John S. Rogers Program

2025
Summer Science Research Poster Conference

Thursday, September 18
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 2025. 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.

Table of Contents

Substrate specificities in *SicTox* venom toxins from sicariid spiders influence cytotoxicity
Finn Watson[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*

The family Sicariidae contain S*icTox* in their venoms, a variant of Phospholipase D (PLD). *SicTox* is known to cause loxoscelism in humans, and fast acting and immobilizing toxicity in insect prey. *SicTox* variants make up more than 50% of the proteins found in *Loxosceles* and *Sicarius* venom, implying an important role in prey capture. Despite this outsized presence in venom, the effects of *SixTox* isoforms in prey systems are poorly understood. Notably, different homologues of *SicTox* show different cleavage specificity towards various phospholipid substrates. The effects of this diverse specificity on prey immobilization remains poorly understood. One hypothesis is that varying phospholipid substrate specificity could allow toxins to target wider varieties of prey, allowing for the generalist hunting behavior of spiders in this family. To investigate the effects of *SicTox* on prey we perform *in vitro* cytotoxicity assays by treating SF9 cells with extant venom toxins and mutants that modify phospholipid binding. We measure cell permeability via a propidium iodide assay in a microplate format. We find that venom toxins with diverse phospholipid specificities result in differing effects on prey cells. Additionally we find that mutations predicted to increase substrate binding to sphingomyelin can cause increased cell permeability. These data are consistent with our hypothesis that varied specificity could broaden the range of physiological effects on prey.

Intestinal morphology guides the placement of the gonad along the left-right body axis in *C. elegans,* Bryn Romig ‘25, Ian Larkin ‘26, Greg Hermann, *Department of Biology, Lewis & Clark College*

The C. elegans hermaphrodite gonad displays prominent asymmetries along both the anterior-posterior and left-right body axes. While much is known regarding the developmental process generating the proximal-distal asymmetries within the gonad that align with the anterior-posterior body axis, we have a more limited understanding of how the gonad becomes positioned asymmetrically along the left-right body axis. The gonad primordium is composed of 4 cells, Z1-Z4, that are initially aligned symmetrically along the left-right body axis during mid embryogenesis. At hatching, the L1 stage gonad primordium is asymmetrically positioned so that Z1/Z2 are located anteriorly along the right side and Z3/Z4 are located posteriorly along the left side of the body. In the adult hermaphrodite, the anterior gonad arm, resulting from the proliferation of Z1 and Z2, lies along the right side of the body and the posterior gonad arm, which is derived from Z3 and Z4, lies along the left side of the body. The mechanisms guiding the asymmetric positioning and morphogenesis of the gonad relative to the left-right axis are unknown. Given the close association between the gonad primordium and the intestine during both embryonic and post-embryonic development, it is likely that interactions between these two organs contributes to asymmetric gonad positioning along the left-right axis. We will present work characterizing the effects of a mutation altering intestinal cell behavior and morphology that impacts gonad development and causes mispositioning of the gonad along the left-right body axis.

In the *C. elegans acdh-11*(-) mutant, gut granules become essential for embryonic viability and expression of the fatty acid desaturase FAT-7. Trent Nause ’26, Hazel Gladish ‘28, Madeline Daniel ’24, Frances Parrott ’22, David Nhek ’22, Greg Hermann, *Department of Biology, Lewis & Clark College*.

Lysosome-related organelles (LROs) are specialized, cell-type-specific organelles derived from the endolysosomal system and have diverse functions and morphologies depending on the host cell. Proper LRO 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. ACDH-11, an acyl CoA dehydrogenase, has been shown to impact biogenesis of the *C. elegans* LRO, called gut granules. ACDH-11 specifically oxidizes 11 carbon β-cyclopropyl fatty acids (CFAs) and regulates the fatty acid desaturase FAT-7. FAT-7 converts saturated fatty acids to monounsaturated fatty acids and impacts membrane composition, impacts lifespan, and promotes survival under various stressors. Our research has found that in *acdh-11(-)* mutant worms gut granules become essential for viability, and influence expression of FAT-7. These findings suggests that gut granules may play a crucial role in membrane composition, lipid metabolism, and may be a critical site of degradation or storage of excess CFAs.

