

**Proceedings of the 2026 Annual Meeting
of the
Oregon Academy of Science**

hosted by

**Western Oregon University
Monmouth, Oregon**

on

Saturday, February 28th, 2026

Meeting Schedule & Highlights

- 8:00-9:00** **Registration:** basement lobby of Werner University Center (WUC)
Continental Breakfast: Pacific Room in the WUC
Poster set up: Lobby and the Columbia Room in the WUC
- 9:00-10:15** **Poster Session & Graduate School Fair**
Location: Columbia Room in the WUC
[Biology](#) (32)
[Chemistry](#) (21)
[Geography](#) (1)
[Health Science & Kinesiology](#) (1)
[Mathematics, Computer Science & Statistics](#) (1)
[Physics](#) (3)
[STEM Education](#) (2)
- 10:15-10:30** **Poster Take-Down and Transition**
- 10:30-12:00** **Awards Ceremony and Plenary Presentation**
Outstanding Educator: Higher Education - Margaret D. Haak
Outstanding Oregon Scientist - Elisar Barbar, PhD (Plenary Speaker)
Beyond the Fold: The Surprising Superpowers of Disordered Proteins
- 12:00-1:00** **Lunch:** Pacific Room in the WUC
- 1:00-1:15** **Transition and speakers check in with moderator**
- 1:15-3:00** **Oral Presentations**
Locations: Richard Woodcock Education Center (RWEC)
RWEC 102: [Molecular, Genetic & Genomic Mechanisms](#) (5)
RWEC 104: [Evolution, Paleobiology & Comparative Biology](#) (4)
RWEC 105: [Ecology, Biodiversity & Environmental Systems](#) (4)
RWEC 106: [Organismal Biology & Physiology](#) (4)
RWEC 107: [Chemistry](#) (4)
RWEC 207: [Physics, Mathematics, Computer Science & Statistics](#) (3)

Important Information

- [Poster and Oral presentation requirement](#)
- [Campus Map & Conference Center Map & WiFi Instructions](#)
- [OAS Leadership Team](#)

Presentation Requirements

Poster Presentations

Poster dimensions must not exceed **104 cm (41 inches) in height** and **145 cm (57 inches) in width**, and posters should be prepared in **landscape orientation**.

During the poster session, presenters will divide their time as follows:

- Students with **odd-numbered posters** should stand by their posters and be prepared to present during the **first half** of the session.
- Students with **even-numbered posters** should stand by their posters and present during the **second half** of the session.

An announcement will be made at the midpoint of the session to signal when presenters should switch. This structure ensures that all presenters have dedicated time to share their work while also allowing time to view other posters.

Oral Presentation Instructions

Presentation Length

Each oral presentation is allotted **15 minutes**, followed by **5 minutes for audience questions**. Presenters should plan their remarks carefully to remain within the 15-minute limit. Session moderators will keep time to ensure the schedule is maintained.

Arrival & Check-In

Presenters must arrive in their designated classroom **at least 15 minutes prior** to the start of their session. This time should be used to check in with the session moderator, upload your presentation, and test any audiovisual equipment.

Presentation Files

Presenters should bring their presentation on a **USB flash drive (jump drive)** or in a format that can be downloaded (e.g., from email or cloud storage), but you are responsible for ensuring reliable access. Bringing a backup copy in PDF format is strongly recommended.

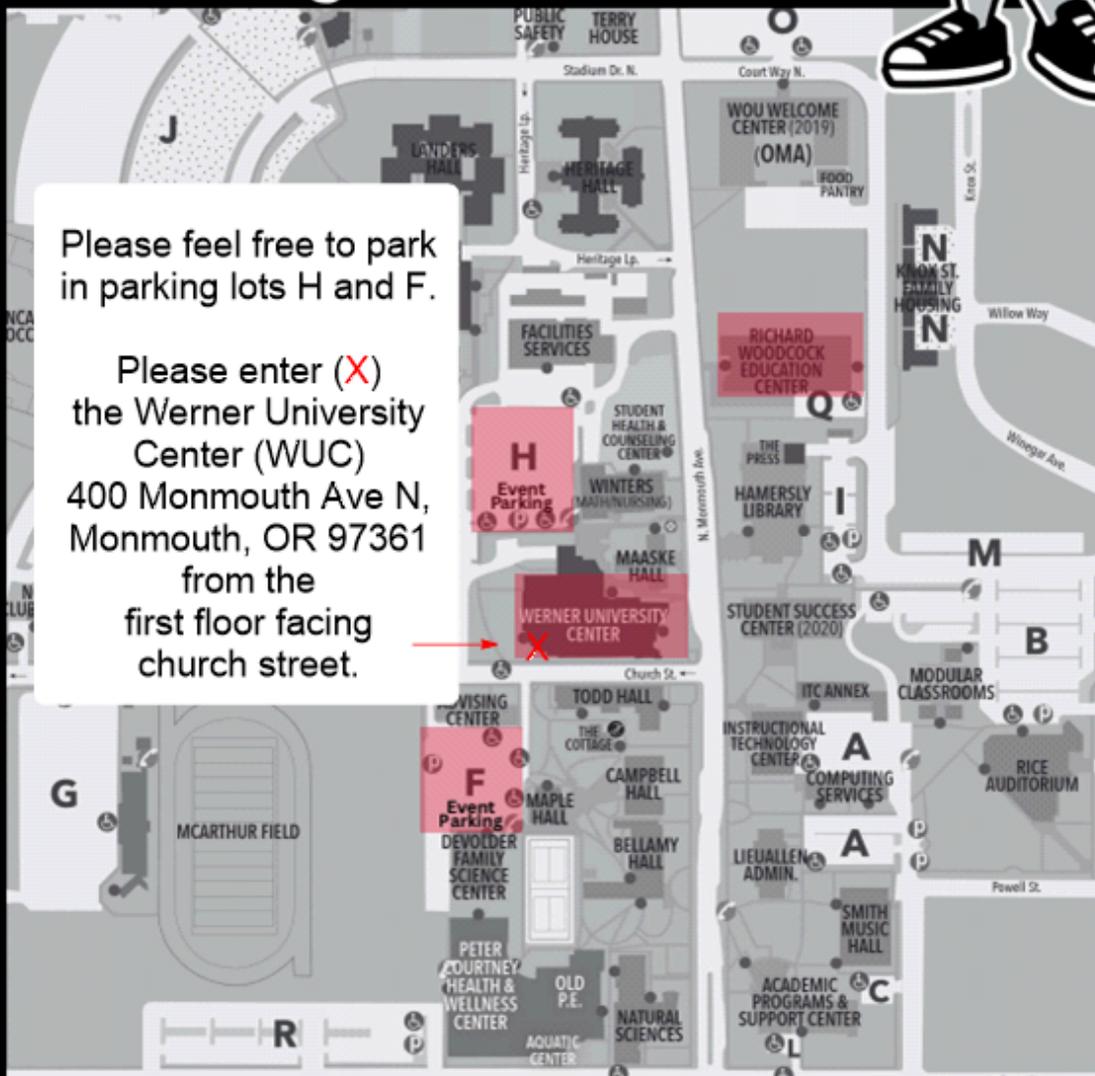
Campus Map

Oregon Academy of Science Conference Map February 28th 2026



Please feel free to park in parking lots H and F.

Please enter (X) the Werner University Center (WUC) 400 Monmouth Ave N, Monmouth, OR 97361 from the first floor facing church street.



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Conference Center Map & WiFi Instructions

Werner University Center Conference Map



How to connect to WOU guest Wi-Fi

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1. Connect to the Wi-Fi network named "wou-guest-open."
2. Once connected, a form will open for you to complete. Fill out the form with the necessary information.
3. After submitting the form, you will receive a username and password via both email and text message.
4. Use the provided username and password to log in to the wi-fi network.

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**Western Oregon
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DESCHUTES LOUNGE	202
KLAMATH ROOM	213
LITTLE D ROOM	136
METOLIUS ROOM	211A
NORTH SANTIAM ROOM	135
PACIFIC ROOM	101
ROGUE ROOM	132
OCHOCO ROOM	131
SOUTH SANTIAM ROOM	133
WILLAMETTE ROOM	214



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Awards & Plenary Presentation

2026 Outstanding Educator- Higher Education:

Margaret D. Haak



Margie Haak has dedicated more than three decades to excellence in chemistry education at Oregon State University. Since joining the Department of Chemistry in 1993, she has played a pivotal role in shaping introductory chemistry instruction, driven by a deep commitment to supporting first-year students as they develop confidence and curiosity in the chemical sciences. Her influence extends across generations of students and has helped define how chemistry is taught at OSU.

A leader in educational innovation, Margie was an early adopter of electronic homework systems, the “Atoms First” curriculum sequence, and active-learning classroom models, all of which have led to measurable improvements in student learning outcomes. She is also the long-time director of *The Mole Hole*, OSU’s chemistry tutoring and collaborative learning center, which now serves students across multiple chemistry disciplines and continues to expand access through increased hours and remote support. Beyond campus, Margie has demonstrated a sustained commitment to STEM outreach through her leadership of Family Science & Engineering Nights, bringing hands-on science experiences to elementary schools across Oregon. Her career reflects an enduring dedication to teaching, mentorship, and broadening access to high-quality science education

2026 Oregon Academy of Science Outstanding Oregon Scientist and Plenary Speaker:

Elisar Barbar, PhD



Seminar: Beyond the Fold: The Surprising Superpowers of Disordered Proteins

Dr. **Elisar Barbar** is an internationally recognized leader in biophysics whose career exemplifies scientific rigor, innovation, and transformative mentorship. As a faculty member and Department Head in the Oregon State University Department of Biochemistry and Biophysics, she has built a highly impactful research program focused on intrinsically disordered proteins (IDPs), a challenging class of proteins that comprise nearly 40% of human genes and play critical roles in health and disease. Guided by her motto, “Insist, Persist, Take Risks,” Dr. Barbar has advanced fundamental understanding of protein–protein interactions, particularly in the dynein motor complex and the LC8 hub protein, and contributed to antiviral research including structural studies of SARS-CoV-2 proteins. Her scholarship includes 100 peer-reviewed publications, sustained federal funding totaling approximately \$14 million, and numerous invited lectures worldwide. Among her most significant achievements was leading a decade-long, statewide effort to secure NIH funding for an 800 MHz NMR instrument—now the highest-field NMR facility in the region—dramatically elevating research capacity and visibility across Oregon.

Equally remarkable is Dr. Barbar’s dedication to mentorship, education, and academic leadership. She has trained and inspired more than 100 scientists, including 87 undergraduates, 16 graduate students, and 6 postdoctoral scholars, many of whom have gone on to successful careers in academia, industry, and public service. Her laboratory is known for its inclusive and supportive culture, where students from diverse backgrounds are empowered to thrive. As Department Head, she has strengthened shared research infrastructure, expanded collaborative facilities, led faculty hiring initiatives, and advanced graduate training programs. A tireless advocate for diversity, equity, and inclusion, Dr. Barbar has actively supported the recruitment, retention, and success of underrepresented scholars across the university. Her career reflects not only exceptional scientific accomplishment, but also a deep commitment to building people, programs, and possibilities in science.

Poster Presentations:

Biology Posters

BP-01

Investigating the meiotic role of Bub1 kinase activity in *C. elegans*

Olivia Herning, India Rosario, David Wynne, Ph.D., University of Portland, Portland, OR.

Accurate chromosome segregation is essential for fertility and development, and depends on proper recruitment of the Chromosomal Passenger Complex (CPC) to chromatin. In *C. elegans*, CPC localization is mediated by two parallel pathways: Bub-1-dependent phosphorylation of histone H2A, which recruits Shugoshin (Yamagishi et al., 2010; Tsukahara et al., 2010), and Haspin-dependent phosphorylation of histone H3 at threonine 3 (H3T3ph), which provides a binding site for Survivin. To investigate the contribution of Bub1 kinase activity to CPC recruitment, we used the *bub-1(lt155)* D814N kinase-dead mutant (Moyle et al., 2014) that retains checkpoint function and viability due to Bub1 is pleiotropic functionality. We generated a strain combining *bub-1(lt155)* with an auxin-inducible *hasp-1::AID* allele and assessed viability, male frequency, and H3T3ph localization. Our findings begin to support the model proposed by Macareg et al. (2022), in which Bub-1 contributes to CPC function in meiosis, though Haspin plays a dominant role. Together, these results aim to clarify the relative importance of Bub-1 kinase activity in meiotic versus mitotic germline contexts and contribute to resolving conflicting models of CPC recruitment (Ferrandiz et al., 2018; Hadders et al., 2020; Macareg et al. 2022).

BP-02

Topoisomerase II α is required to maintain proper chromosome segregation in *C. elegans*

Luke Gunnels, Olivia Herning, David Wynne, PhD / University of Portland Department of Biology, Portland, OR. 97203.

In order to ensure proper chromosome segregation, a number of proteins are required to ensure microtubule spindles attach to a centromeric position. Protein kinase Haspin (HASP-1) is one protein that is activated by a SUMOylated version of Topoisomerase II α , which is required to correctly attach microtubules. An AID system – which conditionally degrades a selective protein – was added to a strain of *C. elegans* in both Topoisomerase II α (TOP-2), and Haspin (HASP-1) to observe the loss of function of these proteins. Strains were created which contained both TOP-2 and HASP-1, as well as TOP-2 alone. The AID strains showed a severe loss of function in the created strains, which indicated HASP-1's activation by TOP-2. In the future, point mutations will be made to attempt to find the residues of interaction between both proteins.

BP-03

Game of Clones: Quantifying the Impact of Aggression on Survival in the Wild of *Anthopleura elegantissima*

Riley Bellows, Trinity Chernoff, Kayla Reed, Lacey Winthorn, Samantha Lengsfeld, Z461 Class, Nathan Kirk

Sea anemones are predicted to benefit from global climate change, but little empirical evidence exists to support this claim. Developing more extensive monitoring programs of these animals will help provide a more holistic understanding of how our oceans will be impacted by potentially irreversible warming. The intertidal sea anemone *Anthopleura elegantissima* is a clonal aggregating species found along the west coast of North America, from Alaska to Baja California. These animals reproduce sexually through broadcast spawning, but primarily reproduce asexually through binary fission, subsequently forming colonies of genetically identical individuals. These colonies then aggressively interact with other anemones in a competition for space. While individual interactions quantifying aggression have been studied, it is less understood how aggression affects long-term population size dynamics. To address this deficiency, we started a long-term monitoring program marking the location of 72 colonies in proximity to each other across two separate field sites on the Oregon Coast. Throughout the past three years, we have collected individuals from each colony to determine their aggression through pairwise aggression assays, and have measured how colony sizes change over time using image and video analysis. We hypothesized that increased aggression would lead to increases in colony size in the field. Overall, the population of sea anemones was relatively stable (n=11,960 in 2022 and n=12,277 in 2024), however there were large changes within the colonies themselves; 6 colonies were extirpated in the 2 year period. Aggression did not correlate with colony sizes changing though indicating that other factors influence their population dynamics.

BP-04

Paper-based Affordable Approach to Detection of Serotonin Syndrome

Dulce P Hernandez, Rachel Edwards / Biotechnology Research Laboratory, Oregon Institute of Technology, Klamath Falls, OR, 97601

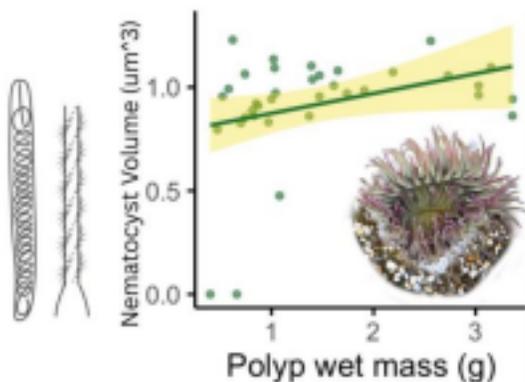
Serotonin syndrome is a life-threatening and underreported condition where poisonous amounts of serotonin are present in your body and there are no known diagnostic methods applicable. Developing a Serotonin Electrochemical Sensor would introduce a definitive test for serotonin syndrome. Made from affordable screen-printed electrodes using filter paper and carbon paste, a circuit composed of different components would function to measure the levels of serotonin present in the blood. When serotonin levels exceed a threshold, an LED light illuminates, giving the patient a formal diagnosis of serotonin syndrome.

