Ecology & Evolutionary Biology
UNIVERSITY OF TORONTO

Undergraduate Research Fair 2021

Program Guide

Contents

EEB Undergraduate Research Fair

Thank you for joining us for the EEB Undergraduate Research Fair 2021! The fair is a great way to experience the diversity of exciting undergraduate research in EEB, to hear about new scientific discoveries made by students, and interact with undergraduates and peers.

The students participating in the fair are competing for the *Corey A. Goldman Prize for Best Research Poster in Ecology and Evolutionary Biology*. The prize is named after former EEB Undergraduate Associate Chair Corey A. Goldman, and recognizes the top students within the department for excellence in their fourth-year independent research projects. Cash prizes will be awarded to the best research poster in each category.

This guide has been prepared to help you navigate the event. We have included items that we believe will be useful for you to know prior to attending to ensure the event runs as smooth as possible. All posters will be available for viewing at https://eebuoft.weebly.com. The site will also showcase posters from other research projects that were conducted this academic year by undergraduate students, but were not available for judging.

Event Details

Date: Friday, April 9, 2021
Time: 2:00PM – 4:00PM EST
Join Zoom Meeting: https://utoronto.zoom.us/j/81226781373
Zoom Meeting ID: 812 2678 1373
Passcode: research

IMPORTANT: It is recommended to use a computer or laptop (not a mobile device, tablet or iPad) and the latest version of Zoom in order to move freely between breakout rooms on your own.

- How to check what version of Zoom you have: https://support.zoom.us/hc/en-us/articles/201362393
- How to upgrade/update to the latest version: https://support.zoom.us/hc/en-us/articles/201362233-Upgrade-update-to-the-latest-version

Event Schedule

2:10 – 2:20 PM Welcome

Opening remarks: Ben Gilbert & Shelby Riskin

2:20 – 3:00 PM Elevator pitches

Student presenters will each deliver short elevator pitches (2 minutes each) of their research project.

1. Alan Bui
2. Anthony Carrozzi
3. Natasha Dhamrait
4. Natasha Djuric
5. Ismay Earl
6. Arielle Earn
7. Sophia Fan
8. Mikayla Ford
9. Angela Gong
10. Asad Hasan
11. Jameson Kunkel
12. Claudia Lacroix
13. Chantelle Lam
14. Teagan Netten
15. Jacy Newfeld
16. Dorsa Nouri Parto
17. Sharon Quan
18. Samantha Ramphal
19. Sarah Ravoth
20. Avery Schwarz
21. Zifang Xiong

3:00 – 4:00 PM All breakout rooms open

Attendees can move through the breakout rooms on their own.

Time	Student	Supervisor
BREAKOUT ROOM 1		
Category: Global Change, Organisms & Ecosystems		
Judges: Nicole Mideo & Rosalind Murray		
3:00 - 3:15	Natasha Djuric	Shelby Riskin
3:15 - 3:30	Mikayla Ford	Shelby Riskin
3:30 - 3:45	Jacy Newfeld	Jonathan Ruppert
3:45 - 4:00	Sharon Quan	Chelsea Rochman
BREAKOUT ROOM 2		
Category: Ecological Interactions		
Judges: Sebastian Kvist & Lea Chibwe		
3:00 - 3:15	Alan Bui	Don Jackson
3:15 - 3:30	Angela Gong	Ben Gilbert
3:30 - 3:45	Chantelle Lam	Helen Rodd
3:45 - 4:00	Teagan Netten	Njal Rollinson
BREAKOUT ROOM 3		
Category: Genetics, Evolution & Environment		
Judges: Matt Osmond & Tiziana A. Gelmi Candusso		
3:00 - 3:15	Natasha Dhamrait	Stephen Wright
3:15 - 3:30	Asad Hasan	Aneil Agrawal
3:30 - 3:45	Jameson Kunkel	Art Weis
3:45 - 4:00	Sarah Ravoth	Art Weis
BREAKOUT ROOM 4		
Category: Biodiversity & Morphology		
Judges: Adriana Bravo & Rafaela F. Gutierrez		
3:00 - 3:15	Ismay Earl	Sebastian Kvist
3:15 - 3:30	Sophia Fan	Sebastian Kvist
3:30 - 3:45	Samantha Ramphal	Rowan Sage
3:45 - 4:00	Zifang Xiong	Luke Mahler
BREAKOUT ROOM 5		
Category: Conservation & Management		
Judges: Megan Bontrager & Katja Kasimatis		
3:00 - 3:12	Anthony Carrozzi	Chelsea Rochman
3:12 - 3:24	Arielle Earn	Chelsea Rochman
3:24 - 3:36	Claudia Lacroix	Njal Rollinson & Marie-Josée Fortin
3:36 - 3:48	Dorsa Nouri Parto	Nicole Mideo
3:48 - 4:00	Avery Schwarz	Emily Darling
BREAKOUT ROOM 6		
Non-Competition Posters		
3:00 - 3:10	Maia Dall'Acqua	Art Weis

3:10 - 3:20	Sydney Gram	Marla Sokolowski
3:20 - 3:30	Rebekah Jolicoeur Alfaro	Jean-Marc Moncalvo
3:30 - 3:40	Fernando Jurado Soria	Rowan Sage
3:40 - 3:50	Nicole Regimbal	Jonathan Ruppert
3:50 - 4:00	Jessie Wang	John Stinchcombe

4:00 PM Closing Remarks – Back in Main Room

Closing remarks: Shelby Riskin

Navigating the Event

Housekeeping

	Audio – When you are not speaking, keep mic muted to avoid any unnecessary background noise.
	Video – Turn on if you can.
Chat	**Chat box –** This is the preferred method to ask questions to presenters. Messages sent in the chat are *not* broadcasted widely to everyone in other rooms. Only the people in your current room will see the messages.
Breakout Rooms	**In breakout rooms** – Move between breakout rooms on your own to view research posters and speak with the presenters.

