute to the mapping tool that growers can access for improved resistance management decision making.

Vincent, Charles, Agriculture and Agri-Food Canada; Tim Dumonceaux, Agriculture and Agri-Food Canada

Auchenorrhyncha associated with cultivated hop in Quebec

In recent years, the production of hop (Humulus lupulus) has steadily increased in the world. Likewise, cultivated surface area of hop has increased in Canada, the demand being notably prompted by micro-breweries. In Canada in 2018, the estimated cultivated surface areas of hop were, by decreasing order: British Columbia (250ha), Ontario (91ha) and Quebec (57ha). In 2017, in spite of insecticidal treatments, leafhoppers were observed in abundance in a hop field located at the Agriculture and Agri-Food Canada experimental farm in lAcadie, QC. The foliage exhibited yellowish marbling. In 2017 and 2018, to document the leafhopper fauna, cultivated hops were sampled in three localities of Southern Quebec: lAcadie, Dunham and Ste-Pie. Among the 1108 Auchenorrhyncha collected and identified, the potato leafhopper, Empoasca fabae (Cicadellidae), was the most abundant (1082 specimens), followed by Cedusa incisa (Derbidae) (6 specimens); Metcalfa pruinosa (Flatidae) (6 specimens); Empoasca esuma (Cicadellidae) (5 specimens); Helochara communis (Cicadellidae) (1 specimen); and Stictocephala taurina (Membracidae) (1 specimen). Several specimens were barcoded and vouchered. Because some of these insect species are suspected to vector plant diseases like phytoplasmas, leaf samples were taken from plants in the fields in which these insects were collected in 2017. Analysis of these samples using nested PCR targeting the 16S rRNA-encoding gene of phytoplasmas revealed that 2 of 5 plants presented evidence of infection across three time points, although very low levels of phytoplasma DNA were found in the positive samples. These results suggest that insect population interventions may be critical for controlling the spread of disease in H. lupulus.

Walker, Leah, Memorial University of Newfoundland; Dr. Carissa Brown, Memorial University of Newfoundland

Reconstructing the long-term fire history and forest composition of coastal boreal forest stands of Newfoundland using soil charcoal

Little is known about the long-term fire history of coastal boreal forests in Atlantic Canada, particularly of Newfoundland. Establishing historical baseline conditions is essential to wildfire management and projecting future wildfire activity. We radiocarbon-dated and botanically identified soil charcoal to resolve the long-term fire history of Terra Nova National Park (TNNP), in northeastern Newfoundland. Typically, dendrochronology or lake sediment cores are used to reconstruct fire histories; yet, a soil charcoal approach creates a longer time-scale and finer resolution, stand-level understanding of past fire events. Charcoal ages ranged from 7528 to 64 years BP, with fires beginning shortly after deglaciation of the island. The fire return interval for the park was consistent with other eastern boreal forest stands. In the charcoal record, we found spruce, balsam fir, pine, birch, maple, and ash. From past to present, spruce and balsam fir proportions have remained relatively stable, increasing by 18% and 8%, respectively. Conversely, deciduous species have notably declined, with birch proportions decreasing by 43% from past to present, likely coinciding with the introduction of moose. Our results directly inform the wildfire management plan in TNNP with the goal of enhancing black spruce regeneration, improving overall forest health, and decreasing fire risk.

Walker, Emma, University of Toronto; Benjamin Gilbert

When Allee effects alter coexistence outcomes of Chesson’s framework

Modern coexistence theory is accredited for creating a fundamental shift for community ecology, bringing generalizable principles to an otherwise highly contingent and system specific mess. However, coexistence theory has largely failed to address evidence that the effects of order and timing of species arrival plays a critical role in shaping communities via priority effects. Priority effects are predicted to occur when destabilizing mechanisms exceed the effects of fitness
differences, where destabilizing mechanisms ultimately may be thought of as occurring any time species experience positive intra-specific frequency dependence when at low-density. This condition is met when populations experience an Allee effect, or positive density dependence when at low densities. We develop a simple and generalizable Lotka-Volterra competition model with an Allee effect and a sufficiently flexible density-dependent form to characterize species that range from showing weak to strong positive density dependence. We demonstrate and analytically solve for conditions under which Allee effects alter coexistence outcomes classically expected by coexistence theory, quantitatively describing when alternate stable states and low-density barriers to invasion emerge, and how likely these barriers are crossed when species experience demographic stochasticity.

Wallace, Shaylyn, University of New Brunswick; Graham Forbes, University of New Brunswick; Joseph Nocera, University of New Brunswick

**Mortality Risk of Wood Turtle (*Glyptemys insculpta*) in a Landscape under Active Agriculture**

Agricultural land and improved agricultural machinery present an ecological trap for some species. The threatened wood turtle (*Glyptemys insculpta*) inhabits riparian buffers and forests but will use agricultural fields if close to nesting habitat, as these fields can provide adequate basking temperatures and feeding grounds. In actively farmed fields, agricultural machinery can present a mortality risk for the species. Mitigation of this risk is difficult, as there is limited information on the effects of agricultural practices on wood turtles. We sought to quantify how different agricultural practices affect wood turtles at levels ranging from individual movement behaviour to population demographics. From May to October of 2017 and 2018, we studied wood turtles in central New Brunswick along a second-order meandering stream surrounded by hay fields and forest. We located 51 wood turtles along a 2-km section and radio-tagged 23 to monitor their habitat use and relative risk to agricultural practices. Almost half of the turtles captured during 2017 and 2018 were found to have injuries on the carapace (45%) and tail (41%), which is likely due to agricultural machinery or predation. We recorded a total of 993 relocations in 2017 and 2018 and from June 15th to July 15th, approximately 50% of relocations were within a hay field. In July and August of 2017 and 2018, we monitored the response of wood turtles approached by agricultural machinery. Results were variant, but none of the turtles would have been undamaged if we did not intervene. Due to the high risk of agriculture practices, implementing early-successional buffer strips along field edges would be ideal to avoid mortality risk to wood turtles. This information will assist several critical knowledge gaps for this species-at-risk and provide management recommendations to land managers attempting to mitigate agricultural impacts."

