

ABSTRACT BOOKLET

2ND ANNUAL CCU SUMMER RESEARCH SYMPOSIUM

CREATING BREAKTHROUGHS • SHAPING THE FUTURE



LOCATION
Thompson Library

DATE
July 31, 2026

TIME
1:00 PM – 3:00 PM



Welcome to the 2nd Annual CCU Summer Research Symposium!

We are thrilled to welcome the entire campus, along with our friends, neighbors, and community partners to celebrate the creativity, determination, and brilliance of our researchers. Throughout the summer, these exceptional scholars have been pushing boundaries, asking bold questions, and conducting remarkable research both here on our beautiful campus and in locations around the country. From environmental studies to cutting-edge computer technologies, the breadth and depth of their work will leave you amazed and inspired.

Bring your curiosity, and join us for this exciting showcase of knowledge, innovation, and the next generation of innovators. Please stop by all the posters and be inspired by the intellectual energy and curiosity that define Coastal Carolina University. Come see why this is a special place; where the breakthroughs and discoveries of the future are being discovered today!

Thank you for attending our symposium.

**To check out more research opportunities at CCU please
check out our website:**

<https://www.coastal.edu/research/>

CCU Summer Research Symposium

Abstract Submissions

Poster #	Name of presenter	Poster #	Name of presenter
Poster#1	Andre Vu	Poster#20	Leila Evans
Poster#2	Shane Krausse	Poster#21	Alexander Ur
Poster#3	Removed	Poster#22	Carson Kopeck
Poster#4	Beverly Nakawatase	Poster#23	Marcos Carvajal
Poster#5	Jayden Ockert	Poster#24	Hudson Furnari
Poster#6	Jackson Greenwold	Poster#25	Inisa Maxhari
Poster#7	Alyssa McKnight	Poster#26	Christian Benz Raymond Zheng
Poster#8	Ansley Link	Poster#27	Jay DeLoria Cody Casey
Poster#9	Lana Silver	Poster#28	Connor Walstrum
Poster#10	Zoe Demo	Poster#29	Ashraf Soltani
Poster#11	Avery Javens	Poster#30	Gabriella Gurreri
Poster#12	Crystal Dudley	Poster#31	Victoria Chen
Poster#13	Mike Szklarzewski	Poster#32	Abigail Aston
Poster#14	Hannah Bendle	Poster#33	Ace Carrasquillo
Poster#15	Zoe Smith	Poster#34	Avery Falco
Poster#16	Paige Mayhew	Poster#35	Ava Hurley
Poster#17	Andrew Giordano	Poster#36	Gavin Smithson
Poster#18	Mollie Cannon	Poster#37	Rim El Belkacemi
Poster#19	Abigail Wood		

Poster numbers assigned by the order the abstracts were submitted

SYMPOSIUM ABSTRACTS

Poster #1

Funding: other

NCN and CNO Facially Chelated Pt(II)-Cl Complexes for the Catalytic H/D Exchange of C-H bonds

Presenter: Andre Vu | **Major:** Biochemistry | **Mentor:** Dr. Morgan Kramer

Three Pt(II) complexes were synthesized for the catalytic H/D exchange of aromatic functionalities in pharmaceutically relevant molecules. H/D exchange is a chemical process in which a hydrogen (H) atom is replaced by its heavier isotope, deuterium (D). Although this transformation represents only a minimal structural modification to the molecular framework, it can have profound effects on drug metabolism, uptake kinetics, and mechanisms of drug action, while also influencing a wide range of other chemical and biological properties influencing a wide range of other chemical and biological properties.

Poster #2

Funding: Los Alamos National Laboratory

Designing Safer C Libraries with Opaque Data Structures and Defensive Programing

Presenter: Shane Krausse | **Major:** Computer Science | **Mentor:** Brian Atkinson (LANL), Migeljan Imeri (LANL), Dr. William Jones (CCU)

C does not provide built-in access modifiers such as public and private, so protecting a data structure's internal representation depends on careful interface and implementation design. This project explores how established low-level programming patterns can provide encapsulation and defensive behavior in C using only native language features. Separate queue and stack implementations were refactored to use a shared linked-list engine, reducing duplicated code and centralizing common operations. Each public data structure was then exposed through an opaque pointer type, allowing client programs to interact with it only through the functions declared in its public interface. Because the complete structure definitions remain private to the implementation files, attempts to access internal fields directly are rejected by the compiler. The library also applies systematic null-pointer checks and consistent status reporting so invalid inputs can be handled without dereferencing unsafe pointers or terminating unexpectedly. Correctness was evaluated through an automated test suite covering queue, stack, and shared linked-list operations. A negative compilation test was also used to verify that external client code could not access private structure members. The resulting GCC/glibc-based library demonstrates how opaque types, shared internal components, narrow public interfaces, and defensive checks can improve maintainability and reduce misuse in C. Although these techniques do not provide the same language-enforced protections available in some higher-level languages, they allow C programmers to achieve meaningful encapsulation and safer API behavior through disciplined software design.

Poster #4

Funding: National Institute of Health

The Synthesis of Novel, Sustainably Resources Block Copolymers, PLLA-b-PmLi, for Degradable Orthopedic Implants

Presenter: Beverly Nakawatase | **Major:** Public Health | **Mentor:** Dr. Wentz

Poly-L-lactic acid (PLLA) is widely used in surgical implants due to its biocompatibility and biodegradability, which eliminates the need for a second removal surgery, decreasing the possibility of overall complications during recovery. However, its clinical use is limited by localized inflammation caused by the acidic degradation products of PLLA. To mitigate this issue, we present the novel synthesis of a block copolymer, PLLA-b-PmLi, incorporating polymethyl lipoate (PmLi as an integrated anti-inflammatory agent). The relationship between the structural composition and the resulting material properties was investigated to evaluate suitability for orthopedic load-bearing applications. The synthesis, characterization, and degradation profile of the PmLi block are presented. By collecting this meaningful data, further research can be conducted to ultimately implement surgical implants with more efficient biocompatibility and biodegradability.

Poster #5

Funding: Horry County Higher Education Commission

Love at First Bite: Employing a Preventative Screen to Detect Heartworm in Mosquito Populations In Horry County Communities

Presenter: Jayden Ockert | **Major:** High School | **Mentor:** Dr Paul E. Richardson

Heartworm disease, a vector-borne illness caused by the filarial nematode *Dirofilaria immitis*, threatens hundreds of thousands of mammalian hosts annually. Although dogs, cats, ferrets, and other household pets are impacted by the disease, dogs are the only animals with an approved treatment. Year after year, South Carolina consistently ranks among the top states in the country for heartworm prevalence, driving an urgent need for widespread parasite control. In order to predict a potential outbreak before onset, the CCU Disease Hunters have developed a molecular screening method to detect *D. immitis* in mosquito populations. This screen utilizes Polymerase Chain Reaction (PCR) to amplify the cytochrome c oxidase (Cox-1) gene that is present in heartworms; leaving a distinct genomic signature band. Two key objectives were established in this study: optimize the screen to detect heartworm DNA in mosquitoes and implement the screen in Horry County residential communities to determine vulnerable areas. Over the course of the summer, the screen was deployed in several regions including Socastee, Myrtle Beach, Conway, and Carolina Forest. Positive samples were found at two locations, indicating that heartworm disease can be detected in mosquito populations and can highlight areas at risk of infection. By implementing this screen in communities, a proactive approach can be undertaken to combat the heartworm epidemic through surveillance and education. This method provides a rapid and low-cost way to combat heartworm infections and has the potential to help animals, pet owners, and the entire community defend against a disease before more animal lives are lost.