To Join the Meeting

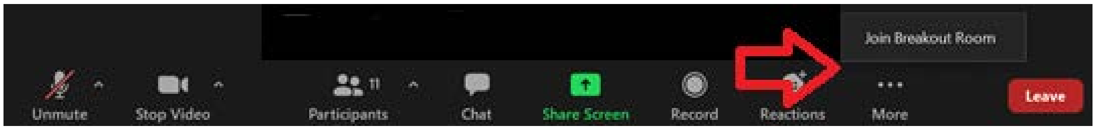
- Click on event zoom link
- Follow the prompts to open Zoom Meetings
- If prompted, enter your name and the meeting passcode
- Click 'Join Meeting' and you will be admitted into the event's main room

How to Move Between Breakout Rooms

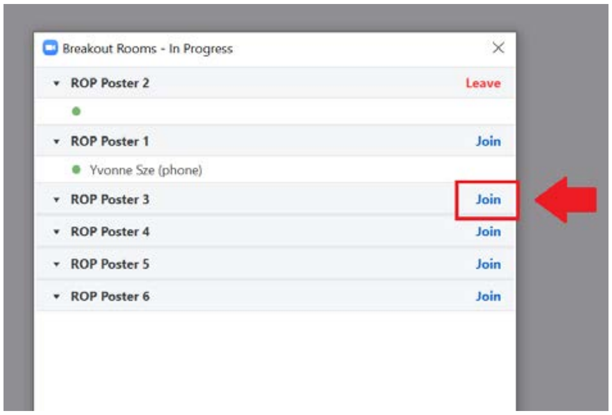
- To move to a breakout room, click the 'Breakout Rooms' button to open a breakout rooms list.
- Judges should go to the breakout room they are judging.

Breakout Rooms

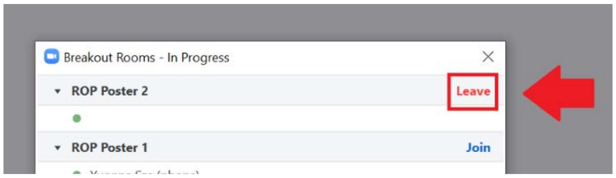
Note: Sometimes the 'Breakout Rooms' button may be hidden. If you do not see the 'Breakout Rooms' button, click 'More (…)' and 'Join Breakout Room'.



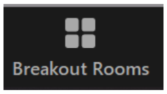
- Select your next breakout room by clicking ‘Join’. ***Note:*** Every time you change rooms, you will be automatically muted.



- You can click ‘Leave’ from the breakout rooms list if you’d like to leave. You will then be redirected to the *main room.*



- To leave the main room and rejoin the breakout rooms, click ‘Breakout Rooms’ and ‘Join’ to be automatically redirected to your previous breakout room.
- From there, you can move into other breakout rooms by clicking ‘Breakout Rooms’ again to view the breakout rooms list and click ‘Join’.



To Leave the Meeting

- When you have finished touring the breakout rooms, you are free to leave at any time.
- Click ‘Leave Room’ and ‘Leave Meeting’ (at the bottom right corner of the screen).

Code of Conduct

All participants, attendees and volunteers are expected to adhere to the following code of conduct to ensure a safe, open, productive, and welcoming environment to promote a positive virtual fair experience for everyone.

Acceptable behavior:

- All participants, attendees, and volunteers are treated with respect and consideration, valuing a diversity of views and opinions.
- Be considerate, respectful, and collaborative.
- Communicate openly with respect for others, critiquing ideas rather than individuals.
- Avoid personal attacks directed toward other participants, attendees, and volunteers.
- Respect the rules and policies of the online platform used.

Unacceptable behavior:

- Making verbal or online comments inappropriate in tone or content, which may include and not limited to those that reinforce social structures of domination related to gender, gender identity and expression, sexual orientation, disability, physical appearance, body size, race, age, and/or religion (or lack thereof);
- Including inappropriate material in oral or poster presentations, networking channels, or posters.
- Physically intimidating or frightening behavior (through threatening, stalking, harassing, abusing, etc.).
- Participating in illegal activities.
- Any activities that violate the policies of the online platform used.

Additional expectations:

- Be mindful of your surroundings and of your fellow participants. Alert organizing team members if you notice a dangerous situation or someone in distress.
- Avoid disrupting presentations.
- Refrain from using socially deemed inappropriate language in any form (textually, visually, and/or orally).
- Unacceptable behavior from any participant, including attendees and presenters, will not be tolerated. If a participant(s) engages in unacceptable behavior, individuals may be removed immediately without warning and may be prohibited from attending future meetings.

Student Poster Abstracts

Breakout Room #1: Global Change, Organisms & Ecosystems

Judges: Nicole Mideo & Rosalind Murray

Natasha Djuric (Supervisor: Shelby Riskin)

Effects of polyester microfibers and their chemical by-products on cherry tomato development (Solanum lycopersicum var. cerasiforme)

Agroecosystems are increasingly being recognized as major basins for terrestrial microplastics. Improper agricultural practices have led to high loading of plastic mulch films, synthetic microfibers, and other microplastics onto fields. These particles have the potential to influence physicochemical soil properties and crop productivity, but their impacts remain unclear. Here, we track the effects of polyester microfibers, a dominant biosolid contaminant, on the development of the cherry tomato (*Solanum lycopersicum var. cerasiforme*). Using soil containing microfibers, or soil watered with isolated leachate from microfibers, we further identify which properties most affect plant growth. We hypothesize that the physical changes to soil with the addition of microfibers may increase plant growth through decreased soil bulk density and increased water holding capacity. This effect may be exacerbated by the chemical additives applied to polyester yarn, most notably UV stabilizers that have been shown to mimic plant hormones. However, we find that neither polyester microfibers nor their chemical by-products affect germination. Growth and productivity during both the vegetative and reproductive phases may be altered, however, which we will assess.