Competition and Predation by Native and Non-Native Ladybird Beetles at Various Temperatures. Michelle Jin ‘25, Suzie Myles ‘26, Julia Thompson ‘25, Dr. Heidi Liere *Department of Biology, Lewis & Clark College*

Rising temperatures due to climate change have been shown to expand the range of insect pests and reduce the effectiveness of natural enemies. Changing temperatures can also affect competitive interactions and differentially affect native and non-native species. Given the pest control services provided by all ladybird beetles (Coleoptera, Coccinellidae) it is important to understand the effects of climate change on their competition and predation dynamics. In this study, we analyzed the competition and aphid predation rates of two ladybird beetles native to the Pacific Northwest of the U.S. (*Hippodamia convergens* and *Cycloneda polita*) and two non-native species (*Coccinella septempunctata* and *Harmonia axyridis*) at three temperature conditions (15-25°C, 20-30°C, and 25-35°C). We ran cage inclusion experiments in climate controlled chambers with aphid-infested plants, measuring beetle weight change and aphid predation rate after 24 hours in 4 treatments: intraspecific groups (native/non-natives alone), interspecific groups (natives & non-natives together), and a control (aphids alone). At room temperature, the predation rate was highest in intraspecific non-native groups, followed by interspecific groups, with the lowest predation rate in intraspecific native groups. Native ladybirds gained more weight in intraspecific groups compared to interspecific ones. Conversely, non-natives gained more weight in interspecific groups compared to intraspecific ones. This suggests that non-native ladybirds are stronger competitors at room temperature than native ladybirds. All ladybirds gained the most weight at 30°C, but showed the highest predation rate at 35°C. This may suggest that ladybirds need to eat more at higher temperatures in order to maintain biomass.

The Systematics of Ringtail Dragonflies (*Erpetogomphus*)
Zack Stack (‘26), *Lewis & Clark College*, Fopé Akanni, Avery Pennington, Ellie Gamett, Violet Onsongo, Jessica Ware, *American Museum of Natural History*

The genus *Erpetogomphus* (Selys 1858) comprises a distinctive group of clubtail dragonflies (Odonata: Gomphidae) commonly known as ringtails, with 24 described species distributed across North and Central America. Despite detailed morphological classification, comprehensive molecular phylogenetic analyses of *Erpetogomphus* are lacking, limiting our understanding of their evolutionary relationships. To address this gap, we generated Anchored Hybrid Enrichment (AHE) data from museum specimens. Using these data, we constructed species trees to clarify phylogenetic relationships and applied fossil-calibrated molecular clock analyses to investigate the genus’s evolutionary history. Here we present the most comprehensive phylogenetic study of *Erpetogomphus* to date, contributing to a larger effort to resolve the Gomphidae phylogeny.

Pollinator-mediated impacts of Impatiens glandulifera on native plants - a Mesocosm Experiment. Natalie Sinclair ’27, Cora Lochner, Alica Lipinski, David Becker, Dr. Mialy Razanajatovo, Prof. Dr. Christine Sheppard, Prof. Dr. Ingo Grass, *Department of Landscape and Plant Ecology, University of Hohenheim*

The Himalayan Balsam, *Impatiens glandulifera,* is an invasive plant that originates from the Himalayas. In southern Germany, it is predominantly found along rivers and in damp forests. It has established itself as one of the dominant plant species in many regions of Europe. The competitiveness of *I. glandulifera* stems from several traits, including its tall stature, rapid germination and growth rate, and tolerance to nutrient deficiency. Its conspicuous flowers produce substantial nectar resources, which are highly attractive to a variety of pollinators. This attraction can have both positive and negative consequences for native plants. As an intern at the Institute of Landscape and Plant Ecology at the University of Hohenheim in Stuttgart, Germany, I supported doctoral student Alica Lipinski in her studies of *Impatiens glandulifera*. For this purpose, 16 different native plant species were grown and placed in mesocosms—in mixed culture with *I. glandulifera* and in monoculture without *I. glandulifera*. In addition, two different pollinator species were introduced into the mesocosms: *Osmia bicornis* and *Bombus terrestris*. To determine which characteristics render *I. glandulifera* so successful, trait measurements were also taken, including nectar depth, flower length, plant height, and related traits.