Wallace, Cory, Wilfrid Laurier University; Philip Marsh, Wilfrid Laurier University; Evan Wilcox, Wilfrid Laurier University; Jennifer L Baltzer, Wilfrid Laurier University

**Predicting fine-scale patterns of shrub recruitment at the taiga-tundra ecotone**

Deciduous shrub productivity is increasing across much of the arctic, though this trend displays pan-arctic and fine-scale variability. Within sites, studies have primarily documented expansion down slopes and valley bottoms, suggesting heterogeneity due to topographic resource gradients. While this expansion is often related to high topographic wetness index, no direct comparison of seedling recruitment and resource availability has been made. Seed dispersal may also drive this pattern, as areas which accumulate water may also accumulate seeds by way of overland flow or snow drifting. Refining our understanding of what drives this heterogeneity is crucial to understanding the ecosystem impacts of shrub expansion in the arctic. Here, we ask: 1) Are patterns of seedling recruitment associated with downslope resource gradients of soil moisture or nitrogen? 2) Can we use physical process models of seed dispersal to explain the spatial distribution of a) seeds and b) seedlings around shrub patches? To answer these questions, we developed seed dispersal models based off remotely sensed data for a taiga-tundra ecotone site. These models were evaluated using seed and seedling counts collected at the site. Preliminary analysis suggests little relationship between either downslope resource gradients or seed density, though moss cover may explain the discrepancy.

Wang, Yue, McMaster University; Himeshi Samarasinghe; Jianping Xu

**Dynamic distributions of mitochondrial introns in the human pathogenic yeast *Cryptococcus deneoformans***
Introns are prevalent in fungal mitochondrial genomes. However, their evolutionary patterns and mechanisms for their distributions in natural populations remain largely unknown. In this study, we investigated the distributions of 11 mitochondrial introns in natural populations of the human pathogenic yeast Cryptococcus deneoformans. Among the 54 analyzed strains from across the northern hemisphere, we found limited evidence for geographic clustering of intron distributions. In addition, mating type plays a minor role in intron distribution, consistent with intron exchange among strains in nature. The mitochondrial intron distributions were further analyzed based on the phylogenetic framework derived from multiple nuclear gene sequences. Our analyses revealed abundant incongruences between strain relationships derived from the nuclear and the mitochondrial genes. Taken together, our results suggest a dynamic pattern of mitochondrial intron distribution in this model basidiomycete yeast.

Wang, Xueqi (Sharon), University Of Guelph; Gustavo S. Betini; Tal Avgar, Ecology/Wildland Resources, Utah State University; John M. Fryxell, Department of Integrative Biology, University of Guelph

How can we better predict population trajectory with a size-structured population model?

Understanding the mechanisms by which populations may respond to environmental changes is of critical importance in preventing extinction and preserving biodiversity. However, the million dollar question in currently population ecology resides in differentiating deterministic processes from stochasticity to better identify key factors that drive population declines. Here, we set up an aquatic mesocosm experiment to test previous model predictions that populations will likely experience a higher level of demographic variability at warmer environment due to synergistic interactions between temperature and food availability on size-dependent growth, survival and reproduction. Using data collected over 260 days, we provided evidence that Daphnia experience faster population growth at higher temperature tanks, overshoot earlier, followed by resource-dependent reproductive limitation. We also observed temperature-dependent reduction in food availability suggesting strong bottom-up regulation on Daphnia abundance. We argue that obtaining information on population size structure is critical in detecting early warning signals of population crash and that temperature-dependent variability in food abundance and individual vital rates can drive different population trajectories.

Wang, Chih Julie, University of Toronto; Marc Cadotte; Scott MacIvor

Improving Extensive Green Roof Functioning using Invasion Theory as a Management Tool

Green infrastructure has become increasingly popular to mitigate the negative impacts of urbanization and to restore key ecosystem functions in cities. They are planted most frequently with species in the genus Sedum (commonly known as stonecrops). However, a positive link between plant diversity and ecosystem function has been well-established in ecological literature, thus questioning the utility of planting green roofs with a single genus. I assess whether extensive green roof functioning is improved by increasing functional diversity with native (non-Sedum) species. Since disturbance and resource addition increases invasibility, they can be used as management tools for increasing native species on constructed ecosystems. In a fully factorial experiment, five native invaders were planted at three diversity levels across 44 extensive green roof modules on six roofs and two ground level controls. Resource addition via irrigation and disturbance treatments, which involves clearing vegetation, were predicted to enhance native invader success and increase green roof functioning. Preliminary results show that plants help cool the roof, however, no statistically significant effect of native invader diversity on soil temperature was observed in the first year. Diversity effects on function theoretically require co-existence mechanisms to play out, thus requiring observation over longer temporal scale.

Waterman, Jane, Dept. Biological Sciences, University of Manitoba; Lauren LaFleche, Dept. Biological Sciences University of Manitoba

Why care? Alloparental care by non-dispersed males in a highly social African ground squirrel

Alloparental care, caring for non-descendent offspring, is characteristic of cooperative breeding. Helpers may gain inclusive fitness benefits by staying with their family and caring for offspring. They may also care to be able to remain in
the group and gain direct fitness benefits (e.g., group augmentation), in essence paying to stay. Cape ground squirrels (Xerus inauris) are highly-social cooperative breeders living in southern Africa. Females live in kin groups, while males disperse at maturity to join all-male groups. Some males delay dispersal and provide alloparental care to offspring in their family group. We tested the hypotheses that males alloparent to increase inclusive fitness benefits and/or as pay-to-stay. We compared rates of alloparental care to 1) offspring relatedness and 2) rates of affiliative behaviours females direct at natal males. The lack of relationship between rates of care and the relatedness of males-juveniles suggests that males did not help for inclusive fitness benefits. We found a positive relationship between rates of alloparental care and affiliative behaviours females directed at males, suggesting males alloparent for pay-to-stay benefits. Further research into the benefit of males delaying dispersal and the benefit of helpers to females are required to better understand alloparental care in this species.

