

51ST ANNUAL FALL SCIENTIFIC PAPER SESSION 2025



The State University of New York at Geneseo
Saturday, November 1, 2025, 8:00 AM to 3:00 PM

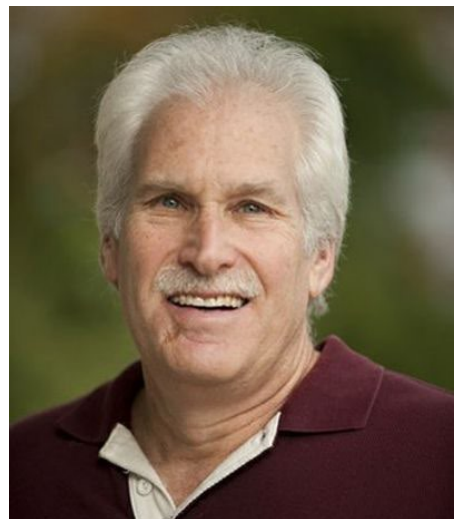
Dr. Lawrence J. King Memorial Keynote Lecture by Dr. Marc Abrams

Dr. Abrams is a Nancy & John Steimer Professor of Agricultural Sciences, and an Emeritus Professor of Forest Ecology and Physiology at Penn State.

Dr. Abrams will lecture on, *Native Americans, Smokey the Bear and the rise and fall of eastern oak forests* from his recent research and 2025 paper.

Saturday, November 1, 2025

Newton Lecture Hall room 202
9:00 a.m. Free & open to the public



Program

Condensed Presentation Schedule

Concurrent Oral Presentations A: 10:15-11:15

Session 1A, Bailey 102

- Gonzalez, Dayana (St. John Fisher Univ): *"Comparing Audio Logger Data to Trap Capture Data for Frogs at Vernal Pools"*
- Coates, Kaelyn (RIT): *"The Assessment of Pollinator Diversity, Floral Use, and Ecosystem Quality Across RIT Green Spaces"*
- Town, Kendalyn (SUNY Brockport): *"Modeling the Richness and Abundance of Non-native Vegetation in Great Lakes Coastal Wetlands"*
- Miller, Sara (St. John Fisher Univ): *"Variability in Capture Rates of Amphibians Within and Between Wetlands in Monroe County, NY"*

Session 2A, Bailey 103

- Gantress, Natalie (St. John Fisher Univ): *"Determining the Influence of Glyphosate on Erythropoiesis using K562 Cells"*
- Champlin, Julian (Ithaca College): *"Roots and Rubber: Impacts of Tire Wear Leachate on Hemp Physiology"*
- Stearns, Charles (Ithaca College): *"Turf: Morphological Effects of Artificial Turf Exposure to Minnow Embryos"*
- Gall, Jack (SUNY Brockport): *"Tracing Hatchery Origin and Lake Diet of New York's Lake Erie Tributary Steelhead"*

Session 3A, Bailey 104

- Hooke, Gail (RIT): *"Polybutylene succinate copolymers with variable degradability"*
- Islam, Muhammad S. (RIT): *"Ink-Process-Structure- Property Relationships in Ambient Slot-Die"*
- Stanek, Veran (RIT): *"Space Radiation Effects in Wide Bandgap Perovskite Solar Cells"*
- Lusignan, David (RIT): *"Role of Ink Rheology in Slot-die Coating of Halide Perovskites"*

Session 4A, Bailey 202

- Lee, Theodore (Cornell University): *"Development of Virokines as Tags for Mammalian Cell Protein Expression Systems"*
- Cookinham, Ariana M. (SUNY Geneseo): *"A Region of the X Chromosome Linked to Meiotic Drive in *Teleopsis dalmanni* is also Drive-Associated in *Teleopsis whitei*"*
- Greco, Michaela (Hobart and William Smith): *"Cracking the Shell – The Effects of CBG Oil on Chicken Embryo Development"*
- Ismail, Mohamed (Nazareth Univ): *"New insights into the Mechanism of Nodal Signal Expansion in Left-Right Axis Determination in the *Xenopus Laevis* embryo"*

Session 5A, Bailey 203

- Habib, Ishtyaq (SUNY Geneseo) *"An Astronomy-Inspired Approach to Tackle Spatial Genomics in Giant Bacteria"*
- China, Sidney (St. John Fisher Univ): *"The Use of Microfluidic Devices for Biosensors and Bacterial Growth"*
- Sabat, Emma. *"Dissecting Cross-Regulation Among Host and Prophage Quorum-Sensing Systems in *Phaeobacter inhibens* T5T"*
- Johnson, Jordan (RIT): *"Survey of Electric Composters on the Market and Their Attributes"*

Session 6A, Bailey 105

- Delnesa, Leah T. (RIT): *"A Python-Based GUI for Perovskite Solar Cell Radiation Testing Protocols"*

- Anderson, Isaac (Houghton University): *"Augmenting Student Learning with AI and Mixed Reality in Higher Education"*
- Over, D. Jeffrey (SUNY Geneseo): *"Tentaculites minutus Hall 1843 – The Adventure Continues"*
- Fahy, Declan (SUNY Geneseo): *"Myological reconstruction of the forelimb of Yutyranus huali and muscular trends within Tyrannosauroida"*

Concurrent Oral Presentations B: 11:30-12:30

Session 1B, Bailey 102

- Molee, Francesca (RIT): *"Green Microbial Communities, Physiology, and Stress Response in Retention Ponds in the Genesee River Basin-Lake Ontario Watershed"*
- Morrison, Caitlin C. (RIT): *"Characterizing Microbial Diversity and Abundance in Biological Soil Crusts"*
- Owens-Rios, Wendy (SUNY Geneseo): *"Linking Microbial Community Structure and Function to Ecosystem Succession in Coastal Salt Marshes"*

Session 2B, Bailey 103

- Geister, Caleb (SUNY Brockport): *"Evaluating Prey Species' Nutritional Quality as a Potential Driver of Thiamine Deficiency in Lake Trout: A Comparative Study of Lake Ontario and Lake Superior"*
- Truscott, Jonathan C. (SUNY Brockport): *"Evaluating thiamine deficiency as a potential driver of recruitment failure in Great Lakes lake whitefish"*
- Berlin, Grace T. (Ithaca College): *"The Effectiveness of Three Fish Species on Plant Growth in an Aquaponic System"*
- Napolitano, Joseph (Ithaca College): *"Components and Toxicity of Artificial Turf Runoff"*

Session 3B, Bailey 104

- Wilkosz, Mikolaj (RIT): *"Roll-To-Roll Printing of Halide Perovskite Inks"*
- Salas, Joel (RIT): *"Polyethylene Mimics With Tunable Degradation Rates"*
- Kum, Tatchen B. (RIT): *"Contrasting Radiation Effects in mixed-cation metal-halide perovskites: The Role of Lattice Chemistry"*

Session 4B, Bailey 202

- Chau, Margaret (SUNY Oswego): *"Quantification of Pigment in the Eggshells of Passerine Birds"*
- Sena, Maleah (RIT): *"Impact of Salt Stress on Growth and Pigment Production in Green Algae"*
- Hernandez-Salazar, Blanca (Nazareth University): *"Work Towards Biocatalytic Synthesis of Human Milk Oligosaccharides (HMOs)"*
- Talcott, Aiden (Houghton): *"Amyloid-beta 1-16 Peptide Homodimer-Regorafenib Complex Revealed by Native Mass Spectrometry, Ion-Source Gas-Phase Top-Down Carbene Footprinting, and GalaxyWeb Modelling"*

Session 5B, Bailey 203

- Butler, Ryan W. (RIT): *"A Gaia Motivated Catalog of Candidate Planetary Nebula Central Stars"*
- Spaziani, Julia (RIT): *"Non- Destructive Characterization of Triple Cation Perovskite Space Solar Cells Using Variable Angle Spectroscopic Ellipsometry"*
- Breitbeck, Ava C. (Syracuse University): *"What Scientists Should Know About Public Opinion"*

2025 Rochester Academy of Science Oral Presentation Abstracts

Concurrent Oral Presentations A: 10:15-11:15

Session 1A, Bailey 102

- **Comparing Audio Logger Data to Trap Capture Data for Frogs at Vernal Pools**

Gonzalez, Dayana N. and Hoffman, Andrew S. (St. John Fisher University)

Abstract: Amphibians are the most endangered vertebrate group on the planet, and the study of their populations is crucial to protect them and their habitats. Since they are sensitive indicators of ecosystem health, studying fluctuations in their reproductive patterns can give insight into environmental health. My research focused on spring peepers (*Pseudacris crucifer*) and wood frogs (*Lithobates sylvaticus*). Annual variation in temperature, humidity, and rainfall can affect their calling behavior and potentially reduce reproductive success. In the spring and summer of 2025, we placed audio loggers at different wetland sites in Mendon Ponds and Powder Mills Parks. We looked at hourly call data from multiple sites collected during the spring breeding season over a few days to better understand the impact that temperature, rainfall, and time of day have on calling intensity. We also compared these results to capture data from the same time of year to estimate the detection rates for these species from call surveys compared to trapping.

- **The Assessment of Pollinator Diversity, Floral Use, and Ecosystem Quality Across RIT Green Spaces**

Coates, Kaelyn and Whitney, Kaitlin Stack (Rochester Institute of Technology)

Abstract: Native bees are vital to ecosystems, yet their populations have been impacted by environmental factors such as habitat loss, limited food resources, and pesticide exposure. College campuses often feature both naturalistic and manicured green spaces, making them ideal settings to study the impact of different landscapes and management systems on native bee populations. Native bees are wild bees that have evolved alongside native plants; many are specialized to pollinate specific plants. They are not domesticated like honey bees and are usually solitary. My research objective was to assess how successfully the RIT Henrietta campus supports native bee populations. To understand how RIT serves as a bee habitat, I used nonlethal sampling methods to assess habitat quality, pollinator abundance and diversity, and floral visitation at four campus sites during summer 2025: the Observatory, Community Garden, Jefferson Pollinator Plot, and Eastman Kodak Quad. These sites represent a wide range of management and landscaping choices. The Observatory and Pollinator Plot experience minimal human disturbance and infrequent mowing, in contrast to the Eastman Kodak Quad, which is mowed daily and primarily composed of ornamental plants. The Community Garden includes both edible and decorative plants and is intensively managed. I found significant variation in pollinator presence and plant-pollinator interactions across sites, as well as critical differences in habitat quality scores. The Community Garden supported diverse pollinator communities and had an abundance of floral resources, earning a high score on the habitat assessment. The Observatory old field yielded similar results, with high bee abundance, diverse plant interactions, and a high assessment score before it was mowed. Conversely, the Eastman Kodak Quad had limited diversity and a small number of plant species, as did the Jefferson Pollinator Plot, despite being a designated area for pollinator-friendly flowers. However, the Pollinator Plot scored the highest on the habitat assessment, while the Quad scored the lowest. Overall, my

results indicate that while some areas of RIT's campus provide high-quality habitats for native bees, there are opportunities to enhance floral diversity and improve habitat resources. This study highlights the potential of campuses to make a positive contribution to urban pollinator conservation.

- **Modeling the Richness and Abundance of Non-native Vegetation in Great Lakes Coastal Wetlands**

Town, Kendalyn and Schultz, Rachel (SUNY Brockport)

Abstract: Laurentian Great Lakes coastal wetlands promote coastal resilience and provide valuable ecosystem services, but they face various threats, including invasive vegetation. These wetlands differ by hydrogeomorphology and experience temporal changes from interannual lake level variation. Additionally, coastal wetlands differ in anthropogenic disturbance levels from both upland and aquatic sources, including land development and hydrologic modifications (dams). Each of these factors may affect the establishment and spread of non-native plant species, and the impacts may vary among different wetland plant zones (wet meadow, emergent, submergent). Previous studies of macrophyte invasion in Great Lakes wetlands have been limited by spatial extent and species of interest. To address these gaps, we used data from the Great Lakes Coastal Wetland Monitoring Program to model the influences of landscape-level predictors on the richness and abundance of non-native macrophytes in 632 Great Lakes coastal wetlands. Of the 1022 plant species observed from 2011 to 2022 across the basin, 177 were non-native. We found that hydrogeomorphic class was often a significant predictor of invasion, though none of the three classes were consistently more invaded than the others. Lake level fluctuation was an important predictor of invasion, as non-native species richness decreased following above-average peak lake levels, while abundance increased following these peaks. Land use/cover disturbance was a strong predictor of non-native plant prevalence, with wetlands in developed areas being more invaded. Damming did not consistently predict invasion, as it showed both positive and negative relationships with non-native plant prevalence. Vegetation zones differed most significantly in non-native prevalence; the submergent zone was consistently the least invaded, while the emergent zone consistently had the greatest non-native abundance. The goal of this work was to identify the wetland characteristics that best predict invasion so that conservation and restoration can be better targeted toward vulnerable wetland sites. Because results vary by Great Lake, wetland managers should use region-specific results for management applications.

- **Variability in Capture Rates of Amphibians Within and Between Wetlands in Monroe County, NY**

Miller, Sara and Hoffman, Andrew S. (St. John Fisher University)

Abstract: Amphibians are the most threatened group of vertebrate animals and being able to effectively sample their populations will be critical to their conservation moving forward. Many amphibians breed in wetlands and studies that focus on better understanding their populations often define wetlands or ponds as discrete sites or populations. However, wetland size can vary from an isolated bathtub-sized pool to an expansive seasonally flooded forest spanning many interconnected acres. Our goal was to examine variability in detection and abundance of amphibians both within and between wetland complexes in order to understand how habitat variability affects amphibian captures at multiple scales. From March to July, 2025, we used trapping stations and standardized dip-nets to sample amphibians within multiple wetland complexes at Mendon Ponds, Powder Mills, and Tinker Parks. During the summer, we collected data on water quality, canopy cover, and vegetation cover to use as covariates of amphibian occurrence. We found considerable variability in both detection and occupancy rates between

spring and summer and within wetlands and observed that the relationship of amphibian captures to different habitat variables was highly specific-specific.

Session 2A, Bailey 103

• **Determining the Influence of Glyphosate on Erythropoiesis Using K562 Cells**

Gantress, Natalie and Murphy, Zachary (St. John Fisher University)

Abstract: Glyphosate is a very common chemical found in herbicides for both agricultural and nonagricultural purposes. It has been linked to several severe health problems in people including cancer, liver disease, kidney disease, reduced fetal growth, and Non-Hodgkin's Lymphoma. There are more links between glyphosate and other biological processes that are being explored or have yet to be, including the effects of glyphosate on erythropoiesis in humans. This research proposes using varying dosages of glyphosate in cell culture to determine how it changes the growth and apoptotic rates of K562 cells. Through dose response testing we will analyze cell morphology, growth, and cell surface changes. Importantly, doses will specifically test at levels based on federal agency acceptable exposures (FDA and EPA), and hemocytometry, microscopy, and flow cytometry will be used to determine the effects. Due to the links glyphosate has with severe health problems, we hypothesize that higher amounts of glyphosate will interfere with erythropoiesis causing a decrease in cell growth, an increase in apoptosis, and deformities in cell shape.

• **Roots and Rubber: Impacts of Tire Wear Leachate on Hemp Physiology**

Champlin, Julian (Ithaca College)

Abstract: Industrial hemp is an increasingly important aspect of agriculture in the United States. There is very little information on how TWP leachate effects terrestrial plant life, despite its importance both medicinally and agriculturally globally. As the concentrations of TWP and therefore the potency of TWP leachate increases over time, more studies must be done to understand the impact of these chemicals on plant growth. Understanding the effects that ecologically relevant TWP leachate concentrations have on industrial hemp will give a better understanding of how TWP leachate is affecting the agricultural industry in the United States. We grew hemp under different ecologically relevant concentrations of TWP leachate. Hemp was grown for 5 weeks and leachate was prepared by adding commercially available tire wear particles to glass jars in a greenhouse to simulate natural conditions. Our results demonstrate the need for regulations regarding tire wear particles in the environment, as it could very well become a detrimental material to the agricultural industry in the US.

• **Turf: Morphological Effects of Artificial Turf Exposure to Minnow Embryos**

Stearns, Charles (Ithaca College)

Abstract: Artificial turf fields are composed of contaminants of emerging concern, including tire crumb rubber. As crumb rubber photodegrades and weathers, it releases a cocktail of toxic compounds such as polycyclic aromatic hydrocarbons (PAH), 6PPD, zinc, and organic contaminants. These compounds are associated with stream toxicity, such as coho salmon mortality syndrome in the Pacific Northwest. This study aims to quantify the effects of artificial turf leachate on *Pimphales promelas* embryo development and characterize each endpoint from the overall toxicity using the OECD's standard methods of a Fish Embryo Toxicity (FET) test. Two of the standard core endpoints were recorded: 1) coagulation and 2) lack of heartbeat, along with many nonspecific morphological impairments related to teratogenicity: 3) edema, 4) eye

disfiguration, 5) abnormal heartbeat, 6) late hatchings, and 7) spinal impairment. Three experimental groups were used: a negative control under normal tank water conditions, a 50% dilution of the artificial turf leachate in tank water, and a solution of 100% leachate; these higher concentrations maximized the potential to record the developmental impairments from 0 hours post fertilization (hpf) to hatching. Overall, a higher frequency of embryo mortality was observed in each concentration of leachate than in the control, with higher concentrations having a higher mortality rate. Hatching success was lower in leachate exposures compared to the control due to embryo mortality and late hatchings. Notably, the blood flow of the embryos was impaired by leachate exposure, causing a higher frequency of pericardial edema in 50% and 100% concentrations. Visually, more spinal impairment (scoliosis, lordosis, kyphosis) was found in hatched individuals exposed to the leachate. Although mass spectrometry tests were not performed to identify the concentration of compounds in the leachate, it's clear that the mixture has effects on embryological development in fish. Additional studies on the morphological effect of environmentally relevant concentrations of tire-derived contaminants are currently underway.

- **Tracing Hatchery Origin and Lake Diet of New York's Lake Erie Tributary Steelhead**

Gall, Jack (SUNY Brockport), Ludwig, Jarrod (NYSDEC), Robinson, Jason (NYSDEC), Evans, Thomas M. (SUNY Brockport), and Rinchard, Jacques (SUNY Brockport)

Abstract: In Lake Erie, steelhead trout (*Oncorhynchus mykiss*) are collaboratively managed by multiple jurisdictions to facilitate angling opportunities, generating millions of dollars in annual revenue. Tributary catch rates have consistently remained above New York's goal of 0.33 fish per hour since its first formal assessment in 2003. However, past work has shown that most steelhead trout returning to New York tributaries originate from Pennsylvania hatcheries. In 2024, Pennsylvania enacted a 20% stocking reduction, and in 2025 they enacted an additional 50% reduction. These reductions could have serious impacts on angling quality in New York. Therefore, evaluating the current proportional contribution of Pennsylvania-stocked steelhead trout in New York's tributaries will provide insight on the influence Pennsylvania's stocking program has on adult returns in New York. Otoliths from hatchery steelhead yearlings will be collected for biogeochemical analysis using laser ablation – inductively coupled plasma – mass spectrometry (LA-ICP-MS). Adults will be collected as they enter New York tributaries, and their otoliths will be analyzed with LA-ICP-MS to determine their origin. Growth rates and the age structure of Lake Erie steelhead will also be evaluated using otoliths. Additionally, fatty acid signature and stable isotope analyses will be used to determine lake diet. This study will provide valuable insights into the influence of Pennsylvania stocking efforts on New York's tributary steelhead fishery.

Session 3A, Bailey 104

- **Polybutylene succinate copolymers with variable degradability**

Hooke, Gail and Miri, Matt (School of Chemistry and Materials Science, Rochester Institute of Technology, Rochester)

Abstract: Polymers, most of which are plastics, are ubiquitous and an integral part of modern life. However, polymers also create massive environmental issues, for example, piling up in landfills and contaminating waterways and the oceans. Polybutylene succinate (PBS) is a commercial polyester that has found many applications, such as in packaging and agricultural mulch films. It has a relatively slow biodegradation rate. In the present study, we added to the base monomers, 1,4-butanediol and succinic acid or its derivatives, comonomers which could break up readily upon hydrolysis and act as “weak links” in the polymer chains. Comonomers

which were applied were dimethyl dicarbonate (DMDC) and methyl-3-hydroxybutyrate (MHB). We varied the comonomer content in the feed between 5 and 15 mol %. Polymer yields, monomer composition, and microstructure of the polymers, determined by ^1H and ^{13}C NMR spectroscopy, were found. DSC (Differential Scanning Calorimetry) and TGA (Thermal Gravimetric Analysis) were used to investigate the thermal properties of the polymers. The hydrolytic degradation of the polymers was measured by immersion in an alkaline buffer solution over a few weeks, while monitoring the weight loss.

• Ink-Process-Structure-Property Relationships in Ambient Slot-Die Coated Perovskite Thin Films

Islam, Muhammad S.; Tomkiewicz, Alex; Stenak, Veran and Kirmani, Ahmad R (Rochester Institute of Technology)

Abstract: The large-scale manufacturing of perovskite solar cells necessitates scalable deposition techniques that produce high-quality films with uniform properties. Slot-die coating has emerged as a promising candidate, offering material efficiency, continuous processing capability, and roll-to-roll compatibility. However, film quality is highly sensitive to processing parameters, particularly substrate temperature, which governs solvent evaporation kinetics and crystallization dynamics. This study systematically investigates the influence of substrate temperature, ink composition, and coating speed on the structural, morphological, and optoelectronic properties of methylammonium lead iodide (MAPbI₃) perovskite films deposited via slot-die coating in ambient air. Two ink compositions were examined: a stoichiometric 1:1 molar ratio of MAI:PbI₂ and one with a 10% excess of MAI. Films were deposited at substrate temperatures of 25, 50, and 85 °C and coating speeds of 5, 25, and 50 mm/s. Comprehensive characterization using X-ray diffraction (XRD), scanning electron microscopy (SEM), atomic force microscopy (AFM), and photoluminescence (PL) spectroscopy revealed a strong dependence of film properties on substrate temperature. Our results demonstrate that a substrate temperature of 50 °C represents an optimal processing window for the 1:1 composition, yielding films with superior crystallinity, improved phase purity, reduced electronic disorder (Urbach energy of approximately 65 meV), and a uniform, pinhole-free morphology with minimal surface roughness. In contrast, films deposited at 25 °C exhibited poor crystallinity, low-intensity diffraction peaks, and incomplete perovskite conversion due to insufficient thermal energy for proper intermediate phase formation and crystal growth. At 85 °C, rapid solvent evaporation led to the formation of dendritic structures, the presence of residual PbI₂, and increased electronic disorder (Urbach energy of 110 meV), which are detrimental to device performance. These findings highlight the critical role of substrate temperature in controlling the crystallization kinetics and establishing a "processing memory" that fundamentally dictates the final film properties. By carefully tuning the substrate temperature, it is possible to balance the rates of solvent removal and crystal growth, thereby enabling the fabrication of high-quality perovskite films via a scalable slot-die coating process. This work provides valuable insights into the careful optimization of perovskite film deposition for the commercial production of highly efficient and stable solar cells.

• Space Radiation Effects in Wide Bandgap Perovskite Solar Cells

Stanek, Veran; Lasko, Cassandra; Kum, Tatchen B. and Kirmani, Ahmad R (Rochester Institute of Technology)

Abstract: Metal-halide perovskites are solution-processed semiconductors with promise for solar cell applications. The recent proliferation of the near-Earth space has necessitated development of a new low-cost solar cell technology, and perovskites have gained attention given their notable radiation tolerance. Going forward, band gaps beyond 1.8 eV are important to the

creation of multi-junction photoabsorber layers that promise higher output powers. Wide bandgap perovskites are vulnerable to phase segregation and their performance under radiation is not known. In this work, we fabricate perovskite films and solar cells with wide bandgaps with the aim of comparing them to more traditional PSCs with lower bandgaps closer to Silicon. These are characterized using techniques such as x-ray diffraction, UV-Vis absorption, and photoluminescence spectroscopy. These studies extend the bandgap range of perovskites relevant for space applications, and will be pivotal in informing future multi-junction solar cell designs

- **Role of Ink Rheology in Slot-die Coating of Halide Perovskites**

Lusignan, David; Islam, Muhammad S. and Kirmani, Ahmad R (Rochester of Technology)

Abstract: Metal-halide perovskites are inkable semiconductors that can be converted into thin film solar cells with minimal energy input using scalable slot-die coating. Ink rheology and colloid size play a key role in regulating the ink-to-film transition and are less-explored areas to unlock high film quality. Colloid size demonstrates the breakdown of perovskite ink as a function of time, providing insight to the lifespan of perovskite inks when exposed to moisture. Inks that do not exhibit shear thinning or thickening can minimize coating defects and are industrially preferred. We systematically investigate perovskite ink rheology and demonstrate that it exhibits shear-independent–Newtonian–behavior across a temperature range of 25°C to 85°C. The viscosity decreases from 2.5 cP to 1.42 cP and 1.1 cP with increasing temperature. Slot-die coating at an industrially relevant speed of 1.5 m min⁻¹ reveals a film thickness decrease from 4 µm to 0.8µm with temperature. The thickness reduction is attributed to lower viscous drag forces, which limit ink entrainment under constant coating speed, highlighting the critical influence of ink rheology on slot-die coating dynamics.

Session 4A, Bailey 202

- **Development Of Virokines as Tags for Mammalian Cell Protein Expression Systems**

Lee, Theodore and Diel, Diego G. (Department of Population Medicine and Diagnostic Sciences, Cornell University College of Veterinary Medicine)

Abstract: Mammalian cell systems are common when researching expression and purification of proteins. These systems are desirable for their ability to produce correctly folded proteins and perform post-translational modifications that regulate the action of these proteins. Transfected cells use a variety of methods to aid protein expression, including inducing expression of anti-apoptotic proteins, arresting cells in growth phases of the cell cycle, and alteration of DNA methylation and acetylation patterns. However, reaching this point comes with many challenges. Mammalian cells have high costs and maintenance requirements, and may produce less protein than their insect or bacterial counterparts. This research thus seeks to develop a reproducible and specific system to reliably express secreted proteins in mammalian cells, utilizing viral proteins known to be expressed extracellularly during infection as secretion tags. The objectives of this project are: 1) to design and generate an expression plasmid for cloning of proteins in fusion with the Orf Virus Chemokine Binding Protein secretion tag, and 2) to validate the mammalian secretion expression system using a diverse array of viral proteins. By developing a virokinase-based system of isolating protein targets, we hope to produce recombinant proteins faster and more efficiently than is possible with existing methodologies, allowing for more effective routes towards their use in therapeutic and research settings.

- **A Region of the X Chromosome Linked to Meiotic Drive in *Teleopsis dalmanni* is also Drive-Associated in *Teleopsis whitei***

Cookinham, Ariana M. (SUNY Geneseo)

Abstract: *Teleopsis whitei* is a species of stalk-eyed fly that exhibits meiotic drive, which causes a gene to be inherited more than the expected 50% of the time. In *T. whitei*, sex ratio (SR) males pass down the X chromosome at least 90% of the time, leading to nearly all female offspring. In a similar species, *Teleopsis dalmanni*, genomic evidence for meiotic drive is only present on the X chromosome. However, prior studies suggest that the mechanism for drive in *T. whitei* may not be confined to the X chromosome. To look for places in the genome that cause drive, 10 standard (ST) males and 10 SR males were sequenced with whole genome sequencing. A whole reference genome for *T. whitei* does not exist, so reads were mapped to the *T. dalmanni* reference genome and to a genome containing fragments of the *T. whitei* genome mapped onto the *T. dalmanni* genome. GATK was used to identify genetic variants from pooled data and assign genotypes to individuals. PCA was performed on the individual genotypes but there was no evidence of genetic clustering by SR status on any entire chromosome. When performed on windows of 3 million base pairs on the X chromosome, some windows around the second quarter of the chromosome showed evidence of drive-associated clustering. Overlapping phylogenetic trees containing 3 million base pairs each were also generated with the pooled data using the program iqtree2. A monophyletic group for drive was found in a singular tree on the X chromosome. Compared to the autosomes, the X chromosome showed more genetic differentiation between SR and ST chromosomes when controlled for population level differentiation. Using SnpSift, fixed polymorphisms for drive were identified. Overall, only a small portion of the X chromosome seems to be associated with drive in *T. whitei* while the entire X chromosome contains drive-associated differentiation in *T. dalmanni*.

