**Poster Session #1**

**The Influence of Habitat and Prey Availability on Female Bat Foraging Behaviour During Reproduction**

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Understanding predator foraging patterns in relation to prey and environmental features is crucial for unravelling links between species and the habitat they live in. A significant knowledge gap exists regarding the foraging behaviour of cryptic and endangered species such as little brown bats (*Myotis lucifugus*). Once abundant in the Great Lakes region of Ontario, little brown bats were listed provincially as endangered in 2014. The key question I will answer is how bat foraging behaviour varies over time and space as a function of habitat and prey availability throughout the reproductive season. My research has two primary objectives: 1) evaluate how spatiotemporal variables influence prey species assemblages and nutritional quality of nocturnal flying insects; 2) quantify shifts in little brown bat diet and foraging behaviour over the reproductive season. By using a suite of methods including DNA Bar Coding of guano and insect trapping, I will identify little brown bat critical foraging habitat and measure prey selection, helping to identify what insect species are essential for population recovery and long-term health. My research will provide a holistic view of how environmental variation, predator-prey dynamics, and reproduction influences the foraging behaviour of an endangered species.

**Lighting Environment and Body Size Influence Activity and Risk Behaviour in a Poison Frog Mimic**

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Antipredator colour strategies are often thought of as fixed traits, but ontogenetic shifts in colouration are common. A transition in colour strategy may be met with a complementary shift in behavioural phenotypes, but this remains under-explored. Similarly under-explored is how light environment perturbations affect behaviour in diurnal animals. To address these questions, we conducted a field experiment using the non-toxic Amazonian frog Allobates zaparo which mimics a sympatric poison frog species. Allobates zaparo metamorphoses into a cryptic phenotype, becoming aposematic and improving mimetic resemblance across development. Human activity exposes Al. zaparo to elevated light intensity through canopy disruption. We used a field arena assay and calibrated photography to evaluate the effects that colour development and elevated light intensity have on exploration and boldness. We find that Al. zaparo improves its mimetic resemblance across development, but that colouration alone does not impact behavioural phenotypes. We find that larger frogs exhibit less-bold behaviour, and that high light intensity reduces frog activity. These results suggest the presence of reproductive-stage based behaviour, and that human activity may impose a novel selection pressure in the species.

**How Can Thermal Image-Detection and Reflectance Determine the Moisture Content in Rockwool Cubes?**

Anna S. Bazangeya1, Michelle Pham2, Parham Jafary2, Lesley G. Campbell1, Habiba Bougherara2

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Rockwool is a widely used medium in soilless protected cultivation, where water deficit stress can pose a challenge to plant health and productivity. Substrate moisture content influences various factors including crop nutrient absorption, and plant stress responses. Due to rockwool’s limited water retention capacity, precise moisture management is crucial for optimal crop growth. We hope to develop an imaging moisture monitoring tool that can estimate how much moisture is contained in a rockwool block at any given time. We aimed to determine the spectral reflectance signatures of rockwool cubes at varying levels of moisture for the development of a spectral library. In turn, drought conditions can be detected before visible signs manifest in plants, allowing for proactive irrigation management. A CARY 5000 UV/Vis-NIR spectrophotometer was used to capture spectral readings of rockwool cubes at varying moisture levels by incrementally adding known volumes of water. Additionally, we plan to use infrared thermal detection via an IR camera to monitor water flow characteristics within rockwool cubes under different watering conditions. The results of the study will be presented, providing insights into the physical properties of rockwool as a medium and elucidating water movement dynamics within it.

**Investigating the Evolution and Genetic correlates of Sleep Consolidation across Cichlid Fish**

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Sleep is essential to every animal studied; but sleep structure varies extensively across the animal kingdom. Sleep may be consolidated all at once (monophasic) or split into multiple bouts throughout the day (polyphasic). Interpreting behavioural diversity of sleep behaviours is difficult due to confounding variation between taxa. As such, I used the model clade of cichlids to understand the evolution of differences in consolidation and identify the genetic signatures associated. I took a comparative approach, integrating behavioural variability, evolutionary histories, and genomic analyses. Our previous work on cichlids has identified that they display high inter-species variation in sleep behaviours, including total duration and circadian timing (during the day or night). My project defined variation in sleep consolidation across cichlids by re-analyzing their activity patterns using 150,000 hours of video from 60 species and calculating metrics I have devised to quantify consolidation. Our analysis suggests that cichlids vary from highly fragmented sleep patterns to very consolidated patterns, and display differences across the circadian cycle. I will use this information to perform genome-wide association studies (GWAS) to identify genetic correlates of sleep consolidation. This will lay the foundation for future research that can investigate how consolidation affects sleep functions.

**Development of an In-lab, Vertical Column Bioassay for Examining Chloride Exposure Modulation Among Endemic Zooplankton to Toronto’s Inner Harbour**

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Application of chloride-based deicers to many Great Lakes cities maintains safe travel conditions but leads to increasing chloride (Cl-) concentrations in streams, lakes, and groundwater. Currently, environmental exposures of zooplankton to Cl- across depth profiles are not well understood. Further, multi-lake mesocosm experiments (in-situ and ex-situ) demonstrated that Canadian Water Quality Guidelines for the protection of aquatic life (chronic: 120 ppm Cl-) are too lenient, leading to reductions (>50% lethality) among various zooplankton. In the environment, water bodies that receive saline runoff may experience stratification. In response, zooplankton may modulate their exposure to contaminants through diel vertical migration (DVM), a predation avoidance response, with coincident benefits to ensure population persistence and regulation of phytoplankton communities. While past work has examined the impact of Cl- on this behavior (e.g. downregulation of circadian genes, decreased DVM amplitude) initial testing used lethality test vessels do not adequately realize a zooplankton species’ vertical niche. The proposed research is on the development of a novel, low-cost behavioral ecotoxicological method for zooplankton DVM testing, utilizing 8-12’ column assays. These columns allow the simulation of thermohaline (salt and temperature-driven) stratification, where users can evaluate the impact of a contaminant on species vertical migration behaviors. (197 words).

