John S. Rogers Program

2024
Summer Science Research Poster Conference

Tuesday, September 17
4:30 – 6:00 pm
Stamm Combo, Fowler Center

John S. Rogers Science Research Program

This program prepares outstanding students for careers in the sciences by supporting collaborative scientific research between students and faculty. In addition, the program aims to attract and retain outstanding students and faculty in the mathematical and natural sciences. Rogers fellows are trained not only as scientists, but as scientists who have a responsibility *to communicate the purpose and results of their work to a general audience.*

The following pages contain summaries of the research projects conducted during the summer of 2024. In these abstracts and in the conference posters, the names of the student researchers are followed by their expected year of graduation; the project director's name is listed last. To get the most out of the conference, ask the student presenters to explain to you the essence and significance of their research projects.

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A Method to Rapidly Pattern Breast Tumor Microenvironment Cells Using a Laser Assisted Bioprinter. Johnathan Pang '26, Haylie Helms, MS, Luiz Bertassoni, DDS, PhD, *Knight Cancer Precision Biofabrication Hub, Oregon Health & Science University*

The tumor microenvironment (TME) is composed of many cell types interacting with one another to either promote or inhibit tumor progression. Current models such as co-cultures and spheroids used to study the TME lack the ability to control the spatial organization of these cells, which has been proven to be a key contributor to clinical outcomes. While our lab has developed a method to pattern different cell types with subcellular resolution, it is limited in throughput by the amount of time it takes to conduct a single print. Here we developed a method to rapidly pattern cells of the breast TME using a laser assisted bioprinter.

Functional Diversity of Phospholipase Ds in the *SicTox* gene family.
Finn Watson '26[1], Lindy Gewin[1], Matthew Cordes[2], Greta Binford[1].
[1]*Department of Biology, Lewis and Clark College,* [2]*Department of Chemistry and Biochemistry, University of Arizona*

Venoms are made up of hundreds of different molecules that serve various functions. The *SicTox* gene family, found in brown recluse spiders and their close relatives, codes for an enzyme known as Phospholipase D (PLD). Variants of these enzymes cleave phospholipid heads from their tails with varying levels of substrate specificity. PLDs are known to be the cause of tissue damage in humans and can cause neurotoxicity in insect prey. PLDs make up more than 50% of the proteins found in brown recluse spider venom, indicating a major biological role, however despite this outsized presence in venom, the effects of PLD substrate specificity on biological systems are poorly understood. Our current working hypothesis is that varying specificity means that these toxins can target wider varieties of prey. In this study we performed in vitro cytotoxicity experiments by treating SF9 cells with both extant venom toxins and their mutants, as well as recombinantly expressed, computationally estimated, hypothetical ancestor reconstructions of *SicTox* and measuring their permeability via propidium iodide staining in a microplate format. SF9 cells have a balanced phospholipid composition making them ideal for testing a broad range of toxins. We find that an ancestral reconstruction of *SicTox* after being recruited into venom shows a higher ability to permeabilize cells in a shorter time frame than a prevenom ancestor. We also find that mutations adjacent to residues in the active site of extant toxins cause little to no change in activity from wild type, and may in some cases increase activity. We continue to work on refining these assays and performing more mutant and wild type comparisons. We also plan to begin work on elucidating the mechanisms of neurotoxicity in insects.

The AP-3 complex plays a role in lysosome-related organelle biogenesis and maintenance in *C. elegans* 1.5-fold embryos.

Bella Root ‘24, Greg Hermann, *Department of Biology, Lewis and Clark College*

Lysosome-related organelles (LROs) are an under researched group of cell type-specific compartments. LROs function in a variety of biological processes such as body pigmentation and healthy lung function. The nematode *Caenorhabditis elegans* has unique LROs called gut granules found in their intestinal cells. These gut granules contain autofluorescent material, allowing for easy identification and visualization of gut granule phenotypes.

The symphony of proteins required for gut granule formation and maintenance is not fully understood. I tested the role of the AP-3 complex in the formation/maintenance of gut granules during the 1.5-fold embryonic stage, when LROs are typically already formed. The AP-3 complex has been shown to mediate protein trafficking to LROs in cell cultures.

In a mutant *C. elegans* strain for which LRO formation is initially abolished, an AP-3 complex knockout rescued LRO formation at the 1.5-fold stage. I found that the loss of AP-3 complex function resulted in reduced LROs in the later pretzel-stage embryos. These findings indicate that the AP-3 pathway is required at 1.5-fold for regular formation of LROs.