- **Cracking the Shell – The Effects of CBG Oil on Chicken Embryo Development**

Greco, Michaela; Wilcox, Kendall; Mozden, Claire; Simms, Justine and Jensen, Thomas (Hobart and William Smith Colleges)

Abstract: Despite a lack of research on the effects of CBG on the developing human fetus, there is a perception that CBG is more natural and therefore a safer alternative to reducing inflammation, pain, or anxiety compared to other prescribed/traditional medications. CBG oil and CBD oil maintain similar effects on the body but target different receptors in the brain. CBG directly attaches to the CB1 and CB2 receptors in the ECS, where CBD influences the ECS by increasing the body's natural cannabinoids and interacting with serotonin receptors to achieve its calming effects. Our goal is to determine the possible effects and influence of CBG oil on human fetal development, using the chicken embryo developmental model. Our hypothesis is that CBG oil has a harmful impact on the heart, brain, and body size of treated embryos. To measure the effects of CBG on embryo development, we injected 5 ul of CBG oil into the air cell portion of a 5-day old chicken eggs. Following euthanasia, we measured the brain, heart, total body weight, arm length, leg length, and eye diameter. We did not detect any significance in our results, but there was a trend towards longer wing and leg length in the CBG-treated group. These results, while they did not support our hypothesis; were still abnormal compared to our controls. Our research shed light on an under-researched topic and the importance of further investigation and understanding the potential implications of taking CBG oil on a developing fetus

- **New insights into the Mechanism of Nodal Signal Expansion in Left-Right Axis Determination in the *Xenopus Laevis* embryo**

Mohamed, Ismail (Nazareth University)

Abstract: Internal organ asymmetry (the left-right axis, L/R) in vertebrates is established through the selective activation of the Nodal signaling pathway in the left lateral plate mesoderm (LPM). The current model assumes that Nodal signaling, starting from two posterior streaks of Nodal expression, is asymmetrically spreading on the left lateral side of the embryo, then moving to the anterior where it conditions heart rotation. Using *Xenopus laevis* embryos, we investigated if dorsal structures are required beyond the posterior segment for anterior progression of Nodal by making sections of axial and paraxial tissues at different antero-posterior positions and embryonic stage and scoring for correct heart position and intestinal coiling. We found that the entire paraxial mesoderm (PM, dorsal side of the embryo) is required for correct left-right axis determination. RT-PCR analysis of lateral expression of the Nodal gene indicated, surprisingly, that in sectioned embryos Nodal is not absent on both sides, but on the contrary bilaterally expressed, in contradiction with the current model for left-right determination. Finally, in search of a mechanism for the role of the entire PM, we used *Xenopus* embryonic explants stained by immunofluorescence for Smad2, the effector of the Nodal signaling pathway, to localize Nodal activity. Our results indicate left-sided Nodal activity along the entire PM, in agreement with our resection observations. Together, our data reveals that left-right axis determination depends not only on lateral Nodal activation but also suggests a role for the entire paraxial mesoderm in the anterior expansion of the Nodal signal.

Session 5A, Bailey 203

- **An Astronomy-Inspired Approach to Tackle Spatial Genomics in Giant Bacteria**

Habib, Ishtyaq; Pellerin, Anne; Hutchison, Elizabeth (SUNY Geneseo) and Anne, Kirk (Rice University)

Abstract: The giant bacterium *Epulopiscium* sp. type B is an outlier in the microbial world. This bacterium houses thousands of copies of its chromosomes whereas most bacteria only maintain a few. Procedurally mapping the location and arrangement of massive numbers of genomes from fluorescence microscopy images presents a data challenge analogous to a one common in astronomy; astronomers must accurately identify and catalog countless points of light within a dense, noisy volume. To address this, our project borrows robust image processing algorithms in astronomy to build a high throughput pipeline for analyzing the spatial distribution of chromosomes. This interdisciplinary approach will provide insight into how extreme polyploids have adapted to large cell size. Furthermore, the resulting workflow will be broadly applicable to other complex, large-scale 3D image analysis in microbiology.

- **The Use of Microfluidic Devices for Biosensors and Bacterial Growth**

China, Sidney and Ontiveros, Fernando (St. John Fisher University)

Abstract: Microfluidic devices allow for the manipulation of fluids, particles, cells, micro-sized organs or organisms in channels ranging from nano to submillimeter scales, with volumes spanning from microliters to picoliters. The use of these micro-sized networks of channels and chambers enables the use of distinctive phenomena characteristic of fluids in small dimensions. Our research group has developed hybrid polyethylene terephthalate laminate (PETL) microfluidic devices that are derived from polymer film and other low-cost materials to fabricate a biosensor. These membrane-based sensors can be used for the rapid detection of infectious

agents contingent on their size and surface antigens in a small amount of bodily fluid. This technology is aimed to provide an affordable and accessible approach for effective pathogen detection in low-resource environments. The detection of red blood cell agglutination was used to test the functionality of the biosensors. The use of PETL devices was further explored through the development of a bioreactor that facilitates the controlled growth of bacteria within a microfluidic architecture.

- **Dissecting Cross-Regulation Among Host and Prophage Quorum-Sensing Systems in *Phaeobacter inhibens* T5T**

Sabat, Emma

Abstract: Bacterial viruses (phages) typically transition from a dormant state in their hosts (lysogeny) to virion production (lysis) in response to DNA damage. However, recent evidence has shown that intercellular communication through quorum sensing also influences this transition. Gram-negative bacteria use N-acyl homoserine lactones (HSLs), produced by LuxI and detected by LuxR, as autoinducers to mediate quorum sensing and regulate gene expression. We have identified two co-resident prophages in a lysogenic strain of the bacterium *Phaeobacter inhibens* that encode unique luxI and luxR homologs, suggesting that the prophages can produce and perceive quorum-sensing signals. Here, we show that the host and prophage quorum-sensing systems exhibit cross-activation and cross-inhibition through non-cognate signaling. We used liquid chromatography-mass spectrometry to isolate and identify the structures of the various HSLs produced by the bacterial host and its prophages, then we utilized biochemical assays to examine the effects of these HSLs on multiple mutant *Phaeobacter* strains. Our findings demonstrate that phages can use quorum sensing to influence gene expression of co-resident prophages or their bacterial host. This contrasts with the earlier view of phage communication as strictly host-dependent and expands our understanding of how chemical communication shapes host-virus dynamics.

- **Survey of Electric Composters on the Market and Their Attributes**

Johnson, Jordan, DeFelice, Hannah, and Whitney, Kaitlin Stack (Rochester Institute of Technology)

Abstract: Every year, about one-third of all food produced worldwide is wasted. Food waste is food that's for human consumption but is discarded instead. This occurs at various stages of the food supply chain. This waste significantly contributes to greenhouse gas emissions and environmental damage. Much of this damage is found in landfills. The making of landfills destroys natural environments that wildlife use to survive. Landfills release methane gas, which absorbs the sun's heat, and the landfill's liquid can leak into water ecosystems, causing irreparable damage. Composting can help reduce this problem by keeping organic waste out of landfills. Compost is a substance made from the decomposition of organic materials. It improves the soil's health when applied by providing it with the essential minerals it needs. Traditional composting can take many months or even years to produce usable compost. However, electric tabletop composters are a recent technology that claim to produce compost much faster, as quickly as just a few hours. These machines are designed to fit on kitchen countertops and are currently marketed to potential buyers as composting without the potential downsides like odor, mess, or pests. In our study, we explored the electric composters currently available for purchase. We then collected detailed information about machines' price, size, composting capacity, electrical requirements (including voltage and power), noise levels, cycle times, and the name of output. In addition, we analyzed customer feedback to understand how users feel about these products. This was done by recording keywords found on Amazon's and the company's pages. We found 25 different models of electric composters currently on the market. Their average price is \$329.98,

and they have a median composting capacity of 3 liters. Consumers reported liking certain features, including ease of use, manageable noise levels, and overall capacity. However, they also reported concerns about the durability of the machines, their value for money, and unpleasant odors. These results help give important insights for anyone considering electric composters as a way to reduce food waste and support sustainable practices.

Session 6A, Bailey 105

• **A Python-Based GUI for Perovskite Solar Cell Radiation Testing Protocols**

Delnesa, Leah T., Kum, Tatchen B., Kirmani, Ahmad R (Rochester Institute of Technology)

Abstract: The expanding global space economy demands sustainable, low-cost power technologies optimized for harsh space environments. Perovskite solar cells (PSCs) have emerged as a promising solution due to their high power conversion efficiencies (up to 26%), specific power exceeding 40 W g^{-1} , and inherent radiation tolerance. To assess their readiness for space applications, robust ground-based testing protocols must accurately simulate the radiation environment. Radiation qualification of PSCs often misses on-orbit damage physics when PSCs are capped by lightweight SiO_2 barriers (1-100 μm). Here we present a Python graphical user interface (GUI) that converts mission specifications into laboratory radiation testing protocols that reproduce the damage expected in orbit. Users provide orbit class (e.g., ISS, upper LEO), mission duration (5-10 years), device stack, and SiO_2 thickness. Under the hood, the engine uses SRIM/TRIM Monte-Carlo stopping and range/straggling outputs in the layered SiO_2 /perovskite stack and enforces a straggling-aware traversal requirement: the incident proton energy is increased by a thickness-dependent, nonlinear correction, ΔE , to ensure barrier traversal and the intended entrance energy into the perovskite. The tool then computes cumulative displacement damage dose (DDD) in the active layer and returns a single recommended proton energy and a single fluence that satisfy two equivalence conditions: (i) DDD match across the perovskite active layer and (ii) close agreement of vacancy-depth distributions with the mission target. The GUI outputs energies and fluences and exports a radiation test plan. We show that ΔE grows non-linearly with barrier thickness and that recommended energies shift above the 70 keV regime suitable for bare devices while preserving in-layer DDD uniformity. Our straggling-aware irradiation simulations will enable reproducible, mission-specific testing of barrier-capped PSCs.

• **Augmenting Student Learning with AI and Mixed Reality in Higher Education**

Anderson, Isaac; Gossman, Ashleigh and Sorinolu, Babafemi G. (Houghton University)

Abstract: Advances in Artificial Intelligence (AI) and Mixed Reality (MR) are opening new opportunities to enhance learning experiences in higher education. However, most existing MR tools are designed for specific subjects and are not easily adaptable to different courses. Additionally, students often face challenges when using digital learning tools without real-time support from teachers. To address this gap, we developed a prototype for a generalized, multidisciplinary learning system made up of two main parts: a Mixed Reality (MR) platform using the Meta Quest 3 with an AI-powered tutor for immersive learning, and a web-based platform for delivering structured lesson content. These two tools are designed to work together to create a flexible and engaging environment for multidisciplinary education. This system enables educators to easily create and customize course content, while providing students with immediate, personalized support through the AI assistant. We anticipate that this approach will enhance learning outcomes across a variety of higher education disciplines by improving both adaptability and independent learner support. To evaluate its effectiveness, we will conduct a usability study

and assess the student learning experience, as well as the platform's performance across multiple academic subjects.

- ***Tentaculites minutus* Hall 1843 – The Adventure Continues**

Over, D. Jeffrey; DeMott, Alyssa; Zaffino, Noah (SUNY Geneseo), and Brett, Carlton (U. Cincinnati)

Abstract: *Tentaculites minutus* Hall 1843, one of three Silurian tentaculitids described by James Hall, was first illustrated in *Geology of New York, Part IV* (Hall, 1843) and described in *Paleontology of New York, Volume II* (Hall, 1852). The type specimen, as indicated by Hall (1852), comes from “the upper green shale at Rochester, associated with *Atrypa hemispherica*.” – the Sodus Formation and *Eocoelia hemispherica* (Sowerby 1839). Curiously, the type specimen of *T. minutus* in the American Museum of Natural History, where much of the Hall collection, initially repositied in the New York State Museum, now resides, a result of financial issues encountered in the publication of the *Paleontology of New York* volumes, is not from the Sodus Formation. The cataloged type specimen – AMNH 1575 – is an external mold preserved on a slab of brown-orange fossiliferous sandstone labeled as “Clinton Oneida”, and lithologically consistent with the Joslin Hill Member of the Herkimer Formation, which is exposed in Oneida County, near Clinton, New York. The type slab also has the brachiopods *Stegerhynchus neglectum* Hall 1852 and *Dalmanella elegantula* (Dalman 1828) – not *Eocoelia*. The holotype of *T. minutus* and other specimens on the type slab closely resemble *Tentaculites niagarensis* Hall 1852, described from the “Niagara shale”; furthermore, they fit the description and illustration of the holotype, and are similar to specimens collected from the Rochester Formation near Middleport – a lateral equivalent to the Herkimer Formation. Thus, the holotype of *T. minutus* is not *T. minutus* in the sense of the original description, referred type locality, and other specimens collected from the Sodus Formation in Monroe County at Rochester Gorge and Palmer Glen that fit the description of *T. minutus* in regard to size, number of primary annulations, and general morphology. A neotype with a revised description of *T. minutus* is to be proposed and a revised description of *T. niagarensis* is in preparation.

- **Myological reconstruction of the forelimb of *Yutyrannus huali* and muscular trends within Tyrannosauroidea**

Fahy, Declan, and Burch, Sara (SUNY Geneseo)

Abstract: Paleontology is a field of comparison and inference. This is evident in the study of theropod forelimb function and evolution, for which there are few modern analogs. Forelimb function in tyrannosaurs is a hotly contested topic, but the overall evolution of the musculature in the clade remains poorly understood. To help fill these gaps, we've undertaken a reconstruction of the forelimb musculature of *Yutyrannus huali*, a basal tyrannosauroid of Cretaceous China. This reconstruction was developed in order to better conceptualize muscle evolution in the tyrannosaur clade as a whole, and was conducted by using morphological comparisons to taxa in multiple lineages. The structure of the *Y. huali* forelimb was illustrated and muscle attachment sites were reconstructed. These locations were inferred using preserved osteological correlates along with prior reconstructions of *Tawa*, a basal theropod, and the tyrannosauroids *Guanlong* and *Tyrannosaurus*. Upon completion of this reconstruction, the forelimb morphology of *Y. huali* was compared with that of other tyrannosauroids, and differences in the shape of bone, presence or absence of specific features, and location of muscle attachment sites were noted. The forelimb of *Y. huali* shows an intermediate muscular morphology between the gracile forelimb of basal tyrannosaurs and the extreme reduction of derived taxa. The humerus, radius, and ulna all exhibit an overall trend in broadening, providing more area for attachment of muscles such as Coracobrachialis and Supinator. In the manus, a trend is evident in the reduction of digit III. In *Y.*

huali, the manus remains robust and digit III is well developed, whereas in derived species, digit III is reduced to only the metacarpal containing a single attachment for the flexor carpi ulnaris. Overall, there is a clear change in proportion as well, with the scapula being relatively larger than the other bones in derived taxa. This suggests proximally located muscles remained important throughout the lineage, even as more distal muscles were reduced along with the forelimb. This in-depth reconstruction allows for a better understanding of the morphological changes in the forelimb of this clade and will serve as an important future reference in other similar analyses.

Concurrent Oral Presentations B: 11:30-12:30

Session 1B, Bailey 102

• Green Microbial Communities, Physiology, and Stress Response in Retention Ponds in the Genesee River Basin-Lake Ontario Watershed

Molee, Francesca; Narayan, Micada; Halterman, Dakota; Rodriguez, Fernando and Peredo, Elena Lopez (Rochester Institute of Technology)

Abstract: Extreme rainfall events in the US are projected to get 20% more severe and 200% more frequent in the coming decades due to climate change ([Swain et al., 2020](#)). This is concerning as urban runoff from precipitation events is a prevalent source of aquatic pollution, carrying chemicals such as herbicides from landscaping and deicing salts from road maintenance into nearby water bodies ([Baker et al., 2022](#)). These disrupt community structure and biodiversity, with fertilizers specifically creating nutrient-rich waters that fuel Harmful Algal Blooms (HABs). Alongside disrupting system stability, HABs pose health risks through the production of cyanotoxins. Retention ponds are constructed to catch and hold this runoff. Yet, this strategy creates runoff-fed ecosystems that expose organisms, including green microbial communities, to high levels of pollutants. Retention systems can therefore be used to explore the consequences of runoff on water and sediment microbial communities, with a focus on those often linked to HABs, such as cyanobacteria and eukaryotic algae. Using high-throughput prokaryotic sequencing of the 16S ribosomal gene, strain isolation methods, and in-lab chemical stress testing under common garden conditions, this research investigates the changes in microbial communities in retention ponds heavily impacted by urban runoff in the greater Rochester area. This includes contrasting these communities with those of non-retention created ponds, as well as considering seasonal variation; samples collected in early spring are exposed to runoff carrying road salts, while samples collected in early summer are exposed to excess nutrients from fertilizers and herbicides. Current results indicate that green algal isolates are susceptible to the presence of NaCl and MgCl₂ road salts, as well as Miracle Gro Lawn Food. Roundup Weed & Grass Killer was able, even at extremely low concentrations, to inhibit growth. However, stress growth response varied more by isolate than by pollution regime. Current Qiime analysis shows rough clustering of diversity by substrate and site. Current efforts focus on increasing replicates with samples from four more sites and further testing, including mixed-culture tests to examine interspecies stress response dynamics. 18s amplicon sequencing will also be conducted to examine eukaryotic diversity.

• Characterizing Microbial Diversity and Abundance in Biological Soil Crusts

Morrison, Caitlin C., Peredo, Elena Lopez and Kulp, Rachel (Rochester Institute of Technology)

Abstract: Biological soil crusts (BSC) are complex communities comprised of a wide range of organisms, including bacteria, cyanobacteria, fungi, green microalgae, diatoms, mosses, and lichens. In desert areas, BSC collect and sequester large amounts of greenhouse gases, while

BSC from temperate regions release greenhouse gases. The BSC samples for this research were taken from a sand barren in the Oak Openings at the Kitty Todd Nature Preserve in Northwest Ohio. This temperate region is extremely arid in the summer but becomes a wetland in the winter and spring due to its proximity to Lake Erie. This location differs from other areas rich in BSC due to its elevated nitrogen deposition from nearby agricultural and urban sources. 16S rRNA V4 & V5 amplicon sequencing was performed on the collected BSC samples, and alpha diversity, beta diversity, and taxonomy were analyzed. Thus far, we have found that there appear to be two distinct groups among the seven sample sites, one with an abundance of Chloroflexota, while the other has an abundance of Actinomycetota. The emerging groupings suggest that temperate BSC may operate through distinct microbial pathways shaped by regional environmental factors that differ from those in desert regions.

- **Linking Microbial Community Structure and Function to Ecosystem Succession in Coastal Salt Marshes**

Owens-Rios, Wendy (SUNY Geneseo), Miller, Avery; McCalley, Carrie; and Tyler, Christy (Rochester Institute of Technology)

Abstract: Coastal salt marshes provide vital ecosystem services such as storm protection and carbon sequestration, yet the factors controlling the microbial communities that underpin their biogeochemical functioning remain poorly understood. Understanding how these microbial communities develop over time is important for predicting marsh resilience and guiding future restoration. At the Virginia Coast Reserve Long-Term Ecological Research (VCR-LTER) site, we examined two natural salt marshes that represent different stages of ecological succession: the Young Marsh (<30 years old) and the Mature Marsh (>170 years old). We compared sediment microbial communities, sediment properties, and vegetation structure across elevation zones (Edge, Meadow, and High Marsh) to understand how microbial community structure and function change through time. Using 16S rRNA amplicon sequencing, we found clear differences in microbial diversity and community composition between the two marshes. The Mature Marsh contained higher pools of carbon and nitrogen, supporting greater microbial diversity and communities dominated by sulfate-reducing bacteria such as Desulfatiglandaceae. In contrast, the Young Marsh is characterized by coarser sediments and lower nutrient content which depict high relative abundances of disturbance-tolerant and pioneer microbial phyla, including Pseudomonadota and nitrogen-fixing Cyanobacteriota. These patterns indicate that younger marshes are characterized by microbial groups that can tolerate nutrient limitation and physical stress, while older marshes host more specialized taxa linked to established vegetation and anoxic sediment conditions. Our findings highlight how microbial community structure mirrors ecosystem development and sediment chemistry across a natural salt marsh chronosequence, illustrating how succession shapes both ecosystem structure and function through links among microbial communities, vegetation, and sediment characteristics. These insights are especially relevant as coastal ecosystems face increasing pressures from sea-level rise and warmer temperatures, emphasizing the importance of maintaining both biological and microbial diversity for long-term marsh resilience.

Session 2B, Bailey 103

- **Evaluating Prey Species' Nutritional Quality as a Potential Driver of Thiamine Deficiency in Lake Trout: A Comparative Study of Lake Ontario and Lake Superior**

Geister, Caleb (SUNY-Brockport), Futia, Matthew (University of Vermont-Rubenstein Ecosystem Science Laboratory), Ludwig, Jarrod (NYSDEC-Lake Erie Fisheries Research Unit), Rowland, Freya; (USGS-Columbia Environmental Research Center), Stricker, Craig (USGS-Fort Collins)

Science Center), O'Malley, Brian (USGS-Lake Ontario Biological Station), Sitar, Shawn (Michigan DNR-Marquette Fisheries Research Station), Yule, Daniel (USGS-Lake Superior Biological Station); Gorsky, Dmitry; Morton, Kyle (USFWS-Lower Great Lakes Fish and Wildlife Conservation Office), Carl, Dray (Wisconsin DNR), and Rinchar, Jacques (SUNY-Brockport)

Abstract: Thiamine Deficiency Complex (TDC) continues to hinder natural recruitment of lake trout in most of the Great Lakes, except Lake Superior. While research has linked alewife consumption to the occurrence of TDC in lake trout and other salmonines, the underlying mechanisms remain unclear and require further investigation. To address this knowledge gap, we initiated a comprehensive study to evaluate prey fish nutritional quality across two contrasting systems – Lake Ontario and Lake Superior – and to examine the relationship between lake trout diet composition and their egg thiamine concentrations. This study will present preliminary results on egg thiamine concentrations and belly flap fatty acid signatures from lake trout collected at three locations per lake, as well as prey species lipid content collected from U.S. waters of both lakes. These data will serve as a foundation for future analyses, including comparisons with fatty acid signatures of prey from both lakes, to estimate lake trout diets. By linking lake trout egg thiamine concentrations to prey nutritional quality, this work aims to improve our understanding of the factors influencing TDC and to better inform lake trout restoration efforts in the Great Lakes.

• Evaluating Thiamine Deficiency as a Potential Driver of Recruitment Failure in Great Lakes Lake Whitefish

Truscott, Jonathan C. (SUNY Brockport); Beech, Sarah (Ontario Ministry of Natural Resources and Forestry); Bonilla-Gomez, Jose (US Fish and Wildlife Service); Davis, Chris (Ontario Ministry of Natural Resources and Forestry); Dey, Kristopher (Little Traverse Bay Bands of Odawa Indians); Dunlop, Erin (Ontario Ministry of Natural Resources and Forestry); Fisk, Aaron (University of Windsor); Hansen, Scott (Wisconsin Department of Natural Resources); Harding, Ian (Red Cliff Band of Lake Superior Chippewa); Johnson, Timothy (Ontario Ministry of Natural Resources and Forestry); Lauzon, Ryan (Chippewas of Nawash Unceded First Nation); Marsden, Ellen (University of Vermont); Michaud, Gary (Little Traverse Bay Bands of Odawa Indians); Olsen, Erik (Grand Traverse Band of Ottawa and Chippewa Indians); Rowland, Freya (USGS - Columbia Environmental Research Center); Schmitt, Joseph (USGS – Lake Erie Biological Station); Smith, Jason (Bay Mills Indian Community); VanDoornik, Tina (Little River Band of Ottawa Indians); Walters, David (USGS - Columbia Environmental Research Center), and Rinchar, Jacques (SUNY Brockport)

Abstract: Lake whitefish play a critical ecological role in the Great Lakes, linking nearshore and offshore food webs. In addition, they are a commercially valuable Coregonid species and hold deep cultural importance for Indigenous and First Nation communities across the region. Over the past two decades, their populations have declined significantly in lakes Huron, Michigan, Erie, and Ontario. Poor recruitment has been linked to multiple factors, including invasive dreissenid mussels and the decline of *Diporeia*, a high-quality prey. As a result, lake whitefish diets have shifted toward nutritionally inferior species like dreissenid mussels and young-of-year fishes including round goby, rainbow smelt, and alewife. Consumption of prey containing thiaminase, an enzyme that breaks down thiamine (vitamin B₁), can potentially lead to thiamine deficiencies that affect embryonic development and contribute to recruitment challenges. Similarly, increased consumption of high-lipid prey like alewife may lead to lipid peroxidation within the cells of salmonids, reducing available thiamine reserves required for transfer to the eggs. This study aims to assess the impact of thiamine deficiency as a potential cause of recruitment failure in lake whitefish. In fall 2024, female lake whitefish were collected from multiple sites throughout the Great Lakes, and several prey species were collected in fall 2024 and spring/summer 2025. Preliminary results of egg thiamine and belly flap fatty acid analyses of lake whitefish will be

presented. These findings will help identify thiamine-repleted and thiamine deficient stocks across the Great Lakes and provide valuable guidance for their conservation and management efforts.

• The Effectiveness of Three Fish Species on Plant Growth in an Aquaponic System

Berlin, Grace T. and Russell, Hayley L. (Ithaca College)

Abstract: Aquaponics is the possible future of sustainable farming and food security, by using fish waste as plant fertilizer. This design reduces water and synthetic fertilizer use in agriculture. However, heavy use of tilapia, *Oreochromis niloticus*, chosen for its rapid growth rates and high waste production, poses a challenge to the industry as their warm water requirement creates high energy consumption and expenses. In this research, we compare the effectiveness of effluent produced by cold-water fish like, catfish, *Ictalurus punctatus*, and bluegills, *Lepomis macrochirus*, to the warm-water tilapia as a way to reduce energy input and cost. Here, we report on basil plants watered by tilapia, bluegills, or catfish excreta, to compare plant quality and waste composition measures. Because nitrate is a macronutrient that plants need to grow successfully, we hypothesize that the fish species that produces the highest nitrate levels (ppm) would lead to faster growth in basil. Over a five-month period, the following experimental factors were measured: nitrate (NO_3^-), food consumption, largest leaf length, root to tip length, diameter of stem, and leaf color. Though results suggest significant differences among the basil quality attributes like root-tip length ($p= 0.001$) and diameter of stem ($p= 0.002$), between the catfish and the other two species, there are no statistically significant connections to nitrate levels ($p= 0.056$) between the three species. The data suggest no nutrient advantage of tilapia when compared to bluegills, presenting a lower energy alternative in the aquaponic industry.

• Components and Toxicity of Artificial Turf Runoff

Napolitano, Joseph (Ithaca College)

Abstract: Artificial turf fields have become prevalent and are typically regarded as the standard for a good sports facility, but what environmental impact can these fields have? The runoff of a turf field's rubber crumbs, layers of fabrics, and artificial grass contains emerging contaminants such as tire wear particles (TWPs), PFAs, and microplastics. These compounds can leach out toxins that include endocrine disruptors, carcinogens, neurotoxins, and mutagens into the environment (Murphy and Warner 2022) (Le Du-Carrée et al. 2024) (Shin et al. 2022). I quantified the concentration of TWPs from the runoff of Ithaca College's Buttermilk Field and compared the concentration to stormwater data from the Ithaca area. A sample was also sent to be tested for PFAs compounds and Nile red dye was used to analyze microplastic prevalence in a sample. I conducted toxicity tests on *Nicotiana benthamiana* to assess sublethal and potentially lethal effects of the turf runoff. Tests were conducted on 10 plant tap water control groups and 10 plant turf water treatment groups. After four weeks I measured differences in average dry biomass, out-of-ground growth, root growth, and total growth length of each group. My toxicity tests showed no statistically significant differences in growth between control and treatment groups. There was a smaller variety of PFAS compounds detected however there were significantly more PFOAs than stormwater. TWP results showed a smaller concentration in runoff when compared to the average of three stormwater sites, however this average was greatly inflated by one site. Microplastics were also found in the turf runoff. As installation of turf fields increases globally and these contaminants are starting to be found in our bodies, the vitality of this research grows (Satyanarayana) (Armada et al. 2022). I am currently starting a new trial in which I will investigate potential differential gene expression along plant defense and stress response pathways between treatment and control groups. In this trial I opted to create my own artificial turf leachate to control for some of the variation I was encountering with runoff samples.

Session 3B, Bailey 104

• Roll-To-Roll Printing of Halide Perovskite Inks

Wilkosz, Mikolaj; Begly, Nathan and Kirmani, Ahmad R (RIT)

Abstract: Halide perovskites are low-cost, solution-processable inks that can be printed as thin films for a variety of optoelectronic applications. This printing capability allows them to be quickly coated onto substrates via various scalable methods, such as blade or roll-to-roll (R2R) coating. R2R coating holds the key for fast, mass production of flexible perovskite solar cells at the industrial level, provided that the numerous and interdependent parameters that affect R2R coating can be refined. Here, we investigate R2R coating of methylammonium lead iodide (MAPI) perovskite on flexible substrates of aluminum and polyethylene terephthalate (PET), focusing on critical processing parameters: ink composition, coating speed, substrate temperature, and air knife pressure during gas quenching. This comprehensive analysis clarifies the complex parameter space required for high quality film fabrication. Films are characterized using a combination of XRD, UV-Vis spectroscopy, and scanning electron microscopy (SEM). As we approach 40 psi with an air knife and faster coating speeds above 1.0 m/min, 2 θ XRD shows a reduction in the unwanted PbI₂ peak near 14° and an increase in peaks near 28° and 32°, corresponding to the (220) and (310) reflections of tetragonal MAPI, respectively. We also note a decrease in Urbach energy and a more uniform film morphology, as evidenced by SEM. We find that Urbach energy (Eu), representative of energetic disorder, is a key determinant of film quality and approaches 60 meV for higher quality films. Our results highlight the importance of establishing ink-structure-function relationships to enable high-speed printing of energy materials.