Poster #6

Funding: National Institute of Health

Dishing the dirt: Establishing a precautionary screen for the detection of Hookworm in local Animal Shelters.

Presenter: Jackson Greenwold | **Major:** Biology | **Mentor:** Dr Paul E. Richardson

Hookworm disease, caused by *Ancylostoma duodenale* and *Necator americanus*, affects over 700 million people worldwide. It is transmitted through direct skin contact with contaminated soil. The infection causes chronic blood loss, which can lead to health complications. Hookworm can also be fatal to young dogs, which poses a major challenge for animal shelters. To combat this, the CCU Disease Hunters have worked to establish a Polymerase Chain Reaction (PCR)-based environmental screen to detect hookworm DNA in soil samples before transmission reaches human or animal hosts. This screen involves using PCR to amplify specific regions of the Cox-1, and COB genes found exclusively in hookworm. Utilizing this technique helps ensure the screen is specific to hookworm in the soil; thus, creating a way to give warning about a possible outbreak before it begins. By establishing a screen to detect Hookworm in the soil, the CCU Disease Hunters are able to assist shelters by directing attention towards proactive prevention.

Poster #7

Funding: National Institute of Health

Don't forget your shoes! Developing a Molecular screen to investigate the community presence of hookworm DNA in soil and water.

Presenter: Alyssa McKnight | **Major:** Biology | **Mentor:** Dr Paul E. Richardson

Nematodes *Ancylostoma duodenale* and *Necator americanus* are parasitic hookworm species that infect more than 700 million people across the globe and are primarily found in tropical and subtropical climates. Hookworm is transmitted through bare skin contact with contaminated soil. After entering the bloodstream, they migrate to the small intestine. This is where they mature and feed off of blood from the intestinal wall causing health complications within the host such as iron-deficiency anemia and nutritional deficiency. This study utilized a molecular diagnostic assay that allowed the CCU Disease Hunters to detect hookworm DNA within soil and water samples collected from the community. Early detection of hookworm identifies potential areas of transmission to support preventative measures. Samples were collected around various residential and community areas and analyzed using DNA extraction, polymerase chain reaction (PCR), and gel electrophoresis to determine the presence of hookworm DNA. Hookworm DNA was not detected over the course of this study, but previous studies have detected the parasite in our community. To improve detection capabilities, future research should include additional sampling locations with greater mammalian activity to further investigate environmental factors influencing hookworm in our environment.

Poster #8

Funding: Horry County Higher Education Commission

More Than a Rainy Day: Detecting Waterborne Pathogens On Campus

Presenter: Ansley Link | **Major:** High School | **Mentor:** Dr Paul E. Richardson

Waterborne pathogens such as *Cyclospora cayetanensis*, *Giardia duodenalis*, and *Shigella* can enter freshwater systems via storm-driven fecal contamination, posing a potential risk to coastal communities that often experience severe weather events. Recent *Cyclospora cayetanensis* outbreaks have emphasized the importance of monitoring weather conditions and understanding factors that influence pathogen movement. This study investigated five freshwater sites located at Coastal Carolina University to evaluate how pathogen presence varied by location and weather conditions. The procedures developed by the CCU Disease Hunters involved sample collection and filtration, DNA extraction followed by polymerase chain reaction (PCR), and analysis by gel electrophoresis to identify target DNA sequences unique to each pathogen and their species. The data revealed that *Giardia duodenalis* was present on campus and became more consistent and widespread as the summer progressed. In contrast, *Shigella* was not detected until after a significant rainfall event, suggesting that precipitation and runoff may influence the presence of waterborne pathogens. Despite recent outbreaks, *Cyclospora* was not detected. These results demonstrate that pathogen distribution varies between organisms and suggest that weather patterns and other environmental factors may influence freshwater contamination.

Poster #9

Funding: Department of Energy

Fate of ISOPOOH: Exploring Cycloaddition reactions with Criegee Intermediates**Presenter:** Lana Silver | **Major:** Chemistry | **Mentor:** Dr Michael Vansco

Isoprene is earth's most abundant atmospheric alkene with emissions measuring to several hundred Tg yr⁻¹ that react rapidly with hydroxyl radicals (OH), which strongly influences the tropospheric oxidative capacity. OH-driven oxidation of isoprene forms the first-generation product 1,2-isoprene hydroxy hydroperoxide (1,2-ISOPOOH) under low-NO_x conditions. Alternatively, terminal alkenes like isoprene undergo ozonolysis via its outermost C=C double bond to generate the simplest Criegee intermediate, formaldehyde oxide (CH₂OO). Due to the proximal abundance of CH₂OO and 1,2-ISOPOOH from isoprene oxidation, their reaction is probable and likely yields novel, currently uncharacterized products. Reaction data was recorded using multiplexed photoionization mass spectrometry (MPIMS) at the Advanced Light Source (ALS), enabling high-resolution, time-resolved monitoring of product signatures. Electronic structure calculations were carried out to investigate reaction pathways of CH₂OO and 1,2-ISOPOOH, including a cycloaddition channel. Two cyclic insertion pathways were found due to the ability of CH₂OO to add to either carbon of the terminal alkene on 1,2-ISOPOOH. Characterizing this previously unstudied chemistry establishes a critical foundation for future experiments exploring the chemical transformation, volatility, and ultimate particulate-forming potential of these products.

Poster #10

Funding: Department of Energy

OH Roaming in the Unimolecular Decay of Methyl Vinyl Ketone Oxide**Presenter:** Zoe Demo | **Major:** Chemistry | **Mentor:** Dr Michael Vansco

After methane, isoprene is the most abundant volatile organic compound in the Earth's atmosphere. Ozonolysis is a significant removal pathway for isoprene and a path to hydroxyl radical (OH) formation. Methyl vinyl ketone oxide (MVKO) is a Criegee intermediate formed from isoprene ozonolysis and has been shown to undergo unimolecular decay via a 1,4 hydrogen shift from the methyl group to the terminal oxygen forming 2-hydroperoxybut-1,3-diene (HPBD). The O-O bond can break forming oxybutadiene and an OH radical. Alternatively, theoretical calculations have predicted an OH roaming mechanism may occur. The mechanism involves a long range interaction between the separating OH and oxybutadiene radicals in which the OH radicals "roam" across an attractive region of the potential energy surface. This roaming leads to reorientation of the OH and addition to the vinyl group of oxybutadiene yielding hydroxybutanone. The unimolecular decay of MVKO was investigated using a combination of synchrotron-multiplexed photoionization mass spectrometry experiments (MPIMS, 298 K and 4-10 Torr) and electronic structure theory calculations. Evidence for the formation of the hydroxybutanone roaming product was found from the high resolution mass, time, and photoionization energy capabilities of MPIMS.