**Has Mating Behaviour Diverged Across an Invasion Front of the noble false widow spider?**

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Understanding how invasive species establish and spread is a key goal of invasion biology. As invasive populations mature, a range of shifts in demography are expected to affect sexual selection, and thus mating behaviours. In this project we compared mating behaviours across an invasion front of the noble false widow spider, Steatoda *nobilis*. Using lab reared offspring of mated spiders collected in England, we characterized mating behaviours within and across two populations. One population is from the northern invasion front in England (Nottingham, England), first reported in 2016. The other population is older (Portsmouth, England) and was first reported in 1978. Recent studies suggest divergence, however, mating behaviour, has not been examined yet. Here, we pair males and females within and across populations in standard lab mating trials to test the hypothesis of mating behaviour divergence. We predict lower courtship rates, mating rates, but increased reproductive output (arising from increased genetic diversity of offspring) in inter-population pairings compared to intra-population pairings. We discuss our findings in the context of population divergence and invasiveness.

**Population Dynamics and Distribution of Methanotrophs in Landfill Cover Soils**

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Landfills are large contributors to global methane emissions. Methanotrophs living in landfill cover soils can reduce these methane emissions. The objectives of this work are to investigate the microbial diversity and community interactions with varying environmental conditions in landfill cover soils to further our knowledge towards mitigating methane emissions. To evaluate the community composition and correlations with specific environmental conditions, we sampled the cover soils of landfills and took measurements of methane flux, and other environmental variables. Sampling sites were distinguished based on the levels of methane flux. The results indicated high relative abundances of methanotrophs at sites with high methane flux values, dominated by the genus *Methylomicrobium*. Sites were also distinguishable based on several environmental conditions measured, with differing pH values and soil chemistry. The distribution of methanotrophs in samples across landfills and sites differed significantly when considering community evenness. Microbial community diversity correlated most strongly to methane flux and to nitrate and nitrite concentrations, of the environmental factors examined. The present results strengthen our understanding of methanotroph dynamics across different methane exposures and geochemical conditions within landfill cover soils. This will inform the use of designer cover soils and/or methanotroph amendments in efforts toward mitigating methane emissions.

**Expression of the Protein Assembly associated with Excitation-Contraction Coupling in Different Life Stages of the Unicellular Choanoflagellate, *Salpingoeca Rosetta***

Hannah Li1

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This project aimed to investigate the protein assembly associated with excitation-contraction coupling in different life stages of the unicellular choanoflagellate, Salpingoeca rosetta, a unicellular eukaryote closely related to animals. Custom polyclonal antibodies targeted against choanoflagellate homologs of key animal excitation-contraction coupling proteins, including SroCav1, SroRYR (Ryanodine Receptor), SroJPH (Junctophilin), SroSTAC (cysteine-rich domain-containing protein), SroMHC11 (major histocompatibility complex), SroBIN (bridging Integrator), and SroSERCA (Sarco(endo)plasmic Calcium ATPase), were employed to investigate their expression patterns. Preliminary data from immunolabelling indicates specific localization and co-localization patterns of these proteins, suggesting a complex and highly specific interaction network that parallels excitation-contraction coupling mechanism found in animals. Through Western blot analysis, it was found that SroSERCA, an essential gene involved in maintaining calcium homeostasis, was only detectable in thecates but not in rosettes, while SroSTAC was present in the cell membrane of starved chains. The protein density of SroMHC11 was found to be within less than a micron of SERCA of the sarcoplasmic reticulum. Additionally, JPH was found to be expressed only in the cell membrane of chains, while RyR was not. Future directions include carrying out Western blotting of SroVAMPa, SroCava2d, and SroRIMbp (Rab3-interacting molecule (RIM)-binding protein) in transfected HEK-293T cells, as well as focusing on triple co-immunolabelling of key proteins.

**Climate and Commerce Convergence for Optimal Strawberry Farming Decisions**

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Ever wonder why the price of strawberries fluctuates at the grocery store? We predict the answer is a complex mix of factors including the cost of fuel and fertilizers, the annual variation in seasonal availability of locally produced vs imported fruits that may be grown either conventionally or organically, indoors or outside, as well as more recent challenges. Mounting evidence indicates large-scale climatic phenomena such as El Niño Southern Oscillation (ENSO) can overwhelm endogenous factors that govern the population (and thus price) dynamics of wild species - we wondered if this would also influence cropped species. We contribute to the evidence by documenting an ENSO-related impact on strawberry wholesale prices at 3 food terminals across Canada. Time series of daily prices (2017-2023) were evaluated for common patterns of response to dramatic ENSO related events. We will share our preliminary results that describe the relative impact of ENSO relative to endogenous factors. Our findings may prove to be symptomatic of geographically broad impacts of large-scale climate on the dynamics of food security, even in global markets. Our findings reinforce the growing recognition that we should not overlook global-scale causal agents on food security practices.

**Are Shorter Species in Herbaceous Vegetation More Shade-Tolerant?**

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Competitive advantages are attributed to taller plants, especially regarding their ability to intercept more sunlight while also shading shorter plants. However, evidence has not clearly linked this “size-advantage” to light competition. Shorter plants are often the most shaded individuals within natural vegetation yet remain abundant and ubiquitous across community datasets and reach reproduction under high shade. Within forests, herbaceous plant survival is attributed to shade tolerance, but this adaptation has not been investigated within natural herbaceous vegetation, like old-fields, where shade conditions are comparable to some forests. We evaluated the incidence of shade tolerance adaptation, and 17 relevant functional traits (e.g., large leaf area, low chlorophyll a:b ratio), for 81 herbaceous species in a non-experimental old-field. We tested the hypothesis that short maximum height is predictive of trait values consistent with shade tolerance and found that 11 of 17 trait regressions were consistent. By assessing a broad scope of plant physiological performance, we provide a novel account of shade tolerance adaptation at the community-level, while also addressing two generalized assumptions in existing literature (i.e., a size-advantage in light competition, and the absence of shade tolerance within herbaceous vegetation), which have lacked robust supporting or opposing evidence.