• Polyethylene Mimics With Tunable Degradation Rates

Salas, Joel and Matt Miri (School of Chemistry and Materials Science, Rochester Institute of Technology)

Abstract: Polyethylene is the most produced synthetic plastic. However, polyethylene waste largely contributes to environmental issues, accumulating in landfills, but also in the oceans, because it does not degrade rapidly over time. Therefore, for certain polyethylene-based products, which cannot be efficiently recycled, a fast biodegradation rate is highly desirable. Nearly three decades ago the late Robert H. Grubbs developed catalysts for ring-opening metathesis polymerization (ROMP) of olefins. Much research has been done on synthesizing polyethylene like materials using ROMP catalysts. However, a well-established method to produce polyethylene grades with tunable degradation rates has not been reported so far. In the present work, we added unsaturated cyclic compounds that bear functional groups, such as carbonates or diether linkages, as comonomers to cyclooctene at different incorporation levels to achieve the tunable degradability. A third generation Grubbs catalyst was applied. After the ROMP products were isolated, they were hydrogenated. The microstructure of the ethylene copolymers was studied by ¹H and ¹³C NMR spectroscopy. Thermal properties of the copolymers were determined by DSC (Differential Scanning Calorimetry) and TGA (Thermal Gravimetric Analysis). Molecular weight properties of the unhydrolyzed polymers were determined by SEC (Size Exclusion Chromatography) in chloroform with polystyrene calibration standards. Degradation tests were performed in a highly alkaline aqueous solution and the weight loss was monitored over several weeks.

• Contrasting Radiation Effects in mixed-cation metal-halide perovskites: The Role of Lattice Chemistry

Kum, Tatchen B.; Wilkosz, Mikolaj; Tomkiewicz, Alex, Hubbard, Seth and Kirmani, Ahmad R (Rochester Institute of Technology)

Abstract: With perovskite solar cells (PSCs) gaining promise for space power applications, understanding space radiation effects on PSCs is essential. Protons and electrons are the primary particles prevalent in the near-Earth space and degrade space electronics over time. To develop space compliant PSCs, impacts of protons and electrons on perovskite chemistries must be carefully and systematically contrasted. This study investigates the effects of 1 MeV protons and electrons on double-cation (FA_{0.88}Cs_{0.12}Pb(I_{0.922}Br_{0.08})₃) and triple-cation (Cs_{0.05}(MA_{0.17}FA_{0.83})_{0.95}Pb(I_{0.83}Br_{0.17})₃) perovskite chemistries. We irradiate PSC thin films with 1 MeV protons and electrons at fluences between 1e12 - 1e15 cm⁻², generally representative of exposures in the near-Earth environment for up to 5 years. Analysis of the irradiated perovskite films show that triple-cation perovskite chemistry is more radiation resilient to both electrons and protons compared to double-cation perovskites. Through structural and optical characterizations, we assert that the presence of three cations at the A-site of the ABX₃ perovskite crystal structure improves its structure enabling lattice stability under irradiation. Critically, we find that electrons create more notable damage in perovskites while protons are appreciably tolerated. This work offers fundamental insights into radiation effects in metal-halide perovskites, a key step towards their space power applications.

Session 4B, Bailey 202

• Quantification of Pigment in the Eggshells of Passerine Birds

Chau, Margaret; Baldassarre, Daniel; Niri, Vadoud and Geetha-Loganathan, Poongodi (SUNY Oswego)

Abstract: Eggshell pigmentation in birds mediates light exposure for the developing embryo by modulating the thermal environment inside the egg. Pigments provide strength to the eggshell and are responsible for the egg's camouflaging property. The study aims to extract and analyze protoporphyrin and biliverdin pigments from the eggshells of Passeriformes perching bird species using high-performance liquid chromatography (HPLC) to quantify the color composition of the eggshell. Experiments were carried out using eggshells from unincubated (eggs from abandoned nests) and incubated eggs (from eggs collected and incubated in the lab, and from hatched nests). Eggshells were thoroughly cleaned with distilled water, rinsed with 70% ethanol, and air-dried in a fume hood overnight. Dried eggshells were stored in clean specimen bottles. Extraction of protoporphyrin and biliverdin pigments from the eggshells was done by homogenizing eggshell fragments with ethylenediaminetetraacetic acid at pH 7.2. The homogenate was then processed to remove CO₂ and centrifuged at 15000g for 1 minute. The pellet was dissolved in acetic acid and acetonitrile. The solution was centrifuged again to obtain the pure extract, which was stored at 20°C in the dark. Standard curves were obtained using the biliverdin and protoporphyrin chemicals, confirming the measuring range of 5x10⁻⁶ M to 5x10⁻⁴ M. Samples were run at a flow rate of 1.5 mL/min, and a solvent gradient was used, with the total run time being 13 minutes. The initial mobile phase consisted of 25% methanol and 75% ammonium acetate, and a linear change to 95% methanol and 5% ammonium acetate at the 8-minute mark was maintained in this state for 2 minutes before returning to the initial conditions. The amounts of eluted biliverdin and protoporphyrin IX were analyzed at the absorbance 377 nm and 405 nm to quantify the concentration of pigments. Comparing the eggshell properties of the Passeriformes birds will provide extended information about the habits, habitats, possible predators, adaptation to habitat, and development of the bird species belonging to eleven families of Passeriformes.

• Impact of Salt Stress on Growth and Pigment Production in Green Algae

Sena, Maleah; Molee, Francesca; Kulp, Rachel; Rodriguez, Fernando; and Peredo, Elena Lopez (Rochester Institute of Technology)

Abstract: Microscopic green algae are unicellular organisms that can thrive in a range of environments, including both terrestrial and aquatic systems. This ability to colonize a variety of environments makes them ideal candidates for the study of responses to environmental stressors, including drought and salinity. Exposure to high salt concentrations is often a consequence of drought, so salt and water-loss stress are likely closely related and may also have influence on the production of secondary metabolites. Here, we examined a suite of algae within the Scenedesmaceae—*Tetradasmus obliquus* (UTEX 72), *Tetradasmus deserticola*, *Enallax costatus*, *Fletcheria rotunda*, *T. obliquus* (UTEX 393), and *Tetradasmus bajacalifornicus*—to compare their physiological responses to water loss and changes in salinity. We used UV/Vis spectroscopy to measure both overall algal growth and color changes indicative of pigment production. We demonstrate that exposure to sodium chloride (NaCl) and magnesium chloride ($MgCl_2$) significantly affects the production of carotenoid pigments, including astaxanthin, a ketocarotenoid known for its antioxidant properties. Finally, we explored the genetic basis of pigment production under stress by analyzing transcriptomic signatures associated with pigment biosynthesis in algae subjected to desiccation. We analyzed a dataset of slowly desiccated algae to examine the expression of astaxanthin-related genes. The aim of this analysis is to identify potential candidate genes as biomarkers for astaxanthin production under other conditions, such as salt stress. Given the close relationship between salt and drought stress, we predict that gene expression patterns (upregulation and downregulation) will be similar for both conditions.

• Work Towards Biocatalytic Synthesis of Human Milk Oligosaccharides (HMOs)

Hernandez-Salazar, Blanca; Stachowski, Jessica, (Nazareth University)

Abstract: Human milk oligosaccharides (HMOs) are naturally occurring sugars found in human breast milk that support digestive health, immune response, and cognitive development in breast-fed infants. Unfortunately, the limited availability and structural complexity of HMOs makes it difficult to further investigate this important class of molecules. The goal of this project is to use the engineered glycosynthase enzyme Bbhl D746E to make HMOs and HMO derivatives which are currently inaccessible using known biosynthetic methods. We have successfully expressed and purified wild-type and mutant Bbhl in *E. coli* and are optimizing the synthesis of the N-acetyl-D-glucosamine 1,2-oxazoline sugar substrate. The activity of this previously reported sugar-enzyme system will be validated before exploring the compatibility of related carbohydrate substrates.

• Amyloid-beta 1-16 Peptide Homodimer-Regorafenib Complex Revealed by Native Mass Spectrometry, Ion-Source Gas-Phase Top-Down Carbene Footprinting, and GalaxyWeb Modelling

Talcott, Aiden; Ulrich, Hayden; Galen, Annika and Martino, Paul A. (Houghton University)

Abstract: Recent Food and Drug Administration (FDA) approvals of immunotherapies target amyloid-beta peptides and their aggregate forms in order to treat Alzheimer dementia (AD) though these medications include frequent incidences of Alzheimer's Related imaging Abnormalities (ARIA) requiring expensive periodic imaging to manage. Many fragmented and modified forms of amyloid-beta peptides have been found postmortem in AD patients and include amyloid-beta 1-42 ($A\beta_{42}$) which is purported to be the most toxic, and include amyloid-beta 1-16 ($A\beta_{16}$) which is considered nontoxic. We have previously reported in-silico and in-vitro experiments including

AutoDock Vina docking simulations, thioflavin T assays, and circular dichroism results showing that the cancer medication, regorafenib, inhibits A β 42 aggregation by reducing its misfolding into beta-sheet assemblies. Since our previous docking results indicated that regorafenib likely specifically binds to A β 42 close to its N-terminus, we decided to explore the interactions between A β 16 and regorafenib using native mass spectrometry, novel gas-phase carbene footprinting, and further in-silico simulations. An Ion Max electrospray ion source on a linear ion-trap mass spectrometer (Thermo Fisher Scientific, LTQ) was adapted in order to perform novel ion-source top-down carbene footprinting experiments on amyloid-beta 1-16 peptide (A β 16) in complex with cancer medication, regorafenib, a candidate to repurpose for treatment of AD. Native mass spectrometry revealed the presence of a stable regorafenib- A β 16 homodimer complex which was both modelled in-silico and investigated in-vitro using a newly developed ion-source top-down carbene footprinting strategy. Footprinting results indicated that regorafenib protects glutamic acid 11, and valine 12 from gas phase carbene derivatization. The carbene footprinting data was consistent with artificial intelligence GalaxyWeb generated models of the A β 16 homodimer and show strand crossover of the two A β 16 strands at those same two residues E11, and V12. Subsequent docking of regorafenib to the GalaxyWeb generated A β 16 homodimer predict that interactions between regorafenib and both strands of A β 16 provide stabilization of the A β 16 homodimer. Regorafenib stabilization of the A β 16 homodimer suggests that a mechanism for its inhibition of amyloid-beta aggregation may proceed through kinetic trapping of the stabilized A β 16 homodimer-regorafenib complex.

Session 5B, Bailey 203

• **Developing Sputtered Indium Tin Oxide Barrier Layers for Perovskite Space Power**

Daum, Ryan; Spaziani, Julia; Kum, Tatchen B.; Kirmani, Ahmad R; Hubbard, Seth (Rochester Institute of Technology)

Abstract: Perovskite solar cells (PSCs) are emerging as a viable option to power the next-generation low-Earth orbit satellite constellations. To keep their overall launch weights down and retain their mechanical flexibility, it is important to explore ultrathin barrier layers that can protect the PSCs from the harsh space environment. To this end, we are developing sputtered indium tin oxide (ITO) films that can serve as both chemical barriers and redox-benign contacts in PSC architectures. ITO is a transparent conductive oxide widely used in photovoltaic and display technologies due to its high transparency and low resistivity. We sputtered ITO films onto glass substrates using a Denton DC magnetron sputtering system with argon as the working gas. Deposition parameters including sputter time (30–150 s) and pre-sputter duration were varied to achieve films between 40–55 nm thick. Subsequent rapid thermal annealing (RTA) under nitrogen at ~530 °C for 60s – 90 s improved film uniformity and lowered electrical resistivity resulting in a sheet resistance value of 250 Ω/\square for the best 50 nm samples. These properties demonstrate the promise of ITO for PSC device integration.

• **A Gaia Motivated Catalog of Candidate Planetary Nebula Central Stars**

Butler, Ryan W. (Rochester Institute of Technology), Moraga Baez, Paula (University of Western Ontario), Ramsey, Benjamin (Rochester Institute of Technology), Ryder, Diana (Rochester Institute of Technology), and Kastner, Joel (Rochester Institute of Technology)

Abstract: Planetary Nebulae (PNe) are the near-end phase of stellar evolution for intermediate mass (1-8 M_{\odot}) stars and have served as rich astrophysical laboratories for more than a century. Each PN yields a snapshot of the brief ($\sim 10^4$ yr) stage in which the outflowing, dusty envelope of an asymptotic giant branch star is ionized by its newly unveiled core, a future white dwarf (WD).

It is often assumed that most, or all intermediate-mass stars will undergo a PN phase near the end of their life, however the exact formation channels and demographics are poorly constrained. In the last decade, the European Space Agency's Gaia space astrometry mission has greatly expanded the science opportunities surrounding PNe and their WD progeny. The Gaia mission alone has expanded the number of known WDs and candidate WDs by an order of magnitude to over 330,000 and provides useful distance measurements to a large subset. Gaia provides accurate photometry for these stars, facilitating the identification of the hot, luminous WD subset that should be dominated by recently unveiled planetary nebulae central stars (CSPN). Here, we apply Gaia DR3 data to compile a catalog of over ~6,000 candidate CSPN. Our preliminary investigation of a subset of these CSPN candidates, based on the available literature as well as H-alpha surveys of the Galactic plane, indicates that only a small fraction can be definitely associated with PNe at present. The WDs in our CSPN candidate catalog hence present ideal targets for wide-field imaging observations by regional observatories with small telescopes equipped narrowband filters, to attempt to discover "fossil" PNe. As an illustration, we present the preliminary results of TTT 0.8m telescope H-alpha imaging of 3 promising candidates from our catalog. Such observations hold potential for placing constraints on PN lifetimes as well as the enrichment of the interstellar medium in intermediate-mass stellar ejecta.

• **Non- Destructive Characterization of Triple Cation Perovskite Space Solar Cells Using Variable Angle Spectroscopic Ellipsometry**

Spaziani, Julia; Kum, Tatchen B.; Teklemariam, Bekele; Polly, Stephen; Kirmani, Ahmad R; and Hubbard, Seth (Rochester Institute of Technology)

Abstract: Understanding degradation in perovskite films is necessary to produce perovskite solar cells (PSCs) for low Earth orbit space power. In space stressors such as proton and electron radiation can induce damage throughout the device stack by means of displacements and radiolysis. Common characterization techniques such as cross-sectional SEM, XPS, or absorption/emission spectroscopies are either destructive to the perovskite material or lack sufficient depth resolution to determine where damage occurs. In this study, we demonstrate the use of spectroscopic ellipsometry as a non-destructive, high resolution optical method to quantify device layer thickness, optical constants, and dictate chemical changes after irradiation. We model each constituent layer in a triple-cation perovskite device stack subjected to proton irradiation. We assess subtle changes in dielectric function and morphology of the various layers of the device stack, ITO glass/ PTAA/ Triple Cation Perovskite/ C60/ BCP/ Silver, relating to changes induced by irradiation. The accuracy of ellipsometry of thin films allows us to determine the most radiation-sensitive layers in the device stack, helping to develop improved design rules. Our study highlights ellipsometry as a powerful non-destructive diagnostic for ex situ analysis of perovskite degradation under extreme conditions.

• **What Scientists Should Know About Public Opinion**

Breitbeck, Ava C. (Syracuse University)

Abstract: In the aftermath of the COVID-19 pandemic, media pundits and government officials alike have raised concerns about whether a rise in self-reported distrust in scientists might shape the public's willingness to comply with science-based regulations, both in relation to COVID and in other areas. This concern is based on the assumption that the distrust expressed in surveys can also impact real-world behavior. Indeed, survey research indicates a rising tide of anti-science sentiment among the American public that coincides with greater withdrawal from science compliance measures. But these findings stand in stark contrast to vocal pro-science voices that emerged from public discourse and the recent March for Science. How do scientists reckon with these seemingly contradictory trends? This presentation will introduce fundamental principles of

public opinion research in order to explain how the American public forms attitudes and behaviors towards science. The presenter will contrast theories of mass opinion such as the Rational Choice Model and the Receive-Accept-Sample Model (Zaller, 1992). Additionally, the presenter will share results from a recent between-groups experimental study that tested the hypothesis that increasing or decreasing trust in scientists causes a corresponding change in compliance with their recommendations across a range of scientific domains. Despite documented homogenous treatment effects by participants' partisanship, the results show that while decreasing trust does decrease compliance, scholars and scientists face greater difficulty in raising public trust in scientists. Implications for scientists will be at the forefront of this presentation.

2025 Rochester Academy of Science Poster Abstracts

Poster 1 • Building Circuits and Understanding Electronics Through Hands-On Soldering

Dong, Chenxi (Vera), Hall, Madeline (Hobart and William Smith College)

Abstract: Electronics serves as a foundation for nearly all areas of modern technology, from biomedical instruments to communication systems, and understanding its principles is essential for anyone pursuing science or engineering. This project helped us to strengthen our understanding of theoretical physics concepts (current, voltage, resistance, ohm's law, frequency, etc), and how they translate into real-world working systems. Very often in class, these ideas exist only as equations or circuit diagrams, but through soldering and assembling the kits, we were able to see how the electrical circuits behave in practice, how energy flows and how timing, oscillation, and amplification are controlled. Our project involves soldering, testing and troubleshooting electronic circuits. Through this project we gained hands-on experience with electronic components such as resistors, diodes, transistors, capacitors, and integrated circuits. This poster presents and discuss the working of metal detectors, dual LED stroboscope, an electronic dice, a radio, and a cricket sound generator. Completing these electronic kits allowed us to see how physics applies to real engineering design. Each circuit demonstrated a different type of system we encounter in technology today: timing mechanisms, sound generation, random number logic, and radio frequency reception. Understanding how these work on a small scale helps explain how larger and more complex technologies are built.

Poster 2 • Analog Circuit Design for Communication and Measurement: NMOS AM Receiver and Auto-Ranging Capacitance Meter

Martinez Barelles, Jose (Dartmouth College and Hobart and William Smith Colleges)

Abstract: Electronics are at the heart of today's world. Whether in communication devices, sensing systems, or everyday consumer technology, analog and digital circuits shape how information is transmitted and decoded. Mastering their design and understanding their behavior is vital for creating efficient and reliable technologies. This poster presents the design and construction of two analog systems that demonstrate the importance of foundational circuit principles in modern technology, a multi-stage NMOS AM radio receiver, and an auto-ranging capacitance meter. Both projects were developed as part of an undergraduate engineering course work to explore the role of analog design in communication and measurement. Through these designs, theoretical knowledge of transistors, amplification, and signal behavior was applied and tested in real hands-on prototypes. While each circuit serves a different purpose, together they emphasize the continued relevance of analog design in an increasingly digital world. The AM receiver transforms high frequency modulated signals into audible sound, illustrating how amplification, filtering, and demodulation form the basis of all modern communication. The capacitance meter uses similar concepts in a measurement context, including oscillators, amplifiers, and logic control to automatically detect and quantify capacitance values across multiple ranges. Equally important, the process of designing, troubleshooting, and refining these systems developed a broad set of transferable engineering skills. This poster presents the process of circuit design and simulation, data analysis, schematic interpretation, and hardware debugging while learning to adapt to real-world component limitations.

Poster 3 • Black Holes as Statistical Systems

Farren, Zackary D. (Hobart and William Smith Colleges)

Abstract: Black holes are incredibly vast and mysterious systems that exist in the limit of what we know about reality. Understanding and modeling these systems can give us powerful insight into the fundamental workings of our universe, by understanding these behaviors in their high limits. Black holes were once thought of as purely gravitational objects, but further research has revealed a lot of thermodynamic properties, such as radiation and entropy. These properties on the macroscopic scale are best understood through statistical mechanics, which bridges the microscopic and macroscopic worlds. Physicist Stephen Hawking was the first to really exemplify this thermodynamic and statistical behavior, where he combined Quantum Field Theory with curved spacetime to discover that blackholes were thermodynamic bodies that emitted heat radiation. This radiation, named Hawking Radiation, causes black holes to slowly evaporate over time, meaning they aren't these perfect, immortal systems as we previously thought. Other strange thermodynamic properties emerge when looking at the system in this new way, such as the negative heat capacity, meaning the system's temperature increases as it loses energy. Since then, new ideas in quantum mechanics such as string theory and quantum gravity have opened the door to better understanding by modeling the microscopic interactions differently, allowing for the macroscopic picture to make more sense. This crossover between general relativity and quantum mechanics is really at the forefront of theoretical physics, where our current systems start to break down. Systems as complicated as black holes give us great insight into what happens when these theories overlap, and that is why this poster aims to highlight the advancements and current understanding about them.

Poster 4 • Gamma-ray Spectroscopy at RIT of a Soil Sample from the Trinity Test Site Eight Decades Later

Mohammed, Farhaanuddin (RIT), Song, Benjamin (Victor High School), McGowan, Aaron (RIT), Kurinec, Santosh (RIT)

Abstract: The first human-initiated nuclear explosion occurred on July 16, 1945, when a plutonium implosion device was tested at a site located 210 miles south of Los Alamos, New Mexico, on the plains of the Alamogordo Bombing Range, known as the Jornada del Muerto. The code name for the test was "Trinity." We visited Trinity Point in October 2024 and obtained a sample of soil containing Trinitite, the resulting radioactive mineral formed during the explosion. We present gamma ray spectroscopy analysis of sample data collected at RIT using a single NaI:TI plus photomultiplier tube detector with no shielding.

Poster 5 • Low-background Gamma-ray Spectroscopy at the Gamma-X Facility at SUNY Geneseo Applied to a Soil Sample Containing Trinitite

Song, Benjamin (Victor High School), McGowan, Aaron (RIT), Kurinec, Santosh(RIT), Mohammed, Farhaanuddin (RIT), Padalino, Stephen (SUNY Geneseo), Tabei, Mitsuki (SUNY Geneseo), Staiger Hau, Alexandra (SUNY Geneseo), Comer, Emerson (SUNY Geneseo), and Piatkowski, Lucas (SUNY Geneseo)

Abstract: Natural sources of background radiation (primarily cosmic ray muons and isotopes present in Earth's crust) often dominate gamma ray spectroscopy performed in an unshielded laboratory environment. We present low-background data collected from the Gamma-X system at SUNY Geneseo, which uses four tons of lead shielding and houses six detectors. We present analysis of three data sets: empty chamber to characterize the local background, control rock sample collected at RIT to characterize isotopes that are naturally occurring in soil, and a rock sample collected at the Trinity site which contains residual radiation produced 80 years ago in the

first test of a nuclear detonation on Earth. Our high-purity Germanium detectors demonstrated superior gamma peak resolution over the NaI:TI detectors, and the low-background environment allowed for identification of several isotopes that we were unable to resolve using our setup at RIT.

Poster 6 • Concatenated Cat Codes and the Ocelot Chip

Goldman, Elijah (Hobart and William Smith Colleges)

Abstract: Quantum Computing, while extremely promising in the future, comes with several big issues that we still need to overcome. Error correction is one of the most notable examples of this. Unlike conventional computers which deal only with bit flip errors, 0 to 1 or 1 to 0, quantum computers also have a more complex type of error, phase flip error. Quantum computers are extremely sensitive to environmental noise and decoherence. As a result, even small interactions with the environment can cause errors in calculations. With this high error rate, it is vital to design a quantum computer with effective error correction. In an aim to create more scalable quantum systems, effective error correction is one of the biggest roadblocks still faced. In the past, quantum error correction codes, such as the surface code, required a large overhead of qubits dedicated to error correction. Often thousands of physical qubits encode a single logical qubit. Meaning thousands of qubits working in error correction for one qubit that is working towards a calculation. Considering the immense difficulty of creating even one qubit, this motivates researchers to find hardware-efficient alternatives, like bosonic codes. This poster looks at the research done to design a new kind of qubit that passively prevents bit-flip errors, leaving only phase flip errors to be dealt with.

Poster 7 • Trick or Treat? LC-MS method development for the Analysis of BeanBoozled Jellybeans

Seipel, Mason; Gretzinger, Nicole and Peterson, Jeffrey (SUNY Geneseo)

Abstract: This project seeks to develop analytical methods that identify unknown analytes in BeanBoozled jellybeans. BeanBoozled jellybeans are a popular novelty, in which jellybeans come in pairs of similar color and appearance, but one jellybean tastes good (YUM) and one tastes bad (YUCK). “Tutti-Frutti” and “stinky socks” is one example of a YUM-YUCK pair. Because the jellybeans in the Beanboozled pair have similar color and appearance, we expect some of the analytes will be the same in the YUM-YUCK pair, for example the dyes responsible for the jellybean’s color. However, some of the analytes that are associated with the taste will be different. We describe recent efforts in liquid chromatography-mass spectrometry (LC-MS) process development towards this goal. These efforts significantly advance the complexity of the group’s analysis capacity and demonstrate the use of these tools in a real-world application.

Poster 8 • Pretreatment and Fiber Content Analysis of Cannabis sativa L.

Wheeler, Kaden; Geyer, Julia; Allocco, Drew; Clute, Mackenzie; Skermont, Elise and Gikonyo, Barnabas (SUNY Geneseo)

Abstract: Hemp and marijuana, both subspecies of *Cannabis sativa* L. are often generalized into one group but are very different in chemical constituent levels of delta-9-tetrahydrocannabinol (THC) and cannabidiol (CBD). Hemp contains only 0.3% THC, compared to marijuana, which contains 17.1% THC. This makes hemp a useful and safe consumer crop, differing from its co-species, which is harvested for psychoactive and pharmaceutical reasons. Comparing hemp to other crops (corn, beets, etc.), this is one of the fastest-growing plants, and its refined products have incredible commercial value, including biofuels, biodegradable plastics, textiles, dietary supplements, paper, clothing, and much more. Additionally, construction and

manufacturing applications have been seen to include hemp to strengthen their composite products. Its status as a high-yielding, sustainable, and environmentally friendly crop due to its various qualities gives it the potential to yield valuable raw materials for a large number of applications. The research evaluates the pretreatment of hemp along with the comparative analysis of the fiber content to determine the suitability and the potential use of ionic liquid-based pretreatment (ionic liquid code name) for the breakdown of hemp lignocellulosic biomass.

Poster 9 • Enhancing Calcium Phosphate Cement: Evaluating the Influence of Collagen Addition

Flick, Lindsay M.; Wesolek, Olivia L. and Bandemer, Joshua R. (SUNY Geneseo)

Abstract: Understanding the composition of bone is critical to the design of materials to be used to repair bone fractures. This study was conducted to create and evaluate chemically modified Calcium Phosphate Cement composites that act as a replacement for bone that can perform the same role as an autograft. The CPC we will be testing will be combined with hydroxyapatite, which is a mineral that is highly bioactive, biocompatible, and has structural similarities close to those of bone. Collagen from bovine tendons was later added to give more mechanical strength to the cement. The biological properties of hydroxyapatite combined with the structural benefits of collagen can potentially lower the risk of donor-site morbidity and infection risk post-surgery

Poster 10 • Density and Viscosity, and Self Diffusion Measurements of the Ternary System, Water, Salt and low Molecular Weight Polyethylene Glycol

Sanchez, David E.; Janikas, J. Caleb; Uzebu, Ohiohen and Hoffmann, Markus M. (SUNY Brockport)

Abstract: Polyethylene glycol (PEG) is widely used in the industrial, personal, and health care industries. It is a biproduct of petroleum refinement and is produced at about 500,000 tons per annum. A large number polydisperse PEGs are commercially available, where the average molar weight is part of the product name such as PEG200. PEGs are nonhazardous, non-toxic, biodegradable, and possess low vapor pressure, which has made them attractive as an environmentally benign attractive green solvent. Two applications of PEG are its use as a chemical solvent and as a crowding agent to mimic crowded environment in biological studies. Most of these biological studies use changing physiological concentrations of sodium chloride. It has been shown that high concentrations of sodium chloride combined with PEG lower the activation energy needed for B-to-Z transition of DNA. Z-DNA typically requires over 4 M NaCl to form without proteins, but PEG can reduce that salt needed for conformation. To better understand PEG and Sodium Chloride interactions, we examined a wide range of concentrations using PEG200. However, experimental data on key physical properties, especially for the ternary system of PEG200, water, and Sodium Chloride, are scarce. While some data exist for density and viscosity, self-diffusion data is nonexistent. These properties are crucial for interpreting molecular behavior and validating theoretical models, such as molecular dynamics (MD) simulations, which are widely used to study aqueous electrolyte systems. Our new measurements of density, viscosity, and self-diffusion aim to fill this gap and support future computational studies of PEG containing solutions. This poster focuses on the density and viscosity results as final self-diffusion measurements are underway.

Poster 11 • Exploring Alternatives to Dichloromethane for Extraction of Oxylipins from Maize

Kerchoff, Bryden A. and Borrego, Eli (RIT)

Abstract: Oxylipins are an important category of lipids with multiple important roles during plant defense signaling. Oxylipins such as jasmonic acid (JA) and the family of jasmonates are highly studied in the field of plant defense signaling due to their implications in plant defenses and stress responses. In the current extraction methodology, dichloromethane (DCM) is often used for extracting oxylipins and phytohormones from plant tissues during their analysis. Recent regulations from the US Environmental Protection Agency have made usage of DCM more restrictive. Therefore, the aim of this work was to find viable alternatives to DCM for use in the current hormone extraction method. This was done by extracting compounds from a homogenized sample of wounded maize with a buffer (1-propanol:H₂O:HCl 2:1:0.002 v/v/v), then using acetonitrile, ethyl acetate, isopropanol, n-hexane, n-butanol, or ethanol in place of DCM. Liquid chromatography- mass spectrometry (LCMS) was used to quantify the oxylipins and other compounds. Of the solvents, hexane and ethyl acetate extractions performed the best, with isopropanol extractions showing the lowest yield of analytes. Six mixtures of 1:1 v/v between hexane, ethyl acetate, acetonitrile, and butanol were also tested, with hexane:ethyl acetate extractions performing the best. It was found that a 1:1 (v/v) mixture of hexane:ethyl acetate resulted in a higher yield compared to DCM for oxylipins that were particularly nonpolar as well as many fatty acids and JA. In cases of more polar compounds such as the JA derivatives, 12-COOH-JA-Ile and 12-OH-JA, the DCM outperformed the mixture. Overall, a mixture of n-hexane and ethyl acetate are a suitable replacement for DCM in extraction of oxylipins.