Mikayla Ford (Supervisor: Shelby Riskin)

The Effects of Air Pollution and Land-use on Lichen Abundance and Diversity in Riparian Zones

Lichens are long lived, slow growing organisms that are extremely sensitive to air pollution due to their ability to absorb nutrients directly from the atmosphere. As a result, they are useful bioindicators to assess air pollution concentrations, especially in areas with different land uses and varying types of human activity such as agriculture and vehicle traffic. Broadly, this study aims to investigate the impact of air pollution on lichen communities near riparian zones along a gradient from urban to rural sites. Even in some urban landscapes, an extent of riparian zone along a stream channel is often protected due to their ecological importance including the maintenance of biodiversity. Since there are more opportunities for lichens to exist in these areas, even when pollution levels are high, they are a valuable study system to use to investigate the effects of air pollution on ecosystems which are subjected to frequent human activity. This study measures lichen diversity and abundance on trees in transects starting at a river's edge and extending orthogonally 50m, at three sites of varying land use classifications (urban, rural, and intermediate) within Southern Ontario, to determine whether lichen communities change along the urban to rural gradient or with proximity to the stream channel. We then use publicly available air quality data from each of these areas to examine the relationship between lichen communities and air quality at each site. These analyses will provide important insight into the unseen impacts of air pollution on riparian areas in human-dominated landscapes.

Jacy Newfeld (Supervisor: Jonathan Ruppert)

Compositional and functional changes in stream fish communities due to urbanization in the Greater Toronto Area

Globally, increasing urbanization poses significant risks for stream communities, including decreased biodiversity and altered community composition. In the Greater Toronto Area, these symptoms have been documented in urban stream communities. However, there has yet to be a multivariate ordination-based approach to urbanization's effects on stream fish communities that incorporates species identity, species traits, and land use. We examine how land use change affects community composition and species traits using a suite of multivariate approaches, including: Principal Component Analysis (PCA), Redundancy Analysis (RDA), and RLQ/Fourth-Corner Analyses on species identity, species identity by land use, and species traits by land use and species identity, respectively. Spawning temperature and thermal tolerance were widely correlated with many land use variables, and maximum fish length was negatively correlated with meadow cover. Most invasive species were present at sites with high wetland and forest cover and low impervious cover, which could be due occurrence in downstream sites with higher forest and wetland cover. Native species tended towards sites with high meadow cover and moderate or high impervious cover, which could be due to occurrence in upstream sites with higher meadow and impervious cover. Biodiversity was highest at moderate-high levels of natural cover and low levels of impervious area, which could be the result of an ecotone where a low-natural cover-favouring community is in contact with a high-natural cover-favouring community. Altogether, this underscores that particular species traits, such as thermal regime and spawning temperature range, may be important in the context of urbanization and particular species with low temperature preference and low spawning temperature range may be at high risk. These results can help to guide and to inform management and conservation decisions by prioritizing species or traits exhibited in species that may be more at risk of local extirpation due to urbanization.

Sharon Quan (Supervisor: Chelsea Rochman)

Using Histology to Determine the effects of Wastewater-Treated and Untreated Cotton and Polyester Microfibers on the Liver and Gonads of Fathead Minnows (Pimephales promelas)

Microfibers are a subtype of microplastics (< 5 mm in diameter) that are flexible, usually tensile, and resistant to breakage. They are shed from both natural (e.g wool and cotton) and synthetic (e.g polyester and nylon) textiles such as clothing and towels. Our common day-to-day practices like domestic washing cause microfibers to shed from textiles. The shedding of microfibers ultimately makes up 95% of the microplastics found in marine waters, sediments, and organisms. Wastewater effluent from wastewater treatment plants (WWTP), which contains a wide variety of organic and inorganic matter, is a prominent pathway for the release of microfibers into the environment from washing. Currently, much of the physiological effects of microfibers, exposed or unexposed to WWTP effluent, on organisms remain understudied. In this study, we investigated the effects of microfibers on the livers and gonads of Fathead Minnows (Pimephales promelas) using five different exposure treatments: 100% polyester fiber, 100% cotton fiber, WWTP effluent + 100% polyester fiber, WWTP effluent + 100% cotton fiber, and negative control (no microfibers, no WWTP effluent). More specifically, we performed histopathological scoring of the liver and gonads of 5 male and 5 female fish from each treatment. For the male gonads, we scored the quality of the gonads by the presence of abnormalities, including intersex. For the female gonads, we scored the quality of the gonads by the presence or absence of atretic cells, abnormal cells, number of eggs at each oogenesis developmental stage and thickness of the egg lining. The livers were scored for signs of lipidosis. The results of this study known to date will be shared.

Breakout Room #2: Ecological Interactions

Judges: Sebastian Kvist & Lea Chibwe

Alan Bui (Supervisor: Don Jackson)

The Role of Lake Shape Complexity on Smallmouth Bass (*Micropterus dolomieu*) Populations in Northern Ontario

With rising global temperatures and introduction of fish, there has been an increase in the northern range of many freshwater fish species. In the case of predators such as smallmouth bass (*Micropterus dolomieu*), this can have heavy impacts on native populations. The focus needs to be shifted towards identifying key factors in lake morphology that can play a key role in creating a suitable thermal habitat for the warmwater species. One such factor is lake size and shape and the role of embayments. This study proposes that lakes having embayments will warm faster during the year, providing smallmouth bass with a warmer habitat and increase incidence rates in complex lakes compared to more regularly shaped lakes. By breaking up complex lakes into a cluster of perfectly circular lakes that are connected, the daily water temperature was modelled for each section. The daily temperature is then inputted into a bioenergetics model to predict the survivability of young-of-year smallmouth bass.

