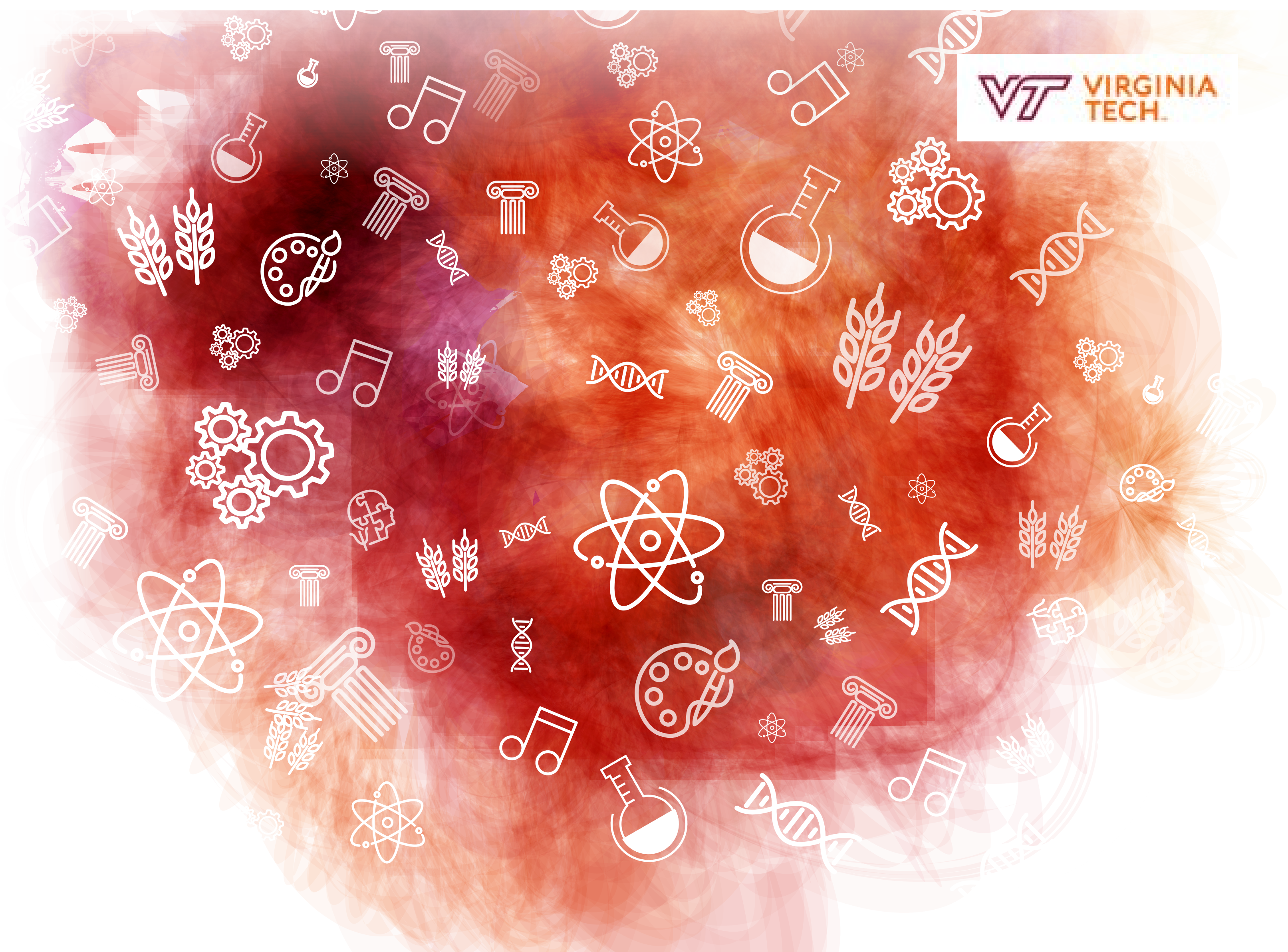

VIRGINIA TECH'S OFFICE of UNDERGRADUATE RESEARCH SUMMER SYMPOSIUM

Virtual | July 29, 2021 | 9am-4pm

ABSTRACTS

www.research.undergraduate.vt.edu

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Jill C. Sible, Ph.D.
Associate Vice Provost for
Undergraduate Education,
Professor of Biological Sciences

Welcome

With great enthusiasm, I welcome all to the 2021 Summer Undergraduate Research Conference at Virginia Tech. This year is particularly exciting to feature both the work of students conducting research remotely as well those who were able to join us in person.