Interplay among features of transcription factor binding sites in an enhancer for the pluripotency gene *Klf4* Srinidhi Sundaresan '27, Dean Pham '27, Sharon Torigoe, *Department of Biology, Lewis and Clark College*

Regulating pluripotency to gain insight into the earliest stages of development allows us to understand more deeply its transcriptional program. *Klf4* is a pluripotency gene expressed specifically in naïve-state pluripotent stem cells (PSCs) but is suppressed in primed-state PSCs. Understanding the mechanisms that carefully regulate *Klf4* expression in the naïve-state can lead to new insights about pluripotency and development. Previous work has shown that the transcription factors OCT4, SOX2, ESRRB and STAT3 assemble at the enhancers for *Klf4* to activate expression. In this lab, we have investigated whether the properties and arrangement of transcription factor binding sites (TFBS) have critical roles for enhancer function, forming the idea of enhancer grammar. We have characterized the grammatical constraints for the ESRRB and STAT3 binding sites in the *Klf4* enhancer E2, such as binding affinity and spatial arrangement. Our prior observation of both suboptimal and constrained features led us to investigate whether there could be interplay among these TFBS features. Here, we present data that demonstrates the interplay between these features in the enhancer E2.

Comparing constraints for ESRRB and STAT3 binding sites between enhancers for the pluripotency gene *Klf4*
Dean T. Pham, Srinidhi Sundaresan, Sarah J. Swanson, Johnathan Pang, Rayne Avery, Sharon E. Torigoe
Lewis & Clark College, Department of Biology, Portland, OR

Enhancers are critical *cis*-regulatory elements that control the transcription of genes, especially during development. A significant challenge to studying enhancers is their identification, due to the long distances from which they can act on target genes. One approach to improve tools for enhancer prediction is to advance our knowledge of enhancer grammar, or the type, number, affinity and/or arrangement of transcription factor binding sites in enhancers. There is increasing evidence that grammar plays significant roles in driving the spatiotemporal activities of enhancers, especially during development. We are particularly interested in the naïve state of pluripotency, which corresponds to the pre-implantation embryo and one of the earliest stages of mammalian development. To gain insight into naïve-state-specific enhancer grammar, we investigate the enhancers for *Klf4*, a critical naïve-state pluripotency factor. Our previous studies of *Klf4* enhancer E2 revealed the importance of the order and spacing of transcription factors to facilitate ESRRB and STAT3 function at this enhancer. We then asked whether these observation apply more broadly to other naïve-state specific enhancers. To this end, we turned to another enhancer for *Klf4*, enhancer E1, which contains binding sites for the same transcription factors utilized by enhancer E2 (OCT4, SOX2, ESRRB, and STAT3). While these binding sites are in the same order in enhancers E1 and E2, these sites differ between the two enhancers in other ways, including the number, binding affinity, and spacing. To elucidate underlying principles for grammar of naïve-state-specific enhancers, we have investigated these differences and how those impact the function of *Klf4* enhancer E1.

Protein Aggregation and Human Mutations Linked to Parkinson's Disease. Abby Yamashita ‘27, Kyle Nguyen, Tamily A. Weissman, *Lewis and Clark department of Biology*

Parkinson’s disease is a common neurodegenerative disorder with no known cause or cure. Parkinson's disease is diagnosed by performing a post mortem autopsy on the brain and identifyingLewy bodies, aggregates of proteins in the cytoplasm of neurons. Out of the many proteins found to be aggregated in Lewy bodies, alpha synuclein is the most abundant. The mechanisms that lead to alpha-synuclein's aggregation are not fully understood, but play a critical role in disease progression. Six known familial point mutations associated with Parkinson’s disease have been found in the N-terminal region of the protein. The main question is, does introducing one of the point mutations change the aggregation patterns of the entire protein? The mutation of this experiment, A30P, changes alanine to proline, and may change the way that the protein is structured and aggregates. Our research focuses on testing how this mutation affects alpha-synuclein mobility and aggregation in neurons. All experiments were conducted in zebrafish (*in vivo)*, a great model organism for visualizing the entire nervous system. We use a combination of approaches including Fluorescence Recovery After Photobleaching (FRAP) and immunohistochemistry staining to assess phosphorylation at site serine-129. We are comparing alpha-synuclein carrying the A30P mutation to the wild type (WT) form of alpha-synuclein. Our experiments aim to understand how the A30P mutation changes alpha-synuclein’s phosphorylation and aggregation patterns. Ultimately we hope our work provides insights into the molecular mechanisms of Parkinson’s disease progression.