Angela Gong (Supervisor: Ben Gilbert)

Incorporating demographic stochasticity into coexistence theory

Ecologists have increasingly recognized the value of integrating niche and neutral perspectives on community diversity to better understand species coexistence and distributions. Modern coexistence theory (MCT) places niche and neutral processes within a single framework, identifying neutrality as the scenario where species are functionally and competitively equivalent. In non-neutral communities, competitive outcomes are theoretically predictable using fitness and niche differences between species, which deterministically structure the community. Here we simulate competition in a stochastic two-species Beverton-Holt model to test whether these predictions are reliable and consistent across a range of community parameters and invasion scenarios. We demonstrate that MCT can most accurately predict competitive outcomes at high species growth rates and large community sizes. We further examine the consequences of removing demographic stochasticity for the resident when one species invades another, to elucidate a potential mechanism by which stochasticity alters competitive outcomes. These results establish the accuracy of MCT as a predictive framework for coexistence in non-neutral communities, and demonstrate when and why stochastic forces such as ecological drift must be further accounted for.

Chantelle Lam (Supervisor: Helen Rodd)

Multivariate analyses of long wavelength genes, colouration, and habitats of fishes reveals an interesting pattern of SPR, a pterin gene

Carotenoids and pterins are two classes of biomolecules that form the basis of long wavelength (LW) (yellow, orange, red) colouration of birds, fishes, and reptiles. There has been much interest in carotenoid-based colouration because in vertebrates the acquisition of carotenoids is solely dietary, making it an honest indicator of mate quality, while, in contrast, pterins can be synthesized autonomously by vertebrates. The underlying reason for why species would utilize both carotenoids and pterins remains unclear. We predicted that habitat would play a role in the distribution of pterin and carotenoid genes across fish species. In this study, we performed phylogenetically-corrected canonical correspondence analyses to investigate the relationships between the colouration, ecological habitats, and the presence of carotenoid- and/or pterin-associated genes for fish species with fully annotated genome sequences. Based on these analyses, as expected, carotenoid-associated genes are associated with the widespread occurrence of LW colours. While most carotenoid- and pterin-associated genes were not affiliated with specific habitat types, we found a positive association between pterin-associated SPR and marine environments. Here, we emphasize the importance of the SPR gene and argue that, because carotenoid availability is low in marine environments, species enhance/replace their carotenoid-based colouration with pterins.

Teagan Netten (Supervisor: Njal Rollinson)

Within-site variation of morph frequencies with respect to temperature and precipitation in the red-backed salamander, Plethodon cinereus

The production and maintenance of intraspecific variation is a fundamental topic in ecology and evolutionary biology. The striped/unstriped colour polymorphism in Plethodon cinereus is maintained by a combination of genetic drift, gene flow, and selection, but the selective processes acting on the morphs are unclear. The frequency of each morph varies both among populations and within populations across time. Physiological differences between the striped and unstriped morphs support correlations between morphotype and environmental factors, with the unstriped morph appearing to prefer hotter temperatures, but potentially requiring wetter substrates. However, the correlations between morphotype and environmental factors in the wild are supported over vast spatial scales, and clear evidence that temperature and moisture broadly influence morph frequencies is lacking. Some evidence suggests that temporal variation in morph frequencies may occur within populations due to individual salamanders retreating underground when conditions are unfavourable. This study aims to elucidate whether morphs have a temperature preference in the wild by examining temporal variation in morph frequency within populations across two years and 66 sites in Northern Ontario. We built six mixed-effects models to examine the relationship between morph frequency, temperature, and precipitation. Model selection showed that none of the models adequately explain variation in morph frequencies. Temperature and precipitation do not appear to drive variation in morph presence within sites over the early active season, and as such this study fails to support a role for temperature and moisture in generating variation in morph frequencies.

Breakout Room #3: Genetics, Evolution & Environment

Judges: Matt Osmond & Tiziana A. Gelmi Candusso

Natasha Dhamrait (Supervisor: Stephen Wright)

A comparative genomic analysis of the rate and drivers of diploidization in angiosperms

Genomic evidence supports the theory that plants regularly experience periodic cycles of polyploidy resulting from whole-genome duplication and subsequent diploidy as redundant genes are lost through a process called diploidization. In other words, diploidization describes the gradual return of a duplicated polyploid genome to a diploid state. Despite the quantitative evidence of diploidization and its mechanisms, the evolutionary forces that drive the rate of duplicate gene loss are still unclear, and only recently have these drivers been studied experimentally. Multiple lines of evidence have supported the theory that diploidization is not random and can widely vary even between closely related lineages and species. The variation in the rate of diploidization is theorized to depend on factors that affect the strength and direction of selection on the retention or loss of duplicates, though there have not been many studies specifically quantifying this. Previous studies of diploidization have not included how life history and effective population size, factors known to influence selection on duplicated genes, can drive the rate of diploidization. This study would be the first to take a genomic approach in comparing the interspecies rate of diploidization in angiosperms while also considering these other drivers of diploidization and genome size evolution. To quantify the rate of diploidization, I used genome-level analyses of available species to estimate the number of duplicated genes and approximate the age of the last whole-genome duplication event by comparing the number of synonymous changes between duplicates. I collected information about effective population size and mating systems through a literature review.

Asad Hasan (Supervisor: Aneil Agrawal)

Examining the sex-specific genetic architecture of fitness in Drosophila melanogaster

Due to anisogamy, where males and females of a species produce different gametes, male and female fitness is optimized differently. Male fitness is limited by the number of available female mates since sperm production is excessive, whereas female fitness is limited by the number of resources they can acquire in order to optimize gamete production. However, there is a lack of research specifically describing the sex-specific genetic architecture of fitness. Using a Genome-Wide Association Study (GWAS) dataset describing male-specific and female-specific fitness of recombinant inbred Drosophila lines in cage and vial environments, this study uses permutation tests and recursive tests as a means to uncover the genetic basis of sex-specific fitness and selection. In accordance with previous research, the permutation tests suggest that most loci are under sexually concordant fitness, where selection operates similarly in males and females. Additionally, the sexually antagonistic loci that are identified have relatively small effects on sex-specific fitness, suggesting that sexually antagonistic selection is weak. The recursive tests suggest that most loci identified are responsible for a very small proportion of the total variation in sex-specific fitness. These results imply that selection is not significantly constrained by differences between fitness optima of both sexes, and provide further evidence for the sex-specific genetic architecture of fitness being highly polygenic.