In the *C. elegans acdh-11*(-) mutant, gut granules become essential for viability when metabolizing cyclopropyl fatty acids. Trent Nause ’26, Madeline Daniel ’24, Frances Parrott’22, David Nhek ’22, Francese Courtemanche ’25, Greg Hermann, *Department of Biology, Lewis & Clark College*.

Lysosome-related organelles (LROs) are specialized, cell-type-specific organelles derived from the endolysosomal system. LROs have diverse functions and morphologies depending on the host cell, and proper formation is crucial to health as defects can lead to genetic diseases like Hermansky-Pudlak Syndrome, which is characterized by oculocutaneous albinism and bleeding disorders. Fatty acid desaturation is crucial for lipid metabolism in metazoans, affecting membrane composition and signaling. *Acdh-11*, an acyl CoA dehydrogenase, is primarily known for its role in fatty acid metabolism, including the oxidation of cyclopropyl fatty acids (CFAs) derived from the food source. My research has found that in *acdh-11*(-) mutant worms, which are unable to effectively regulate cyclopropyl fatty acid (CFA) levels, gut granules become essential for viability. This suggests that gut granules may play a crucial role in storing excess CFAs, highlighting their importance in managing CFA accumulation and ensuring the organism's survival.

The GTPase activating protein ARFGAP1 and the AP3 complex are required for lysosome- related organelle biogenesis. Tevere Loeb ‘25, Caitlin Morris ‘16, Tori Eichten ‘19, David Nhek ‘22, Greg Hermann, *Department of Biology, Lewis & Clark College*.

Organelles are found in all eukaryotic cells, and their proper formation and function are vital for organismal health. Lysosome-related organelles (LROs) are an under-researched organelle family responsible for human body pigmentation, healthy lung function, and blood coagulation. The nematode species *C. elegans* is an ideal model organism for studying LRO biogenesis because they contain optically active LROs. If LRO biogenesis is disrupted, morphological features of LROs can be impacted, and these changes are easily observed in *C. elegans* with fluorescence microscopy.

The Hermann lab has screened for genetic mutations that specifically impact the size of gut granules. Many novel genes involved in LRO biogenesis have been identified through this process. One such gene is *arfgap-1*. Mutants with non-functional ARFGAP1 display an enlarged gut granule phenotype. Further experimentation has shown that *arfgap-1(-)* mutants are defective in protein trafficking to the gut granule. Similarly, the gene *apt-7* encodes a subunit of the AP3 complex, which is also involved in protein transport. Both *arfgap-1(-)* and *apt-7(-)* mutants are defective in delivering cargo with a di-leucine trafficking motif to the gut granule. In addition, the enlarged phenotype of *arfgap-1(-)* mutants is rescued by *apt-7(-)* in *arfgap-1(-);apt-7(-)* double mutants. This data is consistent with ARFGAP1 and the AP3 complex functioning on the same protein delivery pathway to the gut granule.

Ecological Interactions Between Native and Non-Native Lady Beetle Species. Jackson Gamby ‘24, Mairin Thorne ‘24, Heidi Liere, *Department of Biology, Lewis & Clark College.*

Lady beetles (family Coccinellidae) are found worldwide, with 90% of the almost 6000 species acting as agriculturally beneficial predators. Lady beetles are an important biological pest control, commonly consuming aphids, and are also used as a bioindicator species due to their sensitivity to climatic and trophic changes. As an important agricultural resource and a piece of our ecosystem’s diversity, the interactions between native and non-native species warrant further research.

In order to observe these native and non-native lady beetle species interactions, we ran two types of trials with a total of five species: competition and consumption. In the competition trials, we placed the lady beetles in a native/non-native species combination along with three aphids, and recorded their behaviors and weight change over the course of an hour. In the consumption trials, we placed the lady beetles with an aphid infested plant in a native/non-native species combination, and calculated their consumption rates over 24 hours. We also created an iNaturalist page to aid in our understanding of species distributions and seasonality.

The preliminary results demonstrate that *Harmonia axyridis*, a non-native species, is a stronger competitor than the native species tested. From further analyzing our data, we hope to see whether there is potential for coexistence, for which intraspecific competition would measure higher than interspecific competition.

Further research should be conducted to include more than two species per trial, as lady beetles are often found co-existing with multiple other species.