Poster #11

Funding: Los Alamos National Laboratory

Interactive Exploration of Power, Workload, and Cost in HPC Systems

Presenter: Avery Javens | **Major:** Computer Sciences and Mathematics | **Mentor:** Prof. Dakota Fulp, Dr. William Jones, and Dr. Sharmistha Chakrabarti, Los Alamos National Laboratory

High-performance computing systems consume substantial amounts of electricity, making power and energy analysis increasingly important for operational planning, energy-aware scheduling, and cost management. However, comparing HPC systems is difficult because publicly available datasets often differ in their job records, telemetry, hardware descriptions, sampling intervals, workload characteristics, and energy-related measurements. This project develops a comparative framework for exploring data from four HPC environments: Marconi100, Fugaku, NLR's Eagle supercomputer, and MIT SuperCloud. The datasets are evaluated to identify shared variables, structural differences, and limitations that affect their use in power-demand analysis and forecasting. This process provides a foundation for determining which systems and measurements can be compared directly and which require normalization or dataset-specific treatment. An interactive dashboard was developed to make the datasets and analytical results easier to explore. Users can select systems, variables, and time windows to examine workload activity, resource utilization, power behavior, and derived metrics at different levels of detail. The dashboard also provides an interface for comparing forecasting results and identifying temporal patterns, workload relationships, and system behaviors that may be difficult to detect from raw records alone. The next phase of the project will connect these technical analyses to financial scenarios. Planned work includes estimating the potential value of improved power forecasting for workload scheduling, peak-demand reduction, electricity-price variability, and energy-purchasing decisions. By combining comparative data analysis, interactive visualization, forecasting, and financial modeling, this project aims to make HPC energy behavior more understandable and operationally useful.

Poster #12

Funding: National Institute of Health

Testing the Waters: Development of a Biomolecular Detection Screen for Waterborne Pathogens After Tropical Cyclones

Presenter: Crystal Dudley | **Major:** Biochemistry | **Mentor:** Dr Paul E. Richardson

Water is a molecule essential to life, functioning as the core compound in countless physiological and ecological processes. However, it also poses a threat to public health, serving as a highly efficient vehicle for the transmission of infectious diseases, particularly in the aftermath of a Tropical Cyclone, which frequently impacts coastal regions. These extreme downpour events displace infected fecal matter, thus contributing to the contamination of freshwater sources that are crucial to the viability of many communities. Annually, the World Health Organization (WHO) reports 1.4 million preventable deaths as a result of waterborne illnesses, illustrating the dire need for a rapid and reliable method to identify the presence of pathogens in freshwater resources. This project addresses this concern by using biomolecular techniques to develop a preventive screening method capable of detecting waterborne pathogens such as *Giardia*, *Shigella*, and *Cyclospora*. Throughout the summer, this screen was implemented across seven residential sites in Horry County, encompassing Socastee, Conway, Myrtle Beach, and Carolina Forest. Water samples collected from each site were purified and underwent Polymerase Chain Reaction (PCR) to amplify target sequences on selected genes, which were then quantitatively visualized through gel electrophoresis. Positive samples for all three infectious diseases were observed at multiple sites, further emphasizing the need to monitor their presence and assess potential risks. Implementing this preemptive screen in communities would produce key insights that can support regions predisposed to waterborne diseases, furthering preventative resources to minimize risks to public health.

Poster #13

Funding: Los Alamos National Laboratory

From Benchmark to Inspector-in-the-Loop System: Building and Training Anomaly Detectors for Precision Manufacturing

Presenter: Mike Szklarzewski | **Major:** Computer Science | **Mentor:** Dr. William Jones (CCU), Prof. Dakota Fulp (CCU), Dr. Sharmistha Chakrabarti (LANL)

Automated visual anomaly detection often performs well on curated academic benchmarks, yet its reliability can degrade under real manufacturing conditions, where reflective surfaces, subtle defect morphology, and shifting imaging profiles challenge model generalization. Building on our peer-reviewed paper, accepted for publication at the 2026 IEEE International Conference on Machine Learning and Applications (ICMLA 2026), we evaluated 19 unsupervised anomaly detection models on Los Alamos National Laboratory's BowTie dataset and found that model rankings were highly sensitive to acquisition conditions, preprocessing choices, and nominal-data quality, with no single architecture emerging as uniformly robust. This poster presents the follow-on work motivated by those findings. We extended evaluation to a new, recently released dataset containing additional surface parts and previously unseen defect classes. Across tested models, fine surface textures produced elevated false-positive rates, as benign surface variation was frequently misidentified as anomalous structure. These results reinforced the need to move beyond one-time benchmarking toward an adaptive inspection workflow. We are developing and deploying an inspector-in-the-loop system that keeps final disposition under human authority while using machine learning to accelerate review. Detectors flag and localize candidate defects, promptable segmentation refines those regions into editable masks, and inspector accept, reject, and boundary-adjustment decisions become curated training data for subsequent model updates. This predict, verify, and retrain cycle is designed to adapt as parts, surfaces, and defect modes evolve. The next critical step is subject-matter-expert-verified ground truth to validate retrained models and quantify real-world impact on inspection accuracy, consistency, and efficiency.

Poster #14

Funding: National Institute of Health

Biohybrid Brush Polymer, PLi-PLLA, for Skin Grafting and Wound Healing

Presenter: Hannah Bendle | **Major:** Biology | **Mentor:** Dr. Charlotte Wentz

Utilizing the complimentary reactive moieties of the carboxylic acid side chains in poly(lipoic acid) (PLi) and the terminal hydroxyl groups of poly(L-lactic acid) (PLLA), a novel class of PLi-PLLA brush polymers was synthesized. This structural configuration combines a degradable, elastic, and inherently anti-inflammatory backbone of PLi with mechanically robust structural components of PLLA tailored for skin grafting and wound healing. The precise synthesis, macromolecular characterization, and formulation optimization of these biohybrid materials are presented herein.

Poster #15

Funding: Horry County Higher Education Commission

Synthetic Polymer Blends of PLLA, PLI, And PmLi for Biodegradable Scaffolds

Presenter: Zoe Smith | **Major:** High School | **Mentor:** Dr. Charlotte Wentz

Blending distinct homopolymers into homogenous films is an effective and established strategy to engineer hybrid biomaterials with tunable properties that tailor to desired mechanical strength and biodegradability. The core of this project is to generate a diverse library of multicomponent blends leveraging poly-L-lactic acid (PLLA), poly(lipoic acid (PLI), and polymethyl lipoate (PmLi) to optimize mechanical and surface characteristics. These include elasticity, tensile strength, compression strength, and adhesivity, which are characterized for application in biodegradable tissue scaffolds. Following the controlled ring-opening polymerization of the constituent monomers, systemic solution-blending was employed to cast the hybrid films. The physical properties, morphological observations, and performance metrics of these blends are presented.