Watson, Beth, Dalhousie University; Watson, K.B. 1; Bentzen P. 1; Lehnert S.L. 2; Duffy S. 2; Dempson B. 2; Lien S. 3; Kent M.P. 3; Bradbury I 1,2; 1 Dalhousie University; 2 Northwest Atlantic Fisheries Centre, Fisheries and Oceans Canada; 3 Centre for Integrative Genetics, Norwegian University of Life Sciences

CORRELATION BETWEEN ENVIRONMENT AND CHROMOSOMAL STRUCTURAL VARIATION INFLUENCE FINE-SCALE POPULATION STRUCTURE OF ATLANTIC SALMON (Salmo salar)

Chromosomal rearrangements (e.g., inversions, fusions, and translocations) have long been associated with environmental variation. New genomic tools are now providing the opportunity to examine the role of these structural rearrangements in shaping adaptive differences between and within wild populations of non-model organisms. Atlantic salmon exhibit recently identified variation in chromosomal rearrangements that vary across the species natural range. The adaptive role and importance of these chromosomal rearrangements in structuring wild populations remains poorly understood. Here, using a 220K SNP array, we genotype Atlantic salmon from 26 populations within a highly genetically structured region of southern Newfoundland to characterize structural variation both within and between rivers and identify environmental associations. Multivariate analysis suggests a translocation between chromosomes Ssa01 and Ssa23 is the dominant factor driving genetic structure in the region. Preliminary analysis suggests a correlation between this large structural rearrangement and climatic variables including precipitation and temperature. This work highlights potential interactions between chromosomal rearrangements and environmental factors, which may underlie fine-scale local adaptation. As such, this work directly informs the conservation and management of wild Atlantic salmon in the region.

Watson, Christopher, Université du Québec à Trois-Rivières; Léonie Carignan-Guillemette, Université du Québec à Trois-Rivières; Caroline Turcotte, Université du Québec à Trois-Rivières; Vincent Maire, Université du Québec à Trois-Rivières; Raphaël Proulx, Université du Québec à Trois-Rivières

Ecological, social and economic benefits of low-intensity management for urban lawns

Intensive mowing of urban lawns to create a homogeneous aesthetic is common throughout the world. This management generally results in negative environmental impacts, and efforts to promote unmanaged lawns have had limited acceptance. However, recent lawn mortality in Québec suggests that the management status quo not only lowers ecosystem resilience but is also unsustainable, thus prompting reassessment of current management practices. We present a meta-analysis of North American and European studies (2004-2019) to investigate how mowing intensity influences the ecology and functioning of urban lawns. We analysed 40 variables comprising published data and three unpublished datasets from the Québec province, grouped as Invertebrate Communities, Plant Communities, Pest Species and Abiotic Factors within a multilevel random-effects model. Our analysis provides aggregated evidence that invertebrate and vegetation diversity decrease with increased mowing intensity (Hedgesg = -1.05; -0.38). Pest species, including common ragweed Ambrosia artemisifolia and white grubs (Scarabidae) increased with greater mowing intensity (Hedgesg = 0.93). We suggest that adopting low-intensity management may prevent the loss of urban biodiversity, while decreasing the prevalence of unwanted and allergenic species. Economic and social benefits are also realized through decreased operational costs and reduced public health expenses.
Watts, David A., Département de biologie, Université de Sherbrooke; Amanda B. Young, Département de biologie, Université de Sherbrooke; Mark Vellend, Département de biologie, Université de Sherbrooke

Among spring ephemeral plants, species respond individualistically to the timing of snowmelt

In parts of eastern North American deciduous forest where deep (>1 m) snow can last nearly until canopy leaf development begins, the timing of snowmelt can influence the timing of the onset and duration of the growing season, and thus the annual carbon budget, for spring ephemeral understorey plants. We tested the recently proposed hypothesis that the timing of snowmelt might partly explain the elevated abundance of spring ephemerals in proximity to trees by monitoring these species in a factorial snowmelt timing experiment. We transplanted Dicentra cucullaria and monitored preexisting Erythronium americanum, Claytonia caroliniana, and Trillium erectum in a total of 160 plots near tree bases and in the open (~4 m away) in which we removed or added snow. Preliminary results indicate that, unsurprisingly, snowmelt timing affects when plants reach maturity and thus the length of the growing season, but not in the same manner across species. For example, independent of snowmelt timing, Dicentra matured earlier near trees while Erythronium matured earlier in the open. Such results suggest that the importance of the timing of snowmelt, relative to other likely important factors varying with distance from trees (e.g. nutrient availability or soil moisture), differs among spring ephemeral species.

Webber, Quinn, Memorial University of Newfoundland; Christina Prokopenko, Memorial University of Newfoundland; Eric Vander Wal, Memorial University of Newfoundland

Patterns of movement and social network position predict habitat selection patterns in caribou

Patterns of habitat selection can vary based on the social and physical environments experienced by an individual animal. Mechanisms explaining habitat selection are often broad and not typically analyzed simultaneously and with fine-scale measures of movement and sociality. There remains an empirical and theoretical gap linking habitat selection theory, movement ecology, and social networks. We use two populations of caribou (Rangifer tarandus) in Newfoundland to test the hypothesis that movement behaviour and properties of caribou social networks influence habitat selection. Moving to, or with, conspecifics is a by-product of social interactions and we predict that movement and sociality influence patterns of habitat selection where individual caribou will move more slowly in the presence of conspecifics in lichen habitat while individuals will move more quickly in the absence of conspecifics in forested habitat. We use novel implementation of two contemporary methods, social network analysis and integrated step selection analysis, to model socially-mediated habitat selection. We expect our findings will inform classical habitat selection theory by providing context about how fine-scale movement and sociality influence habitat selection patterns for individuals. In summary, our study is among the first to simultaneously examine the effects of movement and sociality on habitat selection.