Tropical Rainforest Ecology: Niche Partitioning of Two Terrestrial Bromeliad Species.
Aeddon Woods ’26, Kai Larson ’25, Margaret R. Metz, *Department of Biology, Lewis & Clark College.*

The western Amazon Rainforest contains the world's greatest plant diversity at local scales of <100 km^2. For example, 1104 unique tree species are found within a 25 hectare study area in Yasuní National Park, Ecuador. Species coexistence is often explained by different competitive abilities for resources and the ability to partition a habitat by occupying different niches. Given plants need the same resources like sunlight, water, and soil nutrients, it is difficult to imagine the dimensions of a niche that could be partitioned to support so many species coexisting. Yet, tropical trees have numerous examples of species partitioning a habitat across environmental gradients, such as from a ridge to valley. This partitioning contributes to maintaining tree diversity but is less studied in herbaceous species which are a significant portion of a tropical rainforest's understory biomass. We censused two terrestrial bromeliad species in Yasuní, *Aechmea rubiginosa* and *Bromelia balansae*, to assess the population structure, spatial distribution and potential habitat specialization of these species in their low resource understory environment. These species have several meter long leaves and appear to occur in large clumps of clonal individuals throughout the 25-ha study area. We mapped and measured each individual, also collecting leaf tissue for trait analysis. We will compare current spatial distributions to historical observations from censuses in 1994 and 2022 to understand population growth rates. We plan to evaluate whether these two species are competing for space and resources or if each occupies its own niche determined by topography, light availability, or moisture

Effects of Adult Nicotine Exposure in *Drosophila melanogaster.* Avi Strok ’25, Jessica Naworski ’26, Norma Velazquez Ulloa, *Department of Biology, Lewis & Clark College*

We have characterized several behavioral and physiological effects of long-term nicotine exposure in adult *Drosophila melanogaster*.

Analysis of survivorship in response to varying concentrations of nicotine revealed concentration-dependent decreases in lifespan. Odor preference assays showed no difference in grape smell preference in response to nicotine exposure. A climbing assay found long-term nicotine exposure depresses locomotion. We also tested whether female flies prefer to lay eggs in a nicotine-laced or control environment. Female flies, regardless of nicotine exposure, laid a majority of their eggs on nicotine. Additionally, nicotine-exposed flies laid fewer eggs.

Decreased survival, egg laying, and locomotion all support the hypothesis that nicotine has systemic negative effects on our model organism. This work will continue with characterization of these behaviors on flies with single-gene mutations to identify nicotine sensitive and resistant phenotypes. Additionally, we developed tests for learning and memory following developmental nicotine exposure.

The Role of Sequences Flanking ESRRB Binding Sites in *Klf4* Enhancer Grammar. Rayne Avery '25, Sharon Torigoe, *Department of Biology, Lewis & Clark College.*

Enhancers are DNA elements composed of transcription factor binding sites (TFBSs) that have a critical role in the regulation of gene expression. In the study of enhancers, it is hypothesized that factors including spacing, order, and orientation of TFBSs in an enhancer influence its function. By studying this enhancer grammar, we hope to eventually be able to predict the location and function of enhancers for a given gene.

As part of an ongoing investigation into enhancer grammar in pluripotent stem cells, we have studied three nucleotide sequences flanking two ESRRB binding sites in the *Klf4* enhancer E2. KLF4 and ESRRB are critical transcription factors for the maintenance of pluripotency, the ability of a cell to differentiate into many different cell types. We find that ESRRB binding site flanking sequences in E2 influence gene expression in luciferase reporter gene assays.

Investigating protein:protein interactions within the Klf4 enhanceosome. Katie Ingersoll '25, Dr. Sharon Torigoe. *Department of Biology, Lewis & Clark College.*

Humans create different cell types by expressing, and then transcribing and translating different genes. Transcriptional regulation is the process of selecting which genes will be expressed out of the thousands of genes present in a cell. To better understand transcriptional gene regulation, we use the Klf4 system. By understanding the rules around Klf4 gene expression, we contribute to our knowledge of gene regulation as a whole, and provide insight into important factors exacerbating genetic disease. Klf4 is a type of protein called a transcription factor found within embryonic stem cells (ESCs) that controls pluripotency. Klf4 itself is tightly controlled by four main transcription factors: OCT4, SOX2, STAT3, and ESRRB. Previous studies have shown that the transcription factors bind each other to form an enhanceosome, a cluster of proteins that facilitates gene expression. However, while the rules governing this system, specifically regarding OCT4 and SOX2, have been widely investigated, we know very little about the physical interactions between the transcription factors, specifically regarding STAT3. While in the Torigoe lab, I investigated the question: does STAT3 directly interact with ESRRB, OCT4, and/or SOX2? I generated stable plasmids expressing tagged transcription factors, and used these to run Co-Immunoprecipitation (Co-IP) experiments. Ultimately, I wasn't able to run a reliable Co-IP, but was able to refine the technique and procedure used in our lab, and set the stage for future Co-IPs to be done.