Poster #16

Funding: Horry County Higher Education Commission

Investigating iodoperoxy radical derived from synthetic MVKO formation

Presenter: Paige Mayhew | **Major:** High School | **Mentor:** Dr Michael Vansco

Isoprene ozonolysis forms the Criegee intermediate methyl vinyl ketone oxide (MVKO), an important source of OH radicals, the primary oxidant in the atmosphere. MVKO was previously characterized following photolysis of 1,3-diiodobut-2-ene in the presence of O₂. Recent evidence indicates that the iodoperoxy radical formed along the reaction pathway is collisionally stabilized, and the yield of MVKO from the photolytic process is less than unity. In this study, multiplexed photoionization mass spectrometry (MPIMS) was used to provide evidence for collisional stabilization of the iodoperoxy radical intermediate through detection of products formed in its self-reaction. Electronic structure theory calculations were performed to aid in the assignment of product signals. Products of the iodoperoxy radical self-reaction were detected at m/z 196, 197, and 198 by 10.5 eV photoionization time-of-flight mass spectrometry at 4 and 10 Torr. Higher signal intensities at 10 Torr indicate enhanced collisional stabilization of the iodoperoxy radical and increased self-reaction at elevated pressure.

Poster #17

Funding: Department of Defense

Investigating the 1,2-insertion reactions of CH₂OO with 1,2-ISOPOOH

Presenter: Andrew Giordano | **Major:** Biochemistry | **Mentor:** Dr Michael Vansco

Isoprene is the most abundant volatile organic compound emitted into the Earth's atmosphere. OH-initiated oxidation of isoprene is its primary removal pathway, and in the presence of O₂ and HO₂ forms 1,2-ISOPOOH as a significant product. Alternatively, isoprene can react with ozone to produce the simplest Criegee intermediate, CH₂OO. Due to the similar formation proximity of 1,2-ISOPOOH and CH₂OO, their bimolecular reaction may be important. The reaction between CH₂OO and 1,2-ISOPOOH was investigated using multiplexed photoionization mass spectrometry (MPIMS). Diiodomethane, O₂, and varying concentrations of 1,2-ISOPOOH were entrained in a helium carrier gas, and CH₂OO was generated from the 248 nm photolysis of diiodomethane in the presence of O₂. Products from the reaction of 1,2-ISOPOOH and CH₂OO were monitored using the high-resolution mass, time, and photoionization energy capabilities of MPIMS interfaced with tunable vacuum ultraviolet radiation from the Advanced Light Source. Multiple reaction mechanisms are plausible due to the three reactive functional groups of 1,2-ISOPOOH, including its alcohol, hydroperoxide group, and terminal alkene sites. Electronic structure calculations were performed to explore the product branching of the reaction.

Poster #18

Funding: Department of Defense

Absolute Photoionization Cross-Section of 2,3-Butanediol and Di-tert-butyl Peroxide

Presenter: Mollie Cannon | **Major:** Chemistry | **Mentor:** Dr Michael Vansco

Peroxy Radicals (ROOs) are reactive organic intermediates that are formed as a product of hydrocarbon oxidation and play a vital role in chemical reactions that occur in oxygenated environments. ROOs are known to undergo self-reaction to form three main product channels: (1) aldehyde/ketone + alcohol + O₂, (2) ROOR (an accretion product) + O₂, and (3) 2 RO• + O₂. To identify products from ROO self-reactions originating from the hydroxyl radical initiated oxidation of hydrocarbons, the absolute photoionization cross-section of 2,3-butanediol and di-tert-butyl peroxide were measured using photoionization mass spectrometry. This was accomplished by comparing the photoionization spectra of each species to known standards where the photoionization cross-section are known. The absolute photoionization cross-sections will aid future data analysis of ROO self-reaction chemistry, including quantification of 2,3-butanediol and understanding the fragmentation pathways of peroxides.

Poster #19

Funding: Horry County Higher Education Commission

Drosophila Based Screening for Marine-Derived Molecules to Improve Polycystic Kidney Disease Pathology

Presenter: Abigail Wood | **Major:** High School | **Mentor:** Dr. Chiara Gamberi

Polycystic Kidney Disease (PKD) remains an incurable genetic disease. Autosomal dominant (AD) PKD affects 1 in every 800 people, while the autosomal recessive (AR) form is rarer and more severe. The renal tubules of PKD affected individuals are lined with multitudes of fluid-filled cysts which progress and lead to kidney failure and other expansive multi-organ symptoms. Current treatments for PKD focus on symptom and pain management. Thus, effective treatments and disease modifying medications are urgently needed. New research models can accelerate drug discovery and mechanistic studies. Specifically, the established genetic model organism *Drosophila melanogaster* can be used to study cyst formation as flies with mutations in Bicaudal C, or BicC exhibit PKD-like renal symptoms. BicC is a gene first discovered in *Drosophila* ovaries which is evolutionarily conserved from flies to humans. Additional evidence for a renal role for the the BicC protein includes the observation that mutation of vertebrate BicC orthologs yield renal cysts, and the human BICC1 protein interacts with PKD-linked proteins polycystin 1 and polycystin 2. Our lab has established a rapid drug-testing pipeline to discover cyst-reducing compounds using the cystic BicC mutant fly model. We applied our mechanistic knowledge of the BicC mutant phenotype to identifying novel candidate cyst-reducing drugs from marine sources to test in the *Drosophila* PKD model. We will present our progress using Trabectedin, an active compound approved for use in oncology. Trabectedin was extracted from *Ecteinascidia turbinata*, an ascidian common in the South Carolina coastal waters.

Poster #20

Funding: National Institute of Health

Screening for New Potential Cyst-Reducing Marine-Derived Molecules Using a *Drosophila* Model of Polycystic Kidney Disease

Presenter: Leila Evans | **Major:** Biology | **Mentor:** Dr. Chiara Gamberi

The oceans are untapped sources of biologically active molecules with drug potential. Polycystic Kidney Disease (PKD) is incurable and one of the leading causes of renal failure. Individuals with PKD develop progressively larger fluid-filled renal cysts and fibrosis. Our group has established a PKD model in the fruit fly *Drosophila melanogaster* Bicaudal C (BicC) mutants and showed that BicC flies recapitulate several PKD defects phenotypically and molecularly. We have previously established assays in the fly to test cyst-reducing molecules in vivo. Our experimental system consists of two BicC allelic combinations, BicC[/YC33] with mild cystic phenotype, and BicC[/IIF34], with a strong cystic phenotype. Here, we will show our progress on testing a seaweed-derived compound, fucoxanthin in the fly cystic model.