Poster 12 • The Serendipitous Discovery of a Potent Antibacterial Agent

Devine, Nicholas W.; Benoit, Kayla M. and Webb, Michael I. (SUNY Geneseo)

Abstract: We are in the midst of an antibacterial crisis with the rise of resistant bacterial strains and the absence of new agents to treat such infections. This creates a great need within the medicinal community for novel agents with unique modes of action such that resistance is not immediately available to the microorganism. Metal complexes are ideal for such studies, given their diverse geometry and unique modes of action, including redox behavior, in contrast to classic organic antibacterial agents. In particular, copper complexes are promising for investigation given their biological utility and established cytotoxicity. We have prepared a small series of 5 copper complexes (CuCl₂L), where L group is a variable 1,10-phenanthroline (phen) group. For the complexes, investigations into their antibacterial activity towards five clinically-relevant pathogenic strains were performed, where substantial activity was observed. Further investigations into the possible mechanism of action were also conducted, the results of which will be presented.

Poster 13 • Detection of Gold Colloid Aggregates Within the Alzheimer's Disease Rat

Donner, Andrew; Chung, Kevin and Yokoyama, Kazushige (SUNY Geneseo)

Abstract: Several brain sections of the Long Evans Cohen's Alzheimer's disease, AD(+), rat model were mixed with gold nano-particles and the gold aggregates were investigated by utilizing the Raman imaging. An examination of normal rat, AD(-), tissues was also performed as a comparison and negative control. In the AD(+) rat tissues, a limited quantity of larger gold colloid aggregates were identified. The SERS spectrum in the hippocampus exhibited nearly identical spectral patterns in the region of Amide I, II, and III bands, as well as distinct spectral patterns in the 300 cm⁻¹ and 1250 cm⁻¹ region that previously could only be observed in AD(+) rat tissue.

The amyloid fibril with a β -sheet conformation, formerly identified and reported in the AD mouse and human brain tissues, was observed to form with gold colloid aggregates. Gold colloid aggregates were significantly found in the hippocampus brain section of AD(+) rats, with unique morphological characteristics. The current study contains a significant potential to conduct a definitive characterization to differentiate the hippocampal tissues in AD(+) and AD(-) rats.

Poster 14 • Investigating the Effects of Propofol on Voltage-Gated Potassium Ion Channels using Molecular Simulations.

Hall, Gabriella I. and Geragotelis, Andrew D. (Keuka College)

Abstract: Voltage-gated ion channels, which are integral membrane proteins that regulate the passage of ions across the cellular membrane, play a vital role in electrical signaling by excitable cells such as neurons. These channels are highly sensitive to binding by various general anesthetics, which can have a wide range of effects. Understanding how anesthetics regulate the function of ion channels at the molecular level is of great importance in describing the cellular mechanisms. In this study, homology models of the Kv1.5 channel in the open and closed states were constructed. Molecular dynamics simulations and small-molecule docking methods will be used to analyze the interactions between the intravenous general anesthetic, propofol, and several voltage-gated potassium ion channels.

Poster 15 • Diadenosine Polyphosphatases of the NUDIX Hydrolase Superfamily in *M. tuberculosis* and *M. leprae*

Bouck, Richard J.; MacLeod, Delila C.; Lynch, Aidan and O'Handley, Suzanne F. (Rochester Institute of Technology)

Abstract: *M. tuberculosis* contains 11 potential Nudix hydrolases, and we are characterizing these enzymes as potential novel antibiotic targets. The diadenosine polyphosphatases (ApnAases) are a family of enzymes within the Nudix hydrolase superfamily. In *M. tuberculosis* there is the primary (more active) Nudix ApnAase and the secondary Nudix ApnAase. There are also orthologs of these two ApnAases in *M. leprae*. The diadenosine polyphosphatases from *Legionella pneumophila* and *Bartonella bacilliformis* have been found to be important in each pathogen's ability to invade its host cells. It is of interest to know whether these enzymes act in the same way in *M. tuberculosis* and *M. leprae*. If they are all found to be involved in invasiveness and thus in virulence, then these enzymes could be novel antibiotic targets. We have cloned and overexpressed each protein and have subcloned each into a HisTag vector to optimize purification. The *M. tuberculosis* enzymes have been purified and their ApnAase activity has been characterized. The primary ApnAase has a second domain, and thus to finish the characterization of this enzyme, we are analyzing this second domain for activity. The *M. leprae* enzymes express too insolubly to purify and characterize, and thus we are working on increasing the expression of soluble protein so that we can study these enzymes as well; currently we know that they each have ApnAase activity (in the crude extract) above that of *E. coli* enzymes alone.

Poster 16 • Investigating G Quadruplex interactions in Oncogenes using Benzothiazole and Benzoquinones

Bulan, Christopher and McKnight, Ruel (SUNY GENESEO)

Abstract: G-quadruplex (G4) DNA has become of increasing interest to the scientific community as anticancer therapies. This intrigue is due mainly to the fact that G4 DNA represents viable targets to both inhibit the telomerase enzyme and to block the expression of cancer promoting oncogenes such as c-MYC, RAS and BCL-2. This makes G4 DNA a viable target for anticancer therapeutics to treat previously "undruggable" genes targets. Inspired by natural

products, researchers have synthesized benzothiazoles and benzoxazoles, heterocyclic compounds that have also been shown to exhibit a broad range of anti-cancer, anti-pathogenic, anti-convulsant, anti-inflammatory, and anti-tubercular bioactivity. The benzothiazole core represents a versatile scaffold that has been found to be a useful framework for creating many stable derivatives. Recent advances in therapeutic screening have identified the benzothiazoles as viable candidates for a novel direction in chemotherapeutic treatment with potentially high selectivity and thus reduced deleterious side effects. In the current study, we have investigated the binding of several benzoquinone-benzothiazole derivatives to a c-MYC G4 DNA sequence. This study was accomplished using a combination of circular dichroism spectroscopy and fluorescence displacement assays. Our data suggests that the identity/nature of the substituent attached directly to the benzoquinone ring component determines the degree to which our compounds bind to the G4 DNA. We have observed that both the addition of an amino group, as well as the location of the amino group influence this interaction. Our findings have implications in the SAR (structure-activity-relationship) when exploring viable drug candidates that targets and inhibits the c-MYC oncogene.

Poster 17 • Targeting G-Quadruplex DNA using Groove Binding Compounds as an Anticancer Study

Lee, AnaSophia; Alabdely, Gadeer and McKnight, Ruel (SUNY Geneseo)

Abstract: This research project investigates the effectiveness of groove binding compounds in binding to G-quadruplex DNA. Previous work by researchers within the field have shown that G-quadruplex (G4) DNA is a viable anticancer therapeutic target. Compounds that stabilize G4 have shown promising antitumor effects in preclinical cancer models. This project seeks to study drug-G4 interactions using fluorescence displacement assays and circular dichroism (CD) spectroscopy. Thioflavin-T (ThT) fluorescence displacement data have shown significant displacement of ThT bound to G4 DNA with certain groove binders, indicating G4 binding and stabilization. Circular dichroism spectroscopy displays the differential absorption of circular polarized light in the presence of chiral carbons such as those that exist in a sample of DNA. Each molecule will have a unique spectra, so when a drug is incrementally added to it, each sample generates a new spectra. We have observed noticeable shifts in the CD spectra when the groove binders of this study were added to G4 DNA. This indicates a change in structure and potential stability of the G4 DNA. Our research lab is currently interested in the drugs/groove binders: DAPI, Hoescht33258, distamycin, and berenil. Upon comparison of the results of CD spectroscopy and fluorescence displacement between telomeric and c-MYC G4 DNA, we have seen a difference in binding affinity and structural change that will be studied further. We plan to add other groove binders (e.g., rapamycin) to our toolbox for future comparisons and evaluations.

Poster 18 • Screening clinically approved kinase inhibitors for dual activity against amyloid-beta and tau pathology in Alzheimer's Disease

Rincon-Guerra, Jorge; O'Brien, Samuel; Mortzheim, Genevieve; Wood, Isaiah and Martino, Paul A. (Houghton University)

Abstract: Objective: Alzheimer's Disease (AD) research has traditionally focused on two separate hallmarks: amyloid-beta (A β) plaques and tau protein pathology. This work describes a screening methodology to identify clinically approved medications that can be repurposed to target both AD hallmarks simultaneously. Methodology: Our workflow involves the following steps: 1. Finding potential inhibitors: Identifying a list of clinically approved kinase inhibitor medications that may inhibit tau hyperphosphorylation and subsequent tau pathology. 2.

In-silico docking: Performing virtual docking experiments against an amyloid-beta target to screen for potential A β pathology treatments. 3. Thioflavin T assay: Using in vitro thioflavin T assays to measure the top candidates' suppression of A β pathology. 4. Competitive binding assays: Conducting in vitro competitive binding assays to measure the relative effectiveness of top candidates in binding the A β target. 5. Individual binding assays: Performing individual binding assays to measure in vitro selective binding and determine the dissociation constant (KD) for the A β target. 6. Phosphoproteomics: Conducting mass spectrometry-based phosphoproteomics measurements on tau-pathology model yeast cultures to measure a candidate's relative potential for treating tau pathology. Focus of this Poster: This poster will focus on the progress and preliminary results from steps 4 and 5.

Poster 19 • Phenotypic Studies of a Phosphoglycolate Phosphatase from *Staphylococcus aureus*

Morgan, Jayla C.; Cullinane, Catherine R.; Soto, Mya; Moreno, Isreal; Blake, Kimbria; Edwards, Jasmine and O'Handley, Suzanne F. (Rochester Institute of Technology)

Abstract: *Staphylococcus aureus* is an opportunistic pathogen that is responsible for over 20,000 deaths annually in the United States. With the continual rise of multidrug resistant strains such as MRSA and VRSA, it is vital to investigate virulence factors as potential novel antibiotic targets. We are studying a phosphoglycolate phosphatase (PGPase) from *S. aureus* that has been established as a virulence factor. Phosphoglycolate is an inhibitor of the glycolytic enzyme triose phosphate isomerase (TPI). TPI is not only involved in glycolysis, but also has a moonlighting function as an adhesion protein, thus inhibition by phosphoglycolate may interfere with *S. aureus*'s ability to attach to host cells effectively. Our enzyme may work as a virulence factor by degrading phosphoglycolate, enabling TPI to adhere more strongly. We have cloned, overexpressed, purified and enzymatically characterized the PGPase from *S. aureus*. Currently, our focus is on understanding how this PGPase is a virulence factor and we are comparing an *S. aureus* knockout mutant to the wildtype strain of *S. aureus*. Thus far we have observed that the knockout strain grows more slowly than the wildtype. Currently we are doing biofilm assays and adhesion assays to test the above theories.

Poster 20 • Biodiesel Production from Algal Lipids

Rupp, Annabel; Grossman, Colden; Klein, Hannah; Doherty, Colin; Hanna, Zoe and Hovling, Theodore (SUNY Geneseo)

Abstract: Fossil fuels are the largest contributors to global climate change, accounting for nearly 75% of total greenhouse gas emissions. A green energy solution can be found in autotrophs, which both sequester carbon in their growth and can be made into biodiesel. *Chlorella vulgaris* has been studied for lipid extraction and biodiesel production. Both of said methods were made more efficient through means of culturing the algae in different growing conditions. Growth of *C. vulgaris* was observed in a variety of media and it was determined that Bold's Basal media fosters the most prolific growth. Growth in BBM was also tested with added nitrogen, phosphorus and magnesium sources to determine if extra nutrients affect yield. *C. vulgaris* was found to have a 25.6% lipid yield per mass, and by testing alterations to growing media nutrients including nitrogen starvation and phosphorus starvation, it is hoped that an increased lipid yield is achieved to make the process more efficient. *C. vulgaris* phospholipids will then be extracted from dead cells and converted into biodiesel using a transesterification process. Finally, we will compare our results from this experiment with previous studies on *C. vulgaris* to determine which growing condition is better for the production of biodiesel.

Poster 22 • qPCR Detection and Quantification of Xenotransferred Donor-Derived Germline Stem Cells within Host Gonads

Wilcox, Kendall; Simms, Justine and Jensen, Thomas (Hobart and William Smith Colleges)

Abstract: Conservation of birds has relied mainly on captive breeding, artificial insemination, and artificial incubation. However, recent advances, including embryonic and adult germline stem cell transfer promise new avenues for introduction of novel germplasm into breeding colonies, or for de-extinction. Our lab focuses on the xenotransfer of germline stem cells, using coturnix quail (*Coturnix coturnix*) and chickens (*Gallus gallus*). We routinely use fluorescent microscopy to detect fluorescent protein (FP) expressing donor cells, or PCR using FP/species-specific primers to confirm successful xenotransfer. Here we describe a qPCR method used to detect donor-derived germline stem cells within host gonads. We used a cell sorter (Propel Labs) to sort 10 to 100,000 quail cells into 100,000 chicken cells followed by gDNA isolation. We used quail and chicken-specific primers to detect donor-derived cells within the host gonad. The standard curve was derived using DCt with chicken as the reference. The calculated qPCR standard curve: $\text{Cells} = 501,829 \cdot e^{-0.779 \cdot \text{Ct}}$ $R^2 = 1$ and DCt ranged from 14.3 to 2.06. 76.9% of host gonads were positive for donor-derived cells, ranging from 19 cells (0.02%) to 23,890 cells (23.9%) per 100,000 chicken cells. However, the majority (90%) of hosts had 1,600 or less donor-derived cells per 100,000 chicken cells. Our assay detected donor-derived cell numbers as low as 19 per 100,000. Most host gonads contained 0.1 to 1.56%, although one host gonad had 24%.

Poster 23 • Chicks in Space: Development of 3D Printed Clinostat to Analyze Effects of Microgravity of Embryo Development

Mozden, Claire; Harrell, Andrew; Simms, Justine and Jensen, Thomas (Hobart and William Smith Colleges)

Abstract: Understanding how microgravity influences early developmental processes is essential for advancing long-duration space exploration and reproductive biology in extraterrestrial environments. Microgravity has been shown to influence cellular differentiation, organogenesis, and overall embryonic development across multiple species. To study the effects on human and food animal development, we modified and 3D-printed a clinostat to simulate a microgravity environment. The original design and software, developed by Dan Dragomirescu (GitHub), provides an accessible and cost-effective clinostat model available to the public. We adapted and customized these files to accommodate quail eggs for our experiments. We will use the clinostat to investigate the effects of simulated microgravity on quail (*Coturnix coturnix*) embryos as a model for the reduced gravitational forces experienced in space. If/when humans reproduce in space, microgravity could have serious effects, including congenital heart defects, which may have to be counteracted with artificial gravity if we (or food animals) are to procreate during space flight. These findings contribute to our understanding of how microgravity influences embryonic development, in both human and food animals.

Poster 24 • *In vivo* and *in vitro* Analysis of Warfarin Embryopathy in Chicken Embryos

Kuhnel, Grace; Magee, Evelyn and Geetha-Loganathan, Poongodi (SUNY Oswego)

Abstract: Warfarin is a highly prescribed anticoagulant used to manage hypertension in pregnant patients with heart valves. Because of its low molecular weight, warfarin can easily pass through the placenta, resulting in various fetal pathologies known collectively as warfarin embryopathy or fetal warfarin syndrome (FWS). The study aims to investigate the mechanisms of warfarin in a chick embryo teratogenicity test *in vivo* and *in vitro*. To determine the effects of warfarin, we overexpressed warfarin sodium at different developmental stages of embryo development, prior to cell specification, to see whether condensation formation and cartilage initiation were affected.

Warfarin-injected avian embryos have pronounced FWS phenotypes consisting of cranial hemorrhage, limb dysplasia, nasal cartilage malformation, and delayed development. In parallel, we turned to micromass culture in which presumptive skeletogenic mesenchyme from limb buds was exposed to warfarin from 4 to 12 days in a temporally-controlled manner. Early condensation was reduced, as shown by Alcian blue staining at 4 days, proving the effect of warfarin on cellular dynamics at early stages of chondrocyte initiation. In cultures at later time points, although there was almost a total loss of Alcian blue-stained nodules compared to controls, ghost nodules were seen in the cultures. The presence of ghost nodules was pronounced when cartilage was exposed to warfarin for a longer time. The cultures also showed reduced stained for alkaline phosphatase, proving that warfarin induced matrix loss. These observations are consistent with incomplete osteogenesis, a causative factor of phenotypes seen in human warfarin embryopathy.

Poster 25 • Sex Estimation of Human Femurs housed in the Keuka College Human Skeletal Remains Collection using Morphometric and Statistical Analysis

Whitney, D.; Saptura, Jade; Lawton, Aurora; Demjanec, Barbara; Geragotelis, Andrew; Palmer, Corey; Cursino, Luciana and Katolik, Jessica (Keuka College)

Abstract: In forensic anthropology, determining the biological sex of skeletal remains is a critical step in the process of individual identification. The femur, as the longest and strongest bone in the human body, exhibits several sexually dimorphic traits that can aid in sex estimation. This study aims to estimate the sex of 8 femurs from the Keuka College Human Skeletal Remains Collection, for which biological sex has not yet been determined. A literature review was conducted to identify femoral features with statistically significant sexual dimorphism. Given that India was a major producer of human anatomical skeletons, the review focused on studies involving Southeast Asian populations. Three papers were selected: Ranaweera et al. (2022), Boonthai et al. (2025), and Purkait et al. (2004), which examined Sri Lankan, Thai, and Indian populations, respectively. Morphometric features highlighted in these studies were measured on the Keuka College femora, and the resulting data were applied to the published linear and logarithmic regression equations to estimate biological sex. Each femur was assessed using all three studies, and an overall sex estimation was determined based on the combined results. Of the 8 femurs analyzed, 3 were estimated to be female and 5 were estimated to be male.

Poster 26 • The Extraction of Dental Amelogenin Peptides from Keuka College Human Skeletal Remains Collection.

Saptura, Jade (Keuka College), Katolik, Jessica (Keuka College), Geragotelis, Andrew (Keuka College), Demjanec, Barbara (Keuka College), Lawton, Aurora (Keuka College), Whitney, Dilyn (Keuka College), Hitch, Juliette (University of Nottingham, UK), Shaw, Barry (University of Nottingham, UK), Layfield, Robert (University of Nottingham, UK), and Cursino, Luciana (Keuka College)

Abstract: Amelogenin is the most important protein found in human tooth enamel. Bioarchaeologists and forensic scientists have leveraged the two isoforms produced by genes on the X and Y chromosomes—AMELX and AMELY—for sex determination of human remains. Peptide specific to the X-chromosome isoform is detected in both males and females, while a peptide unique to the sexually dimorphic Y-chromosome isoform is found only in males. The Keuka College Human Skeletal Remains Collection consists of 875 bones uncovered in 2022. Since then, our group has relied solely on osteological methods to develop biological profiles for the unidentified individuals. In collaboration with the Layfield's group at University of Nottingham, we are now incorporating biochemical approaches to enhance these profiles and identify the sex of unknown individuals. Here, we describe the extraction of amelogenin peptides from the tooth enamel of individuals in our collection, which will be used in subsequent biochemical analyses.

Poster 27 • Sex Determination of Mandibles from the Keuka College Human Remains Collection by Morphometric Analysis

Scaptura, Jade; Cursino, Luciana; Palmer, Corey and Katolik, Jessica (Keuka College)

Abstract: Mandibles have been shown to express a high degree of sexual dimorphism. These variations are caused by males having higher levels of testosterone, a higher bite force compared to females, and having a longer growth period during puberty. Thus, morphometric analysis of mandibles can be used to determine estimated sex of unknown individuals. The Keuka College Human Skeletal Remains Collection has 14 mandible whose sex is unknown. The purpose of this study is to use morphometric analysis to estimate the sex of these mandibles using morphometric analysis. Seven mandibular features were measured and compared to published results where the sex was known. These features included bigonial breadth, bicondylar breadth, maximum ramus height, minimum ramus breadth, and symphyseal height. Each measurement determines indicated is the mandibles were male or female. Then an overall estimation of sex was determined. Of the 14 human mandible studied, 2 mandibles were estimated to be female, while the remaining 12 mandible were estimated to be male.

Poster 28 • Age Estimation of Infant and Adolescent Skulls Using Developmental Juvenile Osteology

Lawton, A.; Cursino, Luciana and Katolik, Jessica (Keuka College)

Abstract: Replace this text with your abstract. Developmental juvenile osteology is the study of bone growth and development in immature skeletons. It studies the progression of bone development from the fetal skeleton to the adult skeleton. The Keuka College Human Remains Collection houses two infants and one adolescent skull. The purpose of this study was to estimate the age of these individuals. To determine the age of the infants, four morphometric features were used: nasal bone height, anterior fontanelle size, sphenoid morphology, and eruption of the primary upper central incisor. To determine the age of the adolescent, five morphometric parameters were used: nasal bone height, the spheno-occipital synchondrosis, and the eruption of the 1st, 2nd and 3rd molars. Infant skull SK-INT-4's age was estimated to be between 0-3 months. Infant skull SK-FRA-5's age was estimated to be between 6-8 months. Adolescent skull SK-INT-1's age was estimated to be between 13-18 years.

Poster 29 • Family History of Alzheimer's Disease and Biobehavioral Responses in Young Adults

Lenchenkova, Emma and Fedorovskaya, Elena (Rochester Institute of Technology)

Abstract: Alzheimer's Disease (AD) is a neurodegenerative disorder primarily occurring in individuals 65 and older and is the most common form of dementia. Though AD is often associated with a decline in memory, it is also linked to impairment in other cognitive processes such as inhibitory control. AD also results in slower information processing, as well as altered connectivity. Both the presence of the apolipoprotein $\epsilon 4$ (APOE4) allele and familial history of AD are known risk factors for AD. Both have also been linked to differences in brain structure in asymptomatic individuals. Familial history has been tied to poorer cognitive performance in associative learning tasks and reduced functional connectivity in healthy individuals. Other factors, such as cognitive reserve, have been considered protective factors against AD. Prior studies investigating the effects of AD familial history on cognitively healthy individuals have primarily focused on older populations. The purpose of our experiment is to compare cognitive performance and neural activity using EEG in young populations (18-30 years of age) with and without familial history of AD. Participants will undergo a Symbol Digit Modalities Test to measure information processing speed, a Paired Associative Learning task, a Cognitive Reserve Test, and

two tasks related to inhibitory control (Stroop and Go/No-Go), with the latter two performed while collecting EEG data. A buccal swab genetic test will also be conducted to check for the presence of the APOE4 allele. Our study aims to determine if familial history of AD and/or APOE4 presence in young adults affects cognitive function, measured via task performance, and neural activity (specifically ERP latency and amplitude as well as effective connectivity) in inhibitory control tasks and resting-state EEG.

Poster 30 • Simulating the Assembly of Branched Actin Networks

Mulligan, Benjamin and Mohapatra, Lishibanya (Rochester Institute of Technology).

Abstract: Living cells contain branched actin networks, such as lamellipodia and patches, which are essential for processes like cytokinesis, motility, and shape regulation. These networks form as actin filaments grow, branch, and debranch from a static nucleation region. We developed a stochastic time-series simulation to model this assembly process and investigated how molecular mechanisms of growth, branching, and debranching influence network size. By analyzing steady-state fluctuations and size distributions, we hope to identify the processes that most strongly regulate network size, offering insight into how actin network architecture may be tuned in various cellular contexts. This work could guide the precise control of actin network size, with implications for targeted therapies and cellular engineering.

Poster 31 • Effects of Red and Infra-Red Low-Level Light Therapy (LLLT) on Differentiated Vascular Smooth Muscle Cell (dVSMC) Wound Recovery

Baciuska, Elijah; Palmer, Risa and Poythress, Ransom (Houghton University)

Abstract: Previous research suggested that low-level light therapy (LLLT) accelerates the recovery of skeletal muscle wounds. This study aimed to investigate whether LLLT produces similar effects on the wound healing process of differentiated vascular smooth muscle cells (dVSMCs). The proposed mechanism of LLLT suggests that photons emitted by Light Emitting Diodes (LEDs) are absorbed in the mitochondria and increase ATP production. Elevated levels of ATP enhance the rate of cellular proliferation. Rat aorta cells (A7r5) were cultured in T-75 vented flasks and subcultured in 6-well plates for a scratch wound assay. The scratch width was measured before treatment intervals of ten, twenty, thirty, and forty-five minutes. The light treatments included constant red, near infra-red (NIR), and mixed red and NIR LED light. Control cell plates received no treatment. Cell width was remeasured sixteen hours post-scratch. The difference between the post-treatment and pre-treatment widths quantified cell regrowth. No significant data was recovered from the NIR light treatment. Similarly, twenty minutes of red, as well as twenty and thirty minutes of mixed LLLT treatment, also yielded no significant data. The thirty and forty-five-minute groups of red LLLT, as well as the ten-minute group of mixed light treatment, did significantly increase cell growth. An ANOVA test of the red LLLT data yielded a p-value of 0.04683, which signified LLLT's effectiveness on regeneration time, specifically with longer treatments of red light.

Poster 32 • Optimizing Thiamine Treatment Timing to enhance Steelhead Trout Egg Viability

Hazard, Owen M. (SUNY Brockport) and Rinchar, Jacques (SUNY Brockport)

Abstract: Thiamine Deficiency Complex (TDC) affects salmonines in the Great Lakes region due to decreased thiamine concentrations. Hatcheries typically mitigate TDC by immersing steelhead trout eggs in a 1,000 or 4,500 ppm thiamine bath for 2 h post-fertilization. However, in California, warm water temperatures make it challenging for hatcheries to maintain eggs in treatment baths for the full duration without expensive cooling systems, limiting the practicality of standard

protocols. The goal of this study was to identify a shorter, yet effective, thiamine treatment duration that would allow California hatcheries to produce healthier steelhead offspring. During fertilization, steelhead trout eggs were exposed to 1,000 ppm thiamine for varying durations: 30 s, 1 min, 1 h, and 2 h. A standard post-fertilization thiamine treatment group (1,000 ppm for 2 h) and an untreated control group were also included. The eggs were sampled at different stages of development: 48 h after collection, at eye stage, at hatching, and after yolk absorption. Results indicated A 2-hour treatment, initiated either at fertilization or post-fertilization, appears necessary to significantly increase thiamine concentrations in eggs sampled 48 h post-fertilization. Further studies are needed to better understand thiamine utilization during embryonic development.

Poster 33 • Structural Responses of Fish Enzymes to High Hydrostatic Pressure

Canter, Samantha; Considine, Rowan; Byer, Amanda (SUNY Geneseo), Daane, Jacob; Le, Katie (University of Houston) and Gerringer, Mackenzie (SUNY Geneseo)

Abstract: The deep sea constitutes 70% of Earth's habitable space yet remains one of the least understood ecosystems. At the deepest depths of 11,000 m, hydrostatic pressure can reach up to 110 MPa, posing physiological challenges for deep-sea organisms. To understand the effects of high pressure on protein folding and function, we investigated the enzymes malate dehydrogenase (MDH) and lactate dehydrogenase (LDH), which are essential for cell metabolism. We studied these enzymes from fishes across a range of habitat depths, including the hadal snailfish, *Pseudoliparis swirei*, and shallow-living lumpsucker, *Cyclopterus lumpus*. We cultured *Escherichia coli* cells containing plasmids with the genes for these target enzymes, induced protein expression, and purified the target enzyme through cell lysis and affinity purification. Enzyme purity, yield, and activity were determined through SDS-PAGE, Bradford assays, and enzyme assays, respectively. High-pressure small-angle X-ray scattering (HP-BioSAXS) at the Cornell High Energy Synchrotron Source allowed real-time monitoring of protein conformational changes in solution across a pressure range of 0 to 300 MPa. Proteins showed structural responses to increased hydrostatic pressure, and these responses were both species and temperature dependent. Studies of protein stability in deep-sea fishes inform understanding of life in extreme environments, potential impacts of climate-driven bathymetric range shifts, and provide insights for biotechnological applications.

Poster 34 • Comparing Lipid and Fatty Acid Signatures of Wild and Domesticated Cisco

Berger, Conner (SUNY Brockport), Roger, Gordon (USFWS), Bartron, Meredith (USFWS), Davis, Steve (USFWS), Sweka, John (USFWS), Rinchard, Jacques (SUNY Brockport)

Abstract: Cisco *Coregonus artedii* was once a key forage species in the Great Lakes, but populations have declined due to overfishing, habitat degradation, and invasive species, prompting restoration and stocking efforts. The objective of this study was to compare neutral and phospholipid contents and the fatty acid composition of eggs from wild and hatchery cisco to identify dietary components that support optimal larval development. Eggs were collected from Drummond Island, Lake Huron, and the Jordan River National Fish Hatchery, in Michigan. Total lipids were extracted from eggs and separated into neutral and phospholipid fractions. Fatty acids were then transmethylated and analyzed using gas chromatography/mass spectrometry. Univariate and multivariate statistics were used to assess significant differences in lipid content and fatty acid signatures between the wild and domesticated eggs. Results showed no significant differences in total, neutral, and phospholipid content between the two sources. However, fatty acid signatures in both lipid fractions differed significantly between wild and hatchery eggs. Future work will examine embryo survival in relation to egg fatty acid composition, with particular focus on how these patterns reflect adult diet.