Investigating the role of phosphorylation in alpha-synuclein aggregation

Sadie Meredith-Andrews ‘26, Nicole Brockway, & Tamily Weissman, *Department of Biology, Lewis & Clark College.*

Parkinson’s disease (PD) is the second most common neurodegenerative disease, affecting nearly one million people in the US. The disease is characterized by the incremental loss of dopaminergic neurons in the substantia nigra, eventually leading to movement disorder symptoms (Jagadeesan, 2017). Alpha-synuclein protein accumulates into aggregates called Lewy bodies; understanding the factors leading to aggregation is essential for developing effective treatments for PD. Although the mechanisms that underlie alpha-synuclein aggregation are not clear, phosphorylation at serine-129 (S129) is likely involved in disease; 95% of alpha-synuclein in Lewy bodies is phosphorylated at this site (Fujiwara et al. 2002). Phosphorylation at S129, however, does not seem to be the only factor causing aggregation (Weston et al., 2021). Nearby site tyrosine-136 could be involved in a combination of phosphorylation events necessary to drive aggregation. It has been shown that when Y136 phosphorylation is inhibited, aggregation may increase, suggesting a potential protective role of Y136 phosphorylation against aggregation (Sano et al., 2021). We are studying Y136 in relation to S129 to understand how phosphorylation of these two sites in conjunction may affect aggregation. We inject DNA plasmids encoding different forms of phosphomimetic and phospho-inhibited human alpha-synuclein tagged with GFP into zebrafish embryos.. We use *in vivo* Fluorescence Recovery After Photobleaching (FRAP) in zebrafish larvae to measure protein mobility and study aggregation. These studies will help us to further understand the mechanisms underlying alpha-synuclein aggregation, which may ultimately allow for targeted treatments and improvements in care for millions of people.

Combined phosphorylation of multiple sites in alpha-synuclein may affect aggregation in Lewy Body disorders. Lily Schainker ‘25, Nicole L. Brockway, Tamily A. Weissman, *Departments of Biology & Psychology, Lewis & Clark College.*

Parkinson’s Disease is a common neurodegenerative disease that affects more than one million Americans today (Yang et al., 2020). Current treatments target symptoms, but are ineffective at preventing the underlying progression of the disease. Although a diagnosis of PD can be made in patients based on symptoms, the disease can only be clinically confirmed with the identification of structures in post-mortem brain tissue known as Lewy bodies (Cabrero & Morrison, 2023). Lewy Bodies are predominantly made up of a 140-amino acid protein called alpha-synuclein (Spillantini et al., 1997). While it is known that alpha-synuclein aggregates into Lewy bodies, the mechanisms that lead to this aggregation are unknown. Phosphorylation may play a role in the change of alpha synuclein’s natively unfolded state. To further test whether phosphorylation drives aggregation, I have used genetic methods to mimic or inhibit phosphorylation at tyrosine-125 (Y125) and serine-129 (S129) in the human alpha-synuclein gene.

Our research aims to measure aggregation of various forms of alpha-synuclein in zebrafish *in vivo*. Forms of alpha-synuclein with sites Y125 and S129 changed to alanine or aspartate tagged with green fluorescent protein were developed and expressed in zebrafish embryos. Zebrafish, which lack endogenous alpha-synuclein and are translucent in early development, are an ideal model for this analysis. Using *in vivo* fluorescence recovery after photobleaching (FRAP), we measure alpha-synuclein protein mobility which may determine the role of certain phosphorylation sites, such as S129 and Y125, in aggregation. We are measuring alpha-synuclein aggregation in multiple neurons at four days as well as six days post fertilization. By analyzing the progression of alpha-synuclein aggregation, its disease-associated mechanisms may be better understood.