Poster #21

Funding: Los Alamos National Laboratory

From XCT Slices to 3D Defect Candidates in Additively Manufactured Specimens

Presenter: Alexander Ur | **Major:** Prospective Computer Science | **Mentor:** Dr. William Jones, Prof. Dakota Fulp, and Dr. Sharmistha Chakrabarti, Los Alamos National Laboratory

Internal defects in parts produced by Laser Powder Bed Fusion can affect quality assurance, component qualification, and structural integrity. X-ray computed tomography (XCT) provides nondestructive volumetric imaging of these features, but subtle planar defects can remain difficult to identify because they may appear as low-contrast regions distributed across large image stacks. This study develops a reproducible workflow for validating, visualizing, and annotating XCT data from ten Laser Powder Bed Fusion 316L stainless-steel specimens. Each specimen contains an engineered planar lack-of-fusion defect, with intended severity increasing from X1 through X10. The workflow verifies image-stack integrity, assembles sequential TIFF slices into volumetric arrays, and supports inspection through axial, coronal, and sagittal views, along with native-resolution slice navigation. Potential defect regions are classified as present, uncertain, or absent and manually contoured across adjacent slices to evaluate their spatial persistence and morphology. Preliminary analysis of the highest-severity specimen, X10, identified a spatially coherent, low-intensity candidate region spanning ten consecutive slices. Lower-confidence boundary slices were retained as uncertain for additional review rather than excluded from the analysis. The same protocol is being applied across the remaining specimens to determine whether candidate visibility, persistence, and morphology correspond with the engineered defect progression. This workflow connects raw XCT image stacks with interpretable, human-reviewed candidate masks that can support three-dimensional reconstruction, comparison across specimens, and future machine-learning-assisted segmentation.

Poster #22

Funding: Los Alamos National Laboratory

Forecasting Hourly HPC Energy Use and Cost

Presenter: Carson Kopec | **Major:** Computer Science | **Mentor:** Prof. Dakota Fulp, Dr. William Jones, and Steven Senator, Los Alamos National Laboratory

High-performance computing facilities consume megawatts of electricity, while their hourly energy use and operating costs vary with workload, system utilization, and electricity prices. Accurate short-term forecasts could support budgeting, workload scheduling, and carbon-aware computing. We present a reusable forecasting pipeline that aggregates scheduler and system data into hourly intervals, generates temporal and utilization-based features, and compares naive baselines with tree-based machine-learning models using 19-window walk-forward validation. Performance is evaluated using weighted mean absolute percentage error. The pipeline is applied to two production supercomputers: Marconi100, for hourly electricity-cost forecasting, and Fugaku, for hourly energy-use forecasting. Model performance was broadly consistent across the two systems. A previous-hour persistence baseline produced the lowest hourly error on both Marconi100 and Fugaku, with errors of 9.8% and 16.7%, respectively. Random Forest was the best-performing machine-learning model, with errors of 15.3% and 17.8%. Its feature importance was dominated by the previous hour's value, which accounted for 94% of the model's total importance. Although hourly forecast errors remained meaningful, cumulative predicted totals were within 0.2% of actual totals. These results show that strong persistence baselines are difficult to outperform at a one-hour forecasting horizon. They also demonstrate the importance of evaluating machine-learning models against simple baselines before introducing additional model complexity.

Poster #23

Funding: Los Alamos National Laboratory

Streamlining HPC Storage Benchmarking: An Extensible Framework for ZFS, Lustre, and xdd

Presenter: Marcos Carvajal | **Major:** Computer Science | **Mentor:** Brian Atkinson (LANL), Migeljan Imeri (LANL), Dr. William Jones (CCU)

High-performance computing file systems are designed to provide many compute nodes with rapid, concurrent access to large scientific datasets. Their ability to deliver high throughput and, ideally, low latency is essential to keeping processors and accelerators performing useful work rather than waiting for input and output operations to complete. HPC storage also supports job checkpointing, which protects long-running computations from hardware or software failures and provides periodic intermediate results that scientists can inspect before a simulation or analysis has finished. Evaluating these complex storage architectures requires rigorous and highly configurable benchmarking methods. This project develops and refines an extensible framework for using xdd to evaluate storage performance in environments that combine the ZFS storage platform with the Lustre distributed file system. The work examines the core operation of xdd, the rationale for its use in HPC storage testing, and the architectural relationship between ZFS, Lustre, and the compute workloads they support. The project also includes substantial refactoring and optimization of the existing benchmarking codebase. Thousands of redundant generated files and elements of legacy technical debt were removed, while the framework was reorganized to simplify configuration, experimentation, and future extension. These changes make it easier to define repeatable benchmark workloads, compare storage configurations, and build additional analyses without duplicating large portions of the existing implementation. The resulting framework supports more systematic investigation of how storage behavior affects scientific computing workflows. By improving both benchmark control and software maintainability, this work provides a foundation for evaluating storage throughput, latency, checkpoint performance, and other input/output characteristics that influence the productivity and reliability of HPC systems.

Poster #24

Funding: National Institute of Health

Synthesis of Novel Amphiphilic Triblock, PEG-PLLA-PLI, with Programmable Degradation for On-Demand Drug Release

Presenter: Hudson Furnari | **Major:** Biology | **Mentor:** Dr Charlotte Wentz

Micellular formation is essential to encapsulation of hydrophobic therapeutics, requiring well-defined amphiphilic structural materials. Established diblock copolymer combining hydrophilic polyethylene glycol (PEG) and hydrophobic poly-L-lactic acid (PLLA) are drug delivery materials but their drug release profiles lack control. Therefore, herein, we design a novel triblock PEG-PLLA-PLI, incorporating a Poly(lipoic acid (PLI) block to enhance dynamic nature of the micelle. By introducing a disulfide-rich backbone sensitive to glutathione (GSH), found in high concentrations in tumor cells, we enable targeted on-demand drug release. This poster presents the synthesis, structural characterization, and redox-responsive degradation behavior of the PLI block.

Poster #25

Funding: Horry County Higher Education Commission

Determining the Presence and Antibiotic Resistance of *Vibrio Vulnificus* in Coastal South Carolina

Presenter: Inisa Maxhari | **Major:** High School | **Mentor:** Dr Megan Cevasco

Vibrio vulnificus is an aquatic, Gram-negative bacterial species that lives in warm coastal and brackish waters and can cause severe wound infections following exposure to contaminated water. The research objective of this project was to assess the environmental abundance and potential health risk of *V. vulnificus* in the coastal waters of South Carolina. Water samples were collected from Huntington Beach State Park, Pawleys Island, and Georgetown in June and July, which were then diluted, filtered and grown on solid media plates selective and differential for pathogenic *Vibrio* species. A subsample of fourteen potentially *V. vulnificus* (blue) colonies were selected for DNA extraction, to screen for the presence of a species specific hemolysin gene using a Polymerase Chain Reaction (PCR) approach with vvhA primers. Gel electrophoresis confirmed the presence of *V. vulnificus* in all Georgetown samples, whereas none were detected in samples from Pawleys Island or Huntington Beach. Moreover, *V. vulnificus* colonies grown on plates containing ampicillin (100 ug/mL concentration) demonstrated a high amount of antibiotic resistance, indicating the need for future work to experiment with a variety of antibiotics in order to evaluate resistance patterns.