BP-05

A novel proportional relationship between nematocyst volume and polyp size and position in *Anthopleura elegantissima*.

Claire Mullin¹, Kat McBride¹, Nathan_Kirk²Rowan McLachlan¹ / ¹Oregon Institute of Marine Biology, University of Oregon, Charleston, OR 97420. ²Hatfield Marine Science Center, Oregon State University, Newport, OR 97365.

Nematocysts, specialized stinging organelles in sea anemones, have traditionally been regarded as species-specific taxonomic markers with fixed size ranges. Recent evidence, however, suggests that nematocyst dimensions scale with polyp body size, raising questions about their reliability in taxonomic classification. *Anthopleura elegantissima*, a clonal aggregating sea anemone, provides an important model for investigating this phenomenon because genetically distinct colonies occur in proximity along the Oregon coast. Whether nematocyst scaling is universal across populations or varies among colonies has remained an open question. To address this, polyps were collected from physically separated colonies at Bastendorff Beach in Coos County, Oregon, representing distinct genetic backgrounds. Polyp mass and volume were recorded, and cnidae from tentacle and acrorhagi tissues were measured using calibrated light-microscopy with randomized capsule selection to avoid sampling bias.



Statistical analyses revealed significant positive correlations between both cnidae length and volume with polyp mass and volume across all colonies. These relationships were consistent regardless of colony size, polyp location within colony, or colony genotype. These results demonstrate that cnidae size reflect fundamental physiological constraints rather than colony-specific adaptations, challenging the use of fixed nematocyst dimensions as taxonomic characters. More broadly, this work highlights how body size influences the scaling of intracellular structures, reinforcing the principle that cellular and organelle dimensions are strongly tied to organismal growth. Such insights contribute to a deeper understanding of cnidarian biology and offer a cautionary perspective on the use of morphological characters in systematics.

BP-06

Human recreation affects transition and transversion rates in aquatic bacteria

Autumn Wienert, Nicholas Stewart / Biology Department, Southern Oregon University, Ashland, OR 97520.

A good indicator of a microbiome's overall adaptability to changes and stress is the presence of genomic diversity and mutation rates, which is driven further by bacteria's ability to spontaneously mutate. In this study, we aimed to look at how stress, specifically human recreation, affects mutation rates in *Priestia magaterium*. Samples were obtained from four lakes in Kansas. The *P. magaterium* present were isolated, and DNA was extracted and sequenced from 5 locations of high human recreation and 5 locations of low human recreation from each lake. Using python we identified all the transition and transversion mutations for each site within two of the four lakes. Transitions were ultimately more common than transversions at all sites, with the average transitions/transversions ratios being in the 2.4 range, but there were on average slightly more mutations in the bacteria sampled from the high traffic sites. These data suggest that high levels of human recreation may be a significant stressor on bacteria, causing more DNA mutations. This leads us to believe that human influence can drive adaptation in bacteria, and, in turn, affect the overall genomic diversity within aquatic environments.

BP-07

Investigating NRF2 Inhibition in Tumor Initiating Cells of Skin Squamous Cell Carcinoma

Cat Thomas¹, Sachiko Oshimori², Naoki Oshimori² / ¹Department of Biology, Willamette University, Salem, OR, ²Departments of Cell and Developmental & Cancer Biology, Oregon Health and Sciences University, Portland, OR 97239.

Tumor initiating cells (TIC) of squamous cell carcinoma (SCC) evade treatments such as chemotherapy and initiate recurrent tumors in response to TGF- β present in the tumoral microenvironment. This evasion of treatment is not only due to their quiescent nature but also their ability to mitigate damage from reactive oxygen species (ROS) produced by chemotherapeutics. TICs utilize nuclear factor-erythroid 2 p45-related factor two (NRF2) as a transcription factor which binds to antioxidant response elements (ARE) within the DNA and upregulates mRNA associated with deactivating ROS and chemotherapeutic drugs. Under normal conditions this binding is regulated by the NRF2-KEAP1 antioxidant pathway but due to oxidative stress present in TICs, KEAP1 is unable to bind to NRF2 and mark it for proteasomal degradation. This study aimed to evaluate the effectiveness of three previously identified potential inhibitors to block NRF2-DNA binding through (1) confirmation of nuclear localization of NRF2 in cell and tissue samples after inhibitor addition, (2) identification of significant downregulation of downstream gene targets, and (3) identification of potential impacts of inhibitor presence on protein expression. This was completed through techniques such as immunohistological staining, qPCR and Western blots.

BP-08

The Role of Meiotic Drive in the Fusion of Chromosomes 2-3 in a *D. americana* and *D. novamexicana* Introgression

Sophia Jetton, Regan Mitchell, Nicholas Stewart / Biology Department, Southern Oregon University, Ashland, OR 97520.

Chromosome shape and structures may vary as a result of translocations, inversions, duplications etc. and the variance in chromosome shape and structure allows for genotypic variety within an organism's karyotype. In most cases rearrangements have a deleterious effect on the organism, however, rearrange are found often. One hypothesis is that meiotic drive facilitates the presence of the neutral or slightly deleterious mutations. Meiotic drive is the phenomena in which a particular allele is inherited more often than predicted by mendelian 50/50 segregation. In this experiment we are studying the chromosomal evolution of *Drosophila americana* due to it have 2 major rearrangements, fusing the X and 4th chromosomes and the 2nd and 3rd chromosomes together at the centromere. Previous research has demonstrated biased inheritance (i.e. meiotic drive) favoring a fused metacentric chromosome in female *D. americana*. To further understand meiotic drive and the role played by the centromere in this process, we inserted the centromere of a *D. americana* into a *D. novamexicana* background. Multiple replicate fly lines were created through an introgression process before DNA was extracted, amplified, and ran through gel electrophoresis to determine genotype of the offspring. Preliminary results show that transmission either matched mendelian expectations or favored the *D. novamexicana* variant. This suggests that meiotic drive and biased patterns of inheritance found within *D. americana* are not caused by the centromere itself, rather, dependent on genomic context. Additionally, these results indicate that meiotic drive may contribute to the maintenance of the acrocentric karyotype of *D. novamexicana*.

BP-09

Using Genomic Sequencing Techniques to Identify Species of Rod Shaped Bacteria Within Lakes Wilson of Northwest Kansas

Linda Webber, Nicholas Stewart / Biology Department, Southern Oregon University, Ashland, OR 97520.

Now more than ever, it's crucial to examine human activity's impact on our biomes' health and status. As temperatures rise and biodiversity struggles to adapt, understanding how these stressors affect bacteria critical to aquatic environments will help us better grasp the evolutionary changes taking place. Under the mutation stress hypothesis, environmental stressors such as human activity can elevate bacterial mutation rates, leading to observable evolutionary responses that reflect ecosystem health at both micro- and macro-scales. Previously, we took samples from four lakes in Kansas at locations of low human activity and high human activity. We isolated, cultured, and sequenced aquatic *Bacillus* genomes. In the summer of 2025, I used computational methods to assess the quality of sequencing and identified 150 species from one of the lakes. Genome analysis from one lake revealed *Shouchella clausii* (n = 21) and *Priestia megaterium* (n = 13) as the most abundant species. While the results show that we have a wide, diverse array of rod-shaped bacteria, our goal was to isolate a higher number of a singular species, indicating that alterations are needed in our isolation step.

BP-10

2D Linear Metrics on First Lower Molar of Bats Reveals Strong Differentiation Between Dietary Guilds

Elise Mitchell¹, Matthew Ebner¹, Sharlene E. Santana^{2, 3}, David M. Grossnickle¹ / ¹Department of Natural Sciences, Oregon Institute of Technology, Klamath Falls, OR, 97601. ²Department of Biology, University of Washington, Seattle, WA, 98196. ³Burke Museum of Natural History and Culture, Seattle, WA, 98196.

In mammals, the molars can be strong predictors of diet. While feeding habits can be observed in extant taxa, dietary information for extinct mammals can be difficult to extrapolate. Our aim is to discover patterns relating to diet in the lower first molar of extant mammals to apply to fossil mammals. We examine the relationship of 2D dental measurements and diet in species of bats comprising almost all families in Chiroptera to examine whether simple measurements can strongly distinguish dietary guilds. We chose bats to begin our study due to their diverse diets and molar morphology. We collected 15 linear measurements on each specimen used and then interpreted the data through phylogenetic comparative methods to examine relationships between molar morphology and diet. Our method suggests that there is a strong, distinguishing relationship between herbivory and faunivory reflected in the morphology of the first lower molar in bats. These results suggest that 2D linear metrics can be strong predictors of diet and can be used as tools for inferring diet in mammals of unknown diets, including fossils. Future avenues for this project include exploring applying 2D metrics to other mammalian groups and then to large fossil samples to study mammalian paleoecological diversity.

BP-11

The Role of MTERF-3 in Mitochondrial Transcription

Reese Jones, Megan Bestwick / Biochemistry Department, Linfield University, McMinnville OR, 97128.

The Mitochondrial Termination Factor (MTERF) family is a protein group of mitochondrial termination factors that are classified as regulators. Each MTERF protein has their own specialized role with respect to mitochondrial transcription, and not all are terminator factors. The protein group is based on sequence similarity, and the MTERF-3 protein is the most conserved of the family showing a crucial role across species. This is supported by the knockout mice exhibiting embryonic lethality when the gene is removed. Understanding the regulatory role of MTERF-3 and its interactions with the mitochondrial transcription machinery is the major aim of this project. To analyze MTERF 3 interactions molecularly, DNA-binding and protein-protein interactions will be assessed. The mitochondrial core transcription proteins are the mitochondrial RNA polymerase (POLRMT), mitochondrial transcription factor A (TFAM), and mitochondrial transcription factor B2 (TFB2M). These proteins exhibit key functions in transcription and have previously noted interactions with MTERF proteins to regulate gene expression. For these assays, MTERF-3 was cloned and the protein expressed and purified. To examine the protein-protein interactions, functional assays including POLRMT, TFAM, and TFB2M, and in vitro transcription will be performed to analyze the role of MTERF-3 in mitochondrial transcription. By understanding the MTERF-3 role in mitochondria, we can better understand its role within disease.

BP-12

From bloom to bacterial boom: effects of environmentally relevant domoic acid concentrations on growth of pathogenic *Vibrio* species.

Dominic Nguyen¹, Amy Segura¹, Alex Baca¹, Kailani Maxwell¹, Ryan Kenton¹, Christine Weilhoefer¹, Cecilia Brothers²/
¹Department of Biology, University of Portland, Portland, OR, 97203. ²Department of Biological Sciences, Walla Walla University, College Place, WA, 99324.

Harmful algal and bacterial blooms (HABBs) pose a continuous threat to marine ecosystems and public health, leading to oxygen depletion, shellfish toxicity, and disease outbreaks. This study focuses on the diatom *Pseudonitzschia*, which produces domoic acid (DA), a neurotoxin responsible for amnesic shellfish poisoning in humans and marine wildlife. Recent studies suggest that pathogenic bacteria, including pathogenic *Vibrio* species, may use domoic acid (DA) as a nutrient source. The objective of this study is to investigate how domoic acid influences the growth of pathogenic *Vibrio* species via optical density, colony counts, and ELISA for toxin quantification. The *Vibrio* species used for this study were *Vibrio alginolyticus*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificus*, and *Pseudomonas aeruginosa* as a control. Growth assays and colony counts revealed species-specific response to DA exposure, suggesting that DA can act as a mild stressor or potential growth signal. *P. aeruginosa* maintained steady growth, *V. cholerae* showed a clear decline in colony counts, *V. parahaemolyticus* showed enhanced growth, and *V. vulnificus* showed variable patterns.

BP-13

Seagrass modulates HABB species in temperate coastal food webs

Alex Baca¹, Kailani Maxwell¹, Dominic Nguyen¹, Amy Segura¹, Ryan Kenton¹, Christine Weilhoefer¹, Cecilia Brothers² / University of Portland Department of Biology, 5000 N Willamette Blvd, Portland OR 97203

P. nitzschia is a species of marine algae responsible for harmful algal bacterial blooms (HABBs) that can produce a neurotoxin known as domoic acid (DA) as a metabolic byproduct, which can be dangerous for human health and has negative impacts on the overall ecosystem. Recent research in the field of microbiology has suggested that eelgrass beds (*Zostera marina*) may play regulatory roles in preventing or limiting the frequency and severity of HABBs from species like *P. nitzschia*. The present study aims to quantify the relationship between the presence of eelgrass in marine ecosystems and the activity of HABB relevant species like *P. nitzschia* and bacteria in the *Vibrio* genus. This was achieved through intensive weekly and biweekly sampling over a 7-month period at Netarts Bay and Tillamook Bay in Oregon. Over this period environmental DNA (eDNA) was collected for sequencing in order to reveal the microorganism species composition of seawater, samples of seawater treated with a formalin preservative were analyzed under a microscope to obtain algal cell counts, and seawater was plated onto *Vibrio* specific media to obtain an estimation on the presence of *Vibrio* in CFUs/mL. This data was then compared to the amount of eelgrass that was found at each specific sample site, on the day. Strong *in vivo* evidence of eelgrass's positive regulatory effects on HABBs can be used to better inform environmental policies that protect vital eelgrass ecosystems along the West Coast of the United States and can help lessen the dangerous side effects of marine HABBs.

BP-14

The Hunger Games: How feeding may fuel competition in *Anthopleura elegantissima*

Thandiwe L Venema, Ziah Barron, Will Swinnerton, Taylor Nollman, Nathan L Kirk / Department of Integrative Biology, Oregon State University, Corvallis, OR, 97331

Aggressive intraspecific competitions can help establish dominance hierarchies that allow the winners more access to resources. However, aggression can lead to injuries to combatants, so determining when to engage is of utmost importance. Some animals use self-assessment (SA) and other use information about opponents (mutual assessment: MA) to determine the duration of aggression, however it is often difficult to empirically differentiate these two strategies. Here we used the local intertidal sea anemone *Anthopleura elegantissima*, which forms colonies through *asexual reproduction*, resulting in aggregations of individuals (polyps) that compete with other aggregations for space. We hypothesized that the outcomes of these competitions are influenced by a polyp's ability to use specialized structures (acrorhagi), as well as its energy budget. Polyps with greater access to food are predicted to show more aggression. We collected anemones from marked colonies that had different aggression levels in past assays and acclimated them to laboratory conditions. To compare how access to food affected aggression and contrast MA and SA strategies, anemones were blocked into 4 paired aggression assays: 1) both individuals were fed, 2) neither were fed 3) only one polyp was fed, 4) only the other polyp was fed. After 7 and 21 days in the 4 experimental groups, individuals were paired in aggression assays. Preliminary data suggests that fed individuals have higher aggression levels than their unfed counterparts. Additionally, fed individuals increased their surface area and lost less weight over 21 days of feeding, indicating that anemones are able to assimilate food into biomass.

BP-15

Armed and Dangerous: Correlation between nematocyst, feeding status, and size of *Anthopleura elegantissima*

Eva Harvey, Olivia Small, Sydney Stubberfield / Department of Integrative Biology, Oregon State University, Corvallis, OR 97333.

Anthopleura elegantissima is a colonial, aggregating sea anemone present on the Pacific coast. As a cnidarian, they have stinging cells containing cnidae that are harpoon-like organelles used in feeding and defense. Spirocysts are a type of cnidae present in tentacles and are used for catching food. While holotrichs are larger, envenomating cnidae used for fighting and defense in larger specialized tentacles called acrorhagi. These organelles are single-use and are triggered when prey or competitors are nearby. Although we know that nematocyst length and volume are correlated with body size, there is limited research on how feeding impacts nematocyst size or how much size variation occurs among different clones. Our results are focused on the envenomating holotrichs in the acrorhagi used in a competition for space. We hypothesized that anemones that were fed over the course of the study (21 days) will have larger nematocysts than those that were not fed, because they have more energy to allocate to nematocyst production. To determine if there is size variation of nematocysts, acrorhagi were dissected out and squashed on microscope slides. Nematocyst lengths and widths were measured using image analysis and converted to volumes. In preliminary results, there was a positive correlation between feeding and nematocyst length in the acrorhagi. Studying the size variation of nematocysts and feeding impacts will allow for further understanding of the behavior of *A. elegantissima* and how they navigate their environment.