Poster 35 • Physiological Responses of Larval Sea Lamprey (*Petromyzon Marinus*) to Density and Food Availability: Insights from Fatty Acid Analysis

Tonner, Maddox (SUNY Brockport); Hume, John (Michigan State University); Sarcy, Trisha (US Geological Survey); Wilkie, Michael (Wilfrid Laurier University); Johnson, Nichols (SUNY Brockport); Goody, Sara (SUNY Brockport); Docker, Margaret (University of Manitoba) and Rinchard, Jacques (SUNY Brockport)

Abstract: Sea Lamprey (*Petromyzon Marinus*) are invasive in the Great Lakes, but ongoing control programs have reduced wild populations, making it increasingly difficult to obtain specimens for research. To address this, the Sea Lamprey Aquaculture Program (SLAP) was created to rear lamprey under controlled conditions. This study investigated the effects of larval density (Experiment 1) and food availability (Experiment 2) on growth and fatty acid composition. Larvae were reared for three months under varying abundances or rations and analyzed for mass, lipid content, and fatty acid profiles. In Experiment 1, high-density larvae had significantly lower mass compared to low and medium-density groups, but lipid content did not differ. Fatty acid signatures shifted between the start and end of the experiment regardless of the treatments, with 12:0, 14:0, 16:1n-7, and 18:1n-9 driving the differences. In Experiment 2, larval mass, lipid content, and fatty acid signature did not differ among ration treatments. These results confirm that larval sea lamprey can be successfully reared across a range of densities and rations, with fatty acid composition remaining relatively stable. Identifying fatty acid signatures provide new insight into larval physiology and supports the development of consistent aquaculture practices to meet ongoing research and management needs.

Poster 36 • Quantifying the Impact of Thiamine Deficiency on Steelhead Trout Embryo Swimming Behavior.

Fermon, Zane (SUNY Brockport) and Rinchard, Jacques (SUNY Brockport)

Abstract: Thiamine deficiency complex (TDC) is a condition impacting salmonids in the Great lakes. It impairs neurologic and metabolic functions, leading to lethargy, confusion, altered behavior, hemorrhage, and high early-life mortality. This study addresses key research gaps by investigating the effects of TDC on movement performance in steelhead trout (*Oncorhynchus mykiss*) embryos from Lake Ontario. Steelhead trout eggs were collected from 20 females at the Salmon River Fish Hatchery (Altmar, NY). Subsamples of unfertilized eggs were kept for thiamine analysis, while the remaining eggs were fertilized and divided into two groups: a treatment group exposed to a thiamine water bath (1000 ppm for 2 hours post-fertilization), and an untreated control group. Ten offspring per female from each group at the swim-up stage and following three weeks of feeding underwent a 5-minute behavioral assay, consisting of a 2-minute acclimation period followed by 3 minutes of motion tracking using the EthoVision software. Movement parameters including distance traveled, velocity, motility state, and activity duration were quantified and analyzed using univariate statistical tests (t-tests, regression). No significant differences were observed between treatment groups, and no correlation was detected between egg thiamine concentration and movement parameters regardless of the stage of development. These findings suggest that TDC does not alter swimming behavior in steelhead trout embryos; however, future research should explore whether thiamine deficiency affects environmental responsiveness or predator-prey interactions to better understand its broader ecological implications.

Poster 38 • Cold Stunned Sea Turtle Diet Analysis in Cape Cod Bay from 2015-2020

McWilliams, Lucy (Hobart and William Smith)

Abstract: As water temperatures drop in November, kemp's ridley, loggerhead, and green sea turtles cold stun in Cape Cod Bay. The foraging ecology of these sea turtles remains an understudied area of research. In this study, I assessed the diet of these turtles using a multi-tissue stable isotope analysis of cold-stunned kemp's ridley, loggerhead, and green sea turtles stranded from 2015 to 2020. A stable isotope analysis of carbon-13 and nitrogen-15 were measured in blood, front and rear flipper, liver, muscle, skin, and scute tissue samples. I observed an elevated level of nitrogen isotope ratios in kemp's ridley and loggerhead turtles compared to green turtles due to the carnivorous diet of loggerheads and kemp ridleys' and the herbivorous diet of greens. In addition, I performed a gut content analysis on samples from cold-stunned kemp's ridley, loggerhead, and green sea turtles. This technique was used to quantify sea turtle diet composition based on the frequency of occurrence of stomach contents in our dataset of stomach samples from cold-stunned sea turtles. The data is influenced by the variety of foraging strategies, migration patterns, and trophic positions between these species. The gut analysis data provides a valuable complement to the stable isotope data, supplying direct evidence of diet preferences. Due to the lethal sampling methods and ethical implications of studying endangered species of sea turtles, this study is only representative of dead sea turtles. Data collected from this study adds to the knowledge of these turtles' prey species and aid managers in the preservation of these species as a mitigation strategy for these turtles' extinction.

Poster 39 • Feeding Morphology and Mechanisms of Deep-Sea Fishes

Aguilera-Fonseca, Jennifer; Kirgan, Chloe; Soper, Zebulun; Wynne, Emily; Spina, Emily; Rose-Morley, Tristin; Billharz, Stephanie; Bohen, Ryan; Tzetzis, Chryssanthi; Oleyourryk, Taylor and Gerring, Mackenzie (SUNY Geneseo)

Abstract: The deep sea is characterized by high pressure, cold temperatures, and low food abundance. To meet the challenges of these environmental conditions, deep-sea fishes have evolved a broad range of specialized adaptations, many of which remain poorly understood. To understand how deep-sea conditions impact feeding in fishes, we examined the skull morphology and feeding structures of marine fishes in five demersal families across the full bathymetric range of vertebrates. Three of these families, the cusk eels (Ophidiidae), snailfishes (Liparidae), and tripodfishes (Ipnopidae) are suction feeders, expanding their buccal cavities to generate a unidirectional flow of water to bring prey into the mouth. In contrast, the cutthroat eels (Synphobranchidae) and rattails (Macrouridae) feed by biting, primarily scavenging on sunken carrion. We examined the three-dimensional functional morphology of these deep-sea fishes using micro-computed tomography (micro-CT) scanning. We compared tooth shape, jaw size and shape in proportion to head and body size, and pharyngeal jaw structure, and we calculated the mechanical advantage of jaw opening and closing. Even in relatively soft-bodied deep-sea fishes, pharyngeal jaws of suction feeders remained well-ossified and well-developed. Our results suggest that the closing mechanical advantage of biting fishes may decrease as depth increases, suggesting that less force may be exerted upon prey at deeper depths. This study sheds new light on evolution and feeding in the deep oceans.

Poster 40 • Diet of Invasive Rudd in Conesus Lake, New York from Stomach Contents Analysis

D'Ambro, Louis; Calus, Jacob; Coronna, Ledis; Batista, Angelina; Meyer, Griffin; Bohen, Ryan and Gerring, Mackenzie (SUNY Geneseo)

Abstract: Invasive species can be a major driver of ecological change, often disrupting food webs and altering ecosystems through their interactions with native species. One such invasive species, the European rudd, *Scardinius erythrophthalmus* (Family Leuciscidae, Order Cypriniformes) was introduced to Conesus Lake in the Finger Lakes region of upstate New York in the 1980s. To understand the impact of this species on the local aquatic ecosystem, we investigated the rudds' diet through stomach contents analysis. From our analysis of forty-six stomachs, we found a wide variety of prey items, including algae, plant matter, invertebrate crustaceans, and macrophytes. Most of the stomach contents in these rudd were either branched or filamentous algae, suggesting that algae play a significant role in the rudd's diet. We also observed the plastics and other debris in multiple stomachs, highlighting an additional human-induced stressor on this ecosystem. Future analyses will compare diet across location in the lake, fish life stage, and season, in addition to obtaining finer resolution taxonomic identification through DNA sequencing of stomach contents. These findings on the diet and ecological impact of rudd can help inform better management plans for understanding and mitigating the impacts of this invasive species in Conesus Lake.

Poster 41 • Exploring the Teratogenic Effect of Caffeine on Chick Embryos

Page, Samantha; Scherfling, Lydia; Simms, Justine and Jensen, Thomas (Hobart and William Smith Colleges)

Abstract: Pregnant women are advised to avoid certain substances during pregnancy. Caffeine is one of the most discouraged yet most vaguely defined substances due to contradictory evidence and the failure to establish a maximum threshold for caffeine intake. Previous studies have associated caffeine exposure with developmental abnormalities, including brain and heart malformation, as well as a significant decrease in total body weight. Our study investigated mid-development embryos exposed to hyper-physiological levels of caffeine to observe potential teratogenic effects. We hypothesized this would lead to a decrease of at least 5% in the relative sizes of the heart and brain, as well as in total body weight. Our study doubled the recommended daily caffeine intake for women, approximately 700 mg which is equivalent to 8.4mg in chicken embryos. We treated chicken embryos with 8.4 mg of caffeine daily from day 6 through 11 of incubation. 100 μ L of a caffeine solution was injected into 10 experimental eggs, and 100 μ L of a PBS solution was injected into 5 control eggs. Our results demonstrate a significant reduction in chick embryo weight and an increase in heart-to-body ratios, confirming our hypothesis that excessive caffeine injections can decrease both metrics by at least 5%. These findings can, along with other studies, help determine a safe maximum caffeine intake during pregnancy.

Poster 42 • In-Ovo Fertilization: A New Breeding Method for Conservation

Scherfling, Lydia; Obrochta, Ariana; Simms, Justine and Jensen, Thomas (Hobart and William Smith Colleges)

Abstract: Breeding techniques play a vital role in animal conservation by helping increase populations of endangered species and maintain genetic diversity. Methods such as artificial insemination, in vitro fertilization, embryo transfer, and cryopreservation allow breeding when natural reproduction is difficult or impossible. In-ovo fertilization, a new breeding technique, is the process of fertilizing an egg within the egg itself. In this process, sperm is injected directly into the germinal disk of the egg through a small opening in the shell. It allows for the fertilization of the egg without the need for natural mating. Unfertilized bird oocytes are widely considered "too old" to be fertilized post-oviposition, making Ovo fertilization impossible in birds. However, we are developing methods to evaluate whether this dogma is true and have begun injecting directly into the germinal disk of quail eggs to assess fertilization potential. We have also been practicing methods to ensure quality sperm collection from males in our colony. If post-oviposition in-Ovo

fertilization is possible, it would have a significant impact on avian conservation projects as artificial insemination is at best difficult due to insemination of timing and behavioral limitations. Researching more advanced breeding technologies is essential to improving management and recovery of threatened species and ensuring the long-term survival of biodiversity.

Poster 43 • Quails Feel Stress Too: Behavioral Observations to Determine Social Hierarchy and Correlated Stress

Cheung, Jasmine; Vit, Gabe; Simms, Justine and Jensen, Thomas (Hobart and William Smith Colleges)

Abstract: Many animal species live in social groups where individuals have different ranks, forming a social hierarchy. These rankings often determine who gets the best food, mates, or resting spots. Those higher in the hierarchy may experience more stress due to the pressure of maintaining dominance. Alternatively, individuals lowest in the social hierarchy may have similar levels of stress as a result of being outcompeted for resources by those exhibiting more dominate behavior. Stress related to placement within a social hierarchy can affect their health at a cellular level. One sign of chronic stress is the shortening of telomeres—protective caps on the ends of chromosomes that naturally wear down as we age. When stress levels are high, telomeres shorten faster, which can speed up aging and increase the risk of disease. Studies of birds, primates, and fish show that social status and the stress it causes can directly influence how quickly telomeres are lost. This means that the social environment itself can play a key role in shaping both health and lifespan in animals. In this study, we observed the behavior of 6 female quail using sequential observations over several weeks to establish the social hierarchy within our colony. We then switched to a focal ethogram to confirm hierarchal placement. It is hypothesized that the female exhibiting the most aggressive behavior (such as resource guarding) towards others will be the most dominant among the flock, while the female showing the least amount of aggressive behavior will be the least dominant. With this data, we plan assessing telomere length to placement within social hierarchy.

Poster 44 • The Rise of An Invasive Species: Genetic Variation in Barred Owls (*Strix varia*) and Spotted Owls (*Strix occidentalis*) Due to Man-Made Corridors

Gross, Sofia A.; Panora, Natalie and Cortes-Rodriquez, Nandadevi (Ithaca College)

Abstract: Slow expansion of the nonmigratory Eastern Barred Owl's (*Strix varia*) habitat has started to butt heads with Northern Spotted Owl (*Strix occidentalis*) populations in the Western United States. This meeting is hypothesized to be due to man-made corridors that have opened the area of livability for *Strix varia* and caused a mass expansion of their inhabitance, directly aligning with the niche that the *Strix occidentalis* occupies. Using this concept, by genetically comparing older and newer populations of both *Strix varia* and *Strix occidentalis* can reveal potential genetic swamping and divergence within both populations. Their hybrid, the Spurred Owl, is also included in these findings, and can possibly be inferred from the variability in DNA. By studying gene locality and haplotype abundance within the Coding Region (C.R.) of the mitochondrial gene, we can see the most potential for differentiation between the two species. Using this information, I can observe how invasive behaviors in *Strix varia* are projected to affect *Strix occidentalis* population density. Phylogenetically analyzing and comparing the genetic links within these owl species can reveal concepts of gene flow, genetic adaptation, and geographical change. This research functions as a snapshot in time of the real-life changes that these two populations are undergoing. Additionally, the shift of *Strix varia* reveals more of the ugly truth of deforestation and anti-climate efforts affecting animal populations around the world.

Poster 45 • Comparing Community Assemblages and Abundances of Aquatic Macroinvertebrate Between Two Sampling Techniques: Surber Sampler and Hester Dendy
Stoddart, Dylan and Graham, Andie (SUNY Brockport)

Abstract: Accurately sampling aquatic macroinvertebrates is an essential tool for assessing the health and biodiversity of ecosystems. This study was conducted to compare two of the most widely used sampling techniques, Surber samplers (SS) and Hester-Dendy traps (HD), within three wetland streams located in Western New York. Hester-Dendy traps mimic aquatic substrate and typically target colonizing invertebrates over time. Surber sampler requires actively disturbing the stream bed which targets the collection of benthic and mobile invertebrates, which could lead to differences amongst taxa between the two trap types. The purpose of this study was to compare both trap types to better understand the community assemblages collected from each, as well as compare the average number of invertebrates collected. Hester-Dendy traps were deployed at six sites in the summer of 2025; trap contents were collected after five weeks. At the time of HD collections, SS surveys were conducted at each site. Samples were preserved in ethanol and identified later in the lab. A second round of surveys were conducted in the fall of 2025. All samples were sorted and identified down to order, and abundance data were compiled for statistical analysis. A Mann Whitney U test showed no statistically significant differences between the abundance of taxa caught with the two different traps ($p = 0.804$, $t\text{-stat} = 0.250$). A PERMANNOVA was conducted using RStudio and running a Bray-Curtis matrix to determine differences amongst community composition between HD and SS. The results of this test were not statistically significant ($p = 0.182$, $F\text{-stat} = 1.399$). It was determined that only 12.3% of the difference in community composition is explained by trap type. These findings suggest that both methods yield comparable results in terms of macroinvertebrate abundance and diversity, however more samples would need to be conducted to confirm these results.

Poster 46 • Benthic Diatom Community Dynamics in Seneca-Keuka Lake Watersheds: Microbial Indicators of Freshwater Ecosystem Health

Modugno, Alana (Keuka College), Derminio, Dominique (SUNY ESF), and MacGregor, Gylla (Keuka College)

Abstract: Diatoms are an important component of freshwater ecosystems, serving as primary producers and bioindicators of environmental change. Benthic diatoms are highly responsive to variations in water chemistry, making them valuable for assessing ecological conditions. This study examines the composition and distribution of benthic diatom communities in Keuka Lake and surrounding streams, measuring pH and water hardness. Field sampling was conducted across multiple sites, including Point Neamo, Assembly Trail Stream, and the Keuka Lake Outlet Trail, where water quality parameters, including dissolved oxygen, water hardness, pH, conductivity, and temperature, were measured. Epilithic algae were collected for chlorophyll-*a* and diatom community analysis. Diatom samples underwent acid digestion, slide preparation, and taxonomic identification using microscopy. At Point Neamo and Assembly Trail Stream, *Cymbella* was the dominant species, a finding consistent with its preference for oligotrophic environments. The Keuka Lake Outlet Trail community was dominated by *Fragilaria* and *Nitzschia*, a species typically found in eutrophic environments. This difference could be due to variations in nutrient inputs or legacy loads. The findings of this study provide insight into how benthic diatom communities respond to environmental gradients and anthropogenic influences in historically oligotrophic lakes. Given increasing concerns over eutrophication and algal blooms in freshwater systems, understanding diatom dynamics can aid in the development of monitoring programs and water management strategies.

Poster 47 • Characterization of Green Algae Isolates from Meromictic Fayetteville Green Lake

Long, Alannah S.; Marnocha, Cassandra and Edwards, William (Niagara University)

Abstract: Fayetteville Green Lake (FGL) in Syracuse, New York is a meromictic lake with a sulfidic monimolimnion. Green algae are photoautotrophs and there are a variety present in FGL. We have isolated two green algae from the photic sulfidic layer. The mechanisms by which these green algae survive and potentially grow in the sulfidic layer is unclear, chiefly because sulfide is toxic to photosystem II. Using microscopy, we identified our isolates as *Granulocystis* and *Pseudococcomyxa*. We characterized the isolates by measuring growth curves and 18S sequence data. An understanding of the metabolic capabilities of these algae in FGL could demonstrate how photosynthesis can be performed by eukaryotic algae in high-sulfide environments. Further research will determine the genetic mechanisms of sulfide tolerance, gene expression changes upon exposure to sulfide, and the generation of growth curves in environments with and without sulfide. Exploring the mechanism by which green algae species grow in sulfide-rich environments can add to what we know about early Earth and the organisms that survived and contributed to the oxygenation of Earth's atmosphere.

Poster 48 • Cryopreserving Algae from the Rochester Area

Goyette, William and Peredo, Elena Lopez

[abstract unavailable]

Poster 49 • Sunscreen Effects on Growth of Alaskan Soil Dwelling Green Algae

Wilson, Olivia R., Molee, Francesca; Narayan, Micada; Kulp, Rachel; Sena, Maleah and Peredo, Elena Lopez (Rochester Institute of Technology)

Abstract: Most studies on the toxicity of Ultraviolet (UV) filters, more commonly known as sunscreens, have been conducted on marine corals to quantify their effects on coral bleaching. However, little to no study has been done to quantify the effects of UV filters on other microorganisms. In this study we will focus on the effect of these chemical compounds on green algae (Chlorophyta). The aim of this study is to quantify the effects of common UV filters on the physiology of soil dwelling green algae. The three samples used for this study were isolated from three sites in Alaska, an area that does not have much exposure to UV filters. Each sample underwent evaluation of morphology and polymerase chain reaction (PCR) to establish taxonomy and ensure single algal isolate samples. Each algal isolate was put under a stress test and evaluated in intervals over one week to track effects on growth and pigment production.

Poster 50 • Dirty Data: Applications of Bioinformatics Pipelines in Soil Metagenomics

Kulp, Rachel, Peredo, Elena Lopez, Rodriguez, Fernando and Kumar, Girish (RIT)

Abstract: Soil microbial communities are incredibly rich and diverse, with shotgun metagenomic sequencing of samples outputting a massive amount of data. Soil metagenomics has not yet been a major focus of mainstream bioinformatics, and as such there are no established pipelines tailored to this type of data analysis. Here, we aim to use bioBakery workflows to analyze biocrust samples collected from the Kitty Todd Nature Preserve in Northwest Ohio. The whole metagenome shotgun (wmgx) bioBakery pipeline includes tools for decontamination (KneadData), taxonomical assignment up to the strain level (MetaPhlAn/StrainPhlAn), and functional profiling (HUMAnN). Our work focuses on customizing each tool for the unique demands of soil metagenomic data, assessing the computational

demands of the pipeline, and cross-comparing results to external tools. Initial results indicate there is potential for the bioBakery wmgx pipeline to be used in soil metagenomics, however further assessment is needed to fully understand its advantages and disadvantages.

Poster 51 • Assessing the physicochemical characteristics of wetland soils impacted by emerald ash borer (*Agrilus planipennis*)

Chang, Joelle; Dawes, Eliza; Flynn, Haley; Hoven, Brian and Owens-Rios, Wendy (SUNY Geneseo)

Abstract: Wetlands are strongly influenced by soil biogeochemical processes which control nutrient cycling and carbon storage. Understanding these dynamics is essential for evaluating how environmental stressors such as emerald ash borer (*Agrilus planipennis*, EAB) affect forested wetlands. Forested wetlands across western New York are undergoing dramatic changes due to the spread of EAB. Until recently, these wetlands were dominated by green ash (*Fraxinus pennsylvanica*), but EAB infestations have led to widespread mortality, perhaps altering wetland function. As plant communities shift due to ash death, we suspect soil biogeochemistry may change. To document this potential change we will measure soil physicochemical characteristics across 24 forested wetland sites. Specifically, we will measure soil moisture, soil organic matter, total carbon, total nitrogen, and total phosphorus to assess how these parameters may respond to widespread canopy loss. Our research aims to provide baseline data for assessing long-term impacts of EAB on wetland soils. Each site consists of three, 400 m² plots, located at least 50 meters (m) from all other plots. In each plot, we collected two, 20 centimeters (cm) depth cores per site. Samples were collected 12 m due north and south from the plot center. Soil moisture was measured in the field using a Dynamax TH300 Portable Soil Moisture Kit. Cores were then divided into 4 depths of 5 cm increments, to test physicochemical characteristics. Soil moisture will be determined gravimetrically by oven-drying subsamples. Soil organic matter (SOM) will be estimated using the loss-on-ignition method. Total phosphorus (%TP) will be measured following acid extraction and colorimetric analysis using the ammonium molybdate method. Total carbon (%TC) and total nitrogen (%TN) will be determined with a Perkin Elmer 2400 Elemental Analyzer. By analyzing the physicochemical properties of forested wetland soils, we aim to assess how EAB infestations influence nutrient dynamics, organic matter decomposition, and carbon storage. This work will clarify whether EAB-caused canopy loss alters soil moisture, nutrient availability, or microbial activity, and will inform evidence-based restoration strategies to improve hydrological stability and nutrient retention in affected wetlands.

Poster 52 • Characterizing soil texture in forested wetlands impacted by emerald ash borer (*Agrilus planipennis*) (EAB) in western New York

Boomhower, Augusta; Ledtke, Adrianna; Skinner, Erin; Hoven, Brian and Owens-Rios, Wendy (SUNY Geneseo)

Abstract: Forested wetlands in western New York are undergoing rapid ecological changes due to green ash (*Fraxinus pennsylvanica*) mortality caused by emerald ash borer (*Agrilus planipennis*) (EAB), first identified in New York in 2009. Green ash serves as a foundational species in these wetlands and their loss could have a severe impact. To assess how these ecosystems respond to ash mortality, we established 24 long-term monitoring sites where there are 3 plots located in each site in the Finger Lakes Region of New York, to document changes in plant communities, soil properties, and soil microbial communities. Previous research has indicated that EAB has had a significant impact in other plant communities. Evaluating soil texture is essential for assessing soil moisture and nutrient availability, which influences plant and soil microbial communities. The interactions among soil, hydrology, and vegetation play a critical role in regulating hydrology supporting biodiversity. Within each plot, three soil cores were

arbitrarily sampled and homogenized to create a composite sample for soil texture analyses. Samples were sieved first to remove coarse material. Given that Forested wetlands have high levels of organic matter which can interfere with particle settling, soils were pretreated with sodium hydroxide (NaOH). After oven drying the soils, the Bouyoucos hydrometer method was used to determine relative percentages of clay, silt, and sand. Knowing the percentages of silt, clay and sand helps determine the effects of soil texture on water and nutrient movement. The size of soil particles influences how water and nutrients move easily through the soil where the larger sand particles allow faster drainage due to bigger space. Smaller silt and clay particles retain water and nutrients meaning it is more effective, reducing their movement. Soil texture results will be compared across sites to evaluate if soil composition can explain variability in wetland conditions. Incorporating soil texture into long-term monitoring will provide a clearer understanding of how these wetlands respond to widespread green ash mortality. Soil texture influences many things such as drainage, water retention, and nutrient availability where understanding it will help explain how different plant communities establish, change, and respond to environmental changes within these wetlands.

Poster 56 • Suppression of *Quercus* Species May Accelerate Transition to a Mesic-dominated Forest Ecosystem

Starego, Katelyn and Ochs, Alexis (SUNY Geneseo)

Abstract: Invasive species can co-occur with native species, and may have varying effects on the forest community. The Michigan Big Woods plot located in Pinckney, MI has a high density of invasive species including *Berberis thunbergii* (Japanese Barberry) and *Elaeagnus umbellata* (Autumn Olive). We analyzed the interactions between invasive and native species using census data for the years of 2003, 2008, and 2014. We found that there was not a substantial change in the effect of invasive species on the growth of native oak and hickory species, despite the rapid influx of Japanese Barberry. These results suggest that adult trees can still acquire sufficient nutrients during this period of invasion and may have a delayed effect on the forest. By constructing maps for each sampling date, we were able to detect changes in population age structure. Our findings indicate that most oak and hickory trees in the forest are mature, shown by their large diameters at breast height (DBH), with a limited presence of young trees. These patterns are consistent with a forest transition characterized by an influx of mesophytic species, including *Acer rubrum* (Red Maple) and *Prunus serotina* (Black Cherry). These species have experienced high instances of regeneration from 2003 to 2014 and may be better suited to capitalize on open canopy space in the forest as a result of the spread of invasive species. These species are shade tolerant and are commonly found in lower elevation areas which may suggest their increase in establishment over time.

Poster 57 • Creating a spatial inventory of campus trees to inform a more holistic approach to management

Lefkowicz, Joshua; Walz, Nathan; Keifer, Hope; Hoven, Brian (SUNY Geneseo)

Abstract: Understanding that native trees and commonly planted street trees may differ in their ecosystem services is crucial in determining what trees offer the greatest ecological benefit to SUNY Geneseo. In the spring of 2024, ecosystem services were assessed for a small sample of planted trees on campus. These trees included newly planted native trees, as well as pre-existing common street trees. Each tree species was evaluated based on how much stormwater runoff prevented, air pollution removed, carbon sequestered, and the number of species of Lepidoptera hosted. These results were compared between native and non-native species, and indicated a trend toward native trees providing greater ecosystem benefits compared to common, established street trees. However, these results were inconclusive, and a larger sample size is needed to

yield more conclusive results. To expand upon these findings, a complete survey of all managed trees on SUNY Geneseo's campus is currently underway. The tree census is being taken using QField, a spatial application that fully integrates with QGIS. For each tree entry, the species and its diameter at breast height (DBH) are recorded for upload to iTree Design. An inventory of campus trees provides insight into the services trees provide to SUNY Geneseo campus sustainability and informs future tree planting selections. As of spring 2025, the survey includes 21 species of trees and 97 individuals, which were assessed on all metrics previously mentioned. Across all metrics other than Lepidoptera species hosted, the native species outperformed the non-native species (per cm of DBH) on a significant level. Wilcoxon signed-rank tests for storm water runoff, CO₂ sequestration and air pollutants removed yielded p-values of 0.003, 0.013 and 0.024 respectively. Currently, the census includes 36 species and 227 individuals who will undergo the same analyses. The goal of this survey is two-fold: to provide the Department of Facilities with an up-to-date campus tree inventory and to enable a comprehensive evaluation of their ecosystem services.

Poster 58 • Changes in Vegetation Over Twenty Years in a Wetland Complex, Implications for Orchid

Populations in Zurich Bog

Ryniec, Kimberly (SUNY Brockport)

Abstract: Terrestrial orchids are an important gauge of ecological integrity due to their high specificity. They require not only specific environmental conditions themselves but are also reliant on relationships with specific pollinators and mycorrhizal fungi, which are also sensitive to changes in environmental conditions. Zurich Bog is a 650-acre wetland complex in Wayne County, NY, containing bog, fen, and swamp habitats that allow for high species diversity within the Orchidaceae family across the preserve. In 2004, a vegetation survey was conducted by Marie Terlizzi of a new area of the preserve that was previously undocumented. The goal of my study was to revisit her original transects and expand the survey to more areas around the preserve to allow for a more complete understanding of where orchid populations are occurring around the preserve. The resurvey allowed us to evaluate how the overall vegetation in that part of the preserve has shifted over the past twenty years to evaluate if successional forces are being exacerbated at all by the muck farm to the north. The new plots allowed us to evaluate conditions that were present where orchid populations were occurring. The last part of this study looks at two shade-tolerant species of Lady's Slipper Orchids: *Cypripedium acaule* (Pink Lady's Slipper) and *Cypripedium parviflorum* (Yellow Lady's Slipper) to evaluate the differences in their phenophases and the environmental conditions behind them. Results show that there has been a change in vegetation since 2004. Within only the orchid species, the one specimen of *Arethusa bulbosa* (Dragon's Mouth Orchid) was not found again, and a small population of *Pogonia ophioglossoides* (Rose Pogonia) was observed that was previously unrecorded. The results of this study will be used to set future management goals for the preserve.

Poster 59 • Early Plant Community Dynamics in a Created Wetland: Assessing the Effects of Leaf Litter Compost Amendments

Weidberg, Talia; Mirza, Aneesa (SUNY Geneseo); Saggese, Lauren (Rochester Institute of Technology). Owens-Rios, Wendy (SUNY Geneseo) and Tyler, Christy (Rochester Institute of Technology).

Abstract: Wetland creation and restoration are important strategies for recovering ecosystem services lost through widespread wetland degradation and destruction. One management approach that may enhance restoration outcomes involves the addition of soil amendments such as leaf litter compost (LLC), which can increase organic matter and improve conditions for plants.