A Bug in the System: Tracking Brain and Behavior Decay in *Drosophila* Alzheimer's Models

Presenter: Christian Benz, Raymond Zheng | **Major:** Biology (Raymond) and Microbiology (Christian) | **Mentor:** Dr. Callie Crawford and Dr. Fang-Ju Lin

Alzheimer's Disease (AD) is a progressive neurodegenerative disorder that causes a cascade of effects including declines in memory, behaviors, and basic bodily function, eventually leading to death. A key molecular hallmark in the development of AD is the accumulation of A β 42 plaques. The detection of these plaques can aid in recognizing the severity of each case. This summer we focused on establishing protocols to track the progression of AD: a histological analysis and a movement tracking software. Histological analysis such as hematoxylin and eosin (H&E) staining can be used for detecting morphological changes in fly brain due to A β toxicity. We aim to apply immunohistochemistry using anti-human A β 42 to detect presence of plaques. In addition, movement tracking programs have been used to find statistically significant variations in behavior in AD flies. These programs track characteristics of fly courtship behaviors such as wing vibration, following, speed/angle of movement, avoidance, and more. Using DeepLabCut, we trained a network to track specific body parts: head, thorax, abdomen, right wing, and left wing which will allow for calculating fly movement and interactions. Our work this summer has established protocols that will be used in the ongoing studies that aim to measure the effects of several candidate genes which showed promising rescue of AD and extend our understanding of Alzheimer's Disease.

Untangling Polycystic Kidney Disease Through the Bicaudal C genetic Network

Presenter: Jay DeLoria and Cody, Casey | **Major:** Coastal Marine and Wetland Studies | **Mentor:** Dr Chiara Gamberi

Polycystic kidney diseases (PKD) like autosomal dominant (AD), autosomal recessive (AR) PKD and nephronophthisis (NPH) are incurable, affect conservatively about 13 million people worldwide, and typically lead to end-stage renal disease and kidney failure. Characterized by divergent severity and progression even in individuals inheriting the same mutations, they present with a constellation of partially overlapping symptoms, or phenotypes, that signal the contribution of multiple genetic and environmental components that affect each other through connected networks. Although current results indicate that ADPKD, ARPKD and NPH display neoplastic features, metabolic remodeling and dysregulation of factors important for renal development, incomplete mechanistic knowledge hinders diagnosis and treatment. Understanding the developmental arc of cystic kidney disease and its complex phenotypes would improve diagnostics and help develop effective personalized treatments. However, this is challenging to study in vertebrate systems due to genetic redundancy, functional overlap, and a dearth of genetic tools. Underused in this context, the fruit fly *Drosophila melanogaster* offers high genomic and pathway conservation, a wealth of genetic tools, and rapid generation times, making it a reliable and sustainable model for mechanistic, genome-wide, and precision medicine studies. One key factor in ADPKD and NPH, the Bicaudal C (*Drosophila* BicC, human BICC1, murine Bicc1) gene encodes an RNA binding protein that is conserved from flies to humans. BicC/Bicc1/BICC1 mutations all cause renal cysts. We have shown that the human BICC1 and mouse Bicc1 orthologs are genetically downstream of PKD1 and that BicC fly mutants display cystic renal tubules and PKD-like markers and are a PKD model. The human BICC1 and murine Bicc1 proteins interact with proteins critical for ADPKD and, NPH respectively. Although these results reinforce the hypothesis that BicC/BICC1/Bicc1 is a key renal factor, both the functions of the BicC/BICC1/Bicc1 protein and the BicC/BICC1/Bicc1-containing complexes are unknown. The genetic, molecular, and phenotypic complexity of both PKD and the BicC fly mutants indicates that gene networks play a large role in how renal diseases manifest in a population. To define the BicC network and gain insight into its function in the normal and cystic renal tubule, we undertake a comparative modeling approach. First, to identify the BicC network, we screened the *Drosophila* Genetic Reference Panel (DGRP) to find modifier variants in the genome and map the corresponding genes and non-coding regions. Second, we apply our mechanistic knowledge of the cystic BicC Malpighian tubules to select potential network modulators, most recently marine-derived compounds, and test their cyst-reducing activity. Third, we undertake a molecular modeling approach and compare the BicC orthologs, most recently in marine vertebrates, to identify conserved domains to be tested functionally.

Poster #28

Funding: National Institute of Health

Warming Waters, Rising Risk: Tracking *Vibrio parahaemolyticus* Abundance Along the SC Coast

Presenter: Connor Walstrum | **Major:** Biology | **Mentor:** Dr Megan Cevasco

Vibrio parahaemolyticus is an opportunistic aquatic pathogen that can cause foodborne illness (vibriosis) from shellfish consumption. Environmental fluctuations, such as temperature, influence the relative abundance of these pathogens in coastal waters. The objective of this research was to characterize the influence of temperature on the composition Gammaproteobacteria and specifically capture the summer abundance of *V. parahaemolyticus* in public South Carolina shellfish collection areas. To this end, coastal water samples were collected in June and July 2026 from three locations (Huntington Beach State Park, Pawley's Island inlet, Georgetown East Bay) and processed via 0.22um membrane filtration. Filters were aseptically transferred to selective and differential CHROMagar media to conduct *Vibrio parahaemolyticus* colony counts. To validate the taxonomic identification, DNA was extracted from twelve presumptive *V. parahaemolyticus* (maroon) colonies across sample dates and locations and confirmed by the amplification of the species-specific primers *toxR* and *gyrB*. To analyze the composition of Gammaproteobacteria, environmental DNA was extracted from sample filters and PCR amplicons of 16S ribosomal DNA pooled into metabarcoded libraries for Illumina iSeq100 sequencing. From these sequenced libraries, Gammaproteobacteria sequences were bioinformatically extracted and compared with data from previous collections to reveal the influence of temperature (seasonality) on the composition and diversity among the samples. These comparisons reveal the influence of seasonal shifts on aquatic Gammaproteobacterial composition, and the potential of temperature to impact the proliferation of *Vibrio parahaemolyticus* in coastal environments.

Poster #29

Funding: National Institute of Health

Testing Presence of *Vibrio Cholerae* in 3 Coastal Georgetown County Locations

Presenter: Ashraf Soltani | **Major:** Biology | **Mentor:** Dr Megan Cevasco

Vibrio cholerae is a motile bacterial species naturally found in aquatic environments around the globe, which thrives in low salinity ecosystems but can still survive in high salinity ecosystems. *Vibrio cholerae* is largely harmless, unless it is infected with the bacteriophage CTX Φ . When integrated as a lysogen in the *Vibrio cholerae* genome, CTX Φ converts the bacteria into a pathogen causing the disease Cholera that is responsible for at least 40 million deaths worldwide since 1817. The objective of this research was to characterize *Vibrio cholerae* present in coastal water samples from Huntington Beach, Pawley's Island, and Georgetown, SC and to screen for the presence of the CTX Φ lysogen within identified *V. cholerae* populations. The results show that from the fourteen sampled colonies selected for taxonomic and pathogenicity screening, none of the 8 colonies identified as *Vibrio cholerae* contained the CTXA genes. Notably, all of *Vibrio cholerae* identified colonies were recovered from Huntington Beach and Pawley's island samples, while highly pathogenic *Vibrio vulnificus* colonies were identified exclusively from the Georgetown collections. These results suggest that there is little risk of contracting cholera from Huntington Beach, Pawley's Island, and Georgetown. Future research is needed to examine the distribution and pathogenic of *Vibrio cholerae* populations in the South Carolina coastal waters.