BP-16

Garlic extracts alter mortality and morphology of northern fowl mites (*Ornithonyssus sylviarum*) collected from purple martins

Patricia Foronda, Isabella Nicoletti, Kathleen O'Reilly / Department of Biology, University of Portland, Portland, OR 97203

Garlic (*Allium sativum*) is a cultivated plant valued for its culinary uses and medicinal properties. This is due to a sulfur-containing compound called allicin, which is released when garlic is crushed. Allicin has displayed acaricidal effects by disrupting neurotransmission, cellular respiration, and cuticular integrity in poultry mites. In addition to its efficacy, allicin in fresh garlic liquid is low in environmental toxicity, making it a safer option for pest management. These effects make allicin a potential natural alternative to synthetic acaricides, which is vital with rising chemical resistance in mites and environmental toxicity.

BP-17

For better or for worse: a volatile breeding season for tree swallows

Avery Weaver, Isabella Nicoletti, Patricia Foronda, Kathleen O'Reilly / Department of Biology, University of Portland, Portland, OR 97203

Tree swallow (*Tachycineta bicolor*) breeding performance at the University of Portland's Franz River Campus in 2025 was characterized by low fledging success and high nestling mortality under unstable summer temperatures. This study demonstrated that frequent temperature fluctuations and nest-based blowfly parasitism constrained reproductive output in the tree swallow population. Post-fledging nest dissections of the 16 active nest boxes quantified relative chick age and positioning within the nest, parasitic (*Philornis downsi*) abundance, nesting material height, and exogenous materials like shells and plastics. Across the breeding season, temperature swings exceeding 13.5°C were not uncommon and coincided with high mortality in 13 of the 16 active nests. Dissections also revealed atypical parental behavior: new nesting material was added atop deceased chicks and unhatched eggs. This created stratified layers that may modify nest sanitation and parasite dynamics, which has not been previously documented for tree swallows.

BP-18

Using Molecular Evolution to Explore Alternative Receptors for SARS-CoV-2

Aemelia Price, Kayden Harris, Ruby Bentz, Dr. John Frank / Department of Biology, Linfield University, McMinnville OR 97128.

SARS-CoV-2, the virus which caused the Covid-19 pandemic and likely jumped from bats into humans, canonically uses the protein ACE2 to infect cells. Recent molecular and cell culture studies have found 22 possible human alternative receptors. However, it is unknown if these receptors represent biologically significant entry mechanisms for SARS-CoV-2 in vivo. Persistent selective pressure between viruses and hosts often drives nucleotide changes in host proteins, including viral receptors. Virus-driven natural selection can be detected by examining the receptor evolution across related species. A signature of natural selection at virus-bound residues of an alternative receptor may indicate historical use by SARS-CoV-2 and its relatives to infect their hosts. To determine if alternative SARS-CoV-2 receptors have been subject to SARS-CoV-2-related sarbecovirus induced natural selection in bats, established computational molecular evolution analysis tools were used to identify sites of positive selection. So far, 8 genes show signs of positive selection, with 2 being particularly promising due to clustering of positive selection in regions accessible by the virus. To determine if these receptors are functionally relevant to the virus, an experimental strategy was established to test the predictions generated by the previous sequence analysis. Human and bat alternative receptor sequences will be cloned into expression plasmids. These plasmids will be transiently expressed in 293T cells, which are naturally resistant to SARS-CoV-2 infection, and then infected with SARS-CoV-2-spike pseudotyped VSV-luc reporter virus. These comprehensive studies will supply a deeper understanding of whether SARS-CoV-2 and related sarbecoviruses are likely to use alternative receptors in bats.

BP-19

Exploring the durability of marine picocyanobacteria micro-colonies

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Picocyanobacteria of the genus *Synechococcus* are widespread aquatic photoautotrophs that play essential roles in primary production, carbon cycling, and water quality. Under environmental stress, some *Synechococcus* strains form multicellular microcolonies, but the mechanisms and structural durability of these microcolonies remain poorly understood. This research investigated the physical durability of microcolonies in two marine *Synechococcus* strains (CC9605 and CC9311) using mechanical disruption treatments. Cultures were subjected to vortexing and sonication treatments, and populations of single cells and microcolonies were quantified using flow cytometry based on differences in measures of size. Results indicated that strain CC9605 showed no significant treatment effect, whereas CC9311 displayed a statistically significant increase in microcolony abundance. Across both strains, physical disruption appeared to increase microcolony frequency rather than decrease it, contrary to the initial hypothesis. Although microcolonies comprised less than 1% of total populations, these preliminary findings suggest that mechanical stress may induce microcolony formation, potentially as an adaptive response. Future work will include larger sample sizes and additional *Synechococcus* strains to further identify the mechanisms and ecological significance of microcolony formation, with broader implications for understanding microbial ecology and carbon cycling.

BP-20

Determining effects of nutrition on growth in the symbiotic sea anemone *Aiptasia* in a CURE course

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Cnidarians form highly productive symbioses with photosynthetic algal symbionts, but this partnership can break down when stressed. The symbiotic sea anemone *Aiptasia*, a model system for coral symbiosis, was used to determine how energy stores and host-symbiont regulation affect host growth and survivorship. Adult anemones were stored for one month, either in the light and fed, allowing for photosynthesis and accumulation of energy, or in the dark and starved, preventing symbiont photosynthesis. We then generated asexual buds (lacerates) by surgically excising tissue from the pedal disc. The lacerates recovered in one of four treatments: light to light, dark to light, light to dark, and dark to dark. We hypothesized that starved animals would have higher mortality and lower growth rates when switched to the light environment, because immune repression during host development disrupts host-symbiont regulation, leading to dysbiosis when nutrition is limited. Data was collected by students in a large enrollment introductory biology course (n=1054) and repeated by two undergraduate fellows to determine data quality from the large class. In the light, lacerates cut from starved parents developed significantly fewer tentacles and had higher mortality compared to those from fed parents. This pattern was also seen in the follow-up experiment, but it was not significant due to smaller sample sizes. Students in the class also felt that the CURE was highly engaging and helped them prepare for future careers.

BP-21

Trans-endothelial Extravasation of Multiple Myeloma via the SDF1-CXCR4 Axis

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Multiple myeloma (MM) is the second most diagnosed hematological cancer in the world and is resistant to treatment. It spreads through systemic circulation before rehoming into healthy bone marrow, where it inevitably causes bone damage and pain. This rehoming is guided by chemical signaling pathways within the body; however, the way in which MM cells respond to these signals under normal blood-flow conditions remains poorly understood. One key signaling molecule, stromal cell-derived factor 1 (SDF-1), acts as a driving cytokine that attracts cells to new bone marrow sites. Understanding how MM cells interpret chemokine cues within the bone marrow microenvironment may reveal critical control points that govern disease dissemination. This work aims to fill a key knowledge gap around the involvement of cellular signaling pathways in the progression of MM. Using CAD software and 3D printing, we have fabricated an endothelium-on-a-chip model that will be seeded with cells to mimic the bone marrow microenvironment. This allows us to use syringe pumps and control fluid flow to mimic relevant MM trafficking conditions. Utilizing this platform, we will investigate cellular behavior and response to the SDF-1 gradients and assess migration under flow.

BP-22

Structural and Swelling Properties of GelMA Hydrogels for 3D Cell Culture Applications

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Gelatin Methacryloyl (GelMA) hydrogels are commonly used as three-dimensional matrices for in vitro cancer models due to their biocompatibility and tunable properties. In pancreatic cancer, the extracellular matrix contributes to the regulation of cellular behavior, highlighting the need for hydrogel systems that can recapitulate key aspects of the tumor microenvironment. This study focuses on the structural and swelling characterization of GelMA hydrogels as a foundational step toward future pancreatic cancer applications. GelMA was synthesized from porcine gelatin and subsequently fabricated into 5% (w/v) hydrogels at Oregon Institute of Technology. Swelling behavior and structural features were examined to assess hydrogel stability and architecture. Both properties are needed to support cells and mimic the extracellular matrix. This work will provide data on how GelMA hydrogels respond to different environments and reveal structural features. Once the material properties of the gels have been characterized, cells will be incorporated into the gels to assess viability and protein expression using MTT assays, western blotting, and immunofluorescence.

BP-23

Non-Vector-Based Synthesis & Delivery of dsRNA for RNAi-Mediated Gene Silencing in *Dugesia dorocephala*.

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RNA interference (RNAi) is a powerful gene-silencing tool that uses double-stranded RNA (dsRNA) to target and degrade complementary mRNA, thereby inhibiting specific gene expression. Traditional RNAi approaches such as vector-based dsRNA synthesis and delivery via microinjection, soaking, or vector-based feeding are often labor-intensive, time-consuming, and inconsistently effective. Optimized RNAi protocols developed for non-native planarian species are frequently impractical due to species availability and regulatory constraints in North America. To address these limitations, this study focuses on *Dugesia dorocephala*, a North American planarian species, and presents a simplified, non-vector-based RNAi protocol suitable for gene function studies. The protocol involves DNA template design, in vitro synthesis of short-hairpin RNA (shRNA), and delivery through feeding, enabling rapid and efficient gene silencing detectable through distinct phenotypic outcomes. The dsRNA synthesis method consistently yielded 2-4 $\mu\text{g}/\mu\text{L}$ of shRNA per reaction. Planarians were starved for 10 days and then fed shRNA-containing liver paste three times, while control groups received RNA-free paste. shRNA was delivered at concentrations of 0.1 $\mu\text{g}/\mu\text{L}$ and 0.5 $\mu\text{g}/\mu\text{L}$, allowing uptake through the digestive system and subsequent diffusion into the cytoplasm, where targeted gene silencing was induced via RNAi. Following the feeding regimen, planarians were transected into head and tail fragments. Regeneration was monitored over several weeks, and the emergence of distinctive phenotypes was recorded. Preliminary results demonstrate effective knockdown of the β -catenin gene during regeneration in *D. dorocephala*. This approach overcomes key limitations of existing RNAi methods and expands the utility of *D. dorocephala* for research in North America.

BP-24

Development of an Integrated Tagging and Metabolic Measurement Protocol for the Northwestern Terrestrial Garter Snake (*Thamnophis ordinoides*)

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The Northwestern Terrestrial Garter Snake (*Thamnophis ordinoides*) is a widespread reptile native to the Pacific Northwest and is commonly used in ecological and physiological research. Long-term population studies require reliable individual identification paired with consistent physiological measurements. This study aims to develop an integrated protocol combining permanent individual tagging with baseline measurements of oxygen consumption (VO_2) in juvenile *Thamnophis ordinoides* under controlled conditions. Individual snakes will be permanently marked using a ventral scale clipping system that produces unique identification codes based on a standardized numerical pattern. This method was selected for its durability, minimal equipment requirements, and proven effectiveness for long-term identification without external tags. All handling procedures follow established herpetological ethical guidelines to minimize stress and injury. Identification codes will be recorded alongside morphometric data to ensure accurate tracking across future capture and measurement events. Following tagging, snakes will be placed in a metabolic chamber to measure baseline oxygen consumption (VO_2) during periods of normal, resting activity. Environmental conditions will be controlled to ensure consistency among measurements. VO_2 data will be used to characterize standard metabolic activity and link physiological measurements to known individuals. Establishing this standardized protocol supports long-term ecological and physiological research on *Thamnophis ordinoides* and contributes to broader efforts in herpetological research and conservation monitoring.

BP-25

Spatial Transcriptomics and Adaptive Multi-Modal Ensemble Encoding: Early Metastasis Profiling and Targeting

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Lung cancer remains the leading cause of cancer-related mortality, primarily due to its high metastatic potential and the difficulty of early detection. Current clinical approaches rely on assessments which have low sensitivity for early-stage metastases. To address these challenges, this project introduces a computational framework to predict metastatic potential directly from the primary tumor site, eliminating the need for secondary site biopsies and enabling earlier intervention. Leveraging spatial transcriptomics, this system captures cellular interactions and sequences missed by traditional methods, identifying high-risk tumor regions and metastatic drivers. The machine learning (ML) pipeline integrates neural networks, autoencoders, and clustering to reveal metastatic signatures with high accuracy. In silico testing aligned the received outputs with known signatures from open datasets. Building on these findings, an ML-guided lipid nanoparticle optimization pipeline was developed to design RNA-loaded formulations for inhibition of the given genetic pathways. A deep learning model was employed to enhance drug delivery candidates for the siRNA gene silencers. In vitro, cellular validation demonstrated high encapsulation efficiency, stability, and biocompatibility, showing potential to deliver therapeutics, offering a scalable, personalized therapeutic solution for metastatic suppression. This study bridges AI-driven profiling and treatment with precision nanomedicine for metastatic cancer at its earliest stages. Shifting cancer metastasis treatment from late-stage intervention to proactive, gene targeted suppression, this work offers a revolutionary, data-driven solution to one of the deadliest challenges in oncology.

BP-26

Population Ecology of Two Species of Terrestrial Bromeliads in Yasuní National Park, Ecuador

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The tropical rainforests of the western Amazon are among the most biodiverse places on Earth. However, understanding the mechanisms behind the coexistence of several hundred species of plants in a single hectare remains a challenge in ecology. Most research of this kind has focused on the co-occurrence of tree, shrub and liana species, while there has been very little research on the richness and composition of the herbaceous plant community. One charismatic component of this understory flora in the western Amazon are large terrestrial bromeliads with leaves that can reach up to 9 m long and stretch into the canopies of nearby trees. In May-July of 2024 we censused 25 ha of forest to understand the distribution and population ecology of two terrestrial bromeliads in the Yasuni Forest Dynamics Plot located in Yasuni National Park in eastern Ecuador. We identified, measured, mapped, and took leaf samples from each individual from two species to assess the population structure and size distribution of each species across topographic gradients. Additionally, we asked whether investment in leaf thickness varied across these same gradients. Finally, we compared the 2024 distribution to censuses done in 2022 and in the mid-1990s when the study area was established to understand population change.

BP-27

Impacts of selective logging as a habitat restoration tool on invertebrate communities in an oak (*Quercus garryana*) woodland

Ella J. Herb, Ava R. Howard, Gareth R. Hopkins / Department of Biology, Western Oregon University, Monmouth, OR, 97361.

Understanding the ecological impacts of forest management practices is critical for maintaining biodiversity and ecosystem function. Invertebrates play many essential ecological roles in forests and woodlands, making them valuable indicators of environmental change. Oregon white oak (*Quercus garryana*) woodlands are a conservation priority habitat in the Pacific Northwest of North America. Due to land-use patterns and environmental change, including fire suppression and competition from coniferous trees, these habitats have declined to 10% of their historic range. To address this conservation problem, habitat restoration activities, including selectively logging competing conifers, have been undertaken throughout the oak's range. While we have some understanding of the effects of this restoration on vertebrates and plants, there is a paucity of knowledge about invertebrates. We address this gap in our knowledge by assessing potential shifts in aerial insect abundance, diversity, and community composition in an oak woodland over six years following selective logging of conifers in this habitat. We sampled the aerial invertebrate community through time-constrained netting immediately prior to and post logging in 2019, and have continued sampling seasonally up to 2025. We have found that community composition has shifted over time in this ecosystem, moving from that typical of a closed-canopy coniferous forest towards that of an open deciduous woodland. We use these data to provide insights into how selective logging as a restoration tool may influence invertebrate communities over time in oak woodlands. Such knowledge will contribute to a broader understanding of the role invertebrates play in ecosystem responses to forest management.