Investigating post-translational modifications of alpha-synuclein and their role in protein aggregation. Aaliya Mehnaz Ahmed ‘27, Lily Schainker ‘25, Nicole Brockway, and Tamily Weissman, *Department of Biology, Lewis & Clark College*.

Parkinson's disease (PD) is the second most common neurodegenerative disease, affecting 1-4% of the US population aged 65 and above. Currently, treatments exist to mitigate certain symptoms but they are ineffective to halt progression of the disease. Although a patient can be diagnosed with Parkinson’s disease based on common symptoms, a definitive diagnosis can only be confirmed through a post-mortem autopsy revealing Lewy bodies. Lewy bodies are therefore the pathological hallmark indicator of Parkinson's disease and are mainly composed of an aggregated form of the protein alpha-synuclein. Alpha-synuclein is a 140 amino-acid long protein that is prone to aggregation. Post-translational modifications of alpha-synuclein such as nitration and phosphorylation at a specific site (serine 129) may promote aggregation. To test this possibility, I successfully performed whole mount-immunohistochemistry using an antibody directed specifically against human α-synuclein that is phosphorylated at serine-129 (anti-phospho-S129) and nitrated alpha-synuclein (anti-nitrated alpha-synuclein). All DNA plasmids were tagged with Green Fluorescent Protein (GFP) and microinjected into zebrafish. The different DNA plasmids used for this research are: wild-type (WT) alpha-synuclein, and a phosphomimetic form of alpha-synuclein with tyrosine 125 and serine 129 altered to aspartate to mimic phosphorylation. Additionally, I investigated the human alpha-synuclein disease mutations A53E and E46K. The data collected from this work will help determine whether post-translational modifications at these sites drive alpha-synuclein aggregation.

Investigating the effects of Parkinson's disease-associated mutations on alpha-synuclein protein aggregation *in vivo*

Willow L. Irving, Nicole L. Brockway, Tamily A. Weissman, *Department of Biology, Lewis and Clark College.*

Parkinson's disease (PD) is a chronic progressive neurodegenerative disorder affecting approximately 1% of the population over 60 years of age (Tysnes & Storstein, 2017). The mechanistic origins of PD remain a mystery, thus therapies can only mitigate Parkinson's symptoms without halting the progression of the disease. A definitive clinical diagnosis requires a post-mortem autopsy revealing Lewy bodies: aggregated alpha-synuclein protein that clusters in the cytoplasm of neurons. Alpha-synuclein is a 140-amino-acid-long protein that regulates neurotransmitter release, vesicle cycling, and has been linked to the DNA repair processes (Cheng et al., 2011, Schaser et al., 2019). However, the mechanisms of aggregation and the role of Lewy bodies in PD remain poorly understood. Familial forms of PD, which make up less than 10% of cases, have revealed at least six alpha-synuclein point mutations, all of which result in autosomal dominant synucleinopathies (Klein & Westenberger, 2012). These mutations have been suggested to either promote or inhibit protein aggregation *in vitr*o. The differences in aggregation tendencies among the various disease mutations suggest a diversity of mechanisms that can affect the formation of Lewy bodies. Research on disease mutations in the complex environment of a living organism is needed to understand better how Parkinson's disease-causing alpha-synuclein mutations impact its aggregation. Our approach uses various forms of transiently expressed human alpha-synuclein tagged with GFP (green fluorescent protein) in live zebrafish larvae. We use *in vivo* Fluorescence Recovery After Photobleaching (FRAP) at 4 days post fertilization to measure and compare the mobility of human A53E-alpha-synuclein, E46K-alpha-synuclein, and wild-type alpha-synuclein. This work will provide real-time insights into the aggregation dynamics of these mutations. This is a crucial step toward developing effective therapies to halt the progression of Parkinson's disease and other synucleinopathies.

Optimizing Human Uromodulin Purification For Urobiome Study: A Tale of Two Methods

Jessica Martin'26[1], Elie Al Khoury'26[1], Jean-Philippe Gourdine[1,2]

[1]Biochemistry & Molecular Biology Program, [1] Department of Chemistry, Lewis & Clark College, Portland OR

Contrary to long-held beliefs, human urine is not sterile. It contains various microorganisms, including viruses, archaea, bacteria, and fungi, collectively known as the urinary microbiomes or urobiome. These microbes thrive in the bladder, an unusual ecological niche rich in salt, urea, and other by-products of digestion. Our lab is particularly interested in understanding bacterial metabolism in this nutrient-poor environment, which presents a unique challenge for these microorganisms. Female urinary bacteria come from the skin, the vagina, and the gut. In these last two body sites, it has been shown that host complex carbohydrates (glycans) can provide a source of nutrients (e.g., glycogen for vaginal microbes and mucin for gut microbes). Our previous bioinformatics work showed that urinary microbes can digest host glycans.