Poster #30

Funding: Horry County Higher Education Commission

Preparing an Image Dataset to Study the Bicaudal C Pleiotropic Phenotypes

Presenter: Gabriella Gurreri | **Major:** High School | **Mentor:** Dr Chiara Gamberi

The Bicaudal C (BicC) gene was first discovered for its function in the ovaries of the fruit fly *Drosophila melanogaster*. It encodes an evolutionarily conserved RNA-binding protein and important negative regulator of translation during egg development. The BicC protein is essential for establishing the anterior-posterior body axis of the embryo, a process that begins during oogenesis in the ovary, and has somatic functions in the epithelium of the Malpighian (renal) tubules. To investigate how BicC functions, we screened the 226-line core set of the *Drosophila* Genetic Reference Panel (DGRP). The DGRP is a collection of over 1,300 fully sequenced fruit fly lines used to study how genetic differences found in natural populations affect phenotypic traits developed in the Mackay laboratory. Unmated DGRP females from each of the 226 lines were crossed to BicC[IIF34]/CyO males, and the BicC[IIF34]/DGRP male and female progeny was isolated, aged to 14-18 days old, microdissected, and 35 sets of Malpighian tubules, ovaries, and testes were imaged for each line. Surprisingly, our original BicC DGRP screen yielded numerous candidate BicC modifier genes that affect several phenotypes in either or both the Malpighian tubules and the gonads. This corroborates the notion that BicC has pleiotropic functions. Building on the results of our DGRP screen, and with the aim to prepare a balanced dataset to study the genetic bases of the BicC pleiotropy via Genome Wide Association Studies, we have dissected additional BicC[IIF34]/DGRP flies and quantified their phenotypes. Here, we will present our progress on the ovarian phenotype analysis.

Poster #31

Funding: National Institute of Health

Study of the effects of Dimethyl Sulfoxide and Ethanol on Bicaudal C and Wildtype *Drosophila melanogaster*

Presenter: Victoria Chen | **Major:** Biochemistry and Molecular Biology | **Mentor:** Dr Chiara Gamberi

The Bicaudal C (BicC) gene, first discovered in fruit fly *Drosophila melanogaster* ovaries, establishes the embryonic anterior-posterior polarity of the oocyte and encodes for a key conserved RNA binding protein that serves as a negative regulator of translation in the germline. BicC loss-of-function mutations produce polycystic kidney disease (PKD)-like cyst in the renal tubules, from flies to humans, further emphasizing the need to understand the biological functions and genetic network of BicC. Our lab has established the fly BicC mutants as a PKD model useful in mechanistic and pharmacological studies. As drug testing with the BicC model continues to expand in search of cyst-reducing compounds, it is essential to establish the baseline effects and tolerable threshold of commonly used solvents such as Dimethyl Sulfoxide (DMSO) and ethanol used to dissolve the many water-insoluble drugs. For example, DMSO is often considered inert, but the commonly used concentrations between 0.1 and 1% affected the cell cycle, apoptosis, and epigenetic regulation⁸. Understanding solvent-induced effects is critical for appropriate experimental controls and accurately interpreting drug responses. Different concentrations of DMSO and Ethanol spiked food were fed separately to female Df(2L)RA5/BicC[IIF34] trans-heterozygotes and Ore[R] wildtype flies 0-2 days old. Flies were aged to 12–14 days-old, microdissected to isolate Malpighian (renal) tubules and ovaries, and imaged on a Leica Ivesta 3 microscope. We will report on the penetrance of the renal and gonad phenotypes in the tested fly populations.

Poster #32

Funding: National Institute of Health

Autosomal Dominant Polycystic Kidney Disease (ADPKD), a genetic degenerative kidney disease

Presenter: Abigail Aston | **Major:** Biology | **Mentor:** Dr Chiara Gamberi

Autosomal Dominant Polycystic Kidney Disease (ADPKD), a genetic degenerative kidney disease, affects 12 million individuals worldwide and is a main cause of end-stage renal disease. ADPKD causes the development of renal cysts, kidney enlargement, reduced renal function, and failure (Chebib et al., 2025). The precise mechanism of ADPKD is unknown. The *Drosophila melanogaster* Bicaudal C gene encodes an RNA binding protein conserved from flies to humans. Our lab has shown that BicC mutations produce PKD-like phenotypes, such as Malpighian (renal) tubules with cysts and extra branching (Gamberi, 2017). Thus, the BicC flies are a PKD model. To identify BicC genetic modifiers, the *Drosophila* Genetic Reference Panel was utilized (Mackay et al, 2012). The DGRP contains ~1,300 stable fly lines, with completely sequenced genomes and transcriptomes. The DGRP collectively contains ~4 million natural genetic variants. We screened the 226 lines of the DGRP core set (~ 2 million variants) by crossing unmated *DGRP/DGRP* females with *BicC[IIF34]/CyO* male flies. For each *BicC[IIF34]/DGRP* heterozygote line, 35 males and 35 females 12-14 days-old were micro-dissected, photographed and scored. We surprisingly found that the seven distinct Malpighian tubule phenotypes are variably associated with gonad phenotypes, which implies polymorphic effects. To define the genetic basis of BicC polymorphism, we increased the image data set to prepare an input matrix for Genome Wide Association Studies. Here, we will share the progress focusing on the Malpighian tubules from female and male flies.

Poster #33

Funding: National Institute of Health

Identifying Bicaudal C in *Drosophila* Genetic Reference Panel

Presenter: Ace Carrasquillo | **Major:** Biochemistry | **Mentor:** Dr Chiara Gamberi

First discovered in the fruit fly *Drosophila melanogaster* ovary, the Bicaudal C (BicC) gene encodes an evolutionary conserved RNA binding protein that establishes the anterior-posterior axis of the oocyte and embryo and has somatic functions in the Malpighian (renal) tubule. We found that BicC mutations also produce phenotypes in the fly testes. To define the BicC functional network, we used the *Drosophila* Genetic Reference Panel (DGRP) which is a unique resource collection of over 1,300 fully sequenced inbred fly lines built to map the genetic interaction networks. The DGRP contains over 4 million genomic variants (or one variant every 50 nucleotides) for extensive genomic coverage. We have screened the DGRP core set (220 lines, ~2 million genomic variants) to identify candidate BicC modifiers in the Malpighian tubule, ovary and testes, define the BicC genetic network, and gain insight into the observed phenotypic variance. To do this, unmated females from the DGRP lines (straight wings) were mated to *BicC[IIF34]/CyO* males (curly wings, dominant) and the *BicC[IIF34]/DGRP* progeny was selected for their straight-winged phenotype. The DGRP screen revealed that the renal and gonad phenotypes assorted variably in the *BicC[IIF34]/DGRP#* heterozygotes, implying pleiotropic effects that can be defined building upon the DGRP screen data. To this end, we expanded the screen data sets with new images of *BicC[IIF34]/DGRP#* heterozygotes. The testes, ovaries and Malpighian (renal) tubules were dissected from the *BicC[IIF34]/DGRP* heterozygote flies and photographed under a Leica Ivesta 3 imaging stereomicroscope. Wild type flies acted as our control reference for organ morphology. We then quantified the phenotypes to build an input data matrix for Genome Wide Association Studies (GWAS) to define the genetic architecture of the BicC pleiotropy. Here, we will present our progress on the *Drosophila* testes phenotypes.