Wegscheider, Bernhard, Canadian Rivers Institute, UNB; Tommi Linnansaari, Canadian Rivers Institute, Department of Biology and Faculty of Forestry and Environmental Management, University of New Brunswick; Mouhamed Ndong, Canadian Rivers Institute, Department of Civil Engineering, University of New Brunswick; Katy Haralampides, Canadian Rivers Institute, Department of Civil Engineering, University of New Brunswick; Andre St-Hilaire, Canadian Rivers Institute, Institut National de la Recherche Scientifique, Centre Eau Terre Environment; Matthias Schneider, sje- Ecohydraulic Engineering; R. Allen Curry Canadian Rivers Institute, Department of Biology and Faculty of Forestry and Environmental Management, University of New Brunswick

Predicting habitat suitability for fish communities and implications for river management

Modelling the linkages between physical habitat and aquatic organisms on multiple spatial scales has become a valuable tool in the management of regulated rivers. Particularly, the distribution and structure of fish communities can be significantly influenced by the physical environment. Traditional approaches are operating at the microhabitat (point)-scale, simulating physical habitat parameters at a high spatial and analytical resolution. The mesohabitat (local)-scale represents an intermediate resolution in modelling that bridges the gap between available resources and conservation efforts for riverine species. In large rivers, a combination of micro-scale and meso-scale analysis has been recommended, acknowledging a higher proportion of functional habitat that may be important for specialized fish species or life stages.
The current study is conducted along a 20 km reach of the Saint John River, downstream the Mactaquac Generating Station and uses a multi-scalar modelling approach to assess spatio-temporal changes in habitat conditions as a function of flow. Mesohabitat types are associated to discrete fish assemblages (i.e. fish habitat guilds). Habitat requirements for fish guilds are defined by local fish experts and habitat suitability is derived using the fuzzy-rule based MesoCASiMiR habitat model system. A fuzzy logic approach is also used to quantify the uncertainty associated to the hydrodynamic and biological component of the model. Specialized habitat requirements at summer flow condition for single species or life stages are analyzed at the microhabitat scale and compared to mesoscale simulations to identify strengths and weaknesses of both approaches. Ecohydraulic metrics are derived from the model and translated into a habitat time series, to discuss potential changes in fish habitat conditions related to different management options of the Saint John River.

Weigum, Emily; Sophie Krolikowski; Ian Scott 1; Pamela MacKinley 2; Sheldon Hann 2; Jess Vickruck 2; Chandra Moffat 2; 1 London Research and Development Centre, Agriculture and Agri-Food Canada, 2 Fredericton Research and Development Centre, Agriculture and Agri-Food Canada

Should Atlantic salmon (*Salmo salar*) scales be acidified prior to stable isotope analysis?

A contradiction exists within peer-reviewed literature regarding whether fish scales need to be acidified using hydrochloric acid (HCl) prior to stable isotope analysis (SIA) to eliminate inorganic carbonates. Carbonates are enriched in 13C and their presence may confound studies estimating the contribution of organic carbon to a consumer from its various prey. Acidification can also affect nitrogen values, causing an enrichment in d15N. This study compared acidified to untreated scales of adult Atlantic salmon (*Salmo salar*) sampled when returning from sea to 9 different locations in North America and Europe to determine if acidification to decalcify scales is required prior to SIA and if the δ15N values of acid-treated scales differs significantly from untreated scales. When samples from all locations were combined, there was a significant difference (p < 0.05) between acidified and untreated δ13C and δ15N values, though this difference was below statistically identifiable levels in 5 of the 9 populations sampled. While these differences were statistically significant, they were too small to be of biological importance as the mean difference between treated and untreated samples was 0.1‰. The discrepancy between the acidification of scales among locations may arise from differences in the balance of metabolically derived bicarbonate and isotopic CO2 exchange of water through the gills. Owing to the differences observed between populations, we recommended that trial comparisons of acidified and untreated scales be done prior to SIA.

Weis, Arthur, University of Toronto; Madeline A.E. Peters

Synergistic Effects of Isolation by Time and Isolation by Distance on Genetic Structure across a Continuous Landscape

Pollen is generally dispersed over short distances, which promotes population genetic structure across continuous two-dimensional space. Similarly, quantitative genetic variance in flowering time structures mating pools in the temporal dimension, at least with respect to the phenology loci. We asked if these two phenomena, isolation by distance (IBD) and isolation by time (IBT), synergistically promote genetic structure in space and time. We constructed an individual-based model that tracked genotype frequencies at flowering time and neutral loci across a uniform landscape, over multiple generations, under four mating schemes: panmixia, IBD only, IBT only, and IBT *IBD. IBT *IBD divided the population into spatial clusters of early-, mid-, and late-flowering genotypes and strongly increased its quantitative genetic variance. Flowering time did not cluster under IBT, but its genetic variance increased moderately. IBD induced mild spatial structure in a non-assortative reference trait but did not change its variance. Importantly, the spatial correlation of genotypes at neutral loci was twice as strong under IBT *IBD compared to IBD alone. IBT *IBD also drew neutral loci into gametic disequilibrium with flowering time loci, structuring them temporally. Temporal and spatial mating pool structure promotes local differentiation. This trend would facilitate adaptation on small spatial scales.
Wellband, Kyle, Université Laval; Claire Mérot, Université Laval; Tommi Linnansaari, University of New Brunswick; Jake Elliott, Cooke Aquaculture Inc.; Allen Curry, University of New Brunswick; Louis Bernatchez, Université Laval