Investigating phosphorylation of alpha-synuclein: a potential cause of Parkinson's disease. Esraa Alkhateeb 27', Kyle T. Nguyen, Tamily A. Weissman, Department of Biology, Lewis and Clark College.

Parkinson's disease (PD) is a neurodegenerative disorder in the nervous system, affecting around 10 million people worldwide, and characterized by the destruction of dopaminergic neurons in the substantia nigra. PD can be diagnosed by the presence of dense, abnormal filamentous bodies known as Lewy bodies. Lewy bodies are mainly composed of an aggregated form of a protein called alpha-synuclein, and they are found in neural cell bodies. The cause of alpha-synuclein aggregation is unknown; however, alpha-synuclein is dominantly phosphorylated at ser-129 in Lewy bodies (Anderson et al., 2006). We are testing whether phosphorylation causes alpha-synuclein's aggregation. Although it has been shown that phosphorylation at S129 alone doesn't cause alpha-synuclein aggregation, four sites in alpha-synuclein's C-terminus can also be phosphorylated. We will test whether phosphorylation at multiple sites simultaneously (S129, Y125, and Y136) causes the aggregation of alpha-synuclein. We will inject two different DNA plasmids coding for alpha-synuclein tagged with Green Fluorescent Protein (GFP) into one-cell stage zebrafish embryos. We have used genetic modification of alpha-synuclein to suppress or mimic phosphorylation at each site. We will compare the aggregation of a phospho-inhibited alpha-synuclein at these sites versus a phospho-mimicked alpha-synuclein in the zebrafish neurons. We will measure aggregation of each form of alpha-synuclein using a Fluorescence Recovery After Photobleaching (FRAP) technique, which examines the mobility of alpha-synuclein tagged with GFP. This will enable us to determine whether phosphorylation of alpha-synuclein at S129, Y125, and Y136 influences alpha-synuclein aggregation. These experiments will test whether phosphorylation of alpha-synuclein influences its aggregation state, exploring its role in disease progression.

Investigating Parkinson's disease: the role of phosphorylation in alpha-synuclein aggregation *in vivo* Sadie Meredith-Andrews, Kyle T. Nguyen, & Tamily A. Weissman
Department of Biology, Lewis & Clark College

Parkinson's disease (PD) is the second most common neurodegenerative disease after Alzheimer's disease, affecting nearly one million people in the United States. The disease is characterized by the incremental loss of dopaminergic neurons in the substantia nigra, eventually leading to motor symptoms and behavioral changes (Jagadeesan, 2017). These symptoms worsen over time as more neurons die, and there are no disease-halting treatments currently. Alpha-synuclein protein accumulates into aggregates called Lewy bodies; understanding the factors leading to aggregation is essential for developing effective treatments for Parkinson's disease. Although the mechanisms that underlie alpha-synuclein aggregation are not clear, phosphorylation at serine-129 (S129) is likely involved in disease. Alpha-synuclein in Lewy bodies is phosphorylated 95% of the time at this site in brain tissue of patients with Parkinson's disease, while the site is phosphorylated only 4% of the time in healthy brain tissue (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 (Y136) could be involved in the 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). I am studying Y136 in relation to S129 to understand how phosphorylation of these two sites in conjunction may affect aggregation. I inject DNA plasmids encoding different forms of human alpha-synuclein tagged with GFP into zebrafish embryos. I 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.

Investigating the spread of pathological alpha-synuclein aggregation in neurodegenerative disease. Elsie Chin ‘26, Kyle Nguyen, Tamily A. Weissman, Department of Biology, Lewis & Clark College.