BP-28

The impact of water quality metrics on physiological stress, immune function, and capture success in Western Painted Turtles and Red-eared Sliders

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Oregon's native turtles are Conservation Strategy species of concern due to habitat loss and degradation and threats from invasive species, including Red-eared Sliders (*Trachemys scripta elegans*). Although population trends have been documented in both native and invasive turtles in Oregon, the physiological health of turtles, and how this might be impacted by habitat quality has been less well-studied. In this study, we examined how common water quality metrics including temperature, pH, and turbidity affect baseline physiological stress (corticosterone levels), immune function, and capture success rate in both native Western Painted Turtles (*Chrysemys picta bellii*) and invasive Red-eared Sliders at Minto Brown Island Park in Salem, OR, in July-September 2024. We used baited hoop nets and recorded water temperature, pH, and turbidity at the time of capture. A blood sample was taken within 5 minutes of capture of each turtle to accurately examine baseline corticosterone levels and immune function (bacterial killing ability and heterophil: lymphocyte ratio). Water temperature positively predicted turtle capture, with a small positive trend of increased corticosterone with increased temperature. Water pH level had a negative trend for predicting bacteria killing ability, and water turbidity negatively predicted turtle capture. These preliminary findings contribute to broader conservation efforts by enhancing our understanding of the factors that affect freshwater turtle capture, as well as how water metrics may influence physiological health in these species.

BP-29

***Wolbachia* prevalence in agricultural pests and toad bugs collected in the northwestern Oregon**

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Wolbachia are maternally transmitted intracellular bacteria estimated to infect 40-60% of arthropod species and are known to influence host reproduction, ecology, and evolution. Despite their widespread occurrence, *Wolbachia* prevalence in many beetles, particularly those in agricultural systems of the Pacific Northwest, remains understudied. The objective of this study was to determine the prevalence of *Wolbachia* infection among insects collected in agricultural settings in the Pacific Northwest, with a focus on cucumber beetles and toad bugs. We hypothesized that approximately 20-30% of insects would test positive for *Wolbachia* based on previous studies. Specimens were collected from multiple sites and preserved in ethanol before DNA extraction. *Wolbachia* infection was determined using co-amplification PCR targeting *W16S rRNA* gene and host *cytochrome oxidase I* as a positive internal control, followed by additional testing of selected samples using MultiLocus Sequence Typing genes *gatB* and *hcpA*. Of the 25 specimens tested 6 were positive for *Wolbachia*, resulting in an overall prevalence of 24%. Infection rates varied among families with Gelastocoidae showing 100% infection, whereas Chrysomelidae and Buprestidae showed 11% and 0%, respectively. Ongoing sequencing and screening will be presented to further characterize *Wolbachia* strains within the infected hosts. These findings contribute to baseline prevalence data for arthropods in northwest Oregon and provide insight into *Wolbachia*-hosts associated within agricultural ecosystems, and potentially be used for biocontrol mechanisms longer term.

BP-30

Fetal sex and intrauterine growth restriction program tumor microenvironment response to cancer.

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Pregnancy complications disproportionately impact male offspring more than females, with an increased risk for certain cancers, including pancreatic ductal adenocarcinoma (PDAC). The differential susceptibility of male offspring is thought to arise from organ-specific differences in fetal DNA epigenetic programming. We hypothesize that variance in PDAC development and lethality may begin with fetal programming in the womb. To test this hypothesis, we injected murine pancreatic cancer cells (KPC) into the pancreatic tails of six groups of genetically identical, age-matched adult C57BL/6 mice in a single-batch experiment (n=36 mice). Ampyrone treatment was used to achieve abdominal skin transparency prior to injection. Intrauterine growth-restricted (IUGR) males and females were used to investigate the effects of fetal growth restriction on tumor growth. Castrated and ovariectomized mice served as hormonal controls, and intact, normal-birthweight males and females served as reference controls. Cancer cells were allowed to grow for 2 weeks before all animals were autopsied to measure primary tumor volume, enumerate metastatic lesions, and perform histologic analysis of tumor microenvironment response. Our findings demonstrate that sex differences in PDAC development are not entirely testosterone or estrogen-dependent and that fetal growth restriction alters the tumor microenvironment independent of testosterone.

BP-31

Bumble Bee (*B. vosnesenskii*) Monitoring and Recovery in a Newly Restored Area

Tara Prestholdt, Charlie DeKlotz, Luke Pettit, Cassie Taimanglo, Hannah Pompeii / Department of Biology, University of Portland, Franz River Campus, Portland, OR, 97203. May 2025 to August 2025

Bumble bees (*Bombus* spp.) are vital pollinators that support both ecosystem biodiversity and agricultural productivity in the Willamette Valley. However, widespread declines driven by habitat loss, pesticide exposure, and climate change highlight the need for long-term monitoring in restored landscapes. Now in year two of monitoring, we initiated a mark–recapture study to establish baseline population data for *Bombus* spp. in a newly restored native plant habitat at the Franz River Campus, Portland, Oregon. We estimated a population size of 3847 bees (95% CI), with a high apparent survival rate of 99% and a recapture probability of 8%. Compared to the previous year's estimate of 698 bees, the population has multiplied by a magnitude of 5.5. Given known colony sizes and foraging ranges of *Bombus vosnesenskii*, the data indicates the presence of multiple healthy colonies within the restored habitat. This study establishes a baseline for long-term pollinator monitoring in an urban river restoration site. Future work incorporating RFID tracking will refine estimates of movement, habitat use, and nest distribution, contributing to broader conservation strategies for native bumble bees.

BP-32

Effects of Cold Exposure and Food Restriction Treatments on Summit Metabolic Flexibility of Two Species of Avian Nomad

Alexis Menson, Hallie Hoffarth, Ben Sonnenberg, Jessica Karr, Jamie Cornelius / Department of Integrative Biology, Oregon State University, Corvallis OR 97331.

Understanding the limits of physiological flexibility in wild populations is important for predicting future responses to environmental uncertainty. Summit metabolic rate (i.e. M_{sum}) measures the thermogenic (i.e. heat producing) abilities of animals in response to cold exposure and is inherently flexible. However, the within-species limits of this trait in response to environmental challenges remains understudied. Long term cold exposure can induce birds to increase their metabolic rate, but the speed and degree of this adjustment is likely species dependent and varies based on location, season, and body size. Our study focused on changes in M_{sum} of two species, red crossbills (*Loxia curvirostra*), and pine siskins, (*Spinus pinus*) across exposure to cold acclimation. These nomadic species are residents of northern latitudes and are known for moving great distances to follow food resources. Thus, we also food restricted one treatment group prior to cold acclimation to look at the thermogenic costs of decreased food availability across species. We measured M_{sum} across four treatment groups: (1) baseline (warm-acclimated; 22°C), (2) after four days of cold exposure (6°C), (3) baseline after four days of food restriction (limited access to food twice daily for 45 minutes; 22°C), and (4) the previously food restricted birds after 4 days of cold exposure. By comparing these two species, we aim to better understand how different species of nomadic birds adjust their metabolic responses to environmental challenges. We found that pine siskins consistently had lower M_{sum} compared to red crossbills regardless of treatment. M_{sum} increased from baseline (1) in both species when placed in the cold exposure treatments (2) and (4). But just food restricted (3) birds did not increase their M_{sum} . Food restriction was found to have no effect on thermogenetic abilities, suggesting that nomadic birds may be able to cope with multiple challenges at the same time.

Chemistry Posters

CP-01

Synthesizing cross-conjugated molecules using Horner–Wadsworth–Emmons reactions

Jennifer Zirkle, Dr. David Cordes / Department of Chemistry, Pacific University, Forest Grove, OR, 97116.

This research focused on synthesizing cross-conjugated molecules using Horner-Wadsworth-Emmons reactions for potential applications in switchable fluorescent sensing systems through the donor-bridge-acceptor pathways. Disubstituted molecules were synthesised to create symmetrical and asymmetrical molecules. The products were analysed by NMR, UV-Vis, and fluorescence-emission spectroscopy.

CP-02

Exploring stability of FRET pair-modified quadruplex molecular beacons.

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The early detection of cancer and other neurodegenerative diseases has shown to lead to increased efficacy in treatment of patients and higher survival rates. This makes the development of accessible early-stage detection methods a desirable area of study. One such method is the detection of micro-RNA (miRNA). There is evidence to suggest that changes in miRNA expression levels occur before protein changes that lead to disease, making miRNA a useful biomarker for early disease progression. Our research focuses on the use of DNA quadruplexes— guanine-based non-canonical secondary structures—modified with a pair of organic dyes to provide fluorescent capabilities and act as sensors for miRNA. These quadruplex molecular beacons (QMBs) exhibit little fluorescence in the absence of their target, and an increase in fluorescence when bound to their target. Our work assessed the stability of QMBs designed to detect a miRNA sequence associated with breast cancer. We determined how different FRET pair attachment methods, as well as chemical environments, impacted their thermodynamic stability as measured by thermal denaturation tests. The sensitivity of the QMBs was measured by fluorescent titration to test how each beacon functions in different concentrations of the target miRNA strand. We found that the internal modification method and a positive ion-rich environment led to the most thermodynamically stable QMBs, and internally-modified QMBs also showed the greatest fluorescent sensitivity.

CP-03

Using water quality to investigate a unique approach to post-fire stream protection.

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For five weeks the 2021 Bootleg fire burned, consuming over 400,000 acres of forest and shrublands in eastern Klamath County and western Lake County, Oregon. It resulted in a dramatic loss of vegetative cover, which serves as essential habitat for diverse terrestrial and aquatic species. Local entities on Gearhart Mountain responded by felling burned trees and placing them in and across stream channels to serve as barriers, mitigating the downstream flow of debris and sediment. This project measures resultant water quality from the placement of these felled trees to better understand the impacts on aquatic species. Water quality measurements were conducted at over twenty sites across seven streams during three sampling trips (spring 2024, fall 2024 and spring 2025). Measured parameters included pH, dissolved oxygen, conductivity, turbidity, nitrate, and phosphorus. Of particular interest is phosphorus, as forest fires are known to significantly increase phosphorus loads in lakes, streams, watersheds, and aquatic ecosystems. This project aims to provide critical data on post-fire impacts on aquatic systems, equipping private landowners, government agencies, and non-profit organizations with the knowledge needed to develop timely and effective mitigation strategies to conserve the habitat of potentially impacted species such as the bull trout (*Salvelinus confluentus*).

CP-04

Accessible CO₂ electrolysis for fuel cell applications and student laboratory kit.

Jacob Maier, Kyra Morris, Travis Owen / Natural Sciences Department, Oregon Institute of Technology, Klamath Falls, OR 97601.

Innovative chemistry labs focused on current topics play an essential role in inspiring and educating students at undergraduate and high school levels. A timely example is the ongoing accumulation of carbon dioxide (CO₂) in the atmosphere. One promising approach to mitigate the increase of CO₂ in the atmosphere is the electrochemical reduction of CO₂ into carbon monoxide (CO), a valuable precursor for renewable fuels. This project examines the development of an accessible laboratory activity that could be utilized by students of all levels of chemistry, by focusing on electrolysis of CO₂ to form CO, with the explanation of how this produced CO can be utilized in a “flow-battery” system reliant on renewable energy-derived fuels. This new laboratory activity empowers all students to actively explore key principles in electrochemistry and current trends in renewable energy, promoting engineering, collaboration and problem solving in a hands-on, innovative and accessible experiment.

CP -05

Oregon State University Mass Spectrometry Center: Enabling Discovery Through Advanced Bioanalysis

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The Mass Spectrometry Center at Oregon State University supports and accelerates scientific discovery by providing access to state-of-the-art mass spectrometry instrumentation, robust analytical workflows, and expert technical support. Our experienced staff offer comprehensive sample preparation and analysis services and actively engage in collaborative research, including the development of investigator-driven workflows and custom assays. Our core expertise spans small molecule analysis, metabolomics, lipidomics, biomarker discovery, and quantitative bioanalytical assay development for complex biological matrices, including pharmacokinetic studies. We provide validated quantitative assays for a wide range of biomolecules, including short-chain fatty acids, bile acids, oxygenated lipids (oxylipins and eicosanoids), amino acids, sugars, and free fatty acids. In addition, we design, develop, and validate custom multiplexed LC-MS assays tailored to specific research needs. The Center also supports diverse protein and proteomics applications, including label-free proteomics, post-translational modification analysis, targeted protein quantification, and molecular mass determination of proteins and protein-antibody conjugates. For collaborative projects, we offer MALDI mass spectrometry imaging for spatially resolved omics with spatial resolutions down to 5 μm . We are actively advancing single-cell mass spectrometry and single-cell proteomics technologies and welcome exploratory collaborations that enable the development and evaluation of emerging workflows and analytical approaches.

CP-06

Spatially Elucidating the Toxicological Impacts of benzo[a]pyrene and 8-methyl-benzo[a]pyrene in Zebrafish Embryos Using MALDI Mass Spectrometry Imaging.

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Polycyclic aromatic hydrocarbons (PAHs) are a group of prominent environmental pollutants and potent carcinogens and mutagens. The toxicological effects of exposure to PAHs have become of increasing concern due to their prevalence in air pollution, and chronic exposure to PAH pollutants has been associated with the development of respiratory diseases, cardiovascular disease and cancers. We aim to use matrix assisted laser desorption mass spectrometry imaging (MALDI-MSI) to spatially characterize and quantify the toxicological effects of exposure to benzo[a]pyrene (BaP) and its methylated derivative, 8-methyl-benzo[a]pyrene (8mBaP) in zebrafish embryo tissues. BaP is a prominent PAH compound and has been the focus of many studies, however research pertaining to methylated derivatives of BaP is scarce in current literature, despite the toxicological effects in some cases being more severe. We imaged 72-hour old DMSO exposed control, BaP exposed, and 8mBaP exposed embryos, spatially mapping the distribution of and quantifying both PAH toxins after exposure. Additionally, we imaged prevalent small molecule metabolite signals, providing insight into the subsequent metabolism and detoxification of both compounds following exposure, which could provide insight into the mechanisms of toxicity associated with exposure to these compounds. Embryos exposed to 8mBaP particularly displayed irregularities in the development of fatty tissue structures, indicating the potential of 8mBaP to alter lipid expression and metabolism following exposure. To understand how lipid expression might be influenced by 8mBaP exposure, MALDI lipidomics imaging was conducted on the tissues to assess alterations in the expression and metabolism of various lipid species following exposure

CP-07

Exploring cellular heterogeneity through single-cell proteomics

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Single-cell proteomics provides a powerful approach to explore cellular heterogeneity and capture subtle biological changes that are often masked in bulk analyses. Two studies were performed to demonstrate its importance. In the first study, MDA-MB-231 breast cancer cells stably overexpressing Bcl-2 were generated by electroporation followed by clonal selection in G418-containing media. Clones with high Bcl-2 expression were identified by Western blotting and analyzed alongside vector control cells during chemical library screening. Single-cell proteomic analysis revealed protein-level changes, including differential expression of BCL2L1, that were not detectable at the bulk population level. In the second study, PC12 cells were differentiated into sympathetic ganglion neuron-like cells using nerve growth factor. Single-cell proteomic profiling was used to monitor differentiation-associated molecular changes and to identify proteins and peptides linked to neuronal differentiation. This analysis further revealed substantial cell-to-cell heterogeneity within the differentiated population that remained obscured in conventional bulk proteomic measurements. Together, these studies demonstrate that single-cell proteomics enables the detection of molecular diversity and biological variability that cannot be resolved using bulk analysis approaches.

CP-08

The characterization of a hypothetical radical SAM enzyme from *Bacillus subtilis*.

Krixia Agtay¹, Annie Crockett¹, Sean Lille¹, Theresa Luu¹, Rachel Hutcheson¹ / ¹Department of Chemistry & Biochemistry, University of Portland, Portland, OR, 97203.

Radical SAM enzymes play an integral role across many different kingdoms of life. They are responsible for catalyzing over 100 different reactions, such as the formation of stable protein radicals, methylation of phosphinate phosphorous atoms, epimerization, and hydroxylation. This research aims to determine whether the target enzyme from *Bacillus subtilis* (RadSAM_10) is a part of the radical SAM superfamily using analytical and spectroscopic techniques. The optimal isopropyl B-D-1 thiogalactopyranoside (IPTG) concentration for the overexpression of the target enzyme from *Bacillus subtilis* was determined. Through the use of the 3-4 L of overnight growths, the average cell pellet obtained was 12.9851 g or 3.25 g/L. Protein purification was performed in an anaerobic chamber where the protein eluted during the 10% buffer B wash. Fractions containing protein were buffer exchanged to prepare for future assays. SAM cleavage assays were performed to test SAM cleavage activity. This included HPLC, iron assays, and Bradford assays.