We hypothesized that Uromodulin (UMOD), the most abundant secreted high-mannose-containing glycoprotein in the urine (~100 mg daily urinary excretion), could be a primary nutrient source for these microorganisms. To test this *in silico*-driven hypothesis, we plan to purify UMOD and use it as the sole carbon source. Nevertheless, financial constraints and biological challenges were encountered. Commercial human glycosylated UMOD is expensive (>$800 for 0.1 mg) and a high concentration is needed for a single urobiome experiment (~5 mg/ml). While bacterial-expressed UMOD would be cheaper, it would result in an unglycosylated UMOD. Hence, this study aimed to use donated human urine specimens to identify a high-yield, time and cost-efficient method for UMOD purification.

Two purification schemes were used: Diatomaceous Earth (DiEarth) column filtration and ammonium bicarbonate (ABC) precipitation. Purified UMOD was analyzed by SDS-PAGE and immunoblot, and its glycosylation was assessed by lectin blots. Results showed that ABC precipitation method yielded in a ten-fold yield of glycosylated UMOD compared to DiEarth filtration. While both methods had comparable costs, ABC precipitation was notably faster, making it a more efficient approach for UMOD purification. These findings provide a viable, scalable method for UMOD extraction, enabling further research into its metabolism by bacteria in the human bladder, with potential implications for understanding bladder health.

Mining Bladder Bacteria Genomes To Explore Complex Sugar Metabolism in Overactive Bladder Syndrome

Nuzhat Hoque '24[1], Nathan Boyer[2], Lisa Karstens[2,3], Jean-Philippe Gourdine[1,4]

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Urine was previously considered sterile until new methods, including new DNA sequencing and culturomics techniques, revealed the opposite. In fact, urinary microbes (bacteria, archaea, fungi, and viruses), collectively known as the urobiome, are found in all humans, in healthy or diseased states from infant to adults, in male, female, and transgender groups. Studies conducted with cohorts of women who suffer from overactive bladder syndrome (OAB) have shown a decrease in urinary bacteria diversity compared to control groups.

Hence, bacteria may play a role in bladder health outside of urinary tract infection (UTI). Our group has focused on the metabolism of urinary bacteria vis-a-vis complex host carbohydrates (glycans) as many microbes forage for host glycans in other body sites (e.g., oral cavity and gut). By exploring bladder microbes' metabolism, we can infer potential molecules that can attract heath-associated bacteria (prebiotics) and understand the ecology of bladder microbes living in a quasi-desertic environment, which is the bladder. We previously used a small set (n=40) of publicly available data from bladder bacteria genomes with a bioinformatics program (dbCAN2) to predict carbohydrate-active enzymes such as glycoside hydrolase (GH) and polysaccharide lyase (PL) and their substrates.

Over this summer, we expanded this study by 1) updating the pipeline with a new version of dbCAN3 and 2) testing dbCAN3 with the old dataset. Our new data with dbCAN3 supported 60% of our previous predictions with dbCAN2, with three carbohydrate-active enzymes (GH25, GH5, and PL12) statistically significant between control and OAB subjects. Substrate-wise, dbCAN3 confirmed that both bacteria found in OAB and control can digest host glycans (mucins, glycosaminoglycans, N-glycans, and O-glycans). Beta-galactooligosaccharide, a new potential substrate, was predicted in fewer OAB patient-derived bacteria than in the control. Interestingly, beta-galactooligosaccharides are abundant in Human Milk Oligosaccharides (HMO). We plan to create a new pipeline with dbCAN3 with a larger dataset (n>1000) encompassing more urogenital diseases and to test bacterial growth with new *in-silico*-suggested substrates such as HMO.

Glyphosate Studies in Benchtop Replications of Real-World Soil. Kenzie Stewart ‘25, Katie Caudill ‘25, Louis Kuo, *Department of Chemistry, Lewis & Clark College.*

In examining glyphosate degradation, this research has found novel ways to increase the degradation rate using molybdenum-based catalysts. Using 31P NMR compounds for both heterogeneous and homogenous catalysis have been developed and proven effective. Further understanding of the degradation of glyphosate in environmental conditions have begun to be studied using HPLC and the key earth mineral Birnessite. Other environmental investigations on possible remediation techniques to limit glyphosate runoff into water have been done using adsorption of the herbicide onto molybdenum adsorbed biochar.