Despite being one of the most well-studied neurodegenerative disorders, the key mechanisms underlying Parkinson’s disease are not fully understood. While it is widely accepted that pathology spreads over the course of neurodegenerative disease, it is unknown how and where this starts, and what dictates it. One key pathological feature of Parkinson’s disease—one that may provide insight into these questions—is the widespread aggregation of a normally monomeric protein called alpha-synuclein. Growing research into pathological alpha-synuclein aggregation has shown that it demonstrates propagation patterns similar to those of the prion protein. This means that aggregated alpha-synuclein may be able to induce aggregation in nearby healthy alpha-synuclein, thereby transforming entire populations of healthy protein. While this hypothesized mechanism explains broad patterns of neurodegenerative disease, more information on the intracellular behavior of alpha-synuclein is needed. This study aims to investigate patterns of alpha-synuclein aggregation within individual neurons. Previous research has suggested that alpha-synuclein aggregates first in presynaptic terminals before spreading retrogradely toward the cell body. I plan to use zebrafish motor neurons to study this hypothesis in vivo. First, microinjections will be carried out to introduce human alpha-synuclein DNA into zebrafish embryos. During larval development, the expressed alpha-synuclein can be visualized in neurons using fluorescence microscopy. We are developing methods to systematically test alpha-synuclein aggregation in different locations within the same neuron. This involves a technique called Fluorescence Recovery After Photobleaching (FRAP), which approximates aggregation based on protein diffusion. By comparing the aggregation levels of presynaptic terminals at varying distances from the cell body, we hope to gain an understanding of how pathological alpha-synuclein aggregation progresses within the cell.

Use of Gold Nanocubes as a Substrate for Shape-Controlled Electrodeposition of Metals
Hunter Powell ‘26, Lindsey G. Stobbs ‘26, and Anne K. Bentley, *Department of Chemistry, Lewis & Clark College*

Gold nanocubes were used as templates to study the electrochemical growth of face-centered cubic (fcc) metals including gold, palladium, and copper. The cubes were synthesized via an aqueous route and then transferred to an indium-tin-oxide-coated glass slide using an airbrush. Electrochemical and solution parameters for electrodeposition of the metals were determined, and deposition of each metal was confirmed using powder X-ray diffraction and energy dispersive X-ray spectroscopy. Gold was electrodeposited using a constant current technique, and chloride ions in the electrolyte (as compared to bromide) encouraged more directional growth. Palladium deposition was achieved by applying a constant potential, and a reduction in deposition time led to more uniform and larger Pd structures. Copper electrodeposited as cubes even without Au nanoparticles on the ITO substrate. When octahedral Au seeds were present, both cubes and flower-like deposits were observed. Although copper was electrodeposited from solution, it quickly oxidized to Cu_2O and CuO.

How do urinary bacteria digest Host-Sugars? Molecular Characterization of GH38 from *Lactobacillus crispatus.* Malia Heien ‘26, Jean-Philippe Gourdine, *Biochemistry and Molecular Biology Program & Chemistry Department, Lewis &Clark College.*

A variety of microorganisms exist in a healthy bladder, collectively referred to as the urobiome. *Lactobacillus crispatus* is a bacterial species present in the female urobiome and is associated with health (Hilt et al., 2014). It is currently unknown what nutrient sources bladder microbes, such as *L. crispatus,* are feeding on to maintain their livelihood. Microbiota in the gut have been shown to feed upon host complex sugars (glycans); however, it is not well understood whether microbiota in the bladder have the same metabolic activity. Bioinformatics data suggest that *L. crispatus* may digest high-mannose-containing glycans with glycoside hydrolase family 38 (GH38) (Gourdine *et al.*, 2025). This study aimed to characterize the enzymatic activity of GH38 from the bacterial species *L. crispatus*.