Structural genomic variation and its relevance for conservation of Atlantic Salmon

The increased availability of genomic tools for species of economic and ecological interest has revealed the importance of structural genomic variation (i.e. large chromosomal rearrangements) in adaptive processes for a wide range of taxa. In particular, structural variation is capable of maintaining important phenotypic or life history variation among populations despite low levels of genome-wide differentiation. North American populations of Atlantic Salmon exhibit three major chromosomal rearrangements relative to the European lineage but their distributions in natural populations are unknown. We produced the first genomic characterization of a fusion between chromosomes 8 and 29 in populations of salmon from the Miramichi River. Fusion genomic features included high LD, reduced heterozygosity in the fused homokaryotes, and strong divergence between the fused and the unfused rearrangement. Population structure in the Miramichi River based on fusion karyotype ($F_{ST} = 0.019$) was five times stronger than neutral variation ($F_{ST} = 0.004$) and the frequency of the fusion was associated with elevation and summer precipitation supporting a hypothesis that this rearrangement contributes to local adaptation despite weak neutral differentiation. It is clear that conservation efforts that seek to preserve adaptive genetic variation must move beyond single locus approaches to characterizing adaptive variation.

Wen, Lina; Dr. Andrew M. Simons

Variable constraints disrupt the relationship between seed count and fitness

Seed count is the most common measure of plant fitness because it is taken as an indication of total recruitment, and it is easily quantified. However, several situations exist where seed number may not be a reliable measure of fitness; for example, when plants reproduce asexually, or when female and male fitness is weakly correlated. Here, we use the herb, Lobelia inflata, to test the hypothesis that variation in seasonal quality experienced among individuals disrupts the relationship between seed count and fitness. Specifically, we predict that individuals experiencing a more constrained season (e.g. flower later) may produce numerous seeds but of low fitness value. We found that manipulated season length had a significant effect on seed number: constrained-season plants produced more seeds than plants under less-constrained seasons; however, as predicted, plants in the constrained season had significantly reduced seedling viability. The relative per-seed fitness was $0.774\pm0.034$ under constrained season length conditions; thus, plants under constrained conditions had higher total fitness according to simple seed count, but not after accounting for seedling viability. We conclude that although seed count may be appropriate under some conditions, more suitable alternatives to this fitness measure should be used under some scenarios, where feasible.

Westwood, Natalie, University of British Columbia; Diane Srivastava, University of British Columbia

Understanding nested ecosystem connections in the context of habitat fragmentation

Ecosystems and their functions are typically studied in isolation from one another. However, the meta-ecosystem assemblage may impact the functioning of a single ecosystem, such as fluxes of energy and nutrient across ecosystem boundaries. Aquatic ecosystems found within terrestrial systems are a special case, especially in the context of habitat fragmentation. These aquatic systems rely on the terrestrial input of nutrients often from leaf litter. There is evidence that fragmentation of forests can influence the types of trees and their leaf chemical quality. Fragmented areas have leaves containing higher nutrient levels and lower secondary compound levels compared to leaves found in intact forest areas. We examined how these potential differences impact decomposition in small aquatic treehole systems in the context of neotropic fragmentation. We performed a reciprocal transplant of leaf litter collected from small fragmented, large fragmented, and intact forests. Leaf litter bags were placed in treeholes for two months and then retrieved to determine mass loss. Leaf litter found in small fragmented forests losses were greater than leaf litter from either large fragmented forests or intact forests. This result emphasizes the importance of understanding the meta-ecosystem that contains a particular ecosystem.
Whidden, Erin, Fundy Model Forest/UNB; Joe Nocera; Nairn Hay

Population Viability Analysis - Protocols for the Acadian Forest

In forested systems, extinction risk can be influenced by forest management strategies. Population Viability Analysis (PVA) can predict current and future potential impacts of forest practices on wildlife populations, as well as illustrate how altered forestry practices might mitigate adverse impacts, but requires region-specific data to make accurate predictions. We sought to develop user-friendly PVA protocols that can be adapted for species in the Acadian forests of New Brunswick. We chose four species to represent a cross-section of habitat use profiles in the Acadian forest: American marten, Ovenbird, Blackburnian Warbler, and Black-backed Woodpecker. Our initial PVA of American marten indicated that if carrying capacity (i.e., quantity of suitable habitat) is managed at 1000 breeding territories in New Brunswick, the population will stabilize at approximately 1500 individuals with a stochastic population growth rate of 0.09 (0.001 SE, 0.25 SD). Sensitivity analyses indicate that population growth in martens is most sensitive to changes in survival (adult, juvenile), proportion of breeding females in the population, and trapping pressure. This first of four analyses illustrates that managers should prioritize monitoring the effects of changing forestry practices on these traits to better predict future population level responses.

White, Easton, University of Vermont

Experimenting with the past to improve species monitoring programs

Species monitoring programs are a cornerstone of conservation and management as well as modern ecological research. Monitoring programs are also expensive and time consuming. Thus, it is essential to design monitoring programs that are both cost effective and have high enough statistical power to answer our questions. Determining the required number of years, samples per year, and the number of replicate sites are all important aspects of a monitoring program. In addition, it might be difficult to clearly distinguish between different species in the field. Yet, little work has explored how this might affect our ability to detect long-term trends in abundance. Here we use both simulations and empirical data to show the effect of not distinguishing between closely-related species. Substantial bias emerges when we cannot clearly identify species, even if we only lump species at the genus level. This has important implications for conservation efforts which typically focus on individual species.

Whitton, Jeannette, The University of British Columbia; Evan Hersh; Jennifer Williams

Life history of sexual and asexual populations of the Easter Daisy, Townsendia hookeri (Asteraceae).