Many students presenting today, have spent ten or more weeks immersed in a research project. Summer affords undergraduates the opportunities to dedicate significant time and effort to the planning, execution and analysis of a research project. They have also had the chance to become authentic members of research teams by working with faculty, graduate students, postdoctoral fellows and research staff. Many thanks to all who have mentored undergraduates this summer. Your commitment to undergraduate research is always commendable, and especially this year given the extra challenges you overcame to offer safe and engaging research opportunities during the COVID-19 pandemic.

Virginia Tech is pleased to offer these summer experiences not only to our own students, but also to undergraduates from all over the country. We hope that you have enjoyed your time working with Virginia Tech research teams, and we appreciate the diversity of ideas and cultures that you have brought to our research programs. Congratulations to all of our presenters!

A very special thank you to Keri Swaby, Nicole Bottass, and our peer mentors for their tremendous work in making this summer symposium happen. We have discovered that this virtual medium has in some ways provided a wider audience for student work and allowed deep exchanges of ideas with our presenters.

So please avail yourselves of that opportunity. I am looking forward to my time learning from our summer research students!

My best,
Jill C. Sible, Ph.D.
Associate Vice Provost for Undergraduate Education

Office of Undergraduate Research

Keri Swaby
Director, Office of Undergraduate Research

Welcome to the annual Summer Research Conference at Virginia Tech!

After cancelling or moving all activities online last summer, we were so excited to be able to welcome students back onto campus *in person* this year. Not everyone could be on campus but today we celebrate ALL researchers- remote and in person- who are part of our vibrant summer research community.

Today we welcome 167 presenters from 20 organized research programs and many independent labs, who will give 154 video presentations. Over the course of the past 10 weeks, these undergraduate students from Virginia Tech and across the country have been engaged in a wide variety of projects tackling real world problems in many disciplines. I am humbled by the quality of work on show today and invite you to enjoy and marvel at the wealth of research that took place both in person and remotely this summer.

In support of our summer researchers, we offered comprehensive professional development programming that would not have been possible without the expertise and time of many folks I would like to thank: Dr. Nikki Lewis (Honors College) and Dr. Donald Conner (VT Environmental Health and Safety) for setting the stage and providing students with critical information during our summer orientation session; Amanda MacDonald (University Libraries) for providing students with valuable training through the online Advanced Research Skills Program, Carrie Kroehler (Center for Communicating Science) for helping to design a brand new and fun communication skill building program, and a number of faculty and students who offered a variety of seminars and workshops throughout the summer including Dr. Justin Grimes (VT Graduate School), Daniel Bird Tobin (Ctr for Comm Sci), Kelsey Reed (PhD candidate in Translational Plant Sciences), Meredith Gerber (Career and Professional Development), Dr. Paul Heilker (Honors College), and Kelsey Hammer (University Libraries) and several research alumni and graduate school panelists. Thank you all for sharing your expertise and insights with our summer students.

This summer was not only about research and professional growth. A special thank you to our energetic and creative peer mentors – Danielle, Jared, Maame and Mackenzie - who offered both in person and virtual activities throughout the summer and were instrumental in building a vibrant research community. They organized a cookout and restaurant visits, hikes to Cascades Falls and Dragon's Tooth, trips to go tubing on the New River and swimming at Claytor Lake, disc golf games, as well as virtual movie and game nights. Without these dedicated mentors, this summer would not have been as fun and engaging for everyone.

I also want to extend an extra special thank you to Nicole Bottass, who has been instrumental in supporting all OUR activities throughout the summer!

The operations of the OUR would not have been possible without generous financial support from the Fralin Life Science Institute. Thank you!

Researchers, congratulate yourselves on a productive summer of *almost* normal! I hope you have been inspired to continue exploring and growing. Good luck next year!