An improved TEV protease variant with increased stability. Bryn Romig ’25, Stella Davis ’26, Nikolas Loening, *Department of Chemistry, Lewis & Clark College*

For recombinant protein experiments, biochemists often use tobacco etch virus (TEV) to cleave off added peptide sequences during purification. The use of the cysteine protease requires adding reducing agents at multiple experimental stages to avoid the oxidation of surface cysteines, and subsequent inactivation of the enzyme. Our research investigated the changes in stability, solubility, and catalytic efficiency of the newly proposed mutant named “TEV Hexa” against the previously improved “TEV Triple.” Results show that TEV Hexa has increased thermal and chemical stability than TEV Triple. Although TEV Hexa does not cleave faster than TEV Triple, the higher stability may allow scientists to more easily store and use TEV Hexa as a cleavage tool without the need to consistently add fresh reducing agents. Additionally, we developed methods to easily acquire high yields of active TEV protease to be used in biochemical purification experiments.

Rehearsing Disaster: Understanding Earthquake Preparedness Behavior in an Interactive Environment. Maggie Giardello ‘25, Scooter Flanagan ‘25, Irene Hilman ‘25, Jake Darnell ‘24 Elizabeth Safran, *Department of Geological Science,* Erik Nilsen, *Department of Psychology,* Peter Drake, *Department of Mathematical Sciences,* Bryan Sebok, *Department of Rhetoric and Media Studies, Lewis & Clark College*

Located inland of the Cascadia Subduction Zone, the Pacific Northwest is poised to experience an earthquake of 8-9 magnitude which is expected to result in numerous casualties and economic turmoil. Nonetheless, many Pacific Northwest residents, particularly those aged 18-29, are unprepared and uninformed. Using video games as a research tool, the current project intends to conduct a total of three experiments: Experiment 1 was completed in 2021, Experiment 2 was conducted over the course of this summer, and Experiment 3 will take place in the fall of 2024.

Experiment 2 was interested in exploring the effects of identification with location (Portland vs. Seattle) and residency type (house vs. apartment) on individual preparedness. A questionnaire was used to assess levels of risk perception, self-efficacy, outcome expectation, and intent to act. Overall, playing the game led to significant increases in nearly all of our measures. However, the results suggest that place and residency identification have little significant impact on disaster preparedness, but have some significant impact on state anxiety.

The final experiment which is currently being conducted focuses on collaboration by introducing a two-player game condition. We aim to understand the relationships between in-game collaboration, real-world collaboration, and measures of efficacy, cohesion, and engagement.

Dependable Computing. Daniel Neshyba-Rowe ’25, Caitlyn Wilde ’25, Wyeth Greenlaw Rollins ‘24, Alain Kägi, Jens Mache, Jorge Martinez *Department of Mathematical Sciences, Lewis & Clark College*.

As computers become increasingly instrumental to modern life, it becomes more important that they are secure and reliable. However, in practice we see errors and bugs proliferating at a startling rate—for example each version of the linux kernel sees a net increase of bugs.

In this project, we attempt to build a system that is bug-free and impervious to certain types of cyberattacks, using a networked temperature sensor as a proof of concept. Our approach is to mathematically prove that each aspect of the temperature sensor behaves exactly as intended. We are developing this sensor on top of a single-board Odroid C2 computer. Its software is written in the C programming language and the plan is to prove the correctness of this program’s implementation against a formal specification with the help of the proof assistant Isabelle/HOL.

This summer, we completed a functional draft of the necessary code for a network stack. Additionally, we began performance diagnostic tests on this draft, achieving competitive performance on lower bandwidths.

Empowering Consumers in the Age of Big Data: A Framework for Privacy Protection. Nate Berol ‘27, Ryder Selikow ‘26, Jens Mache, *Department of Mathematical Sciences, Lewis & Clark College*, Devin Fitzpatrick, *Department of General Education, Lewis & Clark College*

As the sale of personal information becomes increasingly lucrative, firms are more incentivized to keep potentially antagonistic users in the dark regarding the data those firms collect and how they use it. Given this information gap, expecting users to individually leverage their limited time and spending power against large companies is especially unreasonable. To address these power and information differentials, governments must provide user-friendly tools to educate and empower consumers. We review FTC policy recommendations, the California Consumer Privacy Act’s (CCPA) provisions toward these ends, and their respective shortcomings. We recommend creating a system that records and explains privacy policies, stores users’ informed privacy preferences, regulates data exchange, and automatically removes users’ data when privacy policy changes out of compatibility. To verify the usefulness of future government policy of this nature, we also propose a test rooted in the principles of informed consent to grade consumer privacy empowerment and present an experiment to test the policy laid out.

Creating Synthetic Data for Student Success Prediction Models in Hands-on Cybersecurity Exercises. Julia Scott ‘25, Jens Mache, *Department of Mathematical Sciences, Lewis & Clark College.*

Cybersecurity is an ever-evolving field that demands more workers and a wider array of knowledge every year. As such, cybersecurity education remains essential — not just for professionals, but for developers and non-technical roles as well. Due to this, hands-on cybersecurity exercises, such as the ones in the eduRange platform, are increasingly important.

EduRange aims to be a flexible, intuitive cybersecurity platform that allows instructors to tailor pre-existing scenarios to their classes’ needs. However, when students become stuck and annoyed, learning grinds to a halt. To combat this frustration, we want to create an automated hints system that can consistently identify struggling students. Such a hints system, however, requires a large quantity of data, which can be difficult to obtain through classroom testing.

As such, we explored creating synthetic data. We used a sample dataset and stored attempt accuracy in a three dimensional tensor with dimensions students, questions, and attempts. We then used tensor decomposition to fill in gaps in the dataset and identify trends in the relationships between these dimensions. The results showed that generic tensor decomposition is not sufficient for boolean data, but provided us a path forwards using boolean tensor decomposition.

Using Dynamic Assessment in Hands-On Cybersecurity Exercises. Sheperd Thompson ’25, Jens Mache, *Department of Mathematical Sciences, Lewis & Clark College*

One of the challenges that instructors often face is creating exercises that are both multi-level, i.e. accommodate students with different preparation, as well as progress from the start to the finish in a way that accounts for different rates of learning. We explore dynamic assignment/assessment as a solution to these problems.

Dynamic assessment, also known as tiered assignment or differentiated instruction, provides the benefit of catering to students’ educational needs more than a traditional assignment, while also giving the instructor more freedom in the classroom than other modes of instruction. This research investigates the effectiveness of dynamic assessment in hands-on cybersecurity exercises. Using methods from existing research, we will modify hands-on exercises on the cybersecurity education platform, EDURange. Individual exercises on EDURange will be split into three different levels – easy, medium, and hard – allowing students to choose and identify their current skill level. The research consists of two phases, with phase one being the altering of the exercises, and phase two being the distribution of the modified platform. We are currently beginning phase two of this research.

Reconfigurable Bitter-type Electromagnets for Laser Cooling. Emma G. Hataway ‘25, Kaia E. O’Neill ‘26, Emma K. Falk ‘26, Ben A. Olsen, *Department of Physics, Lewis & Clark College*

Many quantum gas experiments using laser-cooled atoms begin with a hot beam of atoms that are slowed using a Zeeman Slower (ZS). A ZS uses a combination of spatially varying magnetic fields and lasers to reduce the atoms’ speed so they can be trapped and cooled. Through a combination of numerical simulations and experimental measurements, we explored a new ZS electromagnet design using stacked, alternating semi-circular copper layers.

To aid in the design of the ZS, we performed a series of simulations of the magnetic field distribution as well as the electrical and thermal properties of the coils. For the magnetic field, we compared simulations using two different techniques. One simulation, using python, calculates the field with a boundary integral method. The other, in the COMSOL simulation package, used finite-element analysis. The predicted fields of the two methods matched well, and the resulting design yielded a magnetic field distribution very close to ideal. We extended the COMSOL simulations to include magnetic field perturbations due to other components of the planned apparatus, and found no significant deviation from the ideal field profile.

We also constructed a prototype of the ZS electromagnet using custom-cut copper layers. Since our design includes many layers, the surfaces where the layers meet can have a big impact on the electrical and thermal properties of the ZS. We tested several surface treatments, with the goal of minimizing the electrical resistance of the layers after exposure to air. We found that electroplating the copper with silver led to the smallest decay of electrical conductivity from air exposure, while nickel-plated and untreated copper led to worse decay. We will also discuss other electrical and thermal measurements of the ZS coil.

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