Sexual diploid and apomictic polyploid populations of Townsendia hookeri occupy distinct ranges in the Rocky Mountain foothills. Sexual diplods occur farther south, in Colorado and southern Wyoming, while apomictic polyploids range from southern Wyoming to southern British Columbia and Alberta. Apomicts are known to have originated repeatedly from sexual progenitors, and their successful spread has been hypothesized to be linked to a colonization advantage (Bakers Law), but our observations in common gardens suggest that apomicts may match or exceed the performance sexuals even in the sexual range. Nonetheless, because these are long-lived perennials, it is difficult to extrapolate from the experimental gardens (for which we have 5 years of data) to a general understanding of persistence over generations. To address this, we conducted a demographic study of seven populations to determine whether there are consistent differences between reproductive types in their demographic transition rates and projected population growth rates. We then ask whether these differences can help explain the distribution and persistence of sexual and asexual populations.

Wilder, Aryn, San Diego Zoo Institute for Conservation Research; Oliver Ryder, San Diego Zoo Institute for Conservation Research; Love Dalén, Department of Bioinformatics and Genetics, Swedish Museum of Natural History; Ian Fiddes, 10X Genomics; Cynthia Steiner, San Diego Zoo Institute for Conservation Research

Deleterious genetic variation and the prospects for genetic restoration of white rhinos
Human activity has left species worldwide on the brink of extinction, where strong genetic drift and weakened selection lead to loss of genetic diversity and the accumulation of deleterious mutations. One of two white rhino subspecies, the northern white rhino (NWR; *Ceratotherium simum cottoni*) has been driven effectively to extinction, with only two non-reproductive females remaining. By contrast, swift conservation efforts enabled the remarkable recovery of the southern white rhino (SWR; *C. simum simum*) from roughly 20 individuals in the early 20th century to 10,000 today. Ongoing efforts to produce NWR embryos from twelve cryopreserved cell lines have prompted questions about the viability of the NWR genome and the prospects for recovery from so few individuals. SWR provides a benchmark for successful recovery, and comparing genomic characteristics of these two closely related but evolutionarily distinct subspecies may provide insight into the potential for recovery of NWR. Whole genome sequence data from 22 white rhinos suggest that NWR actually has higher genetic diversity, but also harbors more deleterious alleles than SWR. Using forward simulations, we are examining the dynamics of genetic load and inbreeding depression in a future NWR population to better understand its potential for genetic restoration.

Wilkinson, Sydney, University of Toronto; Thomas Brown, The Scottish Association for Marine Science; Bailey McMeans, University of Toronto

How does seasonality affect energy pathways across time and space?

Predicting how freshwater fish will allocate (store or deplete) their lipids in response to changing season and prey availability allows for the linking of fish habitat to fish diet and physiology. We are investigating lipid content of three different classes (i.e. fatty acids, sterols, highly branched isoprenoids) and their roles as biochemical tracers in four freshwater fish (i.e. Yellow Perch, Smallmouth Bass, Lake Trout, Burbot) from two Ontario lakes (i.e. Lake Opeongo and Lake of Two Rivers). Patterns of prey quality, prey location (littoral or pelagic), and temporal feeding behaviour are deciphered with the use of these biochemical tracers.

Wilson, Paul, Trent University; Rebeckah Horn, Trent University; Micheline Manseau, Environment & Climate Change Canada (ECCC); Sonesinh Keobouasone, ECCC

Whole genomes assess the roles of parallelism and introgressive hybridization in caribou ecotype evolution

Banfields characterization of Rangifer evolution, based predominantly on skeletal morphology, is an invaluable resource for understanding and conserving an iconic species. We completed the whole-genome sequencing of representative North American caribou subspecies and ecotypes to compare to Banfields work of more than 50-years ago. There was striking concordance in the two evolutionary reconstructions. Genomic demographic reconstruction indicated a major expansion of caribou during the glacial interstitial stage of a largely ice-free North America 120 kya, with subsequent differential population trajectories of emerging subspecies. Timing of subspecies divergence was concordant with Banfields reconstruction, with barren-ground, woodland, and diversification of Arctic Peary and Greenland caribou. Some revisions were notable between the original Banfield and genomic reconstructions. Mountain caribou have a more complex history beyond ecotypic characterization within the woodland subspecies, with lineages related to barren-ground caribou which originated in a separate (Beringian) glacial refugium. Phenotypic convergence of ecotypes was observed in a Beringian derived lineage evolving a boreal ecotype independent of woodland caribou where it is currently placed. Genomic characterization detected admixture among lineages, and while Banfield described intergradation among caribou forms, introgression among lineages is consistent with the recent findings of many mammalian species in that introgression is a more important evolutionary driver than previously thought. Overall, the similarity of Banfields revision from 1961 captured the main patterns of caribou evolution; however, our genomic revision will provide a more accurate characterization of introgression and the complexity of ecotypic divergence relevant to delineating conservation units under Canadas Species-at-Risk Act (SARA).

Wishart, Andrea, Department of Biology, University of Saskatchewan

Here for a grad time, not a long time: Experiences and perspectives of graduate students in long-term research
Longitudinal studies that measure key variables in tractable systems repeatable across years, with some studies running for several decades, are termed long-term ecological research (LTER) projects. LTER projects not only contribute disproportionately to ecology and policy (Hughes et al. 2017 Bioscience 67), they provide critical insights into ecological and evolutionary processes that otherwise could not be captured if monitoring efforts were limited to the shorter timeframes commensurate of typical graduate student projects. As such, LTER projects can provide a wealth of existing data and scientific infrastructure to incoming graduate students. Fine-tuned protocols, a network of multi-institutional collaborators, and an existing body of system-specific literature exemplify some of the obvious attractants graduate students may consider when deciding on a particular avenue of study. However, the nature of many LTER projects can present some unique challenges and difficulties that must be navigated by students learning how to conduct independent research within projects that will long outlast the students individual tenures. In this symposium Collecting data across generations: the inaugural symposium of CSEEs Long-Term Research Section, I will speak to the experience and perspectives of researchers who have been or are presently involved in conducting their graduate thesis work within the frameworks of at least one of the many existing LTER projects by summarising and discussing responses to an anonymous survey. By focusing on the broader range of respondent experiences reflected in the survey, supplemented with my personal experience as a PhD student conducting research in conjunction with the Kluane Red Squirrel Project, I will share strategies and solutions that have already been implemented to some of the more common challenges. I hope to highlight ways in which the respective goals of LTER projects and associated graduate students can be met while ultimately improving the overall satisfaction and success of stakeholders, and encourage discussion around these considerations.