**Attentional Character Displacement: How Search Images Limit Competition**

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Numerous studies in cognitive psychology and behavioural ecology have examined visual search and how foraging animals form search images, almost all focused on individuals. Here, we present an agent-based model simulating collective foraging on cryptic prey in agents that either do or do not form search images. Agents focused on one prey type reduce its local density, biasing other agents to form search images for other prey types, which may reduce competition. We report agents’ success rates as well as their positions and movements across attention-space. We also varied prey crypticity and the proportion of a population that could modulate their attention. We find that the ability to modulate attention increases distance in attention-space and reduces competition, improving success rates. Agents that cannot modulate their attention also benefit from foraging with those that can. These effects are sensitive to prey crypticity. By incorporating the cognition of visual search into a model of collective foraging, our data suggest that competition is a critical driver of the evolution of search images.

**The Good, the Bad, and the Low-abundant: A Review of eDNA Metabarcoding Data Analysis and Curation**

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Environmental DNA (eDNA) metabarcoding is a valuable tool for assessing fish communities and informing environmental management strategies. Given this, well-defined and informed methodologies are necessary to increase repeatability and accuracy of results. This review evaluates 87 eDNA metabarcoding studies with a focus on controls, replicates, and low abundance-read filtration methods. A rubric of 29 criteria was developed to standardize the evaluation process and assess the studies under review. While negative controls were common, their implementation and reporting varied, with limited use of positive controls and replicates throughout studies. Additionally, diverse approaches to low abundance sequence filtration underscore a lack of standardization and justification for threshold selection. Recommendations include the adoption of numerous practices: (1) increasing the application of controls and replicates, (2) providing the rationale behind low-abundance filtering criteria, (3) implementing benchmark studies, (4) improving communication of methods and results, (5) making raw sequence data publicly available, and (6) unifying terminology across the field.  Refined methodologies in eDNA metabarcoding research are imperative to ensure the reproducibility and accuracy of fish community assessment and environmental management practices as this tool continues to integrate into conservation and management efforts.

**Exploring the Role of Frequency-Modulated Bout (FMB) Calls in big brown bat Mate Attraction**

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The male big brown bat (*Eptesicus fuscus*) emits a unique call consisting of 3-4 frequency-modulated sweeps – the frequency-modulated bout (FMB). The FMB has a demonstrated role in food competition, but its exclusivity to males suggests a further function in mate attraction. This is congruent with the ‘songflight’ or ‘social call’ of two other male Vespertilionids, which has a role in both mate attraction and food competition and shares spectro-temporal characteristics with the FMB. In my presentation, I delve into these similarities across the family and outline my proposed procedure for investigating the role of FMBs in mate attraction, a two-alternative forced choice paradigm to test female big brown bats’ responses to a synthetic FMB call during mating and non-mating seasons.

**Classification of Red Raspberry Fruit Development via Spectral Imaging & AI Learning**

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Scheduled deliveries of fresh fruits and vegetables requires communication between farmers and grocery retailers. Raspberry plants undergo multiple growth stages before their final fruit form, with each developmental stage occurring on a predictable schedule. The use of an AI-trained mechanical eye capable of predicting raspberry harvest dates and quantities requires additional research. We aimed to create a hyperspectral signature database of raspberry developmental stages. With phenology data and machine learning, this database can be used to create an automated system capable of distinguishing raspberry stages within the complex agricultural setting.

Individual buds were marked on plants from 2 raspberry cultivars and tracked through developmental stages. Development was classified into 7 phenologies to create a reference standard (bud, flower, green fruit, yellow fruit, transition-stage fruit, ripe fruit, and overripe fruit). The spectral reflectance of each stage was measured using a CARY 5000 UV/Vis-NIR spectrophotometer. Of the 7 phenological stages, the average spectral signatures of 4 stages have been observed: yellow fruit, transition-stage fruit, ripe fruit, and overripe fruit. Data showed each stage with distinct reflectance value readings, with unique peaks along the measured wavelength range. The AI annotation suite has also been able to recognize several phenologies.

Mathematical Approaches for Simulating Epidemic Progression: Addressing Limitations of the Linear Chain Trick in ODE Models

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Simple dynamical models based on Ordinary Differential Equations (ODE) are widely used to forecast infectious disease spread. One issue with this framework is that it implicitly assumes that the residence time in any given state (e.g., the infectious state) is exponentially distributed. This assumption is often unrealistic. A common solution is the application of the Linear Chain Trick (LCT), where the infectious stage is divided into several substages, each following an identical exponential distribution, resulting in a more realistic Erlang-distributed duration. However, the LCT introduces challenges; it limits parametric flexibility and may require comparisons between models with different structures (i.e., different numbers of substages). Here, we propose using a fixed number of substages, but with varying substage transition rates in a geometric sequence. This approach keeps the key advantages of the LCT, while offering greater flexibility and easier fitting to data. We focus here on discussing the SIR (susceptible-infectious-recovered) model, but the potential applications of this approach extend to a wide range of dynamical models, of infectious diseases and other biological systems, offering advantages in terms of computational efficiency, ease of parameter estimation, and flexible time distributions.

**Investigating Freshwater Cyanophage Thermal Stability Within the Context of Climate Change**

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Viruses infecting primary producers such as cyanobacteria play a critical role in shaping aquatic ecosystems. Cyanobacteria thrive in warm surface waters, however, the impact that rising surface water temperatures due to climate change plays specifically on cyanophages, and within host-virus dynamics, remains unclear. This project investigated the thermal stability of two freshwater cyanophages (CrV and Ma-LMM01), which infect two species of invasive cyanobacteria (*Raphidiopsis raciborskii* and *Microcystis aeruginosa* respectively). Cyanophages were subjected to 4-hour temperature exposures ranging from 31 ℃ to 45 ℃ before triplicate MPN (most probable number) infection experiments were conducted, to determine infectious viral particle titer. Both cyanophages remained highly infectious up to 45 ℃, since there was no significant difference in the CrV viral titer between the control (25 ℃ exposure) compared to any of the increased temperatures in the CrV experiments, and only a significant decrease in the Ma-LMM01 titer at 45 ℃. This indicates that like their hosts, cyanophages may have adapted to be stable at warm temperatures, avoiding viral decay. It is likely that these cyanophages will remain stable and infectious for the foreseeable future, since surface water temperatures on average are not predicted to surpass 45 ℃ for over a century.