Jameson Kunkel (Supervisor: Art Weis)

An inquiry into the relationship between spatial and phenological isolation in flowering plants

In flowering plants, limits in seed and pollen dispersal can create spatially isolated pools of genetically similar individuals. Additionally, two flowering plants can only exchange pollen when both plants are in flower simultaneously. Thus mating is assortative with respect to flowering phenology, producing genetically isolated pools of phenologically similar individuals. Only recently have these two forms of reproductive isolation been considered in concert through the use of simulations. Under restrictive assumptions, spatial and phenological isolation were found to synergize, generating persistent spatial clusters of phenotypically similar individuals. Spatial and phenological isolation produced higher genetic variance and pulled neutral and flowering time loci responsible for flowering phenology into linkage disequilibrium. We present a model simulating spatial and phenological isolation in flowering plants that relaxes past assumptions by incorporating true continuous space as well as mutations at flowering time loci in order to assess whether previously observed interactions between spatial and phenological isolation hold under more biologically realistic parameters. We present and compare the spatial and genetic dynamics of a population of flowering plants mating at random, under spatial isolation, under phenological isolation or under both spatial and phenological isolation. Additionally, we highlight limitations of the model and future directions we wish to take it.

Sarah Ravoth (Supervisor: Arthur Weis)

Non-random death and selection on flowering time in seedbanks

Measuring the rate and direction of adaptive evolution in response to global change is essential to ensure persistent populations, species, and ecosystems. Resurrection experiments are valuable tools for this task; ancestral propagules, such as seeds, kept in storage banks and revived and grown alongside descendent generations in a common environment. However, even under the best conditions, long-term storage over years or decades causes mortality of a fraction of propagules. If storage acts as a selective sieve favouring survival of certain individuals, and probability of survival is genetically correlated with a trait of interest, the phenotypic baseline is “moved”, and estimated evolutionary change is distorted. Here, we test whether age of a maternal plant at the time of seed maturation affects survival during storage, and in turn, how this can impose selection on adult flowering time. In this multi-generation experiment, we expose seeds of early- and late-flowering genotypes of Brassica rapa to high heat and humidity to induce 50% mortality, in order to mimic the effects of propagule ageing during long-term storage. We compared survival rates of seeds from the first flowers made by individual maternal plants (which have priority access to maternal resources) to those from her last flowers. These last flowers are also more likely to be pollinated by genetically late-flowering donors. If the poorer condition of last-produced seeds causes storage death, genes from late flowering fathers will be disproportionately lost. Thus, age-related decline in maternal allocation to seeds can impose selection on flowering time through pollen donors, falsely shifting flowering time earlier. The results of this project will help inform methodology for seedbanks and resurrection experiments, such as *Project Baseline*.

Breakout Room #4: Biodiversity & Morphology

Judges: Adriana Bravo & Rafaela F. Gutierrez

Ismay Earl (Supervisor: Sebastian Kvist)

Diversity, phylogeny, and distribution of the leech genus Haemopis (Annelida: Hirudinaria) across North America

Leeches of the genus *Haemopis* are macrophagous predators, playing an important role within freshwater benthic communities. In recent years, DNA barcoding has proven useful in identification efforts within this group, and molecular methodologies have begun to reveal relationships within this genus. Previous studies have repeatedly shown this genus to be monophyletic, though higher level relationships between species of this genus have not yet been concretely resolved. Here, we use phylogenetic approaches to assess species barriers and evaluate evolutionary relationships among *Haemopis* collected across North America. We sequenced the COI locus of 102 specimens, representing 4 of the 8 species from North America and 2 of the 3 species from Europe, as well as the 12S, 18S, and 28S rDNA loci of select specimens. Sequences for the remaining *Haemopis* species not represented in our collections were supplemented using GenBank sequences. To complement our molecular analyses, we dissected a subset of specimens to assess differences in morphology across both genetic and geographic distances. *Haemopis septagon*, *H. terrestris*, *H. kingi*, *H. plumbea*, and *H. grandis* were each resolved as single nominal species. Specimens identified as *H. lateromaculata* and *H. caballeroi* were found to be positioned within the *H. marmorata* species group. Most importantly, our results show *H. marmorata* as having two genetically distant populations broadly grouped into Eastern and Western clades.

Sophia Fan (Supervisor: Sebastian Kvist)

Description and phylogenetic placement of a new species of *Placobdella* (Hirudinea: Glossiphoniidae)

Royal Ontario Museum, University of Toronto Department of Ecology and Evolutionary Biology

Placobdella is a genus of sanguivorous leeches in the family Glossiphoniidae, a group that feeds mainly on turtles but is also known to feed opportunistically on other hosts like amphibians, fish, and humans (de Carle et al. 2017). Its members are distributed largely throughout North and Central America with the exception of one European species (de Carle et al. 2017). To date, Placobdella encompasses 24 nominal taxa with 6 new species described within the last decade (de Carle et al. 2017). As it is currently known, Siddall et al. (2005) define *Placobdella* as all glossiphoniid species with one pair of cecate bacteriomes, bilobate ovaries, and two pairs of fused eyespots. In 2017, de Carle et al. performed the most comprehensive phylogenetic analysis of *Placobdella* to date, and in addition to the known species within de Carle et al.'s analysis, numerous unidentified specimens were recorded and placed within their tree. One of these comprises a novel species, temporarily dubbed *Placobdella* sp. 1, which exhibits a morphology unlike any other *Placobdella* species description to date. This study involves a species description and phylogenetic analyses of these novel *Placobdella* sp. 1 specimens. *Placobdella* sp. 1 displays a variable, buff brown external morphology with a darker brown, interrupted mid-dorsal stripe and five main rows of papillae. Internal morphology shows that it uniquely possesses one pair of compact salivary glands in combination with diffuse salivary tissue. Phylogenetic analysis places *Placobdella* sp. 1 as sister to *Placobdella* kwetlumye. We are to name this species *Placobdella* akahkway, after the Plains Cree word for "leech" in honour of the Indigenous languages spoken at its collection sites.