Wist, Tyler, Agriculture and Agri-Food Canada; Shane Hladun, Agriculture and Agri-Food Canada; Derek Flad, Northern Quinoa Corporation

From lambs quarters to quinoa: insect host shifts threaten quinoa production in Canada

Quinoa, Chenopodium quinoa (Amaranthaceae), cultivated for thousands of years in South America, is relatively new to Western Canada and it has great potential to be a lucrative crop for Canadian farmers. Quinoa production in Western Canada however, is threatened by several insect pests whose original host plants are weedy relatives of quinoa.

Wolf, Jesse, Trent University; Krystal Dixon; Aaron B.A. Shafer

Genetic population structure of Northern British Columbia mountain goats (Oreamnos Americanus)

Genetic diversity varies across geographical distance and between landscape barriers. While large-scale historical events, such as continent-wide glaciation can impact species-wide levels of variation, fine-scale landscape barriers to gene flow result in more localized impacts. The resulting genetic population structure can be continuous and uniform over a large area, or patchy and disjointed, with areas of high abundance separated by areas of where a species is rarely found. Therefore, by quantifying levels and patterns of genetic structure, we can gain insight into the effects of geographic barriers and fragmented environments on gene flow. This is important when it comes to delineating management units and assessing population connectivity. These objectives are of interest when studying species who occupy fragmented habitats and are subject to harvest, as gene flow may be limited, and population management is a multifaceted concern. British Columbia is home to over 50% of the worlds mountain goats and very little is known about northern B.C. specifically, as reflected by uncertainty surrounding population estimates. Our study will evaluate the genetic structure of mountain goats in Northern B.C. and provide data that can facilitate biologically relevant population management.

Wood, Zachary, University of Maine; Laura K. Lopez; Celia C. Symons; Rebecca R. Robinson; Eric P. Palkovacs; Michael T. Kinnison

Evolution can occur contemporaneously with ecology, allowing ecological and evolutionary processes to mutually interact. One important type of contemporary trait change is antipredator adaptation in prey, which can influence the persistence of both predator and prey populations and generate or mediate trophic cascades. Here we assess morphological
and behavioral traits in nine populations of common-garden reared western mosquitofish (*Gambusia affinis*) from three different predator backgrounds to quantify heritable and plastic local and anti-predator evolution. We then use pond mesocosm experiments to examine the ecological consequences of variation in these traits. Evolution in response to two different predators generates a similar mixture of heritable and plastic trait changes, likely focused on predator avoidance and energetic efficiency, but trait variation from antipredator evolution is significantly smaller than that from idiosyncratic local population divergence within predator backgrounds. Among-population variation in several mosquitofish traits associated with heritable and plastic predator naivete causes cascading zooplankton and primary producer change, likely through both top-down and bottom-up pathways. As such, this study provides an impactful example of how contemporary trait change through a variety of genetic and plastic mechanisms can cascade through food webs and alter ecosystem function.

Xu, Cong, Department of Biology, McGill University; Rowan D.H. Barrett, Redpath Museum & Department of Biology, McGill University

The Amazing Spider Web DNA: A New Spin on Noninvasive Genetics of Predator and Prey

Come learn about the amazing spider web DNA! Spider webs act as natural traps of biodiversity. From uncovering trophic cascades on experimental islands in the Bahamas to applications in behavioral ecology of individual black widow spiders in Arizona, spider web DNA is being used all over the world in a variety of fields. What do YOU think spider web DNA can be used for?

Xu, Jianping, McMaster University

Fungal Species Concepts in the Genomics Era

Fungal species are defined by many different criteria, based on macro- and/or micro- morphological, ecological, physiological, metabolic, and/or genetic features. Some groups of fungi are defined based on one or two sets of these features while others are defined based on other features. As a result, it's been extremely difficult to compare different groups of fungi. With the emerging applications of multiple gene sequences and whole genomic sequences to fungal taxonomic and evolutionary studies, some of these difficulties are being resolved. However, additional problems are emerging. In this brief presentation, I will highlight the issues facing fungal species recognition and discuss potential approaches to resolve those issues.

Yack, Jayne, Carleton University

What do Butterflies Hear?

Butterflies have been studied extensively for their sensory ecology, but most research has focused on their visual and chemosensory systems. What about hearing? Many species belonging to the large family Nymphalidae have well developed tympanal ears located at the base of their forewings. These ears are widely distributed within the Nymphalidae, but not all species possess ears. I will summarize research to date on the taxonomic distribution of ears in butterflies, how they work, and why some but not all butterflies have them.

Yadav, Chanchal, Carleton University; Jayne E. Yack, Carleton University; Myron L. Smith, Carleton University

Sociality in caterpillars: what are the mechanisms?