Poster #34

Funding: Unspecified

Assessing the Risk of *Vibrio parahaemolyticus* pathogenic potential from Consuming Oysters Harvested from Northern South Carolina

Presenter: Avery Falco | **Major:** Biology | **Mentor:** Dr Megan Cevalasco

Vibrio parahaemolyticus is an aquatic bacterial species that can cause gastrointestinal infection in humans due to the consumption of raw seafood. The objective of my research was to assess the abundance of *V. parahaemolyticus* in shellfish harvesting areas along the coastal Grand Strand area. Environmental water samples were collected from Huntington Beach and Pawleys Island for selective culture and viable cell counts. The DNA from isolated *V. parahaemolyticus* colonies was extracted, quantified, and amplified by polymerase chain reaction using *toxR* and *gyrB* primers to confirm colony identification. Results showed that the abundance of *Vibrio parahaemolyticus* in the coastal Grand Strand waters tested were below levels known to cause infection, but the public should be advised that improper storage and transport of harvested oysters can result increases in *V. parahaemolyticus* populations, potentially reaching infectious levels.

Poster #35

Funding: Surf grant

Detection of Heartworm DNA in Mosquito Populations at Horry County Animal Shelters

Presenter: Ava Hurley | **Major:** Biochemistry and health Sciences | **Mentor:** Dr Paul E. Richardson

Heartworm disease, caused by the parasite *Dirofilaria immitis*, is transmitted through the bite of an infected female mosquito. It affects various mammalian pets, including dogs, cats, ferrets, and horses. According to the American Heartworm Society, South Carolina has consistently been ranked among the top five states for heartworm disease prevalence. Currently, dogs are the only mammalian pet with approved treatment for the disease and treating heartworm infection can be costly for pet owners, often amounting to thousands of dollars. To combat this endemic, the CCU Disease Hunters team has developed a community-based screening method to detect heartworm DNA in mosquito populations. This screen utilizes Polymerase Chain Reaction (PCR) to amplify the cytochrome c oxidase (Cox-1) gene that is present in heartworms. Then, gel electrophoresis is used to visually determine if heartworm DNA is present in the mosquito populations collected. Animal shelters in South Carolina are at high risk of heartworm infection due to the high volume of mammalian pets and warm, humid conditions. The team has partnered with two animal shelters: All 4 Paws Animal Rescue in Pawley's Island, SC and Kind Keeper Animal Rescue in North Myrtle Beach, SC. Implementing the preventative screen is a valuable tool to help the shelters use their limited resources to protect their furry friends.

Evaluating Metrics for Defect Segmentation Quality

Presenter: Gavin Smithson | **Major:** Computer Science | **Mentor:** Dr. William Jones, Prof. Dakota Fulp, and Dr. Sharmistha Chakrabarti, Los Alamos National Laboratory

Reliable defect localization is essential for manufacturing quality assurance, but manual inspection and annotation can be affected by fatigue, inconsistency, and differences between inspectors. This study evaluates metrics for measuring segmentation quality within a human-in-the-loop inspection workflow that combines MicroSentryAI model suggestions with AnnoMate annotation and validation tools. Unlike image classification, which determines only whether an image contains an anomaly, segmentation identifies the specific image region associated with that anomaly. Using established ground-truth masks from the MVTec Anomaly Detection dataset, we generated controlled perturbations that simulate common annotation errors, including boundary variation, overannotation, underannotation, and severe spatial noise. Each candidate mask was compared with its ground truth using Intersection over Union (IoU), precision, recall, and Euclidean distance between mask centroids. IoU provided the most consistent overall measure of spatial agreement across the tested perturbations. Precision and recall supplied complementary information by distinguishing excessive background inclusion from incomplete anomaly coverage. Centroid distance was less reliable as a general measure because its interpretation varied substantially with anomaly size, shape, and location. These results show that segmentation quality should be evaluated using multiple complementary metrics rather than a single universal threshold. In a human-in-the-loop workflow, combining IoU with precision and recall can provide both an overall measure of agreement and more specific information about the type of annotation disagreement, supporting more targeted review and validation.

Poster #37

Funding: Other (PEG and FSRA 2025/2026)

Beyond Victimhood: Women, Children, and the Untold Knowledge of the Algerian War

Presenter: Rim El Belkacemi | **Department:** Department of Languages and Intercultural Studies | **Mentor:** Internal Grants / Faculty

Some of the most vital knowledge about war exists only in memory and oral testimony. This project explores what rural Algerian women and children know about the War of Independence (1954 to 1962): knowledge about survival, resistance, and how women and children experienced and understood decolonial conflict. Though not combatants, they witnessed war as it interrupted their everyday lives, and they were not passive in that witnessing. Framing them solely as victims is itself a form of epistemic violence: it strips them of agency, flattening complex actors who navigated, endured, and resisted conflict. Through summer fieldwork conducted in Algeria, supported by two internal grants from Coastal Carolina University (PEG and FSRA 2025/2026), I examine the intellectual, ideological, and emotional dimensions of how women and children as subjectivities engaged with war. These testimonies come from rural, non-elite women and children, preserving knowledge that has not been documented before. Their accounts reveal how women and children navigated military operations, maintained households under occupation, and participated in resistance networks. More importantly, they preserve how these experiences were understood and given meaning: the frameworks through which ordinary people made sense of violence, the strategies for protecting communities, the ways communities processed collective trauma, and the ideological commitments that motivated resistance. The project adopts a non-extractive methodology that privileges the narrator's comfort in trauma narrating. This methodology relies on the help of trusted community members trained to conduct interviews in local dialects, allowing access to knowledge that would otherwise disappear with the generation that withstood this war 72 years ago. This is knowledge that lives in bodies, in families, in communities: how fear felt, how decisions were made under impossible circumstances, what children witnessed and carried forward. By collecting these testimonies, this research demonstrates how oral testimony preserves irreplaceable forms of understanding about war's human dimensions while facilitating intergenerational working through of trauma. These accounts fundamentally expand what we can know about conflict, decolonization, and the historiographical exclusion of rural, non-elite communities from both colonial archives and nationalist historiographies.

Special Thanks

We would like to recognize the extraordinary efforts of Eric Resnis! Thanks to his organizational help we were able to host this symposium in the Thompson Library.

<https://libraries.coastal.edu/prf.php?id=5c616f48-7cdb-11ed-9922-0ad758b798c3>



Thanks to all the presenters
that took
part in this scholarly
showcase!!