Samantha Ramphal (Supervisor: Rowan Sage)

The Relationship between Plasmodesmata density, Phloem loading and C4 Photosynthesis

C4 photosynthesis is a carbon concentrating mechanism evolved by plants which improves photosynthetic efficiency over the more ancient yet common C3 photosynthetic pathway. C4 photosynthesis accounts for approximately 25% of global primary production (Wang et al. 2017) and has evolved in over 60 independent lineages, making it one of the best examples of convergent evolution in eukaryotes (Sage et al. 2011). Despite the high number of clades independently evolving the C4 pathway, the pathway is restricted to few taxonomic orders, notably grasses, sedges and Chenpods. This suggests the existence of evolutionary constraints on the pathway, one of which may be the phloem loading mechanism. Specifically, passive symplastic phloem loading may prevent the C4 evolution by interfering with metabolic transport between mesophyll and bundle sheath compartments in leaves that are required for C4 function. The C4 pathway isolates Rubisco to the bundle sheaths cells and leads to a high concentration of metabolites within these cells. Symplastic phloem loading could result in the leakage of photosynthetic assimilates out of the BS through plasmodesmata at the BS/phloem parenchyma (PP) interface (Young et al. 2020). The plasmodesmata density at the BS/PP interface has been used to categorize veins into either Open, type 1 or Closed type 2 groupings. The closed category has been further divided into three subcategories: Smooth companion cell wall (2a), ingrown companion cell wall (2b) or Kranz anatomy (2c) (Gamalei 1991). This has led to an association between plasmodesmata type and phloem loading strategy (Gamalei 1991). This study is using TEM microscopy to investigate whether Kranz anatomy is a type of open phloem loading and whether open phloem loading is associated with apoplastic phloem loading, an alternative form of loading that is distinct and possibly incompatible with widely used passive loading strategies.

Zifang Xiong (Supervisor: Luke Mahler)

The Ecomorphology of Anolis Dentition

The *Anolis* lizards are well known for their adaptive radiation in the West Indies where island species of anoles have repeatedly into a set of similar niche habitat specialists, termed ecomorphs. Spatial niche partitioning of the anoles has been subjected to much research in the past, however, it is relatively unknown whether anoles exhibit dietary niche partitioning, and whether dietary differences are reflected in their dental morphology. *Anolis* dentition has long thought to be conserved among species with little variation. Here, we collected dentition data from microCT images of *Anolis* lizard specimens, and we investigated the following questions. Is anole dentition homodont or heterodont? Do anole teeth vary allometrically? Lastly, does anole dentition differ by ecomorph grouping? By using geometric morphometric and phylogenetic comparative methods, we found anole dentition tend to be heterodont along the tooth row, anole teeth vary allometrically in size and shape, and the dentition of aquatic anole is significantly different from other ecomorphs. This project is the first comprehensive survey of the *Anolis* dentition, findings from this study fill in the gap of existing knowledge in *Anolis* ecology and lay the groundwork for a future study in the dietary specialization of *Anolis* lizards.

Breakout Room #5: Conservation & Management

Judges: Megan Bontrager & Katja Kasimatis

Anthony Carrozzi (Supervisor: Chelsea Rochman)

Examining chemical additives associated with microplastic contamination in drinking water and evaluating their potential impact on human health

Microplastics are a class of emerging environmental pollutants that have been found in freshwater sources and drinking water around the world. They comprise a diverse suite of plastics possessing different colours, morphologies, and polymer types with an array of chemical additives, but they share a characteristic length of 5 mm or smaller. One of the major toxicological risks they pose may be related to their additives, as several of them have already been identified as endocrine-disrupting compounds (EDCs). Since the effects of chemical additives are likely dose-dependent, we must understand the exposure humans receive and their particular hazards to develop a better understanding of the risks they pose. As such, I performed multiple reviews of the literature and relevant databases to determine the quantity and dominant polymer types of microplastics commonly found in drinking water, the chemical additives associated with these dominant types, and the toxicity of these additives to human health. This data is being used to produce a risk assessment of the additives we consume via drinking water. The significance of this work lies in the fact that it is the first of its kind to comprehensively integrate and evaluate all of this information. The consolidated data source produced will provide the public, policymakers, and manufacturers with an initial idea of this ubiquitous hazard and encourage further research on the topic.

Arielle Earn (Supervisor: Chelsea Rochman)

Categorizing Diverse Perceptions of Harm across the Plastics Lifecycle

The perceptions of how plastics cause (or might cause) harm and the terminology to describe these harms vary vastly between fields: namely between scientists, social scientists, public health officials, and economists. Here, we explore the recent work of intergovernmental bodies to understand the diversity in their perceptions of how plastics cause harm across the plastic lifecycle. First, we investigate what might constitute “harm” in different disciplines by exploring the usage and context of the word “harm” in 40 United Nations Environment Programme (UNEP) reports on multiple environmental problems. Second, from these documents, we identify four overarching perceptions of harm that capture different aspects of the impacts of plastics across systems; these are environmental, social and cultural, economic, and human health perspectives. Next, we select and analyze four recent and varied intergovernmental reports on plastics from which we extract and categorize types of perceived harm according to the four overarching perceptions. In this way, we create a typology that summarizes the many ways plastics are perceived to cause harm across their lifecycle: from production to consumption to waste management to pollution. Our typology identifies the wide range of potential forms of harm caused by plastics and highlights that they are understood and weighted unevenly across different intergovernmental bodies. Some of the perceived harms of plastics include gender inequalities, occupational health effects, contributions to climate change, and hidden subsidies. We also find that the intergovernmental bodies are not perceiving types of harm across the full lifecycle of plastic in their reports as currently there is a major gap regarding how waste management (e.g., landfill leakage) impacts the environment. This work helps us uncover which perceptions of harm, and which parts of the plastics lifecycle, should be further researched and considered when forming prevention and mitigation strategies and regulations.