**Nutrient-Rich Solutions: Characterizing Compost and Compost Tea for Applications in Vertical Farming**

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Compost is organic waste that has been converted through digestion by various organisms into a nutrient rich soil that is often used in the agricultural industry as a fertilizer. The organic matter in compost can come from a variety of sources. Including fecal waste, spoiled food, industrial waste, and agricultural wastes. Compost tea is water that has had compost soaked and fermented and separated into a nutrient rich liquid. This experiment aims to determine and compare the nutrient makeup of compost and compost tea produced from four readily available organic waste sources: chicken manure, coffee grounds, spent grain from beer brewing, and raspberry leaves. Each source was processed in compost bins containing *Eisenia fetida,* commonly known as red wigglers. A portion of the compost was used to produce compost tea. Samples from each treatment were analyzed for their nutrient content as well as for the presence of common pathogens like *E. coli* and fecal coliforms. The study seeks to identify whether compost sources have distinct nutrient profiles and to produce sustainable organic fertilizer with ideal nutrient profiles. Preliminary results will be presented at the conference.

**Signal and Quality: Individual Variation in Mountain Chickadee (*Peocile gambeli*) Songs and Spatial Cognitive Abilities**

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This study explores the relationship between song and spatial cognitive abilities in male mountain chickadees (*Poecile gambeli*). Chickadees are nonmigratory, food-caching birds that rely on specialized spatial memory abilities to recover food stores and survive winter. Variation in male song has previously been linked with female mate preference in chickadees. While previous work found associations between song variation and spatial cognitive ability at the elevation level, direct evidence showing that variation in birdsong reflects spatial cognitive abilities is lacking. Using data collected over five years (2016-2017, 2020-2022), we directly tested the prediction that variation in male songs serves as an indicator of their cognitive abilities. We did not find a strong association between individual variation in song structure and spatial cognitive performance. However, differences in cognitive abilities and song between elevations were consistent with previous work. This study contributes to a deeper understanding of the role of birdsong in mate selection and the potential link between acoustic signals and cognitive performance in the context of natural selection.

**Examining the Impact of Polyadenylation Factors PABPN1, PABPC1, and CPSF5 on the Epithelial-to-Mesenchymal Transition in Mammalian Cells**

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Epithelial-to-mesenchymal transition (EMT) is the process in which epithelial cells lose their adhesive properties and convert into migratory mesenchymal cells. Alternative polyadenylation (APA) is a regulating mechanism of EMT in mammalian organisms. APA refers to variance in the polyadenylation sites (PAS) targeted during the polyadenylation process. This variance can generate different mRNA isoforms of the same gene that differ in terms of stability, activity, localization, and protein interactions. This study examines 3 different polyadenylation factors (PABPN1, PABPC1, and CPSF5), and their impact on EMT regulation. It is hypothesized that dysfunction in these genes will upregulate EMT in mammalian cells. In this study, murine mammary cancer cell line Py2T was used to model the effects of gene knockdowns of PABPN1, PABPC1, and CPSF5 on EMT regulation using short-interfering RNAs (siRNAs). EMT for each cell sample was quantified using Fluorescein Isothiocyanate (FITC)-Dextran and Transepithelial/Transendothelial Electrical Resistance (TEER) assays. Results for both TEER and FITC-Dextran assays indicate upregulation of EMT in all three of the knockdown samples relative to controls. While results are insufficient to establish statistical significance, they do support the initial hypothesis and indicate that EMT appears to be upregulated upon downregulation of the PABPN1, PABPC1, and CPSF5 genes.

**Ecological Niche Contributes to the Persistence of the Western x Glaucous-winged Gull Hybrid Zone**

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Hybrid zones occur in nature when populations with limited reproductive barriers overlap in space. Many hybrid zones persist over time, and different models have been proposed to explain how selection can maintain hybrid zone stability. More empirical studies are needed to elucidate the role of ecological adaptation in maintaining stable hybrid zones. Here, we investigated the role of exogenous factors in maintaining a hybrid zone between westerngulls (*Larus occidentalis*) and glaucous-winged gulls (*L. glaucescens*). We used ecological niche models (ENMs) and niche similarity tests to quantify and examine the ecological niches of western gulls*,* glaucous-winged gulls, and their hybrids. We found evidence of niche divergence between all three groups. Our results best support the bounded superiority model, providing further evidence that exogenous selection favoring hybrids may be an important factor in maintaining this stable hybrid zone.

**Poster Session #2**

**Examining the Diversity of Cetacean Temporal Activity Patterns**

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All animals partition their sleep and activity into distinct periods of the 24-hour day cycle. This daily timing of sleep and wakefulness defines a species’ temporal activity pattern, an important aspect of fitness. Species must be well-adapted to their temporal niche, meaning transitioning between activity patterns is often difficult, requiring changes to a confluence of genes/traits. How constrained a species is in this regard appears to depend on life history traits and environment, as the aquatic osteichthyes (bony fish) have been found to have a much higher rate of transitions between temporal niches compared to mainly terrestrial groups like mammals. Using literature meta-analysis, we examine how differences evolved in the temporal activity patterns of cetaceans (whales, dolphins and porpoises), the largest group of fully aquatic mammals. We find that cetaceans have frequently transitioned between activity patterns over their evolutionary history, a stark contrast to other mammalian groups. By modelling the dynamics of cetacean activity pattern evolution and quantifying how it differs from comparable terrestrial groups in the wider order artiodactyla, we can elucidate mechanisms that facilitate frequent transitions, such as exaptation of aquatic adaptations or a stepwise progression through a more arrhythmic intermediate state (a cathemeral/crepuscular bridge).