A pET vector with codon-optimized GH38 was commercially obtained (GeneUniversal). Following their successful transformation, T7 Express *Escherichia coli* were used to overexpress *L. crispatus GH38*. Nickel-NTA affinity chromatography was then used to isolate the His-tagged protein. The purification was monitored by SDS-PAGE. Eluted fractions containing GH38 were used to test mannosidase activity using 4-Methyl-Umbelliferyl-Mannose (4-MU) and a nanodrop Fluorospectrometer. The preliminary results suggest that GH38 from *L. crispatus* can cleave 4-MU-Mannose, suggesting possible high-mannose *N*-glycan digestion. These findings contribute to a greater understanding of how healthy flora in the urobiome can survive in the bladder.

Synthesis of Magnetic Particles for Immobilizing a Urinary Protein

Caroline Mpanganeni ‘28, Elie Al Khoury ‘26, Jean-Philippe Gourdine, and Anne K. Bentley
Department of Chemistry, Lewis & Clark College

The uromodulin (UMOD) protein is a glycoprotein found in human urine that can influence the growth of bacteria in the urine. Purification and isolation of UMOD from human urine can be time-consuming and expensive. The sugars found on UMOD can hydrogen bond with polar surfaces such as diatomaceous earth (DE). Magnetite (Fe_3O_4) nanoparticles were synthesized in the presence of diatomaceous earth (DE) to provide a way to mechanically isolate the UMOD protein from aqueous solution. Synthesis of the Fe_3O_4 nanoparticles was confirmed with powder X-ray diffraction, and the ability of both Fe_3O_4 and Fe_3O_4/DE composites to adsorb UMOD was assessed by measuring the absorption of the supernatant at 280 nm. Both Fe_3O_4 and Fe_3O_4/DE composites removed UMOD from the surrounding solution. In ongoing work, the DE and Fe_3O_4 can be incorporated into agarose beads suspended in water.

Monitoring Urinary Bacteria Growth on Host-Glycans

Elie Al Khoury’26, Jean-Philippe Gourdine, *Biochemistry and Molecular Biology Program & Chemistry Department, Lewis &Clark College.*

Once thought to be sterile, urine is now known to harbor a diverse microbiome, referred to as the urobiome (Hilt *et al*., 2014; Brubaker *et al*., 2023). The urobiome's metabolism remains poorly understood, in contrast to the gut microbiome’s. Preliminary data suggest that urobiome members possess the genetic capacity to digest host glycans (Gourdine *et al.*, 2025), including those present on Uromodulin (UMOD), the most abundant glycoprotein in human urine (Schaeffer *et al*., 2021). We recently demonstrated that a member of the healthy urobiome, also used as a probiotic, *Bifidobacterium longum*, can utilize UMOD-derived glycans, providing evidence of urobiome metabolism toward host glycans (Al Khoury & Gourdine, 2025). Building on this work, we aimed to investigate additional glycans utilization by other urinary bacteria. *Lacticaseibacillus rhamnosus* and *Enterococcus faecalis*, isolated from catheterized female urine samples (gifts from Dr. Wolfe, Loyola University, Chicago), were cultured and tested for growth in minimal medium supplemented with various concentrations (0.1%- 2%) of seven carbohydrate sources (four free sugars, two porcine mucins, Muc II and Muc III, and UMOD). Growth was monitored by measuring the optical density at 600nm over 2 hours. Our results indicate that *L. rhamnosus* metabolized free glycans and *O*-glycans from porcine Mucin II, but showed no growth on Mucin III and UMOD. *E. faecalis* grew on all substrates at low concentrations, but not at higher concentrations of UMOD (1-2%). These results indicate bacterial species-specific glycan utilization patterns, suggesting that host glycoproteins may play a role in shaping the urobiome composition.

The Dynamics of Micro-swimmers. Elan Acevedo ‘27, Ryan Jurischk ‘27, Albert Bae, *Department of Physics, Lewis & Clark College.*