Claudia Lacroix (Supervisors: Njal Rollinson & Marie-Josée Fortin)

Are protected areas an effective measure for the conservation of Ontario's herpetofauna?

Biodiversity is being lost at an alarming rate, and evaluation of effective conservation practices is imperative. Protected areas are a common approach to biodiversity conservation, yet areas of high conservation concern often fail to overlap with protected regions. To assess this concern, we evaluated whether protected areas feature a greater diversity of herpetofauna (reptiles and amphibians) than unprotected areas within Southern Ontario. Specifically, we tested whether species richness (number of species) differed inside and outside parks, by using data of national, provincial and regionally protected areas, and data from the Ontario Reptile and Amphibian Atlas (ORAA), a citizen science-based monitoring program. The ORAA comprises 397 478 observations of 50 herpetofaunal species (23 classified at-risk) within spatially delimited grid cells (10×10 km raster cells). While accounting for environmental variation (e.g., road density, temperature, agriculture, sampling effort), we ran linear-mixed effects models at two different spatial scales (cell level: cells with a park present vs absent, park boundary level: observations inside vs outside protected areas) and three different species richness scales (all species, at-risk species, common species). Overall, we found that species richness was highest within protected areas at the cell level, whereas species richness was highest outside of protected areas at the park boundary level. All results were similar among species richness scales, however species richness of common species at the cell level did not differ inside and outside parks. Overall, our results suggest that species richness is highest in the vicinity of protected areas, where regions surrounding protected areas may be vital to the persistence of species at risk. Our results also suggest that protected areas are less effective at protecting species within park boundaries, however future work should address reasons for this trend and if our results are an artefact of sampling biases.

Dorsa Nouri Parto (Supervisor: Nicole Mideo)

Explaining the variation in culling practices: A Bayesian analysis of data from the World Organization for Animal Health

Culling is the practice of removing infected animals from a population to prevent the spread of pathogens. Theoretical models have shown that culling may affect the virulence of pathogens by changing the background host mortality rate; however, theoretical models are difficult to implement in real-life situations because culling methods vary globally. Our paper focuses on understanding and capturing variation in culling practices using Bayesian models. We used data from the World Organization for Animal Health (OIE), which detailed infectious disease outbreaks and culling rates in the years 2005 to 2011. Our results suggest that health expenditure in a country, the number of cases, and the risk of human-to-human transmission are positively and significantly correlated to culling rate. In addition, the country of the outbreak, the parasite family, and the parasite species explain a significant amount of variation in culling rates. Explaining culling practices using a model can allow us to understand how culling affects the virulence of pathogens and to gauge the efficacy of culling practices at reducing infectious diseases.

Avery Schwarz (Supervisor: Emily Darling)

Evaluating Meta-Refugia for Coral Reef Conservation in Tanzania

Coral reefs are an important ecosystem, providing food and livelihoods to over half a billion people. However, they are among the most threatened ecosystems and are declining at alarming rates. This is mainly due to climate change, which results in rapidly warming and acidifying oceans, exacerbating local stressors such as overfishing. The identification of climate refugia has gained recent focus, defined as relatively stable environments which might provide a safe harbour for threatened biodiversity. Unfortunately, studies suggest that few, if any, long-term reef refugia remain. Building on meta-populations, an emerging theory of meta-refugia suggests that smaller, connected refugia combine into spatial networks to increase the likelihood of maintaining biodiversity at larger scales. As the impacts of climate change accelerate, the application of this theory is becoming increasingly important. Here I seek to apply the theory of meta-refugia to the conservation of coral reefs, evaluating ecological and environmental characteristics of reef refugia using Tanzanian datasets. I hypothesize there will be significant variation across coral reefs in the characteristics used to identify climate refugia, and that an effective network of coral reef meta-refugia will be found in Tanzania. I plan to conduct a literature review to determine the environmental and ecological factors that underpin reef refugia. I will evaluate these factors in existing empirical long-term reef datasets to determine which locations have the highest potential as climate refugia. This study will inform coral reef conservation through the novel application of meta-refugia theory, allowing tropical nations to focus limited conservation resources on areas which have a high likelihood of maintaining reefs.

Breakout Room #6: Non-Competition Posters

These posters are not for judging.

Maia Dall'Acqua (Supervisor: Art Weis)

Natural Selection on Seed Longevity in Agricultural and Riparian Populations of *Amaranthus Tuberculatus*

In riparian environments, seeds typically fall to the ground and germinate where they land. In contrast, seeds in agricultural environments can be buried and resurface years later due to yearly soil turnover by farming machines. Seeds that survive longer have a higher probability of germination after resurfacing, which may introduce a selective pressure for greater seed longevity as native plants evolve into the agricultural environment. We investigate the differences in seed longevity between riparian and agricultural populations in *Amaranthus tuberculatus* by artificially aging the seeds. Seeds were collected from 4 states across the USA from paired riparian and agricultural populations. These were grown up in identical greenhouse conditions to equalize environmental effects on seed quality. Then, the seeds were artificially aged by incubating them at 45°C and 90% humidity for periods greater than 24 hours. Germination trials will be performed with the aged seeds to determine whether seed longevity is greater in agricultural populations. The results from this experiment will further understanding of plant evolutionary transitions from natural to man-made environments.

Sydney Gram (Supervisor: Dr. Marla Sokolowski)

The role of the foraging gene and the evolution of social behavior

The fruit fly foraging gene (for) is one of the first and most extensively studied examples of a gene involved in the regulation of behavioral phenotypes. Due to its high levels of pleiotropy and plasticity, coupled with its high conservation and its shared roles in environmentally responsive behaviors in many animals, foraging is a potentially interesting candidate system for understanding how the cooption of a single gene can facilitate the evolution of a broad array of social behaviors. In this study, I review gene expression data from transcriptomic studies of social behavior and compare the roles (and non-roles) of for in social behaviors across different species. I then review known and proposed mechanisms of action of the foraging gene products and suggest routes whereby this gene could be coopted for use as a regulator of multiple complex and interrelated social behaviors.