What Does qPCR and Marker Sequencing Tell Us About Potential Cyanobacterial Blooms?

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Toxic cyanobacterial blooms pose a threat to the quality and safety of drinking water globally by forming dense surface blooms and producing toxins that are harmful to human health. The aim of this research was to quantify cyanobacterial abundance (16S rRNA gene V4 region) and a potential toxin producing gene (*mcy*E gene) in a northern Ontario forested watershed. Sampling was conducted from May to August 2022 with sequencing and quantitative PCR used for molecular analyses. Cyanobacteria and potential cyanotoxin producers appeared as early as May in this low nutrient, relatively undisturbed lake system. Abundances ranged from 3.597 – 6.299 DNA copies/μL for cyanobacteria and 0.030 – 7.437 DNA copies/μL for the *mcy*E gene. Peak abundances were observed in the months of July and August, without visible blooms during sampling. Abundances ranged from logged values of 4.892 – 5.996 DNA copies/μL for cyanobacteria and 0.300 – 2.786 DNA copies/μL for the *mcy*E gene. Cyanobacterial abundance had variability between the months, days, timepoints, and location in the water column, demonstrating the importance of consistent monitoring and sampling efforts. This highlights that monitoring drinking water sources require appropriate sampling protocols as each water system is unique and can be affected by various disturbances.

**Characterizing Benthic Bacterial Communities in Areas Impacted by Wildfires in Fort McMurray**

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The 2016 wildfire in Fort McMurray deposited nutrients, such as phosphorous and nitrogen, to water systems causing cyanobacterial proliferation not seen prior to this fire. Cyanobacterial proliferation has sustained over several summer seasons due to internal loading of nutrients. The objective of this study was to characterize the previously undescribed bacterial communities in the sediment and benthic water in Fort McMurray, using bioinformatic tools. Sediment and benthic water samples were processed monthly between June and September 2023. Samples were then sequenced for the 16S rRNA gene using Illumina MiSeq technology and analyzed using QIIME2 with the SILVA v.138 taxonomic classifier. Phyla in water throughout the seasonal period were consistently present in similar relative abundances. There was slightly higher relative abundance of Cyanobacteria in water samples in August, and lower relative abundance in September. In sediment, phyla were also consistently present in similar relative abundances, except for Cyanobacteria having a higher relative abundance in September. Cyanobacterial genera in benthic water and sediments shifted from benthic and planktonic genera present in higher relative abundances to entirely planktonic genera present in September. This result indicates the dying off a cyanobacterial proliferation in the water column and settling in the benthos.

**Creating A Reporter To Measure *Sinorhizobium meliloti* *nodD1* Promoter Activity In Response To *Medicago truncatula* Root Exudates**

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Exploring traits involved in legume-rhizobium co-evolutionary history and nitrogen-fixing ability, offers a probe into subsurface ecosystems and a means to develop sustainable agriculture. Legume-rhizobium symbiosis by root nodulation, is highly host-specific and is facilitated through chemical signaling via flavonoids. Unique flavonoid profiles induce the expression of *nod* genes and Nod factors in rhizobia to signal nodulation and intensifies rhizobia competition. Existing methods to investigate both nitrogen-fixation and rhizobia competitiveness are time-consuming and inefficient. A reporter construct using the promoter region of the *nodD1* gene of *Sinorhizobium meliloti* presents a convenient and modular molecular tool to facilitate investigations into legume-rhizobium symbiosis. A 12-hour growth curve of *S. meliloti* with variable exopolysaccharide secretion confirmed relative growth rates. Gibson assembly was used to create two plasmids containing different lengths of the uncharacterized promoter region of *nodD1,* 263bp and 500bp respectively. An experimental design for bi-parental conjugation using a diaminopimelic acid auxotroph, MFD*pir*, was developed to address the lack of competency and selectable traits in *S. meliloti.* Furthermore, previous characterization of flavonoid profiles of *Medicago truncatula* roots inoculated with co-evolved and high-quality nitrogen-fixing strains provided pragmatic flavonoid cocktails to measure variable promoter activity via GFP expression. Upon successful assembly of the reporter constructs, additional assays between co-evolved, novel, high or low-quality, specific or broad-range legumes and rhizobia could revolutionize symbiosis investigations and optimize nitrogen uptake in legume agriculture.

**Local Adaptation to Daylength in the Invasive Plant Species *Mimulus guttatus* of New Zealand**

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Understanding how adaptation and phenotypic plasticity facilitate the rapid spread of invasive species remains a critical question in evolutionary biology. Clines in life-history traits along geographic gradients are a well-established phenomenon that demonstrate how plants synchronize their reproductive window with local conditions. Thus, we investigated whether there was evidence of local adaptation in the flowering and growth of an invasive plant. We used invasive populations of *Mimulus guttatus* from New Zealand, which is native to North America but has spread across other continents within the last 125 years, testing whether populations from across a wide geographic range showed evidence of differentiation or plasticity when grown under varying daylengths. Specifically, we selected nine populations and used seed from 12 maternal families from each population, grown in daylengths of 14, 16, and 18 hours. Given the rapid spread of the species, we expected extensive phenotypic plasticity for flowering and weak evidence of local adaptation. We found evidence of phenotypic plasticity across all populations under the different daylengths but also some evidence consistent with local adaptation to latitude in flowering. By examining how the combination of plasticity and genetic variation facilitates the spread of invasive species, we can better understand fundamental evolutionary processes.