We sought to understand the hydrodynamics of *Chlamydonomas Reinhardtii*, a microscopic single-celled algae, which swims in a Low Reynolds number world. Life at a Low Reynolds number is characterized by the viscous forces completely dominating the inertial forces acting on an object in a fluid. To investigate these hydrodynamic interactions we used an optical tweezer setup which utilizes a laser beam to hold the *C. Reinhardtii* in place, thereby isolating the propulsive forces exerted by the cell. A major limitation of our optical tweezer setup was that all three axes of movement could not be controlled at once. To improve this, we built a motorized translation stage connected to a joystick for multidirectional movement. Using high-speed video cameras and a piezo-electric stage, we captured the trapped *C. Reinhardtti’s* swimming patterns and flagellar movements in addition to the laser’s deflected light. We wrote Matlab programs to analyze and track the movement of the deflected laser light from the series of images taken by the high-speed camera, allowing us to measure the forces at play. We simulated the entire optical setup in Matlab to better understand the role of each component, as well as to gain a better understanding of how the laser deflection depends on the force on a trapped *C. Reinhardtii*. This allowed us to write programs that could track the deflection of the laser light more accurately. Data collected from this project will be used to better understand the dynamics of microswimmers at a Low Reynolds number and if mastigonemes play a role in flagellar movement.

Constructing an Apparatus for Quantum Simulations. Morgan P. Berghof ’26, Emma K. Falk ’26, Emma G. Hataway ’25, Kaia E. O’Neill ’26, Ben A. Olsen, *Department of Physics, Lewis & Clark College*.

Our group aims to study quantum matter using ultracold lithium gases. We will use these quantum gases to emulate other quantum systems, like superconductors and neutron stars. With a series of techniques, generally called laser cooling, we will trap the lithium atoms and slow their motion. The first two phases of laser cooling are a two-dimensional Magneto Optical Trap (2DMOT), which produces a cold beam of atoms, followed by a 3DMOT which results in an even cooler spherical cloud of atoms.

The ingredients of a 2DMOT include laser beams with specific wavelength and polarization, and a magnetic field gradient. In order to stabilize the laser to the correct wavelength, we use a technique called saturated absorption spectroscopy, where two counter-propagating beams are selectively absorbed by lithium atoms in a vacuum chamber. We send a stabilized laser beam through an optical fiber to the 2DMOT Launcher, an optic which alters the beam size and polarization. This beam follows an optical path so that it points towards the center of the 2DMOT from four directions. To create a magnetic field gradient, we use two permanent magnets mounted in custom holders. These holders are designed using a finite element analysis software, COMSOL, to simulate their magnetic field gradient, then printed with a resin 3D printer. The magnet holders and optics will be attached to an ultrahigh vacuum chamber, and are the first steps in creating the quantum gases we will study. Once the atoms are cooled to the quantum regime, we will use radio-frequency coils we designed and built to manipulate the spin of the atoms in the quantum gas.

Geospatial Analysis of Urban Oak Woodland Regeneration. Tova Benson ‘27, Alana Rader, *Department of Environmental Studies, Lewis & Clark College.*

I modeled vegetation canopy in the Santa Monica Mountains before and after the 2018 Woolsey Fire using spatially explicit elevation and height data. I used two computer software programs to produce elevation and height models from this data: RStudio and ArcGIS Pro. With the resulting detailed 3D models I can compare oak tree height and canopy coverage over time to understand how wildfires affect oak tree regeneration.

Initial observations show that some, but not all, oak trees were burned in the Woolsey Fire, and importantly that unburned trees grew taller. Results from this research contribute to a larger project that informs the public and policy on how to manage trees that are regenerating after fire. There currently isn’t any regulation on how to deal with oak trees that have been damaged but are alive and regenerating.

Exploring Executive Functioning, Resilience, and Heart-Rate Variability: A "Sidewalk Neuroscience" Study. Abby Liang '26, Sophie Wong '26**,** & Todd D. Watson, *Department of Psychology, Lewis & Clark College*

In this community-based pilot study in healthy young adults (*N*=17), we examined interrelationships between self-reported cognitive control during stressors, trait and state aspects of psychological resilience (the ability to bounce back from negative life events), and participants' short and longer-term (past five years) stress levels. Separately, we measured dissociable aspects of executive functioning (cognitive/behavioral inhibition, working memory, set-shifting) using computerized versions of the classic Stop Signal, n-Back, and Cued Task Shifting paradigms, respectively. Finally, we recorded participants' resting heart-rate variability (*HRV*, a measure of brain-heart interactions) using low cost, but research-grade hardware and software. As hypothesized, we found higher levels of executive functioning and cognitive control were associated with higher levels of trait resilience, and in turn, these variables predicted lower long-term stress. There were also trends that suggest that inhibitory aspects of executive functioning might be particularly important in these relationships. However, we did not find significant relationships between HRV and other variables. Overall, the data support previous findings in our lab that trait resilience and cognitive/executive control may buffer the effects of long-lasting stressors such as the sequalae of the COVID-19 pandemic. However, the potential relationships between these variables and autonomic nervous system functioning remain unclear.