CP-09

Instrumentation development for studying highly nonlinear properties of lanthanide-doped nanoparticles

Trey Stephens-Cherry, Artiom Skripka / Department of Chemistry, Oregon State University, Corvallis, OR, 97331.

Lanthanide-doped photon avalanching nanoparticles transform invisible low-energy near-infrared excitation into visible high-energy emission, making them promising for applications including deep-tissue bioimaging, temperature sensing, and super-resolution imaging. However, accurately measuring and collecting data on these materials is challenging and requires specialized, custom-built equipment with in-house-manufactured parts and streamlined data acquisition. Using 3D modeling and printing, highly specialized parts can be created that fit specific components within a fraction-of-a-millimeter. To perform highly sensitive measurements on photon avalanching nanoparticles, we have developed a hyperspectral microscope equipped with single photon counting modules that are completely insulated from ambient light, introduced dichroic mirrors to assist with alignment of multiple lasers, and implemented motorized servos to enable remote, automated control of optical elements such as mirrors and filters. We are now testing the setup and preparing to take more advanced measurements to better understand the optical properties of lanthanide-doped nanoparticles at the single particle level.

CP-10

Optimization of Copper-Catalyzed Oxidative Alkylboron Homocoupling

Kenni Proctor, Andrew Baggett* / Chemistry Department, Linfield University, McMinnville, OR, 97128.

Carbon-carbon bonds are one of the most relevant bond types in organic chemistry. Alkyl boron coupling has been heavily studied but there is a gap with Csp^3-Csp^3 bonds made with homocoupling of boron reagents. Csp^3 bonds form key linkages between portions of molecules relevant to medicinal chemistry and products. The goal of this project is to optimize a Csp^3-Csp^3 copper-catalyzed oxidative homocoupling of alkylboron reagents and to generalize the reaction. To develop this reaction the alkylboron reagent was synthesized via a Grignard reaction and the copper catalyzed oxidative conditions were screened. 1H and ^{11}B NMR were applied for analysis of reactants and product. Quantitative 1H NMR was used to determine reaction yields.

CP-11

CPSynthesis and Preliminary Bioactivity of Small-Molecules of Arp2/3 Complex

Jorie Wogmon, Georgia White-House, Andrew Baggett* / Chemistry Department, Linfield University, McMinnville, OR, 97128.

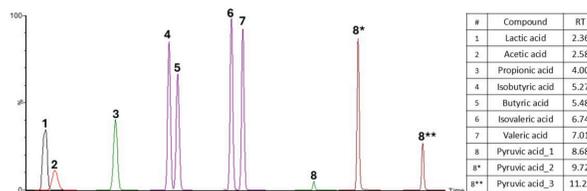
Actin-related protein 2/3 complex (Arp 2/3) is a structural nucleation-promoting factor that initiates nucleation or branching of actin filaments in eukaryotic cells. Arp 2/3 helps build the actin cytoskeleton and promotes cellular movement by attaching to pre-existing actin filaments and nucleating daughter filaments. Numerous human diseases have been linked to hijacked Arp 2/3. Nearly 20 years have passed since the discovery of four significant small-molecule Arp 2/3 inhibitors that have seen widespread use in research but the low potency of these substances has precluded their consideration for preclinical use or beyond. Our research aims to increase potency of small-molecule Arp 2/3 inhibitors via exploration of new chemical space revealed as potentially interesting by *in silico* docking experiments. We present our efforts to recreate synthesis of the 2 most promising potential new inhibitor classes with the goal of following up with derivatization and structure-activity optimization.

CP-12

Targeted LC-MRM-MS quantification of short-chain fatty acids and related microbial fermentation products in human feces.

Jessica L. Etter¹, Liping Yang¹, Jaewoo Choi¹, Jan F. Stevens^{2,3}, Claudia S. Maier^{1,3} / ¹Department of Chemistry, Oregon State University, Corvallis, OR, 97331. ²Department of Pharmaceutical Sciences, Oregon State University, Corvallis, OR, 97331. ³Linus Pauling Institute, Oregon State University, Corvallis, OR, 97331.

Short chain fatty acids (SCFAs) are byproducts of complex carbohydrate fermentation by the gut microbiome. Quantifying SCFAs and related fermentation products in feces provides insight into the interactions between diet, gut microbial activity, and host physiology. This work presents a novel method for the chemical derivatization and quantification of eight fecal metabolites, including six SCFAs, lactate, and pyruvate, using liquid chromatography-mass spectrometry with multiple reaction monitoring (LC-MRM-MS). The method has been validated against all relevant parameters (selectivity, sensitivity, recovery, precision, stability, linearity, and reproducibility of sample preparation) according to the current analytical procedure validation guidelines. The method was successfully applied to quantify endogenous metabolite levels in human fecal samples, demonstrating suitability for metabolomic studies, exploration of microbial activity, and dietary intervention research.



CP-13

Modeling initiation of ruthenium-catalyzed olefin metathesis for greener organic synthesis

Samuel R. Koehler, Buck L. H. Taylor / Department of Chemistry & Biochemistry, University of Portland, Portland, OR 97203.

Commonly used products, including plastics and medicine, are made using simple hydrocarbon chains. These chains, however, are sourced from petroleum. Vegetable oils are a promising alternative, but their length and internal alkene makes cracking them difficult. Through ethenolysis reactions, a type of olefin metathesis in which a transition metal splits the internal alkene into two terminal alkene products, this problem can be solved. Many studies have been conducted to learn more about this process, but they all have the same issue of inefficiency. To compete with the efficiency of petroleum, a catalyst must initiate quickly, be highly selective, and decompose slowly to contribute to a high turnover number. This research used computational methods (density functional theory) to study potential ruthenium catalysts, specifically looking at how they can initiate faster. The faster a catalyst can initiate, the more time it spends in ethenolysis creating desired terminal alkenes. Previous experimental studies by the Grubbs group included measuring initiation rates of several catalysts; however, initiation was conducted with ethyl vinyl ether, rather than the real substrate, ethene. Our computational study set out to compare these two alkenes in initiation. For each catalyst in the different substrates, the rate determining steps of the reaction were modeled to predict free energy barriers. It was found that a catalyst initiated by ethyl vinyl ether was higher in energy than when it was initiated by ethene. This greatly affected the initiation rate and could possibly lead to false conclusions about what contributes to the efficiency of initiation. These findings highlight the importance of using the right alkene during studies of initiation of olefin metathesis catalysts.

CP-14

MALDI mass spectrometry imaging characterizes lipid dysregulations in the 5xFAD Alzheimer's disease mouse model

Phoebe Y. Lee¹, Arpa Ebrahimi¹, Luke Marney¹, Jaewoo Choi¹, Kathy Magnusson^{2,4,5}, Claudia S. Maier^{1,5} / ¹Department of Chemistry, OSU, Corvallis, OR. ²Department of Biochemistry and Biophysics, OSU, Corvallis, OR. ³Department of Biomedical Sciences, OSU, Corvallis, OR. ⁴Carlson College of Veterinary Medicine, OSU, Corvallis, OR. ⁵Linus Pauling Institute, OSU, Corvallis OR.

Alzheimer's disease (AD), a leading cause of death in Americans over 65, occurs in sporadic and familial forms. The 5xFAD mouse model carries five familial AD mutations that drive excessive β -amyloid production and plaque accumulation, making it a powerful system for studying early AD pathology. Dr. Kathy Magnusson's lab has observed significant neurophysiological changes and mitochondrial damage in these mice as early as 1 month of age. Furthermore, spatial transcriptomics in 1-month-old 5xFAD mice have confirmed subregion-specific abnormalities in mitochondrial metabolism and biogenesis. To build upon these metabolic findings, we compared brain lipid profiles of 1-month-old and 8–9-month-old 5xFAD mice with age-matched wild-type controls. Using MALDI mass spectrometry imaging (MALDI-MSI), we developed an on-tissue lipid profiling workflow with near-cellular resolution to visualize lipid distributions across heterogeneous brain regions. Mirroring the early metabolic shifts seen in our transcriptomic data, this approach revealed significant lipid dysregulation in the 5xFAD brain as early as one month of age, well before advanced plaque pathology. Comparisons between young and older mice further demonstrated age-related lipid alterations that parallel increasing β -amyloid burden. Across both age groups, we identified potential lipid biomarkers associated with disease onset and progression. Overall, this work provides insight into the earliest molecular changes in AD and highlights the power of integrating spatial transcriptomics and lipidomics to map the concerted dysregulation defining early neurodegeneration.

CP-15

To float or not to float: proteomic insights into attachment phenotypes of the PC12 cell line

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PC12 cells are widely used in neuroscience to model neurodegenerative disease and neurotoxicity due to their ease of culture, versatility, and ability to differentiate into neuron-like cells upon nerve growth factor stimulation. While undifferentiated PC12 cells can be maintained in either adherent or suspension culture, adherent cells are more commonly utilized, leaving the floating phenotype poorly characterized and often discarded during routine passaging. This study uses mass spectrometry-based quantitative proteomics to identify, quantify, and compare protein expression profiles between floating and adherent PC12 cells. Differential expression and pathway enrichment analyses revealed extensive proteomic reprogramming in floating cells, characterized by upregulation of mitochondrial organization, biomolecule transport, and oxidative phosphorylation. In contrast, downregulated proteins were strongly enriched for processes related to cell cycle progression, DNA replication, and chromosome segregation. These results suggest that when PC12 cells grow in a non-adherent state, they shift away from highly proliferative programs, instead emphasizing mitochondrial and metabolic processes. In a similar manner, neuronal differentiation in PC12 cells involves exiting the cell cycle and reorganization of cellular metabolism, reflecting shifts towards a differentiation-permissive state. Together, these findings indicate that adhesion status on its own can shape the baseline cellular state of PC12 cells, and should be taken into account when interpreting neuronal differentiation and cell-to-cell heterogeneity in PC12-based studies.

CP-16

Untargeted metabolomics detection and machine learning prediction of leaf adulteration in *Withania somnifera* root extract using LC-EAD-QTOF mass spectrometry

Oshoma Erumiseli¹, Emily McDonald¹, Rudranil Dutta¹, Luke Marney^{1,2}, Jaewoo Choi^{1,2}, Amala Soumyanath^{2,3}, Jan F. Stevens^{2,4,5}, and Claudia S. Maier^{1,2,4} / ¹Department of Chemistry, Oregon State University, Corvallis, OR, 97331. ²Botanical Dietary Supplements Research Center, Oregon Health & Science University, Portland, OR, 97239. ³Department of Neurology, Oregon Health & Science University, Portland, OR, 97239. ⁴Linus Pauling Institute, Oregon State University, OR, 97331. ⁵Department of Pharmaceutical Sciences, Oregon State University, Corvallis, OR, 97331.

Ashwagandha (*Withania somnifera*) is a widely used botanical that is increasingly vulnerable to economically motivated adulteration, particularly through the substitution of leaf material for root. In this study, we present an integrated workflow combining untargeted metabolomics and machine learning to detect and quantitatively estimate leaf adulteration in *W. somnifera* root extracts. Samples were prepared along a controlled 0–100% leaf–root mixing gradient and analyzed using liquid chromatography coupled to quadrupole electron-activated dissociation time-of-flight mass spectrometry. A principal component analysis (PCA)–based calibration model showed clear and systematic separation of leaf-enriched and root-enriched samples as a function of adulteration level. Projection of PCA loadings into cosine-similarity molecular networks revealed structurally related metabolite clusters specific to individual plant parts, providing mechanistic chemical context for the observed separation. Machine learning regression using least absolute shrinkage and selection operator (LASSO) and elastic net enabled effective feature selection and accurate prediction of adulteration levels in unknown samples. Overall, these results demonstrate a robust analytical platform that integrates calibration modeling, molecular networking, and machine learning for improved quality control and authentication of botanical products.

CP-17

qPCR Comparison of Cyanobacteria Abundance and Diversity in Upper Klamath Lake over Two Summers

Jesse Leyva, Tyler Leerhuber, Yamini Singh, Adrianna Sulfridge, Miranda Valle, Dr. Ken Usher, Dr. Kamal Gandhi / Department of Natural Sciences, Oregon Institute of Technology, Klamath Falls, OR, 97601.

This research compares cyanobacteria samples from Upper Klamath Lake (UKL) over the course of two summers (2024, 2025). The previous consensus of the yearly algal blooms was an abundance of *Aphanizomenon flos-aquae* (AFA) early in the season and *Microcystis aeruginosa* (MA) predominating later. We collected biweekly samples at two sites around UKL over the last two summers, from June to September. We then extracted and quantified the DNA and used different qPCR primers that we developed to help measure relative amounts of specific cyanobacteria in UKL. Our results show a much broader picture than that previous consensus, including other cyanobacterial species being detected. We currently have qPCR probe/primer sets that quantify three of the species that were detected through 16s sequencing. We are hoping to develop novel primer sets to aid in quantifying the remaining two species.

CP-18

16s Analysis of Cyanobacteria Abundance and Diversity in Upper Klamath Lake Across Two Summers

Miranda Valle, Tyler Leerhuber, Jesse Leyva, Yamini Singh, Adrianna Sulfridge, Dr. Kamal Gandhi, Dr. Ken Usher / Department of Natural Sciences, Oregon Institute of Technology, Klamath Falls, OR, 97601.

This research compares cyanobacteria samples from Upper Klamath Lake (UKL) over the course of two summers (2023, 2024). Historically, two cyanobacteria have been known to dominate UKL blooms, with *Aphanizomenon flos-aquae* (AFA) early in the season and *Microcystis aeruginosa* (MA) later. We collected biweekly samples at two sites around UKL over the summers of 2023 and 2024, from June to September. We then extracted and quantified the DNA and sent our samples for 16s metagenomic sequencing, with those results showing that there were five species of cyanobacteria present in UKL, not just AFA and MA. A similar cycle of growth was detected across both summers. Furthermore, at different times throughout the summer, *Cyanobium gracile*, *Gloeotrichia echinulata*, and *Synechococcus sp.* were the dominant species that were measured.

CP-19

Using X-ray Fluorescence to examine the mobility of topsoil trace metals in Ashland, Oregon.

Jonathan Neill, Wayne Hung, Ph.D. / Department of Chemistry, Southern Oregon University, Ashland, OR, 97520.

Rural communities such as Rogue Valley, Oregon, are experiencing increasing development pressures driven by population growth and raising concerns about environmental quality, particularly in areas with potential legacy contamination. Preliminary soil metal data indicate that several locations exhibit elevated trace lead concentrations; however, the mobility and long-term fate of these contaminants remain poorly understood and warrant further investigation. The objective of this research is to evaluate the mobility of trace metal contamination, particularly lead, in Ashland soils in relation to key soil properties, including pH, organic matter, particle size distribution. Soil samples were processed under conditions designed to approximate natural environmental processes (i.e., neutral aqueous extraction), and solid-phase metal concentrations were subsequently quantified using portable X-ray fluorescence (XRF) spectroscopy as a rapid screening tool. Changes in metal concentrations following extraction were used as a proxy for relative mobility. This approach assesses whether trace metal contaminants remain stable in soils or become mobilized during climatic events, potentially contributing to contaminant transport through stormwater runoff and groundwater pathways. The findings will support a broader research effort examining how increasingly severe wildfire seasons, associated with climate change, influence regional contaminant loading. Collectively, this study will shed light on a practical framework for estimating contaminant mobility using portable, field-applicable XRF measurements as a cost-effective alternative to more resource-intensive laboratory analyses.

CP-20

Investigating the effects of soy protein derived hydrogel environment on breast cancer cell growth and proliferation.

Tori Leyba, Allison Hammer, Michelle Bonilla, Heather Ritter, Ethan Roeloffs, Rachel Edwards /Department of Natural Sciences, Oregon Institute of Technology, Klamath Falls, OR, 97601.