Sincerely,
Keri Swaby
Director, Office of Undergraduate Research

SUMMER RESEARCH PROGRAMS AT VT

PROGRAM DIRECTORS

ARMY RESEARCH OFFICE GRANT

Michel Pleimling

BECKMAN SCHOLARS AT VIRGINIA TECH

Amanda Morris (Director)

The Beckman Scholars Program, supported by the Arnold and Mabel Beckman Foundation, is a 15-month mentored research experience for exceptionally talented, full-time undergraduate students in chemistry, biological sciences, or biochemistry at Virginia Tech. In 2021, Virginia Tech was selected as one of 12 institutions nationwide to host a Beckman Scholars Program. The program leveraged the funding provided by the Beckman Foundation to form a partnership with the Fralin Life Sciences Institute to provide a fully-funded research experience like no other on the Virginia Tech campus. Through unique programming in communication, leadership, grantsmanship, and diversity and inclusion awareness, our goal is to create the next generation of scientific leaders.

Applicants select from 12 principal investigators from across multiple degree programs. The program provides a generous stipend and research support. More information can be found here - https://www.research.undergraduate.vt.edu/ugr-opportunities/vt-programs/beckman-scholars.html.

COMPUTATIONALLY DRIVEN EXPERIMENTAL BIOLOGY

Dr. Kristy Collins

Computationally Driven Experimental Biology is a 10-week NSF-funded summer program. Four students with training in applied mathematics, biology, and computer science developed and analyzed computational models of cellular processes. They developed new algorithms and software to determine whether the properties of simulated gene expression datasets matched those of the underlying biological networks.

CONFLUENCE REEU

co-Directors: Cully Hession, Leigh-Anne Krometis, Brian Badgley, and Erin Ling

This eight week USDA Research and Extension Experience for Undergraduates (REEU) program brings together students representing multiple disciplines from across the country to explore research, outreach, and education in water sustainability. Our 2021 Confluence REEU program cohort includes twelve students representing seven different home colleges and universities and nine distinct degree granting programs ranging from Civil Engineering to Economics. The virtual format of our 2021 program guided fellows through explorations of water resources close to home via data seminars and remote monitoring kits. Fellows were combined into three interdisciplinary multi-university teams that researched common water quality issues in order to develop stakeholder outreach materials. This enabled fellows to both immerse themselves in the pressing water quality issues in their own “backyards” and to link these observations with water sustainability challenges in other fellows’ home watersheds which represent different ecological landscapes.

FBRI NEUROSURF

Dr. Michael Fox (FBRI + VT Biological Sciences)

Dr. Alexandria Pilot (Fralin Biomedical Research Institute)

The FBRI neuroSURF program is a 10-week long program that gives VT and non-VT undergraduate students the opportunity to participate in independent translational neurobiology research at Fralin Biomedical Research Institute at VTC in Roanoke, VA. This year, program participants also included one high school student from Roanoke Valley Governor's School/Salem High School. In addition to independent research, the program includes coursework in translational neurobiology, seminars from VT and Carilion faculty whose research focuses on translational neurobiology, and professional development activities. The 2021 FBRI neuroSURF fellows came from VT, University of Tennessee, University of Florida, Vassar College, Frostburg State, Davidson College, University of Minnesota, The College of William and Mary, Kenyon College, and University of Maryland. The neuroSURF program is funded by the National Institutes of Health.

FRALIN SUMMER UNDERGRADUATE RESEARCH FELLOWSHIP (SURF)

Keri Swaby (Office of Undergraduate Research)

The Fralin SURF program is a 10-week training program designed to give motivated Virginia Tech undergraduates the opportunity to engage in full time research in the life sciences and related professional development activities that mirror graduate training. The goal is to offer students experiences that will help them determine if they want to pursue a career in research while they develop skills for graduate school. For the past seven years, 15 to 30 exceptional students from a variety of majors are selected to participate in this competitive program. We would like to acknowledge the 5 students who had their SURF experience cancelled last year due to the pandemic but were able to defer and join the cohort this year. This program is funded by the Fralin Life Science Institute.

GLYCOMIP SUMMER UNDERGRADUATE RESEARCH

Dr. Richard Helm (Department of Biochemistry)

The National Science Foundation, NSF, funded molecular foundry entitled GlycoMIP (glycomip.org) is pleased to participate in the Fralin Life Sciences Institute *