Rebekah Jolicoeur Alfaro (Supervisor: Jean-Marc Moncalvo)

Identification of Three *Psilocybe* Collections from the Brazilian Amazon and Species Distribution in the Genus *Psilocybe*

The mushroom genus *Psilocybe* is widely known for the characteristic hallucinogenic properties of its species and is being investigated for its aid in therapeutic settings. However, little research has been done on the origins and distribution patterns of species in the genus. In this study, we sought to place phylogenetically three unidentified specimens collected from the Brazilian Amazon Rainforest using sequence data from the ITS and nLSU-rRNA regions. Our results confirmed the placement of the three Amazonian collections in the *Psilocybe* genus and indicated that they probably represent new species. Additionally, our results demonstrated that species in the genus are strongly grouped through climatic patterns, with species being limited more by climate and less by geographic distance. Finally, we discuss the possibility that several species in the genus have diverged recently.

Fernando Jurado (Supervisor: Rowan Sage)

The Edge of the C4 World: Geo-Ecological Distribution Patterns of C4 Plants Species in Ecuador

Through major reorganization of leaf anatomy and physiology, C4 plants assembled the C4 photosynthetic pathway, an energy-dependent CO2-concentrating mechanism that counteracts the inhibitory effects of photorespiration. By reducing photorespiration, C4 photosynthesis could be 40% more effective, allowing plants to reach the full possible growth potential in warm, arid conditions. There is a lot of scientific interest to exploit this potential, including research on C4 insertions into C3 crops, bioenergy, and C4 crops improvement. To understand the evolutionary and ecological dynamics of the C4 flora, it is essential to analyze the environmental conditions that stimulate C4 photosynthesis and its diversification. Ecuador presents a unique opportunity to examine such conditions. Due to its location on the equator, and the presence of the Andes mountain range and the Galapagos Archipelago, Ecuador possesses an extremely high biological and geographical diversity. The Andes likely represented a formidable natural barrier for C4 species coming from regions of origin. As this species established, they evolved in synchrony with the Andes orogenic processes, and the climatic conditions present in this part of the world. The aim of this study is to elucidate the effects of a high elevation barrier to C4 plants distribution throughout their evolution in the Transmontane Andes. We Identify the C4 flora of Ecuador and determine C4 species distribution patterns in Ecuador. We then create a bioclimatic map of the C4 flora of Ecuador and identify the main environmental factors driving its distribution.

Nicole Regimbal (Supervisor: Jonathan L.W. Ruppert)

Road mortality and mitigation measures to reduce impacts on amphibian species in the Greater Toronto Area

Land-use change and increased road infrastructure has resulted in fragmented and degraded surrounding habitats, impeding the fitness of local populations and contributing to biodiversity loss. Amphibians are especially vulnerable urbanization due to specific behavioral and physical traits, such as their size, speed, migratory behaviors, and lack of avoidance behaviors, which increase susceptibility to road mortality. Notably, it is estimated that 1.2 million organisms perish on rural roads every year because of road vehicle collisions within the Greater Toronto Area (GTA) alone. Given continued urbanization in the GTA, there is an increasing need to identify vulnerable species and environmental risk factors to implement effective road mortality mitigation strategies. Using data from 23 sites across the GTA, we assessed concordance between amphibian road mortality and inventory data (within surrounding habitat) to determine if there are disparities in vulnerability. Further, environmental risk factors were assessed between road mortality of varying fauna and surrounding habitat characteristics to determine if any increase in road mortality incidence. Lastly, the effectiveness of a type of several ecopassages at one location was completed to assess the performance of this type of infrastructure. The results indicate that road mortality and inventory datasets are not concordant, thus, species inventory is not reflective of road mortality vulnerability. Environmental factors, notably an increase of wetland are within 500m of the road, act as an additional risk factor to road mortality vulnerability. Lastly, assessing the use of ecopassages at one location appears to facilitate movement of almost all amphibian species surveyed within the surrounding habitat. These results indicate that road mortality mitigation strategies in the GTA should be focused on vulnerable species and environmentally high-risk areas, such as species with large breeding migration distances and low reactivity to oncoming vehicles and areas with surrounding wetlands. Further, mitigation measures, such as ecopassages, appear to be an effective mitigation strategy to reduce risk and impact to most amphibian species.

Jessie Wang (Supervisor: John Stinchcombe)

Project title: Multipartite mutualisms in *Medicago truncatula* are affected by drought stress

Mutualisms are commonly viewed as bipartite systems between two symbionts, predominantly in isolation from other organisms. Interspecific interactions brought about by mutualisms are essential to maintain the structure of ecological systems. Multipartite mutualisms have strong ecological implications due to the number of species involved and the potential for greater complexity in interaction networks, though the dynamics of multiple mutualists are not well-understood. The legume-rhizobium symbiosis is a well-documented example of mutualism. Rhizobia fixes atmospheric N2 to supply the plant with nitrogen resources, while the plant provides the bacteria with organic carbon and shelter inside of root nodules. Legume plants are also known to associate with mycorrhizal fungi which aid plant uptake of low mobility nutrients (such as nitrogen and phosphorus) and water. This association may be costly in situations with minimal nutrient or water stress. Previous investigations on the effects of multiple mutualists on *Medicago truncatula* found synergistic effects on plant performance, suggesting additional benefits induced by the coaction of multiple mutualists. In this study, I examined the fitness consequences of the presence of mycorrhizal fungi in conjunction with rhizobia in *M. truncatula*. I investigated the effects of an additional microbial partner under drought conditions to uncover context-dependent benefits of multiple mutualists. Under conditions of environmental stress, these benefits can counteract the costs of mycorrhizal associations under ambient conditions. These observations can help explain the discrepancy between the prevalence of multipartite mutualisms and the apparent fitness costs on legumes.