Cancer is a complex disease that manages to evade detection by the immune system while co-opting its systems to promote its own growth, survival, and migration. Some tumors can be densely infiltrated by cells of both the innate and adaptive parts of the immune system, which should allow for the immune system to attack the tumor, but it frequently enhances tumorigenesis and progression. Studies have shown that certain foods have anti-inflammatory effects and can affect a range of physiological outcomes, including rate of cancer occurrence and levels of chronic inflammation. These anti-inflammatory compounds are potential agents for cancer prevention and therapy, and so we are investigating soy protein as an anti-inflammatory therapeutic agent. In this study we are: (1) developing soy protein hydrogels at different viscosities to mimic the ECM found in the human body, (2) testing the viability of the hydrogel structure for long-term storage, (3) replicating the hydrogel in mass quantities, and (4) testing the structural integrity at varying temperatures.

CP-21

Creating a Circular Machine Learning Based Platform for Sustainable Agriculture and Climate Change Mitigation

Anisha Dhoot / Westview High School, 4200 NW 185th Ave, Portland, OR 97229.

Greenhouse gas emissions from fossil fuel dependence continue to accelerate global warming, contributing to plastic pollution and food insecurity. This research investigates integrated carbon mitigation strategies through experimental validation and machine learning-based smart agriculture platform. Initial experiments quantified the greenhouse effect by comparing temperature variations in enclosed containers containing oxygen-rich and carbon dioxide-rich environments, with CO₂ filled containers exhibiting significantly higher rates of heating. To evaluate carbon mitigation strategies, kelp seaweed was introduced into CO₂-rich containers, resulting in substantial reduction of heating effect, demonstrating kelp's capacity for carbon sequestration and climate regulation. These findings led to an innovation that we refer to as "Smart Carbon Recycling", a system that maps carbon journey from the atmosphere to sea to agricultural soils. To optimize agricultural implementation, EARTH-ai, a Python-based machine-learning model, was developed to predict optimal crop selection based on soil composition and environmental parameters. In parallel, an organic kelp-seaweed fertilizer, KelpNutriBoost, was formulated and evaluated, demonstrating improvements in soil health, crop yield, nutritional content, at much lower cost compared to conventional fertilizers. Further investigation incorporated biochar typically produced via Microwave Catalytic Pyrolysis of plastic waste and biosolids, yielding cleaner biofuel and carbon-rich soil amendments that enhance nutrient retention and long-term carbon sequestration. Collectively, these integrated approaches demonstrate a closed-loop circular strategy addressing greenhouse gas mitigation, fossil fuel reduction, plastic waste management, and sustainable agriculture. This multidisciplinary approach emphasizes scalability, economic feasibility, and real-world implementation, offering a model for future climate innovation that integrates chemistry, biology, data science, and sustainable engineering solutions globally.

Geography Posters

GP-01

Testing the Efficacy of NDVI enhanced sUAS Imagery for Identification of Invasive Plant Species in the Luckiamute Watershed – Preliminary Findings

Kira Pease, Lua Pierce, David Szpakowski, Bryan Dutton, Steve Taylor, Sarah DeVyldere, Angie Rodriguez / Earth and Environmental Science. Western Oregon University, Monmouth, OR 97361.

Invasive plant species in Western Oregon are posing an increasing threat to native habitats, causing millions of dollars in annual economic loss to public and private lands. Invasive plants are problematic due to their ability to outcompete native species and disrupt natural watershed functions. This poster presents preliminary results from the analysis of sUAS imagery for invasive identification. Our team is working with imagery collected at eight locations within the Luckiamute watershed. We are testing multiple approaches to image alignment and the use of supervised machine-learning classification to establish an effective and efficient approach for rapid identification of invasive plant species at target locations. Previous research done on this topic has found that the use of sUAS imagery for invasive plant species identification shows potential. The sUAS imagery provides a detailed view of vegetation, however sometimes this level of resolution is not sufficient to confidently identify plant cover at the species level without extensive ground truthing. This is where the use of near-infrared sensors and broader-scale image classification for species identification becomes relevant. With the addition of these approaches, we believe we will be able to enhance the accuracy and efficacy of the use of sUAS imagery for these tasks. While our current results are only preliminary, we believe they demonstrate that we are making progress on this goal.

Health Science and Kinesiology Posters

HSKP-01

Advancing opioid overdose intervention: formulating spray-dried naloxone microparticles for pulmonary delivery.

Anvi Singh / Wilsonville High School, Wilsonville, OR, 97070.

In the last decade, the world has plunged into an opioid epidemic, with overdose deaths surging, amplified by the rise of synthetic drugs. In 2019, opioids accounted for 80% of global drug-related deaths, with overdoses claiming 125,000 lives. Naloxone has been critical in reversing overdoses, primarily administered as the intranasal spray Narcan. However, Narcan has limitations, including 50% nasal bioavailability complemented by a short half-life (60-120 minutes), often requiring repeated doses. Additionally, its rapid opioid reversal can trigger acute withdrawal symptoms. This research developed a novel spray-dried microparticle with a drug-entrapping matrix for efficient and targeted delivery of naloxone. These micron-sized particles reach the deep lungs, enabling rapid systemic uptake via the alveolar-capillary membrane. The preservative-free dry powder system also adds to drug stability and shelf life. The polymers sodium carboxymethyl cellulose and carboxymethyl chitosan were selected to optimize mucoadhesion and facilitate controlled drug release. Microparticles were formulated using a Büchi 290 spray dryer with a naloxone hydrochloride-polymer suspension (20% w/w drug loading) with a yield of 70% w/w. Scanning electron microscopy confirmed an average particle size of 1-5 μm , suitable for deep lung deposition. Drug release was evaluated in phosphate-buffered saline at 1, 5, and 10 minutes via UV-Vis with a 40-320 $\mu\text{g/mL}$ standard curve. High-performance liquid chromatography tandem mass spectrometry estimated entrapment efficiency at 55.55% w/w. These findings suggest that dry-powder pulmonary delivery of naloxone is a viable alternative to Narcan, offering improved bioavailability, stability, and longer action to reduce withdrawal symptoms.

Math, Computer Science & Statistics Posters

MCSSP-01

Convergence values for several variants of the tangent inverse series

Stephen Hantzmon / Mathematics Department, Western Oregon University, Monmouth, OR, 97361.

This research was prompted by an introductory mathematics research focused class. Specifically, it involves series, infinite sums of numbers which may or may not add to finite ones. In this instance, we explore series that do in fact converge. To do so, we use an arctangent subtraction identity and telescoping properties of series, finding the specific convergence values of two arctangent series and attempt to generalize thrice; First successfully with a general arctangent series that converges to a real number in a bounded set, the second time unsuccessfully, and the third successfully with a general series that converges to any real number in a real, unbounded function.

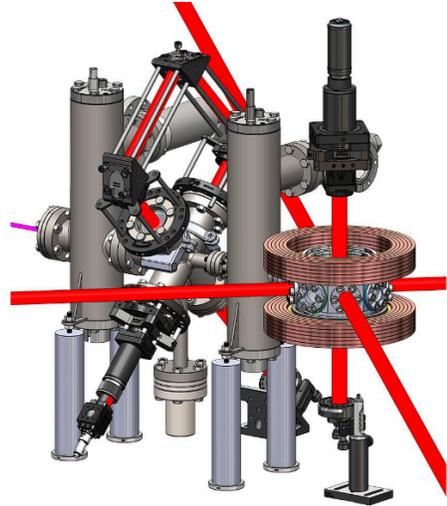
Physics Posters

PP-01

Building a laser-cooled lithium apparatus for quantum gas experiments.

Morgan P. Berghof, Emma K. Falk, Kaia E. O'Neill, Stella R. Kinney, Emma G. Hataway, Ben A. Olsen / Department of Physics, Lewis & Clark College, Portland, OR 97219.

Our group aims to study quantum matter using ultracold lithium gases. We will use these quantum gases to emulate other quantum systems, such as superconductors or neutron stars. With a series of techniques called laser cooling, we will trap the lithium atoms and slow their motion. The first two phases of laser cooling are two-dimensional and three-dimensional Magneto-Optical Traps (2DMOT, 3DMOT), which collect atoms from beams and trap them for loading into subsequent traps. Each MOT requires laser beams with specific wavelength and polarization, as well as a magnetic field gradient. We stabilize the laser wavelength using saturated absorption spectroscopy, then modify the wavelength using acousto-optic and electro-optic modulators. The laser light passes through optical fibers, and is incident on the atoms from several directions. To create a magnetic field gradient, we use permanent magnets mounted in custom holders, which are attached to an ultrahigh vacuum chamber.



PP-02

Optimizing in vitro motility assay protocols to analyze the cellular motor myosin VI.

Michael Ming L. Cotten¹, Sam R. Holmes², Maya G. Ryan¹, David Altman¹ / ¹Department of Physics, Willamette University, Salem, OR, 97301. ²Department of Mathematics, Willamette University, Salem, OR 97301.

Myosins are a family of motor proteins, which are biomolecules that generate force and motion in the cell. Myosins move by travelling along the filamentous protein actin. Myosin VI is a particular class of myosin that is involved in sensory function. The goal of this work is to learn more about how to model myosin VI and determine whether multiple motors interacting through the same filament influence each other. In this study, we examine the behavior of myosin VI in an in vitro motility assay, in which motors are immobilized on a surface, then actin is flowed on top. The binding and moving of the actin filaments are then observed via fluorescence microscopy. To analyze the microscopy data, we used a combination of standard statistical methods and topological data analysis. These approaches analyze the topological characteristics of the actin network, finding persistent voids. Additionally, these methods help reduce the effect of perturbations caused by thermal motion. Here we present preliminary results of these studies, including protocol optimization leading to more reproducible experiments as well as observations of topological differences across different experimental conditions, whose origins we are exploring.

PP-03

Optimal exposure for the Eddington experiment

Anesti Audeh, Benjamin Kerr, Aspen Young, Jesse Kinder / Department of Natural Sciences, Oregon Institute of Technology, Klamath Falls, OR 97601.

The Eddington experiment during the total solar eclipse of 1919 provided the first experimental test of Einstein's theory of general relativity by measuring the gravitational deflection of starlight near the sun. Modern eclipse observations aim to improve the precision and accessibility of this classic test. We analyzed images from the April 8, 2024 total solar eclipse using the MEE2024 data analysis pipeline and compared the data collected with three different camera exposure times: 250 ms, 300 ms, and 400 ms. A single camera tracked the starfield near the sun throughout totality, providing identical starfields for direct comparison of exposure settings. For each exposure, we measured the total number of stars detected, the proximity of detected stars to the sun's limb, the usable area surrounding the sun, and the uncertainties in the measured Einstein deflection coefficient and plate scale. Our analysis provides data-driven insights for optimal exposure in future eclipse observations, balancing the competing demands of detecting faint stars far from the sun against maximizing the usable field near the solar limb where gravitational deflection is strongest.

STEM Education Posters

SEP-01

An Accessible Static Headspace Method for Arson Investigation Using Common Laboratory Materials

Beau Montgomery, Krista Haas, Simon Kimberly, CH 461 class, Keith D. Schwartz / Department of Chemistry and Physics, Western Oregon University, Monmouth, OR 97361.

Static headspace (SHS) enrichment coupled with GC-MS analysis is a widely used technique for the recovery and identification of ignitable liquid residues in arson investigations. However, many traditional enrichment methods rely on toxic organic solvents for extractions and costly carbon strips housed in airtight metal paint cans, limiting their practicality in teaching laboratories. This work presents a low-cost, green chemistry approach specifically designed for arson investigation applications that utilizes activated carbon pouches constructed from common coffee filters and activated carbon, along with green solvents, basic laboratory equipment, standard glass canning jars, and a GC-MS. This accessible method provides a practical alternative for teaching laboratories, undergraduate research, and training exercises in fire debris analysis. It offers a hands-on way to introduce and reinforce fundamental concepts in headspace sampling, adsorption, and forensic arson investigation without reliance on specialized or hazardous materials.

SEP-02

From policing to pedagogy: Guided use of GenAI tools for pre-laboratory preparation in a chemistry laboratory course.

Amila U. Liyanage / Department of Chemistry, Oregon State University, Corvallis, OR 97331.

The use of generative artificial intelligence (GenAI) tools by students has become increasingly common and largely unavoidable in higher education, raising important questions about how these tools can be productively integrated into teaching and learning. This study investigates whether intentionally incorporating GenAI as a guided learning resource can improve student pre-laboratory preparedness in an upper-division chemistry laboratory course. One group of students completed traditional pre-laboratory assignments (prelabs), while another group completed redesigned “hybrid” prelabs that encouraged GenAI use through structured, guided prompts while retaining some elements of traditional prelabs. The educational impact of these hybrid prelabs - positive, negative, or neutral - was evaluated using student self-reported perceptions of conceptual understanding, confidence in performing laboratory experiments, understanding of lab-related calculations, and the number of attempts required to complete prelab assignments. Data analysis revealed that students using hybrid prelabs reported greater conceptual understanding, higher confidence in performing experiments, greater understanding of calculations, and required fewer attempts to complete prelabs. Overall, these findings suggest that guided use of GenAI can support student learning and enhance preparation for laboratory activities.

Oral Presentations

Molecular & Genetic Mechanisms

Moderator: Jeff Duerr

Metacentric vs. Acrocentric Chromosomal Inheritance of the 2-3 Fused Chromosome in the Genetic Background of *Drosophila novamexicana*

Regan Mitchell, Sophia Jetton, Nicholas Stewart / Biology Department, Southern Oregon University, Ashland, OR 97520.

Large alterations of chromosomes are usually deleterious, yet throughout evolutionary time they are common. One hypothesis to explain this apparent paradox is meiotic drive. Meiotic drive is the breaking of traditional Mendelian inheritance, i.e. the chance of any allele transmission rate above 50%. One of our model organisms, *Drosophila americana* has undergone 2 fusion events within the past 500,000 years, the X and 4 chromosomes, as well as the 2 and 3 chromosomes. This contrasts with their sister species, *Drosophila novamexicana*, which has maintained all unfused (acrocentric) chromosomes. Previous research supports the existence of meiotic drive in the inheritance of fused (metacentric) 2 and 3 chromosomes over acrocentric chromosomes in female meiosis within *D.americana*. Our research aims to determine the *D. americana* metacentric 2-3 centromere inheritance patterns within the genetic background of *D. novamexicana*, to determine 1) if meiotic drive favoring the centromere is present independently of genomic background, and 2) if meiotic drive maintains acrocentric chromosomes in the *D. novamexicana* genetic background. Our results do indicate that meiotic drive is not independent of genomic background but are inconclusive as to whether meiotic drive is maintaining acrocentric chromosomes in the *D. novamexicana* genetic background. This indicates that there was an evolutionary change since divergence from *D. novamexicana* that led to this bias in transmission in *D. americana*. These findings highlight the potential of deducing and understanding the regions of genetic background involved in meiotic drive.

Thyroid Hormone Receptor Alpha in Mitochondrial Transcription.

David J Mahrt, Megan S Bestwick / Department of Chemistry, Linfield University, McMinnville, OR, 97128.

Mitochondrial DNA (mtDNA) encodes core proteins in the electron transport and oxidative phosphorylation pathway. The remaining subunits of these protein complexes are encoded in the nuclear genome, translated in the cytosol and imported into mitochondria. Transcription of mtDNA transcription is achieved with three core factors: mitochondrial RNA polymerase (POLMRT), mitochondrial transcription factor A (TFAM), and mitochondrial transcription factor B2 (TFB2M). Regulation of this process requires additional proteins, and likely transcriptional coordination with the nuclear genome. We propose that the thyroid hormone receptor alpha (THRA) acts to coordinate transcription between the two genomes. The thyroid hormone, triiodothyronine (T3), increases mitochondrial biogenesis through the activation of the THRA protein. This protein is a ligand activated nuclear receptor that can also translocate to the mitochondria. We aim to determine if THRA has a direct effect on the rate of transcription of mtDNA. We are currently expressing and purifying the THRA protein for in vitro assays. Understanding the role of THRA in mtDNA transcription will lead to a better understanding of the mechanisms generating of the OXPHOS pathway complexes and mitochondrial biogenesis.

Utilizing bioinformatics to assess genomic diversity of aquatic *Priesta megaterium* in sites of varying human interference.

Kellianne Richardson, Oz Lavering, Nicholas Stewart / Biology Department, Southern Oregon University, Ashland, OR 97520.