Social grouping is widespread among larval Lepidoptera, and while the benefits of group-living are widely recognized, less is known about the mechanisms mediating group formation. Our study explores such mechanisms by testing hypotheses on the roles of vibroacoustics and sociogenomics. We use the non-model organism, the masked birch caterpillars, *Drepana arcuata* (Lepidoptera:Drepanoidea). Specifically, we explore (1) the ontogenetic changes in social
grouping; (2) the role of vibroacoustics in early instar grouping; and (3) the changes in larval transcriptome associated with the transition from social to solitary instars. Results indicate that (a) early instars (I,II) form groups whereas the late instars (IV,V) are solitary, and the third instar is transitional; (b) early instars generate and utilize complex vibratory signals to advertise food and shelter to conspecifics and; (c) there is a significant change in the expression of over 3,000 transcripts during the transition from social to solitary instars, including a number of candidate social genes. Our preliminary RNAi results suggest the association of an octopamine receptor gene with the behavioral transition from social to solitary instars. This research confirms the role of vibration-mediated recruitment in social caterpillars and introduces a sociogenomic approach to understanding social grouping in caterpillars.

You, Man, McMaster University; Jianping Xu, McMaster University

Phenotypic plasticity and genotypic diversity of aneuploid or diploid progeny of the two human pathogenic fungi within Cryptococcus species complex

Cryptococcus neoformans species (CNS) and Cryptococcus gattii species (CGS) can cause life-threatening meningitis in both immunocompromised and immunocompetent individuals. Strains of CNS and CGS are haploid that either reproduce asexually by budding or sexually by mating. They posses a bipolar mating system, with either ± mating type (MAT±) or a mating type (MATa). Mating may occur if cells of opposite mating types meet. In this study, we aimed to study the phenotypes and mitochondrial genotypes of progeny from 34 successful sexual mating crosses. The ploidy levels of progeny were determined by flow cytometry. Phenotypes, including melanin production, growth at high temperature, minimum inhibitory concentrations (MICs) for fluconazole, and self-fertility of progeny were determined, as well as mitochondrial genotypes and mating types. We hypothesized that some progeny would display the increased abilities in these tested phenotypes. We found that the progeny were diploid or aneuploid, with some of them were self-fertile. PCR analysis with primers specific for genes in the MATa and MAT± mating-type loci revealed that these progeny were heterozygous for the mating-type locus. Only progeny were observed that could grow at 42°C rather than the parents. However, most progeny were intermediate between the two parents in the tested phenotypic traits. Consistently with previous studies, most progeny inherited mitochondria from the MATa parent. Our future steps will be to determine the aneuploid chromosomes and nuclear genotypes, study the mitochondria-nuclear interactions among progeny, and identify the temperature-regulated genes.

Zelman, Kaleb, Maliseet Nation Conservation Council; Mary Murdoch & Tim Vickers - Stantec Consulting Ltd.; Aruna Jayawardane - Maliseet Nation Conservation Council; Robert Hanner - Biodiversity Institute, University of Guelph; Matthew Litvak - Biology Department, Mount Allison University; Steve Crookes & Mario Thomas - Precision Biomonitoring Inc.

In pursuit of Pasokos: Weaving environmental DNA monitoring with Traditional Wolastoqey Knowledge to understand changes in habitat use of shortnose sturgeon within the lower Wolastoq

The Wolastoqwiyik (Maliseet) people rely upon fish in the Wolastoq (Saint John River) for food and ceremony, including the shortnose sturgeon, Acipenser brevirostrum, a federally listed species at risk. Construction of a large hydroelectric facility in the 1960s has effectively limited this species to the lowermost 120 km of the 673 km river and has altered habitat downstream of the dam. Maliseet Traditional Knowledge from First Nations elders, knowledge holders and resource users, is vital in understanding changes in downstream habitat use by shortnose sturgeon. Conventional scientific monitoring involves fish capture and is challenging due to cost, logistics, and potential for negative effects to sensitive populations. Environmental DNA (eDNA) provides a new approach to detect species presence without capture, thereby avoiding harm, and the opportunity to increase spatial area and frequency of sampling. This project was initiated by the Maliseet Nation Conservation Council to pilot eDNA sampling paired with Maliseet Traditional Knowledge to learn about seasonal habitat use of shortnose sturgeon along the lower Wolastoq. Scientists from Stantec Consulting planned program design and conducted sampling; scientists from the University of Guelph and Mount Allison University are also participating. This presentation will provide results to date and recommendations for next steps.
Zinck, Christopher, University of Saskatchewan - WCVM

The distribution of tick-vectored Borrelia infections in New Brunswick wildlife

Borrelia burgdorferi, the causative agent of Lyme disease, and Borrelia miyamotoi, are tick-vectored zoonotic bacteria that pose significant health risks to humans and companion animals. To assess the risks of these bacteria wild animal tissue samples were collected and tested via PCR in 2016 and 2017. The levels of infection found in the wild, as well as the animals most commonly found infected, allow for predictions to be made on areas of risk for human infection. Further, by determining what tissues and organs carry the bacteria in the infected animals the spread of these Borrelia species can be assessed through the host and the ecosystem.

Ziter, Carly, Concordia University

Thinking outside the park: a landscape ecology approach to urban biodiversity and ecosystem services

The current era of unprecedented urban growth has markedly changed ecosystem structure, function, and biodiversity, and consequently many ecosystem services that our health and wellbeing depend on. To work towards more sustainable, liveable cities, it is important to understand where there are opportunities to manage cities for increased biodiversity conservation and ecosystem service provision which requires an understanding of urban areas as spatially heterogeneous and temporally dynamic ecosystems. Drawing on synthesis, observational, and citizen science approaches, I will provide an overview of recent research on the effects of landscape structure, land-use history, and biodiversity on ecosystem services in urban landscapes. Examples will be drawn from empirical work in the mid-size city of Madison, Wisconsin, including: the importance of private land in driving soil-based ecosystem services; the interacting impacts of urban canopy cover and impervious surface cover on mitigation of urban heat; and insights into urban invasive species from community science approaches. Results highlight the importance of taking a more expansive view of green infrastructure, and illustrate how considering a more complete mosaic of urban green spaces can shift our understanding of urban ecology.