Validating Thermal Refugia-Seeking Behaviour in Fish During Thermal Agitation

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Ectotherms, such as fish, are highly dependent on the stability of their environment to regulate body temperature, performance, and metabolism. Increasing temperatures cause behavioural changes in fish which can be observed and used as indices for determining upper thermal limits. The thermal agitation temperature (Tag) is a recent, and ecologically significant, sublethal index for the upper thermal limit. Previous studies have described thermal agitation as the endpoint, occurring prior to the critical thermal maximum (CTmax), where fish start exhibiting apparent refugia-seeking and avoidance behaviour. It is an assumption that fish are in seek of colder-water refuge, but evidence for this is lacking. Therefore, this study attempts to validate the assumption that Tag is refugia-seeking behaviour by using zebrafish (*Danio rerio*) and the Loligo shuttle box system. This system is set to provide a colder-water refuge (~27°C) while increasing the temperature of the fish’s environment to the point of Tag (~40°C). The behavioural responses of *D. rerio* will be observed and analyzed during Tag to determine if refugia is sought out. Confirming the behavioural responses associated with Tag will validate it as an additional sublethal endpoint prior to CTmax and help improve understanding of behavioural responses under thermal stress.

**The Influence of Familiarity and Sex on Social Learning in Group Living Fish**

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Social learning, learning via observation and imitation, is an ability that helps animals adapt to their environment. Current research indicates that factors, like one’s sex and familiarity with the demonstrator influence an animal's likelihood of engaging in social learning. The aim of this study is to test how sex and familiarity affect social learning in the matrilineal, group-living cichlid species Neolamprologus pulcher. Such insights may reveal how information spreads within and between groups. A common foraging assay was used to test the learning frequency and speed of N. pulcher depending on the observer’s sex and the familiarity status and sex of their demonstrator. We found that demonstrator sex and familiarity did not have a clear effect on N. pulcher learning. However, female N. pulcher learned faster than their male counterparts. As one of the first experimental studies to examine the factors influencing social learning in N. pulcher, we build upon the existing body of literature that examines how information spreads in groups. Such knowledge can shed light on the behaviours, dynamics, and transmission of cultural traits in cichlid communities. It can also help us further understand behaviour, decision-making, and cooperation in other taxa.

**Sounds of the Water: Studying the Influence of Macrophyte Removal on the Underwater Soundscape in Lake Scugog, Ontario**

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Freshwater lakes provide an array of ecosystem services like fishing, drinking, and swimming opportunities, and lakes can support highly diverse aquatic communities that are surprisingly rich in *sound* producing organisms. Passive acoustic monitoring (PAM), a technology using hydrophones, provides a non-invasive approach to studying underwater ecosystems, and there are many unanswered questions about aquatic bioacoustics – particularly in the ultrasonic frequency range. In the face of declining aquatic biodiversity, it is imperative to thoroughly document and comprehend biotic sound sources and assess any anthropogenic induced alterations. In this ongoing study, I utilize a wide range of sound data (2Hz – 250 kHz) collected from Lake Scugog, a lake in Southern Ontario with abundant macrophyte growth, to investigate the influence of macrophyte removal on the abundance of sounds produced by soniferous aquatic organisms. Biweekly measurements were taken 3 times before and after an aquatic macrophyte removal event using a hydrophone (SM4 Song Meter from Wildlife Acoustics) for acoustic recordings and an EXO2 Multiparameter Sonde for water quality measurements. Preliminary spectral analyses showing the abundance of varying sound frequencies across recordings before and after macrophyte removal indicate a slight decrease in sounds produced, but these results are inconclusive and require further data analysis.

**Dissecting Genetic Architecture for Phenotypic Variations in *Aspergillus fumigatus***

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Human fungal pathogens cause severe infectious diseases, especially in immunocompromised individuals. The rise in invasive fungal infections is linked to increased susceptibility, widespread presence of fungal pathogens, and evolving drug resistance. As a result of recent events, theWHO published the first-ever list of fungal priority pathogens in late 2022. Among them, the ubiquitous mold, *Aspergillus fumigatus,* causes numerous global aspergillosis cases. Research on *A. fumigatus* has primarily focused on single gene effects on virulence and drug resistance, lacking quantification of antifungal susceptibilities and related traits. We aim to fill this gap by analyzing 89 whole genome sequenced (WGS) *A. fumigatus* strains and phenotypic trait quantification. Divergent strains will be crossed, with progeny analyzed for growth at varying temperatures, response to antifungal drugs, and virulence factor production. Genotyping will involve WGS, genetic linkage mapping, quantitative trait loci (QTL) mapping, and genome wide association study (GWAS) to identify single nucleotide polymorphisms (SNPs) influencing phenotypic trait variation. We hypothesize that interactions between SNPs from different genes regulate virulence and susceptibility traits. Additionally, we'll explore correlations among virulence trait expressions to understand their interplay. The work done will provide valuable insights for better treatment strategies during the early stages of infection.

**Investigating the Yield and Light Penetration Impacts of Novel Pot and Trellis Designs in Above-and Below-Ground Competition in Raspberry (*Rubus idaeus*).**

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*Rubus idaeus* (commonly called red raspberries) contain many important micronutrients and dietary fibres for human health. With recent events of the Covid-19 pandemic, food insecurity levels have once again become a key concern for the Government of Canada. This study aims to identify the best possible above- and belowground conditions for raspberry growth in a vertical farming hydroponic platform to maximise yield. The objectives of this study are to measure the impact of below-ground competition in raspberries on yield while the volume of soil substrate remains constant or is reduced. Additionally, this study also aims to measure the impact of above-ground competition in raspberry plants on light interception and yield across multiple trellis designs. In doing so 298 raspberries of the ‘Joan J’ variety were placed in two novel trellis designs and randomised to also have cut and uncut hemp fibre slabs to mimic competition and no competition respectively. This research is pertinent in exploring growing configurations of raspberries to increase yield while maximising vertical farm space. Configurations can then be applied to hydroponic farming techniques in Canada ultimately reducing transport, labour and pest limitations associated with high tunnel raspberry cultivation.