This study examines plant community changes from 2020–2025 at a restored wetland in Bergen, NY where an experimental area consisting of four 4×50m transects was established. Two transects were amended with LLC while two were left untreated as controls (CTR). The two amended transects received LLC each summer from 2019–2024 and we conducted annual plant surveys each year since 2020. These data were used to calculate Shannon diversity, and native and invasive plant cover to characterize early successional trajectories. Initial diversity metrics were not significantly different among treatments, likely reflecting the young age of the system. However, the plant communities have begun to diverge. *Phalaris arundinacea* differed significantly among treatments, with consistently greater cover in LLC transects across all years ($p = 0.0402$). Cover of *P. arundinacea* also varied among years ($p = 0.0009$), with notably higher values in 2024 and 2025 compared to earlier years. In contrast, *Typha* spp. showed strong year-to-year differences ($p < 0.0001$), with greater abundance in the earlier survey years but no significant differences between treatments. Native vegetation also showed encouraging signs of recruitment. *Scirpus* spp. (Bulrushes) and *Sium suave* (Water Parsnip) increased substantially in Compost transects between 2021 and 2024 before leveling off, with significant year-to-year variation ($p < 0.0001$ for *S. suave*) and a strong treatment × year interaction for Bulrushes ($p = 0.0007$). *Alisma subcordatum* showed a rebound in 2025, particularly in CTR transects, with cover significantly higher in 2025 and lowest in 2022 ($p < 0.0001$). These patterns indicate gradual establishment of native plant communities, likely supported by annual seed dispersal efforts conducted by the local community and relevant stakeholders. Overall, the trends suggest that LLC may accelerate early vegetation establishment but could also promote invasive species such as *P. arundinacea* and *Typha* spp. Continued monitoring will be essential to determine whether these early compositional differences lead to long-term divergence between LLC-amended and unamended wetlands.

Poster 60 • Production of axenic plant material to explore the chemical ecology of urushiol in *Toxicodendron radicans*

Kuehnert, Paul; Brooks, Matthew, and Hoven, Brian (SUNY Geneseo)

Abstract: Poison ivy (*Toxicodendron radicans*) is widely recognized for its propensity to induce a rash. This is of growing concern as *T. radicans* prospers in and around human disturbed environments while also being projected to benefit from a changing climate, increasing the chances of human encounters. However, the chemical ecology of the group of compounds responsible for this rash, urushiol, remains largely unknown. One reason for this is the difficulty in replicating the plant in a controlled environment, limiting variables and facilitating focused research on its utilization of urushiol compounds. To address this, 60 individual seedlings of *T. radicans* will be collected and grown in 4-inch pots from three geographically and ecotypically distinct locations. Individuals from each location will be separated into two groups, half will be kept outside and the other half in the SUNY Geneseo greenhouse. We will attempt to end dormancy early, using a growth chamber, to allow work with specimens to continue into the winter months. Non-dormant plants will have active meristematic tissue that may be cultured to produce new axenic samples for testing. From this point, methods of quantifying urushiol compound production of tissue samples can be employed, and genetic expression allowing urushiol production can be explored. By culturing axenic tissue, it will allow for production of many genetically identical samples of the tissue donor. Additionally, tissue culture inherently produces a mass of undifferentiated cells, known as callus. Multiple current methods of plant genetic manipulation utilizing callus tissue will be available to implement adjusting expression of urushiol production in *T. radicans*. Side by side comparative testing can be utilized to determine physiological effects of individuals that retain the ability to produce urushiol vs without.

Poster 61 • Emerald ash borer and forested wetlands: initial community structure and ash decline in the Finger Lakes Region

Haskell, Leena; Bonesteel, Sam; Mooney, Brynn and Hoven, Brian (SUNY Geneseo)

Abstract: First identified in New York in 2009, the emerald ash borer (*Agrilus planipennis*, EAB) is an invasive insect posing a major threat to regional forests. Green ash (*Fraxinus pennsylvanica*), a dominant canopy tree in western New York's forested wetlands, are particularly vulnerable. Widespread EAB-induced ash mortality is expected to have substantial impacts on wetland ecosystems. To establish a baseline for long-term monitoring, we established 24 sites, each containing three circular 400 meters (m²) plots across the Finger Lakes Region. Sixteen sites were established in 2024, and an additional eight in 2025—four in Monroe County and four among the Finger Lakes. Within each plot, all trees ≥10 centimeters (cm) diameter at breast height (DBH) were identified and measured, canopy openness and shrub cover were recorded. The following results refer to the 16 initial sites established in 2024. Across all plots, mean canopy tree abundance, species richness, and species diversity were 26 ± 2 , 3.0 ± 0.1 , and 0.64 ± 0.04 , respectively. For all canopy trees, we assessed crown position. We identified 19 canopy species, dominated by green ash (43%) and swamp maple (*Acer × freemanii*) (50%). Mean stand basal area (BA) for all species was $23,310 \pm 1921 \text{ m}^2 \text{ ha}^{-1}$, per plot, and of that $663 \pm 64 \text{ m}^2 \text{ ha}^{-1}$ was attributed to ash. Ash health (1 = healthy, 5 = dead) averaged 4.7 ± 0.1 in the canopy and 2.7 ± 0.2 in the subcanopy. Canopy stand BA, ash canopy BA, and ash health were used to calculate ash decline and ash mortality indices; the mean was $49 \pm 0.04\%$ and $47 \pm 0.04\%$, respectively. Mean percent canopy openness was $44 \pm 3.7\%$ per plot. There was a correlation between ash size and canopy position and tree rating, where smaller diameter, suppressed trees are more likely to receive a healthier rating. These findings provide a crucial baseline for evaluating future EAB-driven changes in wetland forest structure and composition.

Poster 62 • Using dendrochronology to assess the role of emerald ash borer-caused ash mortality in the potential release of invasive shrubs

Friedel, Bryan; Georgia, Hunter; Hoven, Brian (SUNY Geneseo)

Abstract: The emerald ash borer (*Agrilus planipennis*, EAB) is an invasive wood-boring beetle first identified in New York State in 2009. EAB has caused widespread mortality in green ash (*Fraxinus pennsylvanica*) dominated wetlands, leading to extensive losses. EAB appears to have had a significant impact on these wetlands, but little historical data is available. We will be coring green ash, swamp white oak (*Quercus bicolor*), and collecting cross-sections from invasive shrubs in 24 wetland sites located throughout Monroe, Livingston, and Ontario Counties. Our goal is to construct a chronology with green ash, cross-dated with swamp white oak, which we will use to quantify growth responses to EAB-caused ash mortality. At each site we will core approximately 25 green ash, taking two cores per tree at breast height and the cores will be perpendicular to one another. Approximately, 5-7 swamp white oak will be cored in the same manner as the green ash at each site. Depending on the most pervasive invasive shrubs at each site, we will collect cross-sections from honeysuckle (*Lonicera* spp.), buckthorn (*Rhamnus cathartica*), and multiflora rose (*Rosa multiflora*). Once samples are collected in the field they will be mounted, dried, and sanded in the laboratory. Samples will then be scanned and ring-width measured with CooRecorder. For cross-dating, we will use CDendro to align ring-width patterns between ash and oak to build a reference chronology. We predict that there will be a correlation between EAB-caused ash mortality, and a growth release in co-occurring invasive shrubs. The resulting dataset would add to our understanding of how invasive species can facilitate one another in forests that are becoming increasingly dominated by anthropogenic influences.

Poster 63 • Demographics of *Pogonia ophioglossoides* (Rose Pogonia) and *Platanthera blephariglottis* (White Fringed Orchid) in Zurich Bog

Montione, Justin and Schultz, Rachel (SUNY Brockport)

Abstract: Zurich Bog in Wayne County, NY, has unusually large and understudied orchid populations for the southern Lake Ontario region. To study these populations, the private landowner requires that only non-invasive techniques be used. To address this opportunity and challenge, we developed novel methods using trail cameras to collect daily data on two relatively common orchid species, *Pogonia ophioglossoides* and *Platanthera blephariglottis*, during the growing season in 2025. We gathered data on the phenological changes over time for each species, as well as the percentage of flowering plants and fruiting plants for *P. ophioglossoides* and the number of flowers per stem and percentage of fruiting flowers for *P. blephariglottis*. We analyzed the images using LabKit, a pixel segmentation software included as part of the Fiji distribution of ImageJ. We analyzed data by segmenting individual flowers from the existing background using LabKit, then using per-image area measurements of visible flowers from ImageJ to calculate average density of flowering individuals or flowers per stalk depending on species. For *P. ophioglossoides*, we found a density of 200 stems/m², 39 flowers/m², and 7 seedpods/m². This resulted in an 18% flower rate and a 20% seed-set rate among flowering plants. For *P. blephariglottis*, we found an average of 13 flowers/stalk and an average of 7 seedpods/stalk for a 70% seed-set rate. In comparison to populations in Newfoundland, Canada, *P. ophioglossoides* at Zurich Bog was significantly larger and had a greater percentage of flowering plants, but a lower percentage of plants produced seed. The *P. blephariglottis* population showed similar demographics to prior research from Michigan. Due to year-over-year variations in populations, data collection over multiple growing seasons is needed to inform potential management strategies. Repeat near-field photography appears to be a useful method to study plants in remote or sensitive areas due to the quantity and frequency of data that can be collected automatically, however the methods used in this study had limitations (such as poor camera focus) which would need to be addressed if repeated at a larger scale.

Poster 64 • Mapping Multiflora Rose Infected with Rose Rosette Disease Within Monroe County

Langan, Jayde E., and Amatangelo, Kathryn L. (SUNY Brockport)

Abstract: Multiflora rose (*Rosa multiflora*) is an invasive species originally from East Asia found throughout the United States. Rose rosette disease (RRD) is a viral plant disease that is relatively new to the Finger Lakes area and ultimately leads to plant death. Multiflora rose is particularly susceptible, but this virus can also infect native and cultivated roses and current management strategies favor destruction and removal of infected plants to prevent spread. Prior to my survey the virus was known to be present in Monroe County, but actual location was uncertain. The goal of my project was to map the presence and severity of rose rosette disease in multiflora rose throughout Monroe County. I chose 10 local parks in Monroe County with known multiflora rose populations. Disease presence and severity of infection was recorded on a scale of 0 to 3. Several trails of each park were walked to understand the distribution throughout each park. The virus was found in all 10 parks surveyed with varying presence and severity. Total percent infection rates and severity levels were calculated and compared. These findings can help inform us of the likelihood of disease spread to native roses and can give us insight into future management techniques as this virus continues to broaden its range.

Poster 65 • Analyzing the Impact of Biodegradable Plastic Fragments on Maize

Hampton, Ulysses and Borrego, Eli (Rochester Institute of Technology)

Abstract: Traditional non-degradable plastics resist environmental degradation and fragment into persistent micro- and nano-plastic particles, which accumulate in organisms and the environment. Biodegradable (BD) plastic was developed to mitigate the issue by enabling degradation through microbes already present in the environment. BD plastics have potential applications in film and mulch for agriculture due to their natural degradation, as the backbone chemical structure is derived from natural sources, and in situations where the removal of film and mulch is difficult or expensive. However, recent findings suggest that BD plastic fragments can increase the production of reactive oxygen species in plants, indicating that BD plastic may have unintended biological and environmental consequences. To analyze their effect on plants, we investigated the impact of several biodegradable plastics, poly(butylene adipate-co-terephthalate) (PBAT), polycaprolactone (PCL), Polyhydroxyalkanoate (PHA), polylactic acid (PLA), and Thermoplastic Starch (TPS), on *Zea mays* growth and development. Biodegradable plastic was ground and kneaded into the soil, in which *Zea mays* were planted and grown. Using physical traits, including height, and vegetative stages (VS) progression were evaluated, and root architecture was assessed with RootPainter and RhizoVison software. Along with water loss, transpiration was evaluated. Height and VS measurements revealed that PBAT decreased height and delayed VS in the early stages of *Zea mays*. In contrast, TPS showed increased root development in the root development analysis. The response suggests that the chemical composition of BD plastic influences plant physiology. Understanding these effects would help make an informed selection of BD plastic while balancing the need for biodegradability in agricultural settings.

Poster 66 • Role of Japanese Knotweed Produced Phenolics in Microbial Community Dynamics

Thompson, Jamison W. and Dubiel, Katarzyna M. (SUNY Brockport)

Abstract: Invasive plant species have detrimental impacts on ecosystems, often disrupting native biodiversity, altering soil chemistry, and changing habitat structure. One prominent example is, *Reynoutria japonica*, commonly referred to as Japanese knotweed. This perennial plant grows in dense thickets that crowd out native vegetation. Additionally, Japanese knotweed can regenerate from small root fragments, making eradication difficult. In tandem with its above ground impacts, Japanese knotweed releases phenolic compounds from its roots, including resveratrol and catechin, that seep into the soil and alter microbial communities. This study aims to determine how *R. japonica* produced phenolics impact soil microbial community composition. To this end, soil samples will be collected from a Japanese knotweed patch and a control, diverse flora region. DNA will be isolated from soil samples, and this DNA will be sequenced to determine the overall bacterial composition of the soil. To determine if the presence of phenolics is sufficient to alter the soil bacterial community, a mix of four phenolics (resveratrol, catechin, emodin, and piceid) will be utilized in experiments. These phenolics will be added to cultures inoculated from diverse flora soil samples. These cultures, along with control cultures lacking phenolics, will be part of a long-term study where media will be refreshed and DNA will be extracted and sequenced at set increments to monitor the bacterial community shifts caused by the presence of phenolics. This will serve as a model of Japanese knotweed invasion of diverse plant ecosystems. This work aims to expand our understanding of the role Japanese knotweed plays on microbial systems in ecosystems where it is invasive.

Poster 67 • Impact of Japanese Knotweed Produced Phenolics on Bacterial Growth

Spezio, Matthew; Morgan, Daniel; and Dubiel, Katarzyna M. (SUNY Brockport)

Abstract: Invasive species are any non-native organism that establish and integrate themselves into a new environment, disrupting ecological balance and spreading rapidly by outcompeting native populations. Some invasive plants have evolved chemical strategies, such as the production of phenolic compounds to inhibit competition and alter soil ecosystems. Japanese knotweed (*Reynoutria japonica*), a plant native to East Asia, is a highly problematic invasive in western New York. Japanese knotweed utilizes phenolic warfare, releasing allelopathic compounds that may inhibit the growth of native plants and microbes. This project aims to explore the inhibitory factors that phenolics serve in altering the soil microbiome and disrupting native plant populations. To test this, we monitored bacterial growth after exposure to three phenolic compounds (catechin, resveratrol, and emodin). These compounds are produced by Japanese knotweed and secreted into the surrounding soil. In this study, we tested bacteria previously isolated from either diverse plant-associated soil or Japanese knotweed-associated soil. These bacterial species were tested against various concentrations of phenolic compounds on a 96-well plate and analyzed for growth patterns via a microplate reader. Preliminary tests indicate signs of inhibited bacterial growth at 1mM resveratrol. This work will help us to better understand the chemical defense mechanisms utilized by these invasive plants.

Poster 68 • Nuclear Genetic Variation and Endosymbiont Variation in the Introduced Ant-Mimicking Spider, *Myrmarachne formicaria*

Huchro, Abigail; Rose, Sophie R.; Miller, Milo R.K.; Sikora, Brooke; Dunn, Brenna and Apple, Jennifer L. (SUNY Geneseo)

Abstract: We are examining nuclear genetic variation and endosymbiont variation in *Myrmarachne formicaria*, an ant-mimicking jumping spider native to Eurasia that has been introduced to North America. Analysis of genetic diversity in the invaded range can inform us about the history of *M. formicaria*'s introduction in North America. Previous work found little genetic variation within several mitochondrial genes of North American samples. We have found more variation with several nuclear genes, 28s rRNA and the histone H3a. In previous research, one of the 28s rRNA primers produced low-quality sequences, so a new primer set was designed using *M. formicaria* sequence data. We are testing this new primer set to see if it yields longer, higher-quality sequences, and have expanded our sample size to detect any geographic patterns better. In addition to nuclear genome sequencing, we are also assessing the incidence of and genetic variation among bacterial endosymbionts among our samples. Two endosymbionts detected in *M. formicaria* samples include *Cardinium*, which was present across all samples and showed little genetic diversity, and *Wolbachia*, which has been found sporadically among samples. The sequencing of a surface protein-encoding gene in the *Wolbachia* bacteria (*wsp*) may help us identify the strain of this bacterium, as well as reveal any geographic patterns in endosymbiont genetic variation. Analysis of these genetic sequences will provide more information about the pattern of introduction and spread of *M. formicaria* into North America.

Poster 69 • Identification and Characterization of Bacterial Microbiomes in the Northern Pitcher Plant (*Sarracenia purpurea*) at Moss Lake Nature Preserve, Caneadea, NY

Fluent, Alliah; Krum, Jenika and Potter, Jamie (Houghton University)

Abstract: The northern purple pitcher plant (*Sarracenia purpurea*) represents a unique microcosm in which carnivorous plants rely upon inquiline organisms, namely macroinvertebrates and microbes, to supplement their limited digestive enzyme activity. This study aimed to identify and characterize the bacterial communities inhabiting individual pitcher cups at Moss Lake Nature

Preserve in Allegany County, NY over several months of a growing season. Pitcher fluid samples were collected from early summer through late fall and processed using culture-dependent techniques on LB (Luria Broth) and PCA (Plate Count Agar) medias. Colonies were characterized by their morphological and biochemical traits, including colony characteristics, Gram stain, starch-, lipid-, and DNA- degradation, sugar fermentation, and motility. Selected isolates underwent colony PCR for 16S rRNA gene amplification for Sanger sequencing. From three rounds of sampling, 332 viable isolates were obtained from distinct pitcher plants, with morphological and biochemical diversity observed across collections. 16S rRNA genomic sequencing of representative morphotypes identified bacteria belonging to phyla Proteobacteria, Bacteroidota, Actinomycetota, and Firmicutes. Within these groups, isolates of *Undibacterium jejuense* and *Microbacterium imperiale* were sequenced and their observed biochemical traits were compared to published literature. Additional taxa from genera, including *Pseudomonas*, *Chromobacterium*, *Gordonia*, *Xylophilus*, *Mucilaginibacteri*, *Leifsonia*, and *Sphingomonas* were identified; this data supports previous research identifying similar phyla and genera. Several isolates demonstrated an ability to degrade DNA, lipids, and various sugars, suggesting functional roles in the turnover of nutrients within pitcher cups. The persistence of some taxa across multiple collections points to their potential ecological importance, while other isolates appeared to be seasonally variable. Although DNA extraction techniques from pooled fluid samples did not yield sufficient results for whole-community sequencing, Sanger-based identification confirmed the presence of diverse and metabolically active taxa. Future work will focus on improving approaches to DNA extraction and sequencing, broadening biochemical assay testing, and analyzing community dynamics to distinguish potential keystone species in early-season microbes from conserved taxa present throughout the growing season. This study provides new insight into the microbial ecology of *Sarracenia purpurea* in western New York and underscores the ecological significance of bacterial inquilines in supporting plant nutrition.

Poster 70 • Multi-year Analysis of Bacterial Populations in the Rochester Lake Ontario Embayment

Brown, Nathaniel W.; China, Sidney; Duran Botero, Andres F.; Ontiveros, Fernando and Herman, Maryann A.B. (St. John Fisher University)

Abstract: Freshwater bacterial communities are shaped by a range of environmental factors, including temperature, pH, organic matter, and pollutants. Given the ecological and public health significance of these ecosystems, systematic identification of microbial flora—especially pathogenic species—is essential. Over the past decade, our team has collected water samples from the Rochester Lake Ontario Embayment, isolating over 1,100 bacterial specimens. This effort supports our long-term goal of developing a predictive model that uses satellite imagery to forecast the presence of specific bacterial taxa. In this study, we present and analyze 16S rDNA data from these samples to characterize bacterial populations, map their geographic distribution, assess genus-level prevalence, and identify pathogenic species of concern. We also outline the progress towards full-genome sequencing of water samples to include unculturable species.

Poster 71 • Digging Deeper: Microbial Community Shifts in Response to Leaf Litter Compost Amendments in a Created Wetland

Tomidy, Avelin; Engle, Grace; Barclay, Sophia; Owens-Rios, Wendy (SUNY Geneseo) and Tyler, Christy (Rochester Institute of Technology)

Abstract: Wetland creation and restoration are essential to offset the loss of natural wetlands that provide ecosystem services such as carbon sequestration and flood mitigation. However, many created wetlands fail to fully achieve functional equivalence with natural wetlands. Because

microbial communities are key drivers of biogeochemical processes, monitoring their structure and function can reveal why restoration outcomes vary. One promising approach is the use of leaf litter compost (LLC) as a low-cost carbon amendment, which can enhance soil biogeochemistry, stimulate microbial communities, and promote the recovery of ecosystem functions characteristic of natural wetlands. However, LLC may also shift microbial and biogeochemical dynamics in ways that drive the system toward an alternative stable state, emphasizing the need for long-term monitoring to assess its ecological trajectory. The purpose of this project was to evaluate how microbial community structure and function have changed in the deeper soil layers (10–11 cm) of a created wetland as part of a larger research analysis. In 2020 and 2024, we sampled microbial communities from the Mill Seat Wetland Restoration Area in Monroe County, NY, where two transects were treated with leaf litter compost (LLC) and two were left as controls (CTR), along with a nearby reference wetland (REF). Samples were collected from surface (0–1 cm) and deeper (10–11 cm) soils, as well as from pure LLC obtained from a municipal yard waste composting facility, to assess whether compost additions influence microbial communities. The samples analyzed in this study represent an extension of a larger dataset that included samples processed last year from the 2024 surface soils and pure LLC. Amplicon sequencing is being conducted by SeqCenter, and results will include relative abundances, alpha and beta diversity metrics, and statistical analyses performed in QIIME2 and R. Previous research suggests that LLC amendments are altering microbial community structure compared to the REF. Analysis of the deeper soil profiles may help determine whether leaf litter compost accelerates or redirects microbial succession in created wetlands.

Poster 72 • Characterization of *Synechococcus* Isolates from Fayetteville Green Lake

Wronska, Kinga; Hemmingway, Cassidy; Moll, Ally; Marnocha, Cassandra; Edwards, William

Abstract: Fayetteville Green Lake (FGL) is an extensively studied meromictic lake that is used as an early Earth analog due to the sulfidic layers, which are dominated by anoxygenic photoautotrophs, including the cyanobacterium *Synechococcus*. It has been hypothesized that the oxygen generating capability of photoautotrophs during the Great Oxidation Event was primarily related to mat-forming cyanobacteria along ancient ocean shores. To potentially extend this hypothesis to planktonic algae, we study photosynthesis and growth in two planktonic *Synechococcus* isolates from FGL. To characterize these isolates, we conducted temperature- and light-dependent growth experiments, and compared them to two model strains, UTEX625 and UTEX2470. The growth curves at 20°C show a steady increase in optical density measured at 730 nm across all cultures, indicating a progressive rise in cell number. The absorbance values appear highest under the lowest light intensity (20 $\mu\text{mol m}^{-2} \text{s}^{-1}$). These low light levels are comparable to the light levels at ~20 m depth in FGL, where the photic zone meets the sulfide layer. With further experiments, we aim to further characterize the growth of our isolates in sulfidic conditions and determine their photosynthetic mechanisms in such conditions – specifically, how they interact with sulfide and how it influences their photosynthetic machinery, gene expression, and overall photosynthetic activity. This research will shine light on the photosynthetic activity in the early Earth’s open ocean which is currently understudied.

Poster 73 • Localization of Sonic Hedgehog (Shh) Pathway in Zebrafish Retinal Regeneration

Allam, Sarah; Karimi, Sarah; Conover, Lauren; Deda, Gloria; Brodeur, Kathleen; Parisi, Charles and Bailey, Travis (SUNY Geneseo)

Abstract: The Sonic Hedgehog (Shh) gene is one of three genes in the Hedgehog (Hh) signaling family. This gene encodes for the Shh protein, a signaling molecule essential in embryonic development across species. The Shh signaling pathway, in particular, is responsible

for cell differentiation in retinal development. It has been previously shown that when the Shh pathway is pharmacologically inhibited, the rate of cell proliferation decreased significantly; therefore, the pathway plays a key role in generating new cells. Locating where the Shh protein is in a developing embryo would aid in locating the cells that the protein originates from. Western blotting is a laboratory technique used to confirm the presence of a specific protein using antibodies. We will use this technique to validate the fidelity of anti-Shh protein antibodies for use in zebrafish (*Danio rerio*) embryos. Immunohistochemistry (IHC) is another laboratory technique used to confirm the location of a protein using antibodies. We will use IHC to locate the cells that the Shh protein originates from. The stages of retinal development are similar among vertebrate creatures; however, many of these species do not possess the ability to regenerate. Zebrafish, unlike humans, possess the ability to regenerate their retinas after being damaged. Zebrafish regenerate other parts of their body, including brain and spinal cord. Looking into how their retinas develop may provide insight into how they are able to regenerate other central nervous system tissues. Using zebrafish as a model to understand the mechanisms of regeneration has the potential to be applied to other mammalian species without regenerative capabilities.

Poster 74 • Genomic Analysis of Bacteriophage Against *Staphylococcus aureus*

Shaibi, Finune T.; Bodulovic, Mia; Evans, Isaac; Smith, Mychena; Roloson, Ross; Blachowicz, Arrianna; Long, Matthew; Smith, Haley and Gallo, Mark A. (Niagara University)

Abstract: Antimicrobial resistance is a growing clinical problem. Therefore, it is imperative to identify alternative ways to address this crisis. *Staphylococcus aureus* is a major pathogen affecting both human and animal health. The use of bacteriophage against *Staphylococcus* represents a novel approach with exciting potential, as it provides highly specific activity against a particular microbe. In this study, bacteriophage were isolated from exotic animals and white-tailed deer. Their DNA sequences were determined, and we conducted alignment-based annotation and analysis to identify potential genes and examine overall genome structure.

Poster 75 • Field Testing of Molecular Diet Methods in *Daphnia galeata*

Macartney, Elizabeth A.; Marnocha, Cassandra; Edwards, William and Edwards, Coleen T.

Abstract: Zooplankton, a diverse group of animals within the plankton community, serves as an indicator to the overall health of their ecosystem. Additionally, they contribute significantly to the movement of carbon, nutrients, and energy through the aquatic food web. We developed a method to determine the diet of the zooplankter *Daphnia* by processing the whole organism, separating the *Daphnia* and prey DNA. Here, we field tested this method by collecting *Daphnia galeata* from the Niagara River, which we fed cyanobacteria, *Synechococcus*, and green algae, *Scenedesmus*, in controlled laboratory experiments. Using our method, we were able to detect diversity in the diet of *D. galeata* from the Niagara River. When fed *Scenedesmus*, there were remnants of their river diet, however most 18S reads were *Scenedesmus*. Much of the 16S diet was composed of chloroplast reads and a mix of freshwater and terrestrial heterotrophs. When we fed *D. galeata* lab-grown *Synechococcus*, they preferred the heterotrophs from the culture. This method will allow us to understand the feeding patterns of zooplankton in different bodies of water, and how they contribute to the overall nutrient cycling within their environment.

Poster 76 • Characterizing Motility in *Janthinobacterium lividum* and *Serratia marcescens*: Implications for Astrobiology

Garrell, Caitlin M.; Ashbaugh, Sierra M. and Marnocha, Cassandra

Abstract: The search for extraterrestrial life depends on distinguishing biological activity from abiotic processes. Microbial motility is a potentially useful agnostic biosignature but identifying true biological motility in extraterrestrial environments requires understanding how living movement differs from non-living motion. This study investigates the motility of *Janthinobacterium lividum* and *Serratia marcescens* to characterize biological movement patterns that could inform biosignature detection in future NASA missions. We cultured both species in liquid media, monitored their growth through optical density (OD) measurements and direct cell counts, and identified key growth phases. Using a Zeiss Axio Imager microscope with phase contrast and cell-counting chambers, we tracked individual cells and quantified their movement. The data collected reveal patterns of directional movement and tortuosity that can help refine biosignature criteria for detecting microbial motility in extraterrestrial environments, including on icy moons such as Europa and Enceladus, where liquid water in subsurface oceans may harbor extant microbial life.

Poster 77 • Scents and Sensitivities: Exploring *C. elegans* Response to Essential Oils

Cotteleer, Coral A.; Hamm, Bailey June; Andracki, Alyssa; Burczak, Grace and Lo, Te-Wen (Ithaca College)

Abstract: Reactive Oxygen Species (ROS) are a class of negatively charged oxygen compounds that can damage the cell by increasing DNA and protein degradation. In healthy systems, cells have safeguards to combat the level of ROS so that it does not reach a toxic level, and low levels of ROS have even been shown to be beneficial in maintaining mitochondrial homeostasis. These small molecules that protect against oxidative damage are called antioxidants, and work to neutralize the negative charge before it becomes harmful. Essential oils are a class of naturally derived plant products, and many of them are antioxidants. There is an understanding that these natural compounds may be helpful to humans, but the specific effect of essential oils in a disease scenario is largely unknown. *C. elegans* have also been shown to respond to essential oils such as carvacrol, eugenol, thymol, and vanillin (Fuentes, et al., 2022). To begin to extend these studies, we tested how *C. elegans* respond to 28 different essential oils. Based on this data, we selected six essential oils to move forward with: four attractants (eucalyptus, cherry blossom, chamomile, frankincense), one repellent (black pepper), and one neutral compound (lavender). Ongoing studies are focused on determining if exposure to coffee (caffeine) sensitizes *C. elegans* response to essential oils. We hypothesize that after ingestion of coffee, chemoattractant and chemorepellent responses will increase. Preliminary data suggests that exposure to coffee or caffeine increases *C. elegans* chemoattraction to lavender and chamomile in a dose-dependent manner.