Priesta megaterium, previously known as *Bacillus megaterium*, is a species of rod-shaped, Gram-positive bacteria prevalent in marine and terrestrial environments globally. Recognized for their impact on carbon flow as well as endophytic and nitrogen fixative abilities, they play crucial roles in the habitats they occupy. As human marine interference continues to grow through recreational and industrial means, like boating, fishing and hydropower, understanding impact on the aquatic biotic environment is important in understanding the future health of the ecosystems affected. Genomic sequencing provides insight into evolutionary divergence within populations through real-time genetic analysis. Utilizing bioinformatics and comparative genomics to identify changes within the genome in relation to location can help determine if marine microbiomes may be changing more rapidly in response to human obstruction. The proposed method of aquatic microbiota analysis is through examining the unique mutation rates of *P. megaterium* samples from 2 Kansas lakes, each sampled at 10 different locations. Each location within their respective lake is subject to differing amounts of human interaction, ranging from high levels (near boat docks, etc.) to minimal interference. Deep sequencing of each genome to identify genomic diversity has thus far identified differences between areas of high human interference and those with minimal interference in unique single nucleotide polymorphism count, but with relatively equivalent spread across the genome. Further inter and intrapopulation comparisons between both lakes and their sampling sites may reveal if specific locations are driving mutation rates within their respective lakes.

Using Molecular Evolution to Explore Alternative Receptors for SARS-CoV-2

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SARS-CoV-2, the virus which caused the Covid-19 pandemic and likely jumped from bats into humans, canonically uses the protein ACE2 to infect cells. Recent molecular and cell culture studies have found 22 possible human alternative receptors. However, it is unknown if these receptors represent biologically significant entry mechanisms for SARS-CoV-2 in vivo. Persistent selective pressure between viruses and hosts often drives nucleotide changes in host proteins, including viral receptors. Virus-driven natural selection can be detected by examining the receptor evolution across related species. A signature of natural selection at virus-bound residues of an alternative receptor may indicate historical use by SARS-CoV-2 and its relatives to infect their hosts. To determine if alternative SARS CoV-2 receptors have been subject to SARS-CoV-2-related sarbecovirus induced natural selection in bats, established computational molecular evolution analysis tools were used to identify sites of positive selection. So far, 8 genes show signs of positive selection, with 2 being particularly promising due to clustering of positive selection in regions accessible by the virus. To determine if these receptors are functionally relevant to the virus, an experimental strategy was established to test the predictions generated by the previous sequence analysis. Human and bat alternative receptor sequences will be cloned into expression plasmids. These plasmids will be transiently expressed in 293T cells, which are naturally resistant to SARS-CoV-2 infection, and then infected with SARS-CoV 2-spike pseudotyped VSV-luc reporter virus. These comprehensive studies will supply a deeper understanding of whether SARS-CoV-2 and related sarbecoviruses are likely to use alternative receptors in bats.

Fetal sex and intrauterine growth restriction program tumor microenvironment response to cancer.

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Pregnancy complications disproportionately impact male offspring more than females, with an increased risk for certain cancers, including pancreatic ductal adenocarcinoma (PDAC). The differential susceptibility of male offspring is thought to arise from organ-specific differences in fetal DNA epigenetic programming. We hypothesize that variance in PDAC development and lethality may begin with fetal programming in the womb. To test this hypothesis, we injected murine pancreatic cancer cells (KPC) into the pancreatic tails of six groups of genetically identical, age-matched adult C57BL/6 mice in a single-batch experiment (n=36 mice). Ampyrone treatment was used to achieve abdominal skin transparency prior to injection. Intrauterine growth-restricted (IUGR) males and females were used to investigate the effects of fetal growth restriction on tumor growth. Castrated and ovariectomized mice served as hormonal controls, and intact, normal-birthweight males and females served as reference controls. Cancer cells were allowed to grow for 2 weeks before all animals were autopsied to measure primary tumor volume, enumerate metastatic lesions, and perform histologic analysis of tumor microenvironment response. Our findings demonstrate that sex differences in PDAC development are not entirely testosterone or estrogen-dependent and that fetal growth restriction alters the tumor microenvironment independent of testosterone.

Evolution, Paleobiology & Comparative Biology

Moderator: Melissa Kelley

From bones to behavior: reconstructing locomotion in fossil mammals.

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Understanding how early mammals moved (locomotion) requires bridging modern biological data with the fossil record. Although both living mammals and their extinct relatives show diverse locomotor behaviors, including repeated origins of treeclimbing (arboreality), the timing and frequency of these shifts remain debated. A major obstacle is the limited postcranial fossil material available for many early mammal groups. To address this challenge, we apply a comparative framework that links simple 2-D anatomical measurements in living mammals to locomotor behavior, allowing us to infer movement patterns in fossil taxa. Our approach integrates linear measurements from the limb skeletons of roughly 60 Mesozoic mammals with a large comparative dataset of 285 extant species. Using regression models trained on modern mammals, we use anatomical predictors that reliably distinguish arboreal from terrestrial locomotion. These models are then used to estimate locomotor modes in fossil species and to evaluate whether arboreality was likely ancestral for major early mammal lineages. Across most groups, we find weaker support for arboreal adaptations than recent interpretations have suggested. One notable exception is the Jurassic gliding haramiyidans, which consistently exhibit traits associated with climbing and aerial locomotion. Overall, our results challenge the idea that arboreality was widespread or ancestral among early mammals. By emphasizing quantitative comparative methods, this study provides a more rigorous framework for reconstructing locomotor evolution and highlights the value of integrating modern biological datasets with the fossil record.

Hips Don't Lie: Reinforcement Learning allows T. rex to walk again

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Dinosaurs were often orders of magnitude larger than non-dinosaurs from elsewhere in time, and almost all groups evolved quadrupedal bodyplans, with stout, pillar-like legs to manage the bulk of their bodies during locomotion. Whale-sized sauropods were quadrupeds, as were the armored thyreophorans, the horned ceratopsians, and even the duckbilled ornithomimids were facultatively quadrupedal for ostensibly the same reason. But theropods were obligate bipeds, and the only such animals in Earth's history to achieve multitonne gigantism. They had long tails, heavy thoracic cages, and large heads, often weighing hundreds or thousands of kilograms of largely unsupported bodyweight, carried against a significantly offset center of mass. Despite these obvious challenges, the bodyplan was highly advantageous for them, and remained almost unchanged for over 130 million years, across multiple lineages and in different environments. Strangely, this bodyplan has never re-evolved in any group, so we have no observable reference to compare how individuals may have adjusted their tails when changing direction, or how they carried their torsos at different speeds, or when feeding, or how they reacted to flexibility needs associated with other life circumstances. They may have bobbed their heads as do modern turkeys, or waddled as do ducks, or sauntered like herons, or, their great size and long tails may have forced them to use a gait unique to large theropods that, until now, has been lost to speculation. But reinforcement learning can finally allow us to answer this question empirically with the use of simulations. Artificial intelligence and machine learning promise to radically improve how we understand all disciplines, including paleontology, and in this case were used to scientifically replicate the standing posture and gait of the most exemplar theropod, *Tyrannosaurus rex*. It was among the very largest of all theropods at ca. 9 tonnes and ~12 m in length, and has been popular in both public and scientific attention since first described by HF Osborn in 1905. *T. rex* remains an enduring global icon, and the ongoing debate about its running and walking abilities make it the ideal model for research about postural stability and locomotion in dinosaurs.

What is a mammal? Insights from recent fossil discoveries

David M. Grossnickle / Natural Sciences Department, Oregon Institute of Technology, Klamath Falls, OR 97601.

Extant (living) mammals are easy to distinguish from non-mammals – they evolved from a single ancestral lineage and share common traits such as hair, mammary glands, and endothermy. However, when investigating the fossil record of mammals, especially those of extinct lineages, and their close relatives (mammaliaforms), it becomes much more challenging to distinguish mammals from non-mammals. This is largely due to the lack of preserved soft tissue structures (e.g., hair) in most fossils. From a paleontological perspective, there emerges two central and related uncertainties: 1) the presence of shared traits in extinct mammalian lineages and 2) the evolutionary relationships of early mammalian lineages. I review recent fossil discoveries and paleontological studies that contribute to (and sometimes blur) our understanding of mammalian origins and early evolution. I argue that there remains considerable uncertainty concerning which fossil lineages are mammals, and I advocate for continued paleontological and developmental biology research to help investigate the evolutionary origin of mammals.

Early Evidence of Chaparral-like Vegetation from the Latest Miocene Anaverde Flora, Palmdale, California.

Jeffrey A. Myers¹, and Diane M. Erwin² / ¹Western Oregon University Department of Earth Science, Western Oregon University, Monmouth, OR 97361. ²University of California, Berkeley, Museum of Paleontology, 1101 Valley Life Sciences Bldg., Berkeley, CA, 94720.

Expansion of the Antelope Valley Land Fill (AVLF), Palmdale, CA, exposed the basal member of the Latest Miocene (~5-6 Ma) Anaverde Formation, which holds plant fossils that reflect an early precursor to California chaparral vegetation. The flora, in total, includes twenty-two taxa, reflecting moderate-diversity coastal riparian, oak woodland, and chaparral-like vegetational communities that grew during a period of profound global cooling and environmental change. The Anaverde Flora has, in the past, been considered important to understanding the role of neotropical taxa in the evolution of California flora and vegetation. Instead, our study concludes that all taxa known from the Anaverde Flora represent families and genera present in early Tertiary temperate North American vegetation, almost all of which occur in coastal California plant communities today. The 2023 AVLF expansion produced fossils of *Arctostaphylos* (Manzanita), *Cercocarpus* (Mountain Mahogany), *Philadelphus* (Mock Orange), and *Holodiscus?* (Ocean Spray). These, along with previously identified fossils of *Ceanothus* (California Lilac), *Rhamnus?* (California Coffeeberry), *Malosma* (Sumac), and *Quercus pliopalmeri* (Scrub Oak), contribute a fuller picture of plants that grew in a chaparral-like habitat on poorly developed, well-drained soil. Taxa that today are limited to Neotropical vegetation have not been recognized in the Anaverde flora. Instead, its taxonomic composition closely resembles that of other southern and central California paleofloras of comparable age, and reflects a widespread, moderate diversity Late Miocene vegetation type, lacking diverse thermophylls present in older California assemblages but predating the explosive diversification of families such as Rhamnaceae, Ericaceae, and others dominant in modern California chaparral vegetation.

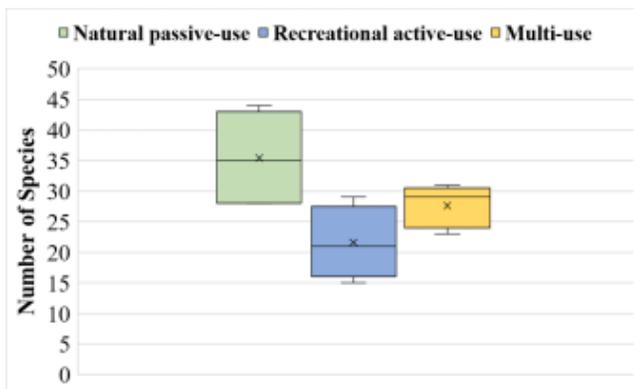
Ecology, Biodiversity & Environmental Systems

Moderator: Margaret Metz

Monitoring Local Plant Biodiversity Patterns in Parks of Salem, OR.

Ellie Scott, Asia Scott, Arthur Taylor, Michelle Talal, Willamette University, Salem, OR 97301.

Urban nature provides many benefits for people and the environment, but there is limited information on plant biodiversity patterns across park types. Using a case study in Salem, Oregon, we hypothesized that there would be a difference in species richness across park types, with natural passive-use parks having the greatest number of species, especially native species because they are adapted to local conditions and may require less intensive management. We also predicted that multi-use and recreational active-use parks would have a greater number of non-native species due to human preferences for their aesthetics. Using a random stratified sampling design, we selected five of each park type, totalling 15 parks. For each, we



collected data within five randomly selected 400m² plots and recorded the species and cover of trees, saplings/shrubs, and woody vines. We sampled five randomly selected 1m² subplots within each 400m² plot for herbaceous species and cover. We found 157 species from 122 genera and 54 families, which included 19% trees, 32% shrubs, 46% herbs, and 3% vines species. Of these species, there were 45% native, 41% non-native, 8% invasive, and 6% unknown species. The Kruskal-Wallis tests revealed significantly more trees in natural passive-use parks ($p < 0.05$), higher species richness, and higher numbers of native and invasive species compared to recreational active-use parks. This study highlights key improvement areas in park management, including encouraging additional invasive species removal and monitoring in natural passive-use parks, as well as promoting more native species in multi-use and recreational active-use parks.

Assessing Lepidoptera biodiversity using morphological and DNA barcoding approaches

Elise Johnston, Sarah Comstock / Science Department, Corban University, Salem, OR 97317.

Butterfly and other Lepidoptera species are experiencing rapid declines worldwide. Moth species in particular, because of their primarily nocturnal lifestyle, have not been as closely monitored. Corban University boasts 203 acres of the last temperate broadleaf and mixed forest biome in the western United States, making it an excellent place to observe Lepidoptera populations. This ongoing study seeks to catalog all Lepidoptera species found on campus using two different techniques. Butterflies and diurnal moth species were spotted and captured actively all over campus, and UV light trapping was used for nocturnal species. All specimens were photographed for morphological identification and released when possible. When morphological identification was inconclusive, DNA barcoding was used to confirm species identity. DNA was extracted from specimens, and the cytochrome c oxidase subunit I (COI) gene was amplified by PCR and sequenced using Sanger sequencing. Resulting sequences were compared against reference databases using BLAST and MUSCLE alignment to determine species-level matches. Over the course of a year, more than 30 species have been identified. Lepidoptera are vital species as pollinators, members of the food chain, and bio-indicators. Insights into their diversity will not only give an idea of the species still present and thriving, but also provide valuable information on the health of the Corban University campus ecosystem at large.

Seagrass modulates HABB species in temperate coastal food webs

Alex Baca¹, Kailani Maxwell¹, Dominic Nguyen¹, Amy Segura¹, Ryan Kenton¹, Christine Weilhoefer¹, Cecilia Brothers² / University of Portland Department of Biology, 5000 N Willamette Blvd, Portland OR 97203

P. nitzschia is a species of marine algae responsible for harmful algal bacterial blooms (HABBs) that can produce a neurotoxin known as domoic acid (DA) as a metabolic byproduct, which can be dangerous for human health and has negative impacts on the overall ecosystem. Recent research in the field of microbiology has suggested that eelgrass beds (*Zostera marina*) may play regulatory rolls in preventing or limiting the frequency and severity of HABBs from species like *P. nitzschia*. The present study aims to quantify the relationship between the presence of eelgrass in marine ecosystems and the activity of HABB relevant species like *P. nitzschia* and bacteria in the *Vibrio* genus. This was achieved through intensive weekly and biweekly sampling over a 7-month period at Netarts Bay and Tillamook Bay in Oregon. Over this period environmental DNA (eDNA) was collected for sequencing in order reveal the microorganism species composition of seawater, samples of seawater treated with a formalin preservative were analyzed under a microscope to obtain algal cell counts, and seawater was plated onto *Vibrio* specific media to obtain an estimation on the presence of *Vibrio* in CFUs/mL. This data was then compared to the amount of eelgrass that was found at each specific sample site, on the day. Strong *in vivo* evidence of eelgrass's positive regulatory effects on HABBs can be used to better inform environmental policies that protect vital eelgrass ecosystems along the West Coast of the United States and can help lessen the dangerous side effects of marine HABBs.

DNA-Barcoded Nanoparticles for Environmental Tracing.

Madelynn Satter, Elaine Slifer, Dr. Sarah Comstock / Department of Math and Science, Corban University, Salem, OR, 97317.

This study investigated novel DNA tracers for detecting water flow in a freshwater system, focusing on their synthesis, stability, and environmental application. The DNA nanoparticle tracer technology developed by our group consists of an encapsulated DNA bound to an iron oxide core coated in silica. After developing a synthesis protocol that produced fully encapsulated particles with exposed amino groups, tracer stability was assessed using ICP-OES to evaluate tracers under neutral aqueous conditions by immersing samples in tap water for one week. No detectable leaching of transition or heavy metals relative to baseline measurements was observed. Multiple inputs of DNA tracer were introduced into distinct water sources converging into a single output source. These streams had a shared drainage system, allowing tracer recovery at a single downstream collection point. An additional DNA tracer was introduced at an upstream location within the drainage network. Tracer transport, concentration and retention were monitored over time, and connectivity of water sources was verified using qPCR. These results demonstrate the potential of DNA nanoparticles as effective and stable tools for tracking water flow dynamics. Future studies involving longer deployment periods, larger water volumes and additional input sources would further validate their applicability in environmental systems.