**The Influence of Resource Quality on the Optimal Temperature for Population Growth in Flour Beetles**

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As global environmental change continues to alter ecosystems, understanding its impact on population processes has become increasingly important. These global changes influence factors such as resource quality and temperature, and our study aimed to investigate the combined effects of these two factors on the population growth of flour beetles (Tribolium castaneum). We tested a novel prediction from recent theory (Thomas et al. 2017) that the optimal temperature for population growth (Topt) declines with decreasing resource quality. Specifically, we tested the hypothesis that increasing resource quality would increase Topt up to a plateau. We exposed flour beetles to a fully crossed experiment consisting of four levels of resource quality and five temperature levels (27.5, 30, 32.5, 35, 37.5°C), allowing us to examine the interactive effect of these two factors on population growth. We manipulated nutrient quality using varying ratios of whole wheat and rice flour, and we counted population sizes every two weeks to track growth rates across treatment conditions. Our results revealed a saturating relationship between nutrient quality and Topt, with Topt decreased under low-nutrient and low-temperature conditions. These findings highlight the importance of considering resource quality alongside temperature when predicting population responses to environmental change.

**Dietary Composition and Partitioning in Ecuadorian Hummingbird Communities**

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Hummingbirds (Trochilidae) are a highly diverse and primarily nectivorous group of birds. However, they also feed on small invertebrates to supplement their diet with protein and other nutrients. Despite this, invertebrate consumption and how invertebrates fit into the food network of hummingbirds is largely unknown. As such, our study aims to use DNA metabarcoding, a DNA-based identification method, to determine the diet of 29 hummingbird species from Ecuador. With this information, our goals are to 1) determine if beak morphology (length, width, shape) or habitat elevation impacts invertebrate composition in the diet, and 2) explore whether hummingbirds partition their invertebrate diet similar to their floral diet. It is expected that the results from this study will emphasize tropical hummingbird dietary networks and the factors which influence resource use between species. With this information, we hope to aid in combatting the population decline of at-risk hummingbird species and the plants which rely on them for pollination. In addition, this study will allow for further examination of tropical hummingbird community dynamics and add to the current set of primary literature concerning their ecology and evolution.

**Can Duckweed Remain a Viable Superfood Despite Climate Change?**

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*Wolffia globosa* is a tropical duckweed native to Southeast Asia, where it is used as a food source. This aquatic plant reproduces rapidly and contains important nutrients. With cultivation commonly occurring outdoors, *W. globosa’s* reproduction is dependent on ambient temperatures. Thus, climate change could affect production and information regarding optimal temperatures for indoor production could be valuable. Reproduction, count of dead individuals and area coverage of *W. globosa* was measured at realistic increases to mean temperatures during its growing season (~1.5-2 ℃ in the next 40 years). As well, a thermal performance curve was created to understand the thermal tolerances of *W. globosa*, which can be beneficial in colder locations where indoor cultivation would occur. I found no significant effect of the predicted increase in mean temperature on the reproduction, count of dead individuals and area coverage of *W. globosa*. The frond count thermal performance curve indicates that the optimal temperature range is ~ 27-32 ℃, while the area difference thermal performance curve indicates the optimal temperature range is ~ 23-27 ℃. Therefore, in areas of Southeast Asia, like Laos and Myanmar, the mean temperature is expected to rise closer to optimal temperatures of *W. globosa*, which could increase production.

**Effect of Population-Specific Mating Preferences in the Context of Male Competition and Female Mate Choice in the noble false widow spider**

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As an invasive species spreads through a region, the isolation of newly established populations may occur due to founder effects and local adaptation. Even when these populations have some geographic overlap, divergence can still occur due to premating isolation and mating preferences. However, if mating preferences are weak and hybridization costs are low, the populations may occasionally interbreed. In previous experiments using two populations of Steatoda *nobilis* from a northern and southern latitude of an invasive distribution in the United Kingdom, we observed that in one-on-one interactions, mating rates were the same whether males and females were from the same (‘local’) or different (‘exotic’) populations. While spiders from different populations may mate if they have no other choice, females may exhibit preferences if simultaneously exposed to local and exotic males, and males may be less likely to engage in fights with locally adapted competing males, compared to exotic males. To test whether population-specific mating preferences are intensified in competitive contexts, we matched two males from different populations in weight and age and introduced them to the web of a female from either population and observed the interactions. We discuss our findings in the context of perceived mate quality and competition.

Declining Ice Duration Alters Key Ecosystem Parameters in Lakes Worldwide

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Lake ice duration is declining worldwide, which will affect the structure and function of ice-covered lake ecosystems. However, lake ecosystem responses to ice loss remain poorly studied. A global analysis of changing under-ice ecology is necessary to understand how lakes will respond to declining ice duration. We examined 21 lakes in North America, Europe, and Antarctica. We find that shorter ice durations are weakly correlated with warmer under-ice water temperatures (R2 = 0.35), reduced dissolved nitrogen (R2 = 0.37) and phosphorus (R2 = 0.35) concentrations, higher under-ice chlorophyll *a* concentrations (R2 = 0.34), and higher zooplankton abundances (R2 = 0.07) in lakes worldwide. These parameters represent key ecosystem processes in lakes, and changes in these processes can alter lake ecosystem function over time, particularly under more severe climate warming. This global analysis improves our understanding of how lake ecosystem parameters change in response to ice loss and provides information that may help preserve lakes and the ecosystem services they provide under future climate warming.

Big Brown Bat (*Eptesicus fuscus*) Spatial Memory

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The study of bat movement focuses greatly on echolocation as the animal’s method to orient, navigate, and forage. Interestingly, it has been shown that bats also rely on spatial memory for these tasks. Big brown bats, which produce frequency-modulated echolocation calls, also learn to rely on acoustic landmark locations to accurately navigate. Furthermore, after repeatedly flying through a cluttered environment, big brown bats learn the layout and where to orient their sonar beam while flying. This beam orientation persists even when the environment layout is changed. Finally, big brown bats can develop stereotyped flight paths in the wild and the laboratory. The proposed study aims to further our knowledge of big brown bat spatial memory by testing whether they can learn a food source’s location, and whether changing its location has effects on feeding accuracy and echolocation call rate. The first attempt of this study was unsuccessful due to the inability/unwillingness of captive big brown bats to fly. However, we aim to complete a second attempt with newly-captured big brown bats.