Poster 78 • Fungal Microbiota and Biodeterioration in Seneca-Iroquois Basketry Heritage: Integrating Microbiology and Cultural Heritage Conservation

Formaniak, Brooke D. and Novikova, Olga (SUNY Buffalo State)

Abstract: This project investigates the fungal microbiota associated with Seneca-Iroquois basketry, a centuries-old indigenous art form deeply rooted in cultural identity, environmental stewardship, and artistic tradition. These handcrafted baskets woven from black ash splints and sweetgrass are preserved within the Seneca-Iroquois National Museum, where they serve as vital cultural artifacts. However, due to their organic composition, these artifacts are highly susceptible to fungal colonization, leading to staining, discoloration, and structural degradation that threaten their long-term preservation. The primary goals of this research are to (1) isolate and identify fungal species colonizing Seneca-Iroquois baskets, (2) evaluate their biodeterioration potential, and (3) develop conservation strategies to mitigate fungal damage. Using a combination of culture-based isolation techniques and molecular methods including DNA barcoding and next-

generation sequencing, the study aims to generate an accurate and comprehensive profile of fungal biodiversity specific to these artifacts. Preliminary sampling of two museum housed baskets involved sterile surface swabbing and cultivation on selective media (MEA, PDA, and FDA) to obtain morphologically distinct colonies. Future work expanded sampling across additional baskets to establish a broader microbial survey. Identified fungal taxa will be assessed for their enzymatic activity and potential to cause material deterioration, providing insights into species specific risks. Anticipated outcomes include a fungal biodiversity catalog unique to Seneca-Iroquois basketry, identification of high-risk taxa contributing to biodeterioration, and evidence-based conservation guidelines for museum professionals. By integrating microbiology with cultural heritage preservation, this project contributes both to the safeguarding of indigenous material culture and to broader scientific understanding of fungal biodeterioration in organic-based artifacts. Ultimately, the work holds great value in interdisciplinary collaboration linking science, culture, and community to protect the Seneca-Iroquois heritage for future generations to enjoy.

Poster 79 • Evaluation of *Bacillus safensis* C3 for Hydrocarbon Degradation and Bioremediation Potential

Bolton, Clara; Noronha, Reuben and Hammers, Daniel E. (Houghton University)

Abstract: Oil pollution poses severe ecological and economic challenges due to the chemical complexity and resilience of petroleum hydrocarbons (PHCs). Bioremediation is a promising alternative to conventional cleanup methods using hydrocarbon-degrading microorganisms. *Bacillus safensis* has been reported in prior studies to degrade PHCs, yet the capacity of the recently identified endophytic C3 strain in this context remains unexplored. This study evaluated the ability of *B. safensis* C3 to use aliphatic or polycyclic aromatic PHCs as carbon sources under controlled conditions. Minimal M9 medium containing individual PHCs or diesel as the sole carbon source was developed. C3 cultures were inoculated and monitored for growth using optical density measurements, and hydrocarbon degradation was quantified through solid-phase extraction followed by GC-MS analysis. Our results indicate that C3 can grow in the presence of certain PHCs, with preferential utilization of some PHCs over others. Under our conditions, C3 exhibited the most growth on and degradation of the aliphatic PHC hexadecane. These findings provide initial evidence that *B. safensis* C3 holds potential as a hydrocarbon-degrading bacterium. Further optimization of conditions and elucidation of metabolic pathways through genomic analysis are necessary to establish its practical application in bioremediation of hydrocarbon-contaminated environments.

Poster 80 • A Multi-Omic Approach to Exploring the Amphibian Microbiome

Thompson, Emma (Rochester Institute of Technology)

Abstract: Amphibians are one of the most at-risk vertebrate groups on the planet. One of the biggest threats to amphibians is the wildlife disease chytridiomycosis. Chytridiomycosis is caused by chytrids, which are aquatic fungi. Both Bd (*Batrachochytrium dendrobatidis*) and Bsal (*Batrachochytrium salamandivorans*) are pathogenic; however, Bd has caused decline in frogs, while Bsal has caused declines in salamander populations. Currently, amphibians have a natural defense, their skin microbiome, which could help to inhibit chytrid infection; however, much is unknown about the genetic mechanisms of inhibition in these microbes. In addition to natural defenses, mitigation methods have been proposed to slow the spread of chytrid. These methods capitalize on the thermal optimum mismatch of the chytrid fungi and their hosts and include warming the host to help overcome the infection. While these methods have proven successful, they do not consider the microbiome, an essential part of defense against chytrid fungi. This study uncovers genes that may be involved in inhibition by using whole-genome sequencing. In

addition, synthetic communities representative of the skin microbiome were co-cultured with chytrid fungi to determine inhibition rates and how temperature affects the microbiome. It was found that several of the inhibitory bacteria shared genes involved in utilizing carbohydrates found in the fungal cell wall. Synthetic communities inhibited Bd more regularly at higher temperatures, which was not shown in the Bsal trials. Next steps include 16S sequencing and qPCR to monitor the community composition of the microcosms and transcriptomics to determine which genes are up- or downregulated during chytrid infection.

Poster 81 • Biological Evaluation of Indolylfuranones as Potential Anti-Cancer Agents

Staunton, Aidan (Hobart and William Smith Colleges)

Abstract: Tubulin polymerization is crucial to cancer growth as it requires constant cell division. During cell division, microtubules, made up of tubulin subunits, polymerize and depolymerize to organize and segregate sister chromatids. This dynamic instability also plays roles in cell shape, organization, and transport. To target this property of cancer cells, tubulin inhibitors either promote or inhibit microtubule stabilization. However, most microtubule inhibitors are often large, complex molecules, leading to solubility, toxicity and multi-cancer efficacy problems. Two known tubulin inhibitors, combretastatin A-4 (CA-4) and colchicine, are both natural compounds that bind to the colchicine binding site (CBS) on tubulin. However, CA-4 easily isomerizes into an inactive form, and colchicine is too toxic to be used in humans. In this research, we investigated compounds with similar structures to CA-4 and colchicine, that were potentially less toxic and effective for human cancer therapy. We investigated the differences between di- and tri- methoxy aryl rings, the difference between a cis oxygen and a trans oxygen on the furanone, and the differences in indole substitutions. Using an MTT assay we assessed the cytotoxicity of each developed compound through EC50. Then to confirm binding at the CBS, we developed a Western Blot assay. We found that tri-methoxy compounds with oxygen trans to the indole ring were the most potent compounds, that indole substitution did not impact potency, and anhydrides had showed no potency. The poster presents our methods and research results.

Poster 82 • Understanding the influence of different intermediate filaments on the morphology of the vulvar cancer cell line, A431D.

Gopal, Avinash; Mongelli, Sara; Stevenson, Abby; Trojanowski, Trinity and Lewis, Jani (SUNY Geneseo)

Abstract: Vulvar squamous cell carcinoma (VSSC) is a rare yet aggressive cancer, primarily affecting women over 60, with early stages often masked by vulvar lichen sclerosis (VLS). VLS is typically treated with ultrapotent corticosteroids like clobetasol. Our previous work showed that clobetasol treatment of A431 vulvar cancer cells leads to a loss of the cell-cell junction protein E-cadherin and a gain of the intermediate filament protein vimentin. These changes are associated with an epithelial-to-mesenchymal transition (EMT), a process linked to cancer progression and the acquisition of a more aggressive phenotype. Interestingly, A431D cells, derived from clobetasol-treated A431 cells, do not lose expression of the epithelial intermediate filaments, cytokeratins 8 and 18. This study explores the roles of vimentin, cytokeratins 8 and 18, and adherens junction components (E-cadherin and plakoglobin) in driving the morphology of these vulvar cancer cells. Using molecular and cellular biology techniques, including plasmid transfections and immunofluorescence microscopy, we introduce E-cadherin-plakoglobin constructs into A431D cells to assess their impact on the intermediate filament network. We hypothesized that E-cadherin-plakoglobin constructs, which reestablish adherens junctions and desmosomes, will restore a cytoarchitecture pattern typical of epithelial cells. In contrast, constructs lacking essential domains for adherens junction and desmosome formation

will fail to alter the distribution of cytokeratins and vimentin. This study aims to deepen our understanding of cytoskeletal remodeling in cancer progression.

Poster 83 • Combination of L-DOS47, KRAS Inhibitors, and Anti-PD1 in Pancreatic Cancer Cells Proposal

Gottstine, Lillian L. and Millen, Jonathan (Saint John Fisher University)

Abstract: Pancreatic cancer is driven by distinct genetic mutations that make it more aggressive than other cancers. The KRAS mutation, found in about 95% of cases, promotes uncontrolled cell growth and tumor development. Other mutations, such as CDK2A, TP53, and SMAD4, also contribute but are less specific, appearing in various cancers. What sets pancreatic cancer apart is its vague early symptoms and late detection, often after tumors have become invasive. The most common and aggressive form, pancreatic ductal adenocarcinoma, arises from the exocrine lining and grows rapidly. Because of this late detection, conventional treatments effective for other cancers—like early-stage breast cancer—are often ineffective. Ongoing research seeks new therapeutic strategies that target the underlying biology of pancreatic cancer. Among these are targeted treatments for specific pathways, including the KRAS G12C mutation. However, such therapies are limited due to their narrow scope. Another approach under study uses L-DOS47, a compound that increases extracellular tumor pH, potentially reducing acidity that hinders immune cell function. While preclinical results are promising, the mechanisms and compatibility of L-DOS47 with immunotherapies remain unclear. My fall research focuses on testing L-DOS47 with anti-PD1 immunotherapy to evaluate their combined effects on pancreatic cancer cells. In addition, I plan to explore the potential synergy between KRAS G12C inhibitors and L-DOS47. These studies will assess how each treatment works alone and in combination, followed by the addition of anti-PD1 therapy. I hypothesize that increasing tumor pH through L-DOS47 will enhance KRAS inhibition and improve immune checkpoint therapy effectiveness. A less acidic tumor microenvironment is expected to boost T-cell activation, decrease immune suppression, and improve overall survival outcomes.

Poster 84 • Structural Modeling of Viral Proteins to Enhance Oncolytic Therapy Design

Hardaway, Jalyn and Mirlano, Rebecca (RIT)

Abstract: Oncolytic virotherapy has emerged as a new approach for targeting and destroying cancer cells while sparing normal tissue yet optimizing viral discrimination of host and cancerous cells remains a significant challenge. In this project, we employ three dimensional computational modeling of viral proteins to guide the design and engineering of viruses with enhanced oncolytic potential. Using structural bioinformatics tools, we generated high resolution models of key viral surface and functional proteins, focusing on regions that mediate host cell recognition, entry, and immune evasion. Protein-protein docking simulations in a waterbox simulation for accuracy were used to predict interactions with tumor associated cellular receptors, and molecular dynamics analyses evaluated the stability and flexibility of engineered variants. By comparing structural features across multiple viral strains, we identified conserved motifs critical for selective targeting of cancer cells and proposed modifications to improve binding affinity while minimizing off-target effects. This modeling approach enables the rational design of viral proteins prior to experimental validation, reducing the time and resources required tedious trial and error wet lab testing. Additionally, we considered potential immunogenicity and safety concerns, assessing how structural changes may influence recognition by the host immune system. The resulting computational framework provides a pipeline for predicting which viral modifications are most likely to enhance tumor specificity, cytotoxicity, and replication efficiency in a controlled and safe manner. Overall, our work demonstrates that integrating three dimensional structural modeling with oncolytic virotherapy design can accelerate

the development of targeted cancer treatments, providing a foundation for experimental testing and future translational applications.

Poster 85 • Investigation of Cytoskeletal Protein Reconstruction of Vulvar Cancer with Surface-Enhanced Raman Spectroscopy

Kurian, Anjana E.; Tabei, Mitsuki, Yokoyama, Kazushige and Lewis, Jani (SUNY Geneseo)

Abstract: The A431 vulvar cancer cell line undergoes a defined cellular transformation when treated with the corticosteroid clobetasol, marked by changes in cytoskeletal protein biomarkers indicative of epithelial-mesenchymal transition (EMT). Replicated experiments demonstrate that this transformation provides a valuable model for studying protein interactions from a chemical perspective. To quantify these interactions, we employed surface-enhanced Raman spectroscopy (SERS) combined with gold nanoparticles, enhancing the detection sensitivity of cytoskeletal protein changes. By tracking protein dynamics and surface composition throughout the cellular transformation, we aim to elucidate the mechanisms underlying EMT. We have completed the data collection of A431 and A431D cells. Spectral analysis provided insights into the sequence of protein gains and losses, and comparison with established data revealed structural information related to protein folding, binding, and interactions. In addition a three-dimensional SERS imaging technique was used to characterize alterations in the cytoskeletal proteins of individual cells. We conclude that a subtle differences were found in spectral features in the region between 250 cm^{-1} and 1250 cm^{-1} , reflecting the presence or absence of vimentin or cyto kelatins.

Poster 86 • Examining the involvement of p27 and p57 in clobetasol induced quiescence in the vulvar cancer cell line, UMSCV-4.

Marsello, Claudia and Lewis, Jani

Abstract: Quiescence is a reversible cellular state where a cell exits the cell cycle and ceases replication in response to stress. Cells can re-enter the cycle once the stress is alleviated. Emerging evidence suggests that cells in a quiescent state may contribute to the long-term dormancy of cancer cells. Vulvar squamous cell carcinoma (VSCC) is a rare form of female genital cancer, and while its treatment and diagnosis remain poorly understood, ultrapotent topical corticosteroids like clobetasol are commonly used to treat vulvar lichen sclerosis (VLS), a skin condition that can precede vulvar cancer development. Our studies show that a subpopulation of the vulvar cancer cell line, UMSCV-4, enters a state of quiescence upon clobetasol exposure. After removal of clobetasol, this subpopulation re-enters the cell cycle. Using BrdU incorporation, a measure of DNA synthesis, we quantified the clobetasol-induced decrease in proliferation and assessed how quickly cells re-enter the cycle post-treatment. Notably, many cells did not re-enter the cell cycle, prompting us to use a caspase-3 assay to determine if these cells were undergoing programmed cell death or apoptosis. Finally, we examined the expression of two proteins, p27 and p57, which are linked to quiescence induced by glucocorticoid receptor activation in lung cancer. Both proteins are tumor suppressors that regulate cell proliferation by inhibiting complexes that drive progression through the cell cycle. Since clobetasol acts through the glucocorticoid receptor, we measured the expression levels of these proteins using western blot analysis of cell extracts after clobetasol treatment.

Poster 87 • Impact of Genotype and Age on Segregation Distorter Meiotic Drive Strength and Spermatid Viability in *Drosophila melanogaster*

Douglas, Clare (SUNY Geneseo); Edvalson, Logan and Larracuente, Amanda (University of Rochester)

Abstract: Meiotic drivers are selfish genetic elements that distort Mendelian inheritance and bias their own transmission to the next generation. *Segregation Distorter* is a well-studied male-specific autosomal driver found on the 2nd chromosome of *Drosophila melanogaster*. Males heterozygous for *SD* and a sensitive wild-type chromosome (+) transmit the *SD* allele to over 95% of their offspring, while female heterozygotes transmit *SD* at the expected Mendelian rate of 50%. The *SD* system includes a driver and its target, *Rsp*— a block of tandem satellite repeats in the pericentric heterochromatin. *SD* targets *Rsp*-bearing + sperm for destruction. Drive strength depends on *Rsp* copy number: *SD* chromosomes carry few copies and resist distortion, while sperm with many copies are disabled. The role of *Rsp* in this process and the mechanism by which it is targeted by *SD* is poorly understood. *Rsp*-bearing + sperm have problems with nuclear condensation and chromatin remodeling during late spermatogenesis, leading to their elimination. It is well established that heterochromatin is progressively lost as flies age, which may compromise the chromatin-based mechanisms underlying *SD*, altering drive strength over time. Here, we examine how genotype and age affect sperm chromatin and drive strength to better understand the chromatin phenotype of drive. We hypothesize that aging influences drive strength and may vary between *SD* haplotypes. To test this hypothesis, we visualized protamine incorporation and measured drive strength in young and old males of six haplotypes with and without drive. While we do not detect an age-dependent trend in drive strength in our experiments, we do detect differences in the cytological defect with age. The cytological defects did not align with k-values. As a future direction, DNA-FISH targeting *Rsp* offers mechanistic insight into distorted spermatids, and future studies should optimize cross schemes, expand sample sizes, improve age control, and include more genotypes to clarify aging's role.

Poster 88 • Gene Expression and Sequence Differences in Male and Female Reproductive Tissues

Linked to Meiotic Drive in Stalk-Eyed Flies

Lee, Sophia J. and Reinhardt, Josephine A. (SUNY Geneseo)

Abstract: The sex-ratio meiotic drive (SR), a trait in an X-linked selfish genetic element (SGE), causes carrier males to produce mostly female offspring, violating the law of segregation. One species known to exhibit SR is the stalk-eyed fly, *Teleopsis dalmanni*. To understand the genetics underlying SR, RNA sequencing was performed on reproductive tissues (ovaries and testes) from five SR, four standard (ST), and three heterozygous *T. dalmanni* individuals. We used the RNA sequencing data to identify drive-associated sequence differences (SNPs) and gene expression differences. To compare differences in gene sequences, we mapped reads to the reference genome using STAR Aligner and identified genotypes in each individual using GATK. SNPsift was used to identify drive associated SNPs. Applying recommended GATK hard filtering parameters resulted in significant read count loss, particularly due to the ReadPosRankSum criteria. Even after adjusting for the ReadPosRankSum criteria, a large proportion of SNPs were lost when filtering out reads with low depth and low quality. We will conduct further analysis into filtering criteria and filtering order to see if meaningful data can be produced. FeatureCounts was used to measure the level of gene expression for each gene in each sample, and DESeq2 was used to identify genes that were expressed differently. Consistent with prior results, many genes were differentially expressed in the gonads of SR males, but there were also 109 genes expressed differently in the ovaries of SR females, suggesting that females could be indirectly impacted by the presence of SR.

Poster 89 • Investigating the Phenotypic Impacts of Overexpressing Ribosomal and Stress Response Genes in *Caenorhabditis elegans*

Riley, Natalie and Morton, Elizabeth (SUNY Brockport)

Abstract: The information stored in genes is used to make proteins, and changes in how much the gene is used can lead to changes in the levels of proteins made. Such changes can affect physical traits and lead to disease. Studying how gene overexpression impacts physical traits in model organisms such as *Caenorhabditis elegans* is useful for learning more about the role of genes in many disorders. *C. elegans* is a small roundworm that is often used in genetic investigations due to its fast growth and recently-developed tools allowing for overexpression of genes. In this study, we will use a CRISPR-based system to target select genes for overexpression in *C. elegans* and assess the impact on disease-relevant traits. These genes include RPL genes, which encode information to make structural components of ribosomes, the cellular structures that make proteins, and HSP genes, which are involved in protecting proteins from environmental stress. Previous undergraduate students have overexpressed multiple RPL and HSP genes and the project described here screens these results for replicability and further study. The initial student results were used as the preliminary screen of 20 total genes; of these, five were chosen for further investigation. The genes chosen had exhibited impact on protein aggregation, the clumping of protein molecules, which is a frequently observed characteristic of neurodegenerative diseases such as Huntington's, Alzheimer's, and Parkinson's disease. Studying how the overexpression of certain genes impacts aggregation may further knowledge of the genetic basis of these diseases. To build on these preliminary observations, we are first reproducing the original experiments with the addition of blinding the conditions of growth during the scoring to prevent bias. We will look at the effect on polyglutamine aggregation and quantify the aggregates to determine if overexpression of RPL and HSP genes impacts protein aggregation. If results can be validated for the chosen genes, we hope to apply their overexpression to different genetic backgrounds to study how the interaction between these genetic differences and gene overexpression impacts physical traits.

Poster 90 • Exploring Connections between Dystrophinopathies and Autism Spectrum Disorder: Investigating the Role for *dys-1* in *C. elegans* Social Feeding Behavior

Remoll, Ava (Ithaca College); Ellison, Casey (Ithaca College); Trenholm, Ryan (Elmira College); Warden, Brett (Elmira College); Butler-Furlong, Gili (Ithaca College); Davir, Olivia (Ithaca College); Hamm, Bailey June (Ithaca College); Lo, Te-Wen (Ithaca College) and Paulson, Abbi (Elmira College)

Abstract: Autism is a neurodevelopmental disorder that affects social interaction, communication, and behavior. Of interest, about 19% of patients with dystrophinopathies, caused by mutations in the dystrophin gene, are reported to have autism¹. Dystrophin links the muscle cell actin cytoskeleton to the extracellular environment, facilitating signal reception necessary for motion². Dystrophin also has roles in Purkinje cells of the cerebellum (coordination and muscle tone), and Schwann cells (myelination)¹. We are utilizing *C. elegans* to better understand the role of dystrophin in autism spectrum disorder (ASD). *C. elegans* has one ortholog of the human dystrophin gene, *dys-1*, expressed in body wall muscle, head, pharynx, and vulva^{3,4}. Mutations in some *C. elegans* autism-associated ortholog genes have been reported to alter social feeding behaviors⁵. To examine the link between muscular dystrophy and ASD, we have been studying if dystrophin knockdown also affects the social feeding behavior of *C. elegans*. Feeding RNA interference was used to deplete *dys-1* expression, and social feeding assays⁶ performed. Experiments were conducted in two strains: N2 and CB4932, which has increased social feeding behaviors compared to N2s. Worms were assessed for bordering (worms within 2 mm of the lawn edge) and clumping (worms touching others along 50% or more of their body length). Clumping was also assessed in *dys-1* mutant strains BZ33 (0.5%, n=748) and LS292 (4.5%, n=806). Multiple conditions were manipulated and evaluated for effect on RNAi outcome: L1 condition (starved vs. fed immediately), induction with IPTG vs. lactose, and whether P₀ or F₁ was assayed. In CB4932 mutants, *dys-1(fRNAi)* (63.9%, n=427) did not affect bordering in comparison to

L4440(RNAi) controls (60.9%, n=448). In most combinations of experimental conditions, both N2 individuals and CB4932 individuals saw a decrease from the *L4440(fRNAi)* negative controls and the *dys-1(fRNAi)* experimental group. L1 condition, induction method, and generation assayed did not have a significant effect on outcome. This data indicates that *C. elegans* could be a productive model for examining the link between autism spectrum disorder and dystrophinopathies. Future directions could include determining where and when *dys-1* expression is needed to promote social feeding and the molecular mechanisms involved.

¹Simone et al., 2021. JCM. 10(19):4370. doi:10.3390/jcm10194370

²Nowak and Davies, 2004. EMBO Reports. 5(9):872. doi:10.1038/sj.embor.7400221

³Ellwood et al., 2021. IJMS. 22(9):4891. doi:10.3390/ijms22094891

⁴*dys-1* (gene) - WormBase : Nematode Information Resource. [accessed 2025 Feb 26]

⁵Cowen et al., 2024. Nat. Commun. 15(1):9301. doi: 10.1038/s41467-024-53590-x

⁶de Bono and Bargmann, 1998. Cell 94(5):679. doi: 10.1016/s0092-8674(00)81609-8.

Poster 91 • Visualizing *Chlamydia* Infection with *C. elegans* Through TGF- β Signaling

Ryann, Tanner; Gondek, David C. and Lo, Te-Wen (Ithaca College)

Abstract: The *Chlamydia trachomatis* infection is a leading cause of preventable blindness (Trachoma) and a common sexually transmitted bacterial infection worldwide. The cervical epithelium is the site of initial infection, and if left untreated, infection can ascend into the upper genital tract, increasing the risk of reproductive complications such as pelvic inflammatory disease, ectopic pregnancy, or infertility (Adachi et al. 2016; Mohseni et al. 2025). A 2023 study estimated that approximately 1.8 million people worldwide suffer from visual impairment due to the disease (Asmare et al. 2023). To date, *Chlamydia*, a gram-negative bacterium, has been successfully studied using cell culture and mouse models. However, these systems have limitations. To expand the available experimental approaches for studying *Chlamydia*, our lab aims to establish *Caenorhabditis elegans* as a model organism for this pathogen. Previous studies have shown that *C. elegans* activates the Transforming Growth Factor-Beta (TGF- β) pathway in response to certain bacterial infections (Madhu et al. 2023). When exposed to gram-positive and negative bacteria, TGF- β signaling (as measured with a GFP reporter) was more strongly induced by gram-negative pathogens (Tian et al. 2010). We hypothesize that *C. elegans* will exhibit increased TGF- β signaling when exposed to *Chlamydia*, similar to its response to other gram-negative bacteria. While previous studies have used quantitative PCR to detect *Chlamydia* infection of *C. elegans*, they have not identified a distinct infection phenotype (Reigada et al. 2024). Our approach represents a critical step towards using *C. elegans* as a model organism for *Chlamydia* research, enabling studies that are not feasible in current models. Specifically, this system would allow us to leverage well-established molecular genetic tools that have been instrumental in studying human diseases in *C. elegans*.

Adachi K, Nielsen-Saines K, Klausner JD. 2016. Biomed Res Int. 2016:9315757.

Mohseni M, Sung S, Takov V. 2025. Chlamydia. In:

StatPearls. StatPearls Publishing [accessed 2025 Feb 25].

<http://www.ncbi.nlm.nih.gov/books/NBK537286/>

Asmare ZA et al. 2023. PLoS Negl Trop Dis. 17(8):e0011573.

Madhu B, Lakdawala MF, Gumieny TL. 2023. Cochella L, Sengupta P, editors. eLife. 12:e75831.

Tian C et al. 2010. Development (Cambridge, England). 137(14):2375.

Reigada I et al. 2024. Biomedicine & Pharmacotherapy. 177:116956.

Poster 92 • i6A tRNA Modification Allows Efficient *Vibrio cholerae* Virulence Gene Expression

Cordero, Abby and Kimura, Satoshi (Cornell University)

Abstract: Cholera is an infectious and deadly disease characterized by severe diarrhea and dehydration. This disease is an ongoing threat to public health, particularly in regions with limited access to clean water. Cholera is caused by a gram-negative bacterium, *Vibrio cholerae*, which colonizes the human intestine and leads to severe diarrhea. The two critical virulence factors responsible for the cholera disease state are toxin co-regulated pilus (TCP) and cholera toxin (CT). TCP facilitates efficient colonization in the gut and CT elicits severe diarrhea. These virulence factors are regulated by a cascade of gene regulation, composed of multiple transcription factors. While the transcriptional regulation of virulence factor expression is well established, their translational regulation is largely unclear. One type of translational regulation is tRNA modification, which is crucial for optimizing cellular processes via protein synthesis from mRNA sequences. We focus on one tRNA modification, 6-isopentenyl adenosine (i6A), which is synthesized by the enzyme MiaA. A genetic screen in the literature showed that *V. cholerae* lacking *miaA* gene exhibited attenuated colonization ability, suggesting that *miaA* and i6A are crucial for *V. cholerae* virulence. However, how i6A facilitates *V. cholerae* virulence is unclear. In this study, we aim to uncover what role i6A plays in the virulence of *V. cholerae* with the underlying hypothesis that i6A facilitates the efficient production of *V. cholerae* virulence factors. We found that the *miaA* deletion strain showed a significant decrease in CT production, strongly suggesting that *miaA* and i6A are necessary for optimal induction of the *V. cholerae* virulence gene expression cascade. A series of experiments suggested that *miaA* is necessary for efficient protein production but not mRNA production of ToxT. ToxT, a virulence gene regulator, controls the transcription of TCP and CT mRNAs. Our findings suggest that tRNA modification is a crucial factor for optimal induction of *V. cholerae* virulence factor production. Currently, we are focusing on how this tRNA modification facilitates the production of ToxT protein and aim to uncover the novel mechanisms that contribute to the production of virulence factors in a critical bacterial pathogen.

Poster 93 • Mechanobiological Regulation of Vesicular Stomatitis Virus Replication in Human Lung Fibroblasts

Valov, Anton; Russell, Tori; Ferran, Maureen C. and Wuertz-Kozak, Karin (Rochester Institute of Technology)

Abstract: Cells don't live in stillness; they stretch, pull, and adapt to forces around them. Yet, existing research rarely examines how those same mechanical cues might influence the outcome. Our work examines this intersection, focusing on how the mechanical environment of human lung fibroblasts affects infection by vesicular stomatitis virus (VSV). Using two recombinant VSV strains expressing mCherry and RFP, higher MOIs led to rapid fluorescence saturation and earlier cytopathic effects, while lower MOIs revealed a slower, wave-like spread pattern. Building on that foundation, we are now comparing infection across substrates that mimic the stiffness of healthy and fibrotic lung tissue, specifically 10, 65, and 240 kPa polydimethylsiloxane (PDMS) matrices. This approach allows us to probe whether a stiffer or softer environment shifts viral replication rates or alters cell behavior after infection. In parallel, we are exploring the contribution of mechanosensitive ion channels, including TRPV4 and TRPC6, which may act as molecular "translators," converting physical strain into biochemical signals through calcium flux. Taken together, these experiments aim to reveal how mechanical stress, a defining feature of lung physiology, affects viral replication efficiency and host response. We will present data characterizing VSV replication kinetics under these varying mechanical conditions and discuss how these results will clarify how the physical microenvironment modulates viral replication

efficiency, offering new insight into how tissue stiffness in fibrotic lungs could alter susceptibility to respiratory viruses.