Organismal Biology & Physiology

Moderator: Nathan Kirk

Knives Out: Natural variation in nematocyst length and density across colonies of *Anthopleura elegantissima* on the Oregon coast

Itzel Delgado Lopez¹, Eva Harvey¹, Nathan Kirk¹, Caitlin Plowmann², Rowan McLaughlin² /¹Department of Integrative Biology, Oregon State University, Corvallis OR 97330. ²Oregon Institute of Marine Biology, University of Oregon, Charleston OR 97420.

Sea anemones are great examples of animals that develop weapons and neurotoxins to defend territory. *Anthopleura elegantissima* is an abundant intertidal anemone along the Western United States. These colonies then engage in intraspecific competition for space using specialized structures called acrorhagi that are laden with nematocysts, single-use organelles, which can inject neurotoxin into conspecific anemones. Although we know the result of these aggressive interactions is the retreat of one or both combatants, less is known about what traits predict the outcome and which colonies will ultimately prevail in the field. Here we examined variation in nematocyst length and density in acrorhagi of multiple clones from colonies on the Oregon coast hypothesizing that increased weaponry could contribute to the success of certain clones: some of the clones have grown in population size over the last 3 years while some have decreased. To determine the density, part of the body column containing the acrorhagi was dissected out and prepared for histological sectioning. Slides were made of the acrorhagi and densities were calculated and standardized for body size. Preliminary results show that there are differences among the nematocyst densities of 10 colonies examined so far ($p = 1.66 \times 10^{-9}$). These will then be correlated with changes in colony size over the last 4 years to determine how the numbers of weapons predicts change.

Effects of habitat disturbance on wildlife stress and immune function

Diana Hutchings¹, Jillian Holtcamp¹, Laurie Dizney PhD¹, Elizabeth Addis PhD², & Ashley Beck PhD³ /¹ Department of Biology, University of Portland, Portland, OR 97203. ² Department of Biology, Gonzaga University, Spokane, WA 99258. ³Department of Biology, Carroll College, Helena, MT 59625.

As natural landscapes are increasingly transformed by human development, wildlife faces new challenges. Most research has focused on ecological impacts of these changes, including increases in establishment of non-native species, increased competition, and changes in biodiversity. Fewer studies have examined the impact of abiotic changes, such as artificial light and anthropogenic noise on wildlife. These alterations can interfere with many physiological processes, including those that regulate stress responses and immune function. We examined the relationship among habitat disturbance, anthropogenic light and noise, chronic stress, and immune function in Western deer mice (*Peromyscus sonoriensis*), predicting that increased levels of disturbance would be associated with an increase in anthropogenic light and noise, which in turn will elevate stress and reduce immune function. We captured deer mice for three years across twenty field sites ranging from a national forest to city parks, allowing us to compare a single species across varying levels of disturbance. At each site, we collected data on light (lux) and noise (dB) using a HOBO data logger. Chronic stress was assessed from hair corticosterone via radioimmunoassay analysis. Immune function was assessed using total white blood cell (WBC) counts per mL of blood and percent of B220+ cells. By integrating measures of abiotic factors and physiological stress with immune metrics, this study provides valuable insight into how anthropogenic environmental changes and habitat disturbance directly impact wildlife health, as well as why some species can tolerate high levels of disturbance while others cannot.

Ecology, Behavior, and Morphology of Rough-skinned newts (*Taricha granulosa*) in dynamically saline environments.

Sophia K Espinoza , Dr. Gareth Hopkins^{1/1}Department of Biology, Western Oregon University, 345 Monmouth Ave N, Monmouth, OR, 97361.

Aquatic ecosystems can range from freshwater to saline depending on their proximity to natural (e.g., oceanic) or anthropogenic (e.g., road salts) sources of salt. This variation in salinity often excludes many osmotically-sensitive freshwater organisms, such as amphibians, from brackish habitats. However recent evidence documents amphibians around the world breeding in habitats that differ greatly in salinity. How amphibians navigate this aquatic stressor is not well understood. This study aimed to document the spatial and temporal variation of salinity using a tidally-influenced system on the Oregon coast, and record Rough-skinned newt (*Taricha granulosa*) distribution, behavior, and morphology at this site compared to a constantly freshwater system. Two sites in western Oregon (coastal/saline and inland/freshwater) were selected for their water dynamics and abundance of newts, then surveyed for salinity fluctuations and newt presence, size, and distribution along short (hourly) and long (monthly) term spatiotemporal scales. Coastal newts were found in salinity ranging from 0.29ppt up to 12.80ppt (seawater ~35ppt). Morphological data recorded significantly smaller newts in the coastal population suggesting a possible trade-off scenario, as seen in other amphibian species. Site salinity was directly impacted by tidal events and displayed non-uniform stratification behavior, suggesting that predictable oceanic ebbs and flows are only one piece of complex coastal freshwater ecosystems that vulnerable amphibians navigate.

LEA Symptom Screening in a Collegiate Cheer and STUNT Team

Erin Mitchell, Makaylee Kuiken, Alyse Webberley, Tyler Whited, Matthew Miller / Department of Kinesiology, George Fox University, Newberg, OR, 97132.

Low energy availability (LEA) places athletes at risk for relative energy deficiency in sport (RED-S), a multifactorial condition that affects physiological health, psychological well-being, and athletic performance. Research on LEA has primarily focused on endurance athletes, with limited data on resistance-trained populations. This highlights the need for research in sports such as Cheer and STUNT. The objective of this study was to screen for symptoms of LEA among George Fox Cheer and STUNT athletes, and to briefly assess the usefulness of educational team lectures focusing on topics of LEA. Forty female athletes voluntarily completed a survey including the LEAF-Q, SCOFF, GAD-7, ASSQ, and APSQ. The survey also briefly assessed athlete awareness of LEA and athlete confidence in management of overall health. Symptoms of anxiety, sleep difficulty, and psychological strain were present across the team, with position-specific trends observed. A brief educational intervention significantly improved athletes' confidence and awareness related to energy availability and strategies to optimize their health. These findings highlight the importance of position-specific screenings and education for resistance-trained athletes. The study's results support the need for further research on LEA and RED-S in Cheer and STUNT populations.

Physics, Mathematics, Computer Science & Statistics Talks

Moderators: Corban Harwood and Scott Prahl

Convergence values for several variants of the tangent inverse series

Stephen Hantzmon / Mathematics Department, Western Oregon University, Monmouth, OR, 97361.

This research was prompted by an introductory mathematics research focused class. Specifically, it involves series, infinite sums of numbers which may or may not add to finite ones. In this instance, we explore series that do in fact converge. To do so, we use an arctangent subtraction identity and telescoping properties of series, finding the specific convergence values of two arctangent series and attempt to generalize thrice; First successfully with a general arctangent series that converges to a real number in a bounded set, the second time unsuccessfully, and the third successfully with a general series that converges to any real number in a real, unbounded function.

Developing microrheology techniques to probe myosin's role in cellular mechanics.

Ben M. Weisz, Cole DeBois, David Altman / Department of Physics, Willamette University, Salem, OR, 97301.

Myosin is a molecular motor inside cells that walk along actin, a protein filament. They can create order in the cells by generating forces that can be used to move cargo. An understudied function of myosin is their ability to create structural linkages in the cell cytoplasm. We hypothesize that one of the ways they regulate intracellular trafficking is by affecting the material properties of the cell through actin crosslinking. We are investigating myosin's role in controlling material properties in retinal pigment epithelial cells using microrheology techniques that probe the material properties of fluids utilizing microscopic tracer particles. Here we detail two such approaches, active and passive microrheology. In both approaches, a probe particle in the cell is tracked while experiencing perturbing forces. In passive microrheology these forces primarily come from thermal motion, while in active microrheology we apply these perturbations with an optical trap. We expect these techniques to yield different results for systems out of equilibrium, such as cells. Here we will describe our implementation of these two techniques and present proof of principle data.

A semiclassical approach to rainbows

Jesse M. Kinder¹, Philip C. Nelson² / ¹Department of Natural Sciences, Oregon Institute of Technology, Klamath Falls, OR 97601. ²Department of Physics and Astronomy, University of Pennsylvania, Philadelphia, PA 19104.

Rainbows are familiar optical phenomena, but an accurate description of their detailed structure—including faint supernumerary arcs inside the primary bow and the dark band between primary and secondary rainbows—has relied on sophisticated mathematical treatments that obscure the underlying physics. We present a conceptually simple theory of rainbow scattering based on interfering ray optics using concepts familiar from introductory physics: reflection, refraction, and interference. This approach successfully predicts experimental features including the positions and intensities of supernumerary bows, the shape of the primary rainbow's peak intensity, and the intensity distribution within the dark band. Our theory agrees with brute-force numerical calculations while providing physical insights into rainbow formation that connect ray optics to wave optics. The framework bridges classical geometric optics (rays and Fermat's principle) with quantum electrodynamics (Feynman path integrals), offering a conceptual pathway from classical to quantum theories of light.

Chemistry Talks

Moderators: Andrew Baggett and Cooper Battle

Assessing stability and sensor response of FRET pair-modified quadruplex molecular beacons.

Sheridan Donovan-Stauder, Cooper H. Battle / Department of Chemistry, Willamette University, Salem, OR, 97301.

A mechanism for the early detection of disease is through the presence of small biomolecules known as micro-RNA (miRNA), which have been shown to be up- or downregulated in the early stages of disease. MiRNA's usefulness as a biomarker has led to the development of nucleic acid-based sensors—called quadruplex molecular beacons (QMBs)—which can detect specific miRNA strands. The addition of a FRET pair modification allows for the QMBs to exhibit a detectable fluorescence signal in the presence of a target miRNA strand; however, this FRET pair can affect the overall stability and sensitivity of the sensor. Our project focuses on examining the impact of FRET pair positioning on structurally diverse QMBs under varying chemical environments. UV-Visible thermal denaturation curves were used to assess stability of QMBs, while sensor response was determined via relative fluorescence increase over the course of a target strand titration. Our results suggest that internal FRET pair modifiers provide more stability and a more significant increase in fluorescence than terminal modifications.

The impact of holmium and ytterbium dopant concentrations in double perovskites on light upconversion.

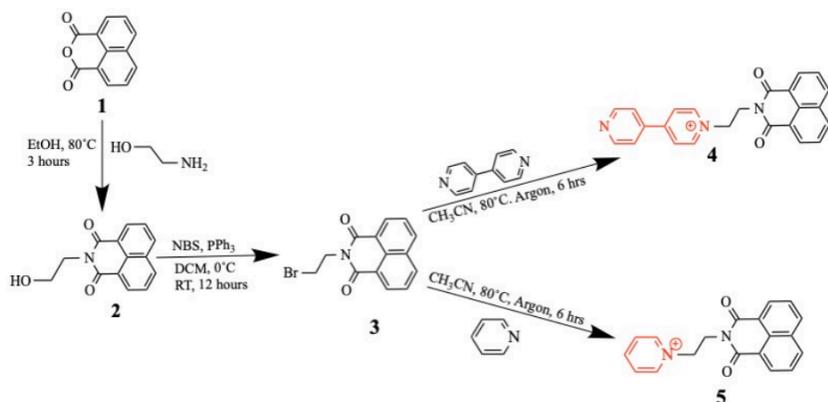
Eva Conour, Abigale Puccini, Artiom Skripka / Department of Chemistry, Oregon State University, Corvallis, OR, 97330.

Lanthanide-doped materials have become promising candidates in a variety of optical applications, due to their ability to convert longer wavelengths of light into shorter wavelength emissions (upconversion) and perform photon avalanching. Engineering an optimal host material with optimal lanthanide doping concentrations is vital to maximizing the performance of light-upconverting materials. We found that $\text{Cs}_2\text{NaInCl}_6$, prepared via hot-injection synthesis, facilitates light upconversion with ytterbium as a sensitizer and holmium as an activator. Critically, the presence of chloride, a heavy halide, in the lattice decreases multi-phonon relaxation and increases the contribution of higher excited states to the overall emission spectrum. Ratios between the two dopants affect the material's optical properties. Increasing the holmium concentration while maintaining 20 mol% ytterbium resulted in a sharp decrease in the orange-to-red emission ratio under near-infrared excitation. Meanwhile, increasing the ytterbium concentration from 5 mol% to 50 mol% at a constant holmium concentration of 20 mol% led to an unexpected change in the excited-state population mechanism. Our current studies focus on understanding these photoactivation dynamics of lanthanide-doped heavy halides to tailor optical properties for applications such as medical imaging, sensing, and photonics.

Synthesis of Rylene Dye Derivatives for use as Fluorescent Supramolecular Sensors

Mckenzie Lee, Mika Boston, Cooper Battle / Department of Chemistry, Willamette University, Salem, OR, 97301.

Rylene imide dyes are useful chromophores that have the potential to be used as fluorescent sensors to test the effectiveness of molecular capsules for drug delivery purposes. These dyes display good photochemical stability, tunable photophysical properties, and structural versatility, which allows them to be used as the base fluorophore for a sensor to detect formation of host-guest complexes in aqueous mediums. For this study, we are conjugating a 1,8-naphthalimide to a series of cationic amines acting as electron acceptors for photoinduced electron transfer (PET), quenching fluorescence emission. On



Scheme 1. Synthesis of bipyridine and pyridine sensors.

encapsulation of the cationic amine in a hydrophobic host molecule (e.g., cucurbit[7]uril), an increase in the energy of the charge-transfer state turns off PET and restores fluorescence. In this talk, we will discuss our success in designing a divergent synthesis generating a 1,8-naphthalimide able to be differentially substituted with different amines. The current focus of this research involves bipyridine and pyridine acceptors, with future goals to further diversify the scaffold before testing photophysical properties. Our key intermediate was synthesized in two steps from 1,8-naphthalic anhydride, with an average yield and purity of 89% in step 1, and 70% in step 2.

Untargeted metabolomics detection and machine learning prediction of leaf adulteration in *Withania somnifera* root extract using LC-EAD-QTOF mass spectrometry

Oshoma Erumiseli¹, Emily McDonald¹, Rudranil Dutta¹, Luke Marney^{1,2}, Jaewoo Choi^{1,2}, Amala Soumyanath^{2,3}, Jan F. Stevens^{2,4,5}, and Claudia S. Maier^{1,2,4} / ¹Department of Chemistry, Oregon State University, Corvallis, OR, 97331. ²Botanical Dietary Supplements Research Center, Oregon Health & Science University, Portland, OR, 97239. ³Department of Neurology, Oregon Health & Science University, Portland, OR, 97239. ⁴Linus Pauling Institute, Oregon State University, OR, 97331. ⁵Department of Pharmaceutical Sciences, Oregon State University, Corvallis, OR, 97331.

Ashwagandha (*Withania somnifera*) is a widely used botanical that is increasingly vulnerable to economically motivated adulteration, particularly through the substitution of leaf material for root. In this study, we present an integrated workflow combining untargeted metabolomics and machine learning to detect and quantitatively estimate leaf adulteration in *W. somnifera* root extracts. Samples were prepared along a controlled 0–100% leaf–root mixing gradient and analyzed using liquid chromatography coupled to quadrupole electron-activated dissociation time-of-flight mass spectrometry. A principal component analysis (PCA)–based calibration model showed clear and systematic separation of leaf-enriched and root-enriched samples as a function of adulteration level. Projection of PCA loadings into cosine-similarity molecular networks revealed structurally related metabolite clusters specific to individual plant parts, providing mechanistic chemical context for the observed separation. Machine learning regression using least absolute shrinkage and selection operator (LASSO) and elastic net enabled effective feature selection and accurate prediction of adulteration levels in unknown samples. Overall, these results demonstrate a robust analytical platform that integrates calibration modeling, molecular networking, and machine learning for improved quality control and authentication of botanical products.

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