**Is Batman Bruce Wayne?: Using a Pattern Recognition Software to Identify Individual Big Brown Bats via Unique Collagen-Elastin Bundle Patterns**

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Collagen-elastin (CE) bundle patterns in bat wing membrane have been used for identification (Amelon et al. 2017); however, the laborious nature of manually comparing images adversely affects this methods practicality. We tested the efficacy of a feature-based pattern recognition software —HotSpotter©— in automating this process by comparing wing membrane photos (n = 328) within a database of adult (n = 24) and juvenile (n = 34) big brown bats (Eptesicus fuscus). The ventral surface of the wing membrane was illuminated with ultraviolet light during imaging. Upon running a match comparison on a selected reference image, HotSpotter© ranks every other photo based on an assigned similarity score. Ranked images in HotSpotter© outputs were classified as either matches of (1) the same animal, (2) a related bat (mom/sibling), or (3) an unrelated individuals and whether matches were of the same or opposite wing as the reference image. Higher similarity scores were afforded for same-individual, same-wing matches relative to other match types. The proportion of correct matches increased as the number of top-ranked images included when selecting a possible correct match increased. The results demonstrate that HotSpotter© has potential to accurately identify individual E. fuscus using photos of CE patterns in the wing.

The Early Bird’s Advantage: Proactive Mitigation Strategies to Improve Habitat Quality for Avian Species at Risk.

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In conservation biology, timing of conservation efforts can be as critical as the mitigation measures themselves. Utilizing advanced ecological tools, this study revealed the critical range of the Red-headed Woodpecker (*Melanerpes erythrocephalus*) and Eastern Whip-poor-will (*Antrostomus vociferus*) in Pinery Provincial Park, Ontario, Canada. This allowed for the implementation of proactive conservation strategies to improve habitat quality; embracing the expression that the early bird gets the worm. Combining the data collected from 14 autonomous recording units, breeding bird surveys, and community science data, we mapped these two species’ presence within the grounds of the park. From there, we tailored resource management strategies to address the specific threats these species face, ensuring the preservation and enhancement of their habitat within the park. By deploying early conservation measures and integrating advanced monitoring techniques with traditional field surveys, this project offers a comprehensive approach to address the conservation requirements of avian Species at Risk in Pinery Provincial Park, and in Ontario. The data collected from this project not only contributes to the understanding of habitat preference for these avian species, but it also offers actionable insights for effective park management strategies aimed at mitigating threats and conserving the unique ecosystems that Pinery possesses.

**Examining links between copulatory postures, sexual size dimorphism and the risk of sexual cannibalism across spider species**

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We tested hypotheses about the influence of the risk of cannibalism on mating behaviour and copulatory postures across species of spiders. Spider copulatory postures are species-specific, categorized into six positions that vary in whether the male is exposed to the female’s fangs during copulation or protected. We hypothesized that males would be more likely to evolve protected postures in species where females are likely to be cannibalistic, or where females are much larger than males and able to kill them with little cost. We extracted data on mating for 51 species from 110 papers. In line with our predictions, spider species with more extreme female-biased size dimorphism were more likely to show invulnerable mating postures. However, no significant relationship was found between body size ratio and cannibalism occurrence or frequency. These findings suggest additional factors such as variation in female hunger or the timing of sexual cannibalism might be important. Limitations of this study include a lack of standardized body size measurements across papers, and the relatively narrow range of species that have been well-studied (primarily Theridiidae and Araneidae). Addition research will be necessary to gain a deeper understanding of the evolutionary forces shaping mating success and species diversity.

**History of the Ontario Ecology, Ethology, and Evolution Colloquium**

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The Ontario Ecology, Ethology, and Evolution Colloquium (OE3C) is a provincial conference organized by students for students that is hosted at a different Ontario university each year. The history of OE3C is undocumented with the founding year and location unknown. I searched the internet and emailed emeritus and current professors at universities across Ontario to assemble a history. My poster will summarize OE3C history and include historical documents and logos. The Colloquium was founded at York University in 1974 and was initially called the Ontario Ecology Colloquium. The name was changed to the Ontario Ecology and Ethology Colloquium in 1977, and finally to OE3C in 2011. The impetus for starting the Colloquium was to increase communication among professional ecologists at Ontario universities and government agencies. For many years OE3C was organized by a Steering Committee composed of professors but is now primarily organized by graduate students. The Colloquium has been hosted by thirteen different universities in Ontario, most commonly by the University of Guelph, Western University, and Queen’s University. The Colloquium has been held every year since its founding except for 1975. The 2024 Colloquium at the University of Waterloo marks the 50th gathering of OE3C!

**Beyond the Signal: Using Digitally-Coded Radiotransmitter Frequency to Predict Temperature**

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Digitally-coded radiotransmitters allow for the simultaneous tracking of multiple animals but don’t explicitly report temperature data. The precise frequency of individual pulses deviates from their nominal frequency, recorded as frequency offset. I hypothesized that frequency offset of digitally-coded transmitters is correlated with temperature and could be used to document temperatures in free-living animals. I first conducted calibration experiments exposing transmitters to controlled temperatures resulting in a strong relationship between frequency offset and temperature. Next these transmitters were attached to free-living Silver-haired Bats (*Lasionycteris noctivagans*). Using only inferred temperature from frequency offset, torpor and homeothermy were observed under environmental conditions known to induce these strategies. However, predicted temperatures were inconsistent suggesting limitations for inferring exact temperature. Data from American Tree Sparrows (*Spizelloides arborea*) tagged with the same model of transmitter was explored with no evidence of heterothermy detected. Furthermore, the predicted temperatures were far below normal bird temperatures. My research indicates that digitally-coded transmitters can detect changes in temperature of free-living animals but is best used to document temperature patterns rather than measuring precise temperatures. Further studies should be conducted on known heterothermic birds to know if this method works for birds and can be used to detect heterothermy in new species.