Poster 94 • DNA Methylation Variation and Demethylation Effects in Rotifers

Alford, Andrew and Rodriguez, Fernando (Rochester Institute of Technology)

Abstract: Bdelloids rotifers (phylum Rotifera) are microscopic microinvertebrates able to survive extreme environmental stressors such as desiccation for long periods of time and ionizing radiation. The bdelloid class is well known for their lack of sexual reproduction (no males have been described and females produce parthenogenic eggs). Rotifers live in limnoterrestrial environments and commonly feed on microalgae, bacteria and microparticulates. Bdelloid rotifer species are also known for their ability to collect foreign DNA in these environments from other organisms through Horizontal Gene Transfer (HGT). Recent bdelloid rotifer genome annotation has shown that 8-10% of their genes originated from non-metazoan (predominantly bacterial) sources. HGT has also allowed for Bdelloids to uptake genetic information to encode for the enzyme N4-Cytosine Methyltransferase, an horizontally transferred enzyme of bacterial origin, responsible for the addition of 4mC marks to DNA in bdelloid rotifers. DNA methylation is a crucial part of the epigenetic regulation, allowing for the activation or deactivation of genes. Knowing which genes are activated and deactivated using this process and why could help us better understand how genes are regulated in the environment. This study includes three bdelloid species: laboratory strains of *Adineta vaga* and *Adineta ricciae*, and environmental *Rotaria* sp., as well as one monogonont environmental *Lepadella* sp. Clonal cultures of laboratory-cultured strains and environmentally collected samples will be procured to compare low and highly methylated sites within rotifer species. Our research aims to investigate changes in DNA methylation in both laboratory-cultured strains and environmentally collected samples, examine how these methylation changes can affect fitness, and compare the methylation responses between lab strains and environmental samples. DNA methylation levels will be assessed using methylation-dependent endonucleases, which cut DNA based on whether specific sites are methylated or unmethylated. Cultures treated with demethylation agents (5-aza-2'-deoxycytidine, sinefungin) will also be observed and tested using modification-dependent endonucleases. We expect to find changes in variation between laboratory-cultured and environmentally collected rotifers, as well as a change in fitness within rotifer species based on changes in variation of methylated DNA.

Poster 95 • Impact of the DNA Methylation Inhibitor CM-272 on *Escherichia coli* Growth and Morphology

Funk, Abigail; Militello, Kevin and Hutchison, Elizabeth (SUNY Geneseo)

Abstract: The goal of this project is to determine how CM-272, a DNA methyltransferase inhibitor, impacts bacterial physiology. Although experiments indicate that CM-272 does not block DNA methylation in *Escherichia coli*, CM-272 unexpectedly has antibacterial activity. To further characterize its antibacterial activity, bacterial growth curve experiments were performed in the absence and presence of CM-272. Bacterial cell numbers were quantified by A600 readings, and indicate CM-272 blocks *E. coli* growth. At various points in the bacterial growth phase, bacteria were observed via phase contrast microscopy at 1000x magnification. Images were captured through the microscope and the lengths of one hundred cells were measured on ImageJ. At logarithmic phase, the cells grown in the absence and presence of CM-272 were similar in length. Preliminary experiments indicate that bacteria grown to stationary phase in the presence of CM-272 are longer, suggesting that CM-272 blocks cell division. Future experiments will be designed to elucidate the exact mechanism by which CM-272 blocks bacterial cell division.

Poster 96 • An Undergraduate Laboratory to Detect MHC Class Ia Gene Expression in *Xenopus laevis* Cell Lines

Dibble, Olivia M.; Lasher, Alexis; Slimak, Cole and Nedelkovska, Hristina (Nazareth University)

Abstract: Understanding gene expression is essential in the study of genetics and molecular biology. One of the important components of molecular biology that students often struggle with is the central dogma, the direct flow of genetic information from DNA to RNA to protein. To better understand these concepts, we developed an undergraduate laboratory activity that demonstrates differential gene expression of a specific gene, Major Histocompatibility Complex Class Ia gene (MHC class Ia). The activity uses two *Xenopus laevis* cell lines; the A6 kidney cell line, which expresses MHC class Ia, and the B3B7 tumorigenic cell line, which does not express this gene. Students will gain experience in extracting DNA and RNA from the cell lines, synthesizing cDNA, and performing PCR/RT-PCR reactions. Students will also perform gel electrophoresis to analyze their PCR products. In doing so, students will be able to interpret that although all *Xenopus laevis* cells contain the same genes in their genome, not all cells express the same genes. Student learning will be evaluated through pre- and post-activity questions to determine if learning objectives are achieved.

Poster 97 • Long Term Study of the Use of Test-Taking Behavior as an Indicator of Self-Efficacy in an Introductory Biology Undergraduate Course

Frank, Olivia and Cursino, Luciana (Keuka College)

Abstract: Historically, studies on self-efficacy, a student's confidence to successfully perform a task, rely on self-reporting questionnaires and surveying instruments to acquire data that later are used for result assessment. Our work focused on using test-taking behavior as an indicator of self-efficacy as the test content confidence and its correlation with student's course success. Long-term student data (n=274) was acquired between 2018 and 2024 in a first semester Introductory Biology course taught by the same instructor at a small rural liberal arts college in upstate New York. Here we assessed the student's ability to answer the same questions across 4 exams and correlated the data with their course's performance. Students that had not completed all 4 exams were excluded and a final sample size of n=258 was obtained. We also evaluated 4 socio-demographic characteristics of the participants and the pre- and post- pandemic impact. Statistical analyses are currently underway.

Poster 98 • Biology Beyond Medicine: Guiding Pre-Med Students Towards Fulfilling Careers in Healthcare and Science

Garbarini, Karissa (University at Buffalo); Tripoli, Marissa (University at Buffalo); Gonzalez, Roxana (University at Buffalo); Loyola Irizarry, Héctor G. (Florida International University); Uzcátegui, Mia (Ohio State University); Benabentos, Rocio (Florida International University); Liberles, Jessica (Florida International University) and McCartney, Melissa (University at Buffalo)

Abstract: Around 70% of undergraduate biology students are pursuing medical school, a highly competitive pursuit with an average acceptance rate of ~45% (AAMC, 2024). Whether students who are not accepted into medical school persist in the STEM workforce is unknown. We are guided by the following research questions: 1) How are undergraduate biology students currently preparing for their career goals? and 2) How can we provide effective, realistic, and targeted career guidance for undergraduate biology students? Grounded in Social Cognitive Career Theory (SCCT), we analyzed responses from undergraduate biology students at a public R1 institution (n=1,161) using assessments on career goals, career development strategies, and science identity. Additional data included students' likelihood to learn about additional biomedical careers and likelihood to change their career goal (1-6 point Likert, high score of 6). Since GPA

is a strong predictor of medical school matriculation, we grouped students based on career goals and GPA, as it relates to their likelihood of matriculating into medical school. Around 50% of our students are in the medium and low GPA categories. The percentage of students participating in most career development strategies decrease as GPA decreases. Most students are willing to learn about additional careers, and not many are likely to change their goals. About 50% of all students have a secondary career goal. Since medical school admissions have shifted towards a holistic application, we discuss ways that students can improve their application through career development strategies. Our data will open a dialogue on providing effective and realistic career guidance for undergraduate biology students. We focus on how current educators and advisors can provide pre-health and pre-med students with career advising based on their current career development trends and the recent shift to holistic medical school applications. We invest heavily in these students and have a responsibility to guide them to attainable careers, as there are many ways to contribute to the STEM workforce.

Poster 99 • Child Maltreatment and Bipolar and Depressive Symptomatology in Young Adulthood: The Moderating Role of Maternal Attachment

Burkle, Jeannette; Johnson, Morgan R; Pabon, Briana and Schenkel, Lindsay S. (Rochester Institute of Technology)

Abstract: The aim of the present study was to explore the role of maternal attachment as a potential risk or protective factor in the relationship between Child Maltreatment (CM) and depressive and bipolar symptomatology in a sample of young adults. Participants (N=291) were college students who completed Childhood Trauma Questionnaire (CTQ), the General Behavior Inventory (GBI), and an abbreviated version of the Inventory of Parent and Peer Attachment (IPPA). CM severity, as measured by the CTQ, was significantly correlated with greater depressive and bipolar symptoms on the GBI, and negatively associated with more secure maternal attachment on the IPPA. In addition, more secure attachment on the IPPA was associated with lower depression and bipolar symptoms ($p < .001$). Two separate regression analyses were conducted to determine whether maternal attachment was a significant moderator between CM and depressive and bipolar symptoms. For depressive symptoms, results indicated significant main effects for sex (covariate) ($\beta = -0.15$, $p < .05$), CM ($\beta = 0.14$, $p < .05$), and for attachment ($\beta = -0.28$, $p < .001$), such that being female, and reporting more severe CM and poorer maternal attachment, were all related to greater depressive symptoms. A significant interaction was found between CM and maternal attachment ($\beta = -0.12$, $p < .05$). Using simple slopes analyses to probe the interaction, results indicated that CM severity was significantly associated with depressive symptoms in college students with low maternal attachment ($\beta = 0.21$, $p < .001$), but was not associated with depressive symptoms among those with high maternal attachment ($\beta = 0.07$, $p = .43$). For bipolar symptoms, there was also a significant main effect for attachment ($\beta = -0.16$, $p < .05$), indicating that lower maternal attachment was associated with greater bipolar symptomatology. There was also a significant interaction between CM and maternal attachment ($\beta = -0.17$, $p < .01$). Simple slopes tests indicated that CM severity was significantly associated with bipolar symptoms among participants with low maternal attachment ($\beta = 0.18$, $p < .01$), but was not significantly associated with bipolar symptoms among those with high maternal attachment ($\beta = -0.02$, $p = .87$) or at mean values of the interaction term ($\beta = 0.08$, $p = .25$). These findings highlight the importance of secure maternal relationships as an important protective factor in the development of depressive and bipolar symptoms among emerging adults with histories of CM.

Poster 100 • The Role of Black Seed Oil (Thymoquinone) on Repetitive Behavior and Neuroinflammation in Spinning Mice

Biondi, Ashley and Bechard, Allison (SUNY Geneseo)

Abstract: Repetitive behavior is defined as repetitive actions with no purpose and is a common characteristic of Autism Spectrum Disorder (ASD). Our goal is to assess whether environmental interventions can reduce repetitive behaviors in mice. Previous research has shown that a Ketogenic Diet (KD) effectively reduces repetitive behaviors in mice, potentially due to its anti-inflammatory properties. Neuroinflammation offers a link between diet and ASD and other disorders. In a convergent approach, this study uses another known anti-inflammatory, Thymoquinone (TQ), to reduce repetitive behaviors. TQ, the main component in black seed oil, has traditionally been used as an anti-inflammatory, antimicrobial, and antioxidant. Prior literature indicated that TQ has positive effects on neurological problems such as epilepsy, Parkinsonism, anxiety, and improvements in learning and memory. If TQ successfully reduces repetitive behaviors, it will provide insight into novel therapeutic remedies for conditions exacerbated by neuroinflammation, such as repetitive behaviors in ASD.

Poster 101 • Military Veterans, PTSD, and Psychedelics

Ophelia, Corrina (SUNY Geneseo)

Abstract: This research project qualitatively explores veterans' motivations for seeking out and their perceptions of psychedelics as a healing method. Veterans of the post 9/11 wars often face significant health challenges, including treatment-resistant posttraumatic stress (PTSD), depression, addiction, and more. Many veterans find tremendous value in psychedelic treatments, usually accessing the substances illicitly or out of the country due to strict regulations within the U.S. Due to their unique biopolitical status and cultural positionality, veterans' use of psychedelics raises interesting questions around healthcare and healing: Why are veterans, who have access to low-cost VA healthcare, seeking out potentially expensive and illicit psychedelic treatments? How do they perceive those experiences? Here, I approach these questions by engaging anthropological theory on biopolitics and healing and through a systematic content analysis, in-depth interviews with veterans, and ethnographic fieldwork.

Poster 102 • New studies in the Los Monos, Iquiri, and Itacua formations, Chaco Basin, Bermejo (Lajas) section, Devonian, District of Santa Cruz, Bolivia

Britt, Ryan; Gilfus, Ethan; McCarthy, James and Over, D. Jeffrey (SUNY Geneseo); Gilleaudeau, Geoffrey J. (George Mason University); Ramirez, Mariano and Strandberg, Bastian (Kobenhavns Universitet); Ortiz, José Luis and Riglos, Mario Suarez (Museo Noel Kempff Mercado); Farjat, Alejandra Dalenz; Segessenman, Daniel and Nana Yobo, Lucien (Texas A&M University)

Abstract: In the tropical to sub-tropical epeiric seas of North America and Europe, the Devonian-Carboniferous transition is recorded by metal- and organic-rich transgressive black shales corresponding to the Hangenberg mass extinction event overlain directly by coarser-grained, organic-poor strata deposited during eustatic lowstand, marking a major climatic shift at the onset of the Late Paleozoic Ice Age. Little is known, however, about this key transition of extinction and glaciation at high paleo-latitudes, which would be expected to respond earlier than equatorial basins to a cooling climate. Here, we investigate dark gray and black shale of the Los Monos and Iquiri formations overlain by glacial diamictites of the Itacua Formation in the Chaco Basin of southcentral Bolivia, collected in the Bermejo (Lajas) section. Preliminary observations and magnetic susceptibility (MS) results from the Iquiri-Itacua transition show decimeter- and meter-scale cyclic patterns in the silty gray shales, while clay-rich black shales, presumably deposited farther offshore, have remarkably uniform MS values. The overall MS values in the shales and

diamictites are positive, similar to values from the Pando X-1 core from similar age strata in northern Bolivia. This is in contrast to Upper Devonian black shale strata in Alberta and Oklahoma which are generally negative, approximately 1 to 1.5 lower in δMS values, indicating distinct sediment sources and local climatic conditions between these equatorial and high-latitude sites. Black shale of the Iquiri Formation contains numerous dropstones indicative of sea ice prior to the Devonian-Carboniferous boundary. A tephra bed in the upper Los Monos Formation yielded numerous zircons which, when dated, may better resolve the absolute age of the formation. Future work will involve high-resolution redox geochemistry of Iquiri Formation black shales, as well as Re-Os geochronology to determine if the Iquiri-Itacua transition is equivalent to the Hangenberg Event as recorded in North America and Europe.

Poster 103 • Preliminary Paleomagnetic Analysis of a Diabase Dike in the Scottsville Basin, VA

Rayburn, Chloe; Salter, Rory and Giorgis, Scott (SUNY Geneseo)

Abstract: The Scottsville Basin, located near Scottsville and just south of Charlottesville, Virginia, is a Mesozoic-aged half graben formed during the breakup of Pangea and the opening of the Atlantic Ocean. This study focuses on a diabase dike exposed within the basin. Fieldwork consisted of drilling approximately 30 1-inch long core samples from an outcrop and orienting each core using Brunton compass and a sun compass. In the lab, remanent magnetization was measured using an AGICO JR6A Spinner Magnetometer. Stepwise thermal demagnetization was conducted in a Schonstedt TSD-1 oven, revealing two distinct magnetization components. The low-temperature component was removed by 400°C. The high-temperature component persisted from 400-600°C and was interpreted as the thermal remanent magnetization. The thermal remanent magnetization exhibits a consistent east-northeast declination and moderate negative inclination ($N = 13/15$, $D = 73^\circ$, $I = -42^\circ$, $k = 24$, $\alpha_{95} = 8.7$). The negative inclination suggests emplacement during a period of reversed geomagnetic polarity. The declination implies $\sim 90^\circ$ of clockwise rotation post-emplacement, although alternative explanations include systematic orientation errors or sampling of a displaced outcrop.

Poster 104 • Dacryoconarids from the Genundewa Limestone, Frasnian (Upper Devonian), western New York

Johnson, Emma E.; Linne, Allison K.; Magerle, Kaitlyn P.; McAneney, Liam T.; Rayburn, Chloe; Salter, Rory; Strong, Colleen R.; Gilfus, Ethan; McCarthy, James and Over, D. Jeffrey (SUNY Geneseo)

Abstract: The Genundewa Limestone, "The Styliolina Limestone" of (Grabau 1898-1899) is a 30-50 cm thick carbonate bed between the Penn Yan and West River formations of the Genesee Group that outcrops from the shores of Lake Erie to the western Finger Lakes of western New York State. The Genundewa Limestone consists almost entirely of current aligned dacryoconarids that represent a winnowing of fine clastic material and concentration of pelagic shelly fossils, interpreted as a very offshore accumulation during a deepening phase in the Appalachian Basin. The dominant taxon is *Styliolina*, also recovered were *Nowakia*, *Striatostyliolina*, and *Viriatella*. There were no significant differences between taxa from the western or more offshore samples collected along Eighteenmile Creek and the eastern or more shoreward samples collected in the Genesee River Valley.

Poster 105 • Dinosaur Soft Tissue and the Issues with Shrink Wrapping

Boufford, Matthew (Sutherland High School, Pittsford, NY)

Abstract: Shrink wrapping is the act of reconstructing extinct fauna without taking into account the presence of soft tissues such as feathers, fat, skin flaps, and other features. When reconstructing extinct fauna, it is vital to ensure that soft tissues are accounted for; otherwise, we risk misrepresenting what these animals truly looked like. Shrink wrapping makes paleo reconstructions of animals look diseased, malnourished, or even dead. Shrink wrapping is considered to be a recent occurrence, as early paleo artists (whilst not very accurate) gave dinosaurs bulk and accounted for soft tissues in their representations. Only come the 1970s did shrink wrapping gain traction as a viable way of reconstructing dinosaurs, as supporting the osteological information contained in the fossils. Examples of living animals with distinct soft tissue features are numerous: in bighorn sheep, the horns of the animal are covered in a keratinous sheath, protecting the bone from the blunt force trauma of slamming into other bighorn rams. A similar keratinous sheath may have existed on many dinosaurs such as members of *Megalocephalia*, the group including ceratopsians and pachycephalosaurians. In addition, despite none of the dinosaurs' relatives—birds and crocodiles—having lips, scientists still believe that dinosaurs, specifically theropods, had lips. The evidence for such lips is seen in anatomical similarities between species such as *Tyrannosaurus rex* and lipped lizards. The presence in dinosaurs of some soft tissues is harder to demonstrate: wattles similar to modern-day turkeys, or sails and frills like the ones seen on crested newts; camouflage-based protrusions like in tasseled wobbegongs or in stick bugs; and the presence of quills and feathers has not been proven in all genera of dinosaurs. Understanding soft tissue depictions depends on finding imprints, wear on bone and attachment points, modern animal behavior, and anatomical comparison.

Poster 106 • Describing Freshwater Temporal Acoustic Patterns of Western NY

Tessier, Anna and Hannam, Kristi (SUNY Geneseo)

Abstract: Freshwater acoustic ecology is a very understudied branch of biology which we chose to focus on this Summer by recording in 6 ponds throughout Geneseo. We recorded across three different sites in each pond over four day time intervals beginning in June and ending in August. We are interested in comparisons between day and night, one pond vs. another overtime, and between different locations in one pond. We are using the Acoustic Diversity Index, the Normalized Difference Soundscape Index, and the Bioacoustic Index to analyze the data to answer these questions. Our initial data analysis using R studio for the Acoustic Diversity Index, showed no significant results when comparing sites A, B, and C at Indian Fort Pond during day or night, as well as no significant results when comparing site A across all ponds over the entire recording season for day or night. We will continue data analysis work to address more of our research questions in the future. Our ultimate aim is to be able to identify water quality based on changes in diversity of a soundscape over time.

Poster 107 • Identifying Coleopteran Vocalizations in a Western New York Pond

Tucci, Maya; Hicks, John and Rumsey, Caroline (SUNY Geneseo)

Abstract: The field of bioacoustics is still relatively new and methods for analyzing ecosystem health through soundscapes are constantly evolving. Within the field, freshwater soundscapes are particularly understudied. A large body of research supports the use of freshwater insect assemblages as indicators of disturbance and pollution extent. The shifts in insect species richness and diversity that accompany changes in these abiotic factors have been documented mostly through observational research methods. Soundscape analysis provides an

alternative, minimally-obtrusive angle for studying these phenomena. As more and more insect species are recorded, both on-site and in isolation, we gain the ability to determine community composition and diversity. By extension, we become able to gauge the state of the environment in its totality. Acoustic indices are widely used in the field, and help with making general assessments of terrestrial soundscapes, but have limitations for freshwater soundscapes. Expanding the limited library of aquatic insect species-level acoustic descriptions allows for more local and specific assessments of freshwater ecosystem health from underwater recordings. In an effort to contribute to the still-underdeveloped body of freshwater insect acoustic data, we collected multiple insect species from local ponds and obtained several days' worth of isolated recordings in the summer and fall of 2025. These include several species of Coleopterans, Hemipterans, and Odonates. At this point, we have pinpointed vocalizations of different types from one Coleopteran species. We continue to analyze their vocalization patterns with the goal of providing species-level resources for machine learning and/or general public use.

Poster 108 • Stream Water Quality in Wyoming County, New York: A Comparison of Trends by Watershed

Kenney, Ciarán and Yang, Suann (SUNY Geneseo)

Abstract: Wyoming County, New York lies on the boundary between the Lake Ontario and Lake Erie watersheds, and contains small headwater streams for both lakes. We examined existing water quality data for the county and found that on average, water quality remained relatively stable, with few issues of concern. However, we identified clear differences between the two watersheds, with water quality being consistently better in the western (Lake Erie) watershed than in the eastern (Lake Ontario). Data indicates that bank vegetation has been declining slowly on the eastern side of the county over the past fifteen years, while remaining unchanged on the western side. Along with this slow decline, we see significantly higher pollution levels, higher pollution tolerance among macroinvertebrate communities, and slightly lower oxygen levels in the eastern streams than in the western. As the eastern side of the county contains much more densely settled land and heavier agricultural use than the western side, these results are consistent with the interpretation that human land use on the eastern side of the county is slowly but steadily degrading local stream quality. If left unchecked in the long term, this has concerning implications for both the eastern streams in their own right, and the larger system into which they flow.

Poster 109 • A Low-Cost, Automated, and Adaptable System for Field-Based Measurement of pCO₂, pCH₄, and Associated Variables in Groundwater

Every, Madeline M.; Dugan, Jesse T. and Kessler, John D. (University of Rochester)

Abstract: Groundwater plays a crucial role in the global carbon cycle, acting as a sink and a point of emission at groundwater-surface water interfaces. Groundwater is generally viewed as a stable and slow changing aquatic environment relative to surface water, though active sources and sinks of carbon dioxide (CO₂) and methane (CH₄) can lead to significant variability in their dissolved concentrations on timescales ranging from hours to seasons. The system presented here reduces the need for discrete sampling of groundwater and expands the spatial and temporal scales possible in field study, so the variables controlling environmental processes can be uncovered. The Groundwater Automated Chemical Examiner (GrACE) is an automated analytical system of integrated sensors for the field-based measurement of chemical and physical properties of groundwater. The GrACE system uses open-source code and low-cost, low-power 5V sensors, several of which are “plug-and-play”, enabling (i) modifications to the design presented here for changing experimental conditions and (ii) deployments in remote locations lasting weeks-to-months using solar powered batteries so both short-term (hours-to-days) and longer-term

processes can be explored. The GrACE system was designed to explore parameters influencing $p\text{CO}_2$ and $p\text{CH}_4$ in groundwater, incorporating one of two equilibrators designs (a Weiss style equilibrator and a groundwater well) to measure dissolved gas partial pressures passively and non-destructively. The $p\text{CO}_2$ sensor has an operating range of 200-100,000 μatm with an accuracy and precision of 17% and 27.5%, respectively, while the $p\text{CH}_4$ sensor has a range of 800-8,000 μatm and an accuracy and precision of 3% and 3.2%, respectively, over a month-long measurement campaign without recalibration. The e-folding response times to changes in $p\text{CO}_2$ and $p\text{CH}_4$ are 41.7-50.3 sec and 103-173 sec, respectively. Field trials using the GrACE system found fluctuations in CO_2 and CH_4 concentrations of over 1270 $\mu\text{mol/L}$ and 12 $\mu\text{mol/L}$, respectively, in a 24-hour period strongly correlated with variability in groundwater volume. These results reveal that the response times of the analytical system are >30 times shorter than short-term environmental variations measured. Complementary measurements of water temperature, electrical conductivity (EC), pH, turbidity, water depth, and dissolved oxygen ($p\text{O}_2$) are also conducted by the GrACE system.

Poster 111 • Generalization May be Common Between Insect Parasites and Their Fruiting Plant Hosts in Forested Communities

Miller, Nolan and Yang, Suann (SUNY Geneseo)

The interactions between species in ecological communities can have a wide range of negative and positive impacts for the species involved. Both invasive species and parasites are examples of organisms that negatively affect other species. In this research I have been studying the relationship between parasitic insects and both indigenous and invasive non-indigenous plant species within forest communities in Western New York. When a parasitic insect lays its eggs on a host plant's berry, the larvae that emerge enter the berry to eat and grow before dropping to the ground to develop into adults. Some insect species may parasitize both cultivated and forest plants, while others may specialize on a small number of species. In these forests, interacting plants and insects may be either invasive or indigenous. Identifying the plant and insect species involved in these host-parasite relationships allows us to assess both the level of specialization in forest communities and the potential role of these interactions in the population growth or decline of invasive species. This research has implications not only for understanding natural plant populations but also for informing pest management on farms, where insect parasites such as spotted wing drosophila can cause significant crop loss. The purpose of this project is to identify insect parasites to the genus or species level using DNA barcoding techniques. These results will allow me to evaluate how specialized certain insect species are and determine the proportion of host-parasite interactions involving invasive species. Along with a previous member of this project, I have been quantifying the incidence of parasitism by mapping host plant species, collecting fruit, and identifying insect larvae to the order level. Most larvae were found in one plant species, Glossy Buckthorn, which hosted all three identified insect orders. Diptera appeared to be more generalized in their plant associations than Lepidoptera or Coleoptera. I plan to build on these results by using DNA barcoding to identify larvae to the species level. Funding for this project will support the necessary supplies for DNA extraction and amplification. This work will contribute to our understanding of species interactions in forest ecosystems and provide valuable experience that supports my goal of becoming a research scientist.

Poster 112 • Cavity-Nesting Bees and Wasps: Patterns in Phenology and Habitat Use

Lingenfelter, Julia; Stang, Sophia J.; Wick, Carly and Apple, Jennifer L. (SUNY Geneseo)

Abstract: Cavity-nesting bees and wasps lay eggs in hollow stems or other pre-made cavities to provision their larvae with food to then overwinter until their emergence in spring. To observe the nesting patterns of these insects, we placed nesting boxes containing "bee tubes" made of hollow

reeds in five locations around the SUNY Geneseo campus. This summer, we added eight new nesting boxes in various locations in the Island Preserve, a 57-acre local nature preserve of native grasslands, wet meadow, and woodland. We photographed the tubes once a week throughout the summer and early fall as the cavities were gradually sealed off by insects to form larval cells. We took note of the type of material used to fill the tubes and analyzed the trends in phenology and site preferences of different occupants using the photographic record. This summer we began performing plant surveys near the bee boxes to potentially determine the influence of blooming vegetation on cavity-nesting species. The dissections of the bee tubes in the spring of 2024 and 2025 allowed us to identify immature occupants based on their morphology and materials used to provision the young. We kept some specimens as vouchers for identification to the species level, and we released the rest. This process will be repeated in 2026 for the bee tubes we photographed this summer. Some of the more commonly observed bee taxa from tubes colonized in 2023 include leafcutter bees *Megachile pugnata*, *M. rotundata*, *M. relativa*, and the mason bee, *Osmia caerulea*. We also observed wasp taxa including the grass-carrying wasp, *Isodontia mexicana*, the spider-hunting wasp *Trypoxylon lactitarse*, and potter wasps *Ancistrocerus capra*, *A. spinolae*, and *Euodynerus foraminatus*. Identifications of 2024 tube occupants are underway. In this study we connect the identities of occupants to the cavity fill type, site preferences, and timing of occupation. We will also compare data trends across years and under different ecological conditions. This information gives us a better understanding of our local native bee and wasp ecology and the conservation efforts necessary to support their populations.

Poster 113 • Developing Behavioral Assays to Assess Personality in the Ant-Mimicking Spider, *Myrmarachne formicaria*

White, Emily M.; Bleier, Sierra A. and Apple, Jennifer L. (SUNY Geneseo)

Abstract: The ant-mimicking spider, *Myrmarachne formicaria* (Salticidae), was introduced to North America from Eurasia over 25 years ago. *M. formicaria* has behavior and morphology that are incredibly similar to ants, including body shape, gait, and lifting of its front legs to mimic an ant's antennae. Our study aims to determine if *M. formicaria* exhibit repeatable behaviors that differ between individuals that can be categorized as personality. To explore this, we are performing several assays for assessing aspects of personality. One behavioral assay we are using to examine boldness is a closed arena trial in which the path of *M. formicaria* is tracked using AnimalTA software to record the time spent at the outside of the arena and at the inside of the arena, with the expectation that bolder spiders will spend more time at the inside. We also measure the time *M. formicaria* takes to leave a safe shelter in the arena after acclimation, with the expectation that more exploratory spiders will leave the shelter sooner. The third assay we plan on using is the amount of time spent displaying in front of a mirror, an action meant to appear more threatening or attract mates, with the expectation that more aggressive spiders spend more time displaying. In the future, we will perform two trials of each assay per individual to determine the statistical repeatability of the results, which will indicate if *M. formicaria* exhibits consistent personality traits. The results of the three assays will be compared to see if individuals show consistency in personality across all tests. These traits may contribute to the outcomes of interactions between individuals, such as male-male confrontations or courtship displays.

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