An Analysis of the Moran Model: Fixation Metrics, Eigen-analysis, and Continuous Time Dynamics. Hayley Kreps '25, Thoan Nguyen '27, Sam Rudderow '26, Dr. Yung-Pin Chen, *Department of Mathematical Sciences, Lewis & Clark College.*

We analyze the Moran model, a birth-death Markov chain, for any population size N. We present formulas for absorption probabilities and mean absorption time to understand the model's fixation dynamics, derive a second order differential equation to find expressions for the eigenvalues and left eigenvectors of the transition matrix, and generalize the model into an irreducible Markov chain. Additionally, we explore the continuous time dynamics of the model as N becomes large. Our findings offer insight into the stochastic behavior of allele frequencies and long-term evolutionary outcomes.

Dependable Computing: Verifying a Network Stack Correctness Felix Gibeault ‘27, Wade McDermott ‘26, Daniel Neshyba-Rowe ‘25, Ellen Whalen ‘25, Elias Williams ‘26, Alain Kägi
Department of Computer Science, Lewis and Clark

In a world where networks span from smart fridges to life support systems, security is paramount. However, today’s systems are flawed and unreliable, leaving the door open for malicious interference. In an effort to provide a verified solution, our objective was to mathematically prove that our implementation of the network stack was flawless, i.e. completely reliable. Utilizing the interactive proof assistant Isabelle, we’ve developed methods and a roadmap towards this goal.

Small Language Models Meet GraphRAG: A Structured Approach to Context-Aware Cybersecurity Hint Generation
Ishan Abraham ‘26, Jens Mache
Department of Computer Science, Lewis & Clark College

Our research this summer was focused on improving the current hint generation system called EDUHints. EDUHints is a fully local human-in-the-loop hint generator that teachers can use to create cybersecurity related hints for students, speeding up their ability to help students in need. It was observed that the hint system needed improvements to make hints more effective so this summer we focused on employing a more nuanced retrieval augmented generation approach called GraphRAG. GraphRAG leverages knowledge graphs and graph-like data to turn complex cybersecurity data into simple data points that relate to one another. We developed a custom system built on a cybersecurity-education focused ontology and knowledge graph by AISecKG. We as well extended this ontology to let us incorporate natural language-to-bash command mappings, a valuable feature as students tend to ask questions regarding command-line use. Graph data is extracted using multiple algorithms to ensure useful data is not missed. We also semantically score extracted graph data to prioritize only the most relevant results. While internal testing showed solid baseline results that improve the SLM’s cybersecurity hint generation capabilities, we plan to further evaluate the design using more student data and testing.

Generative AI integration in a Web Development course

Maxim Gorgan ‘27, Jens Mache
Department of Computer Science, Lewis & Clark College

The availability of Generative AI is transforming how students engage with college courses. In the context of a Web Development course, students report using AI tools to generate ideas, debug code, or even generate complete solutions [citation needed? Available]. However, unrestricted access to such utilities can also impact learning, causing students to over-rely on external solutions, and therefore reducing their quality of learning.

Combining the perspective of a recent Web Development course student, and an instructor having taught the course for ten years, this poster aims to present one possible solution to the disadvantages of Gen AI tools highlighted above. Namely, we suggest instructors could make use of Gen AI to enhance students’ learning by allowing the use of such tools for coding projects, while testing students using in-class quizzes and exams on the implementation of core skills associated with Web Development. This methodology would have the dual advantage of allowing students to solve the set task using any tools available to them, mirroring real-life scenarios of Web Development, while assessing them for key learning objectives (e.g. cookies, event listeners, database interaction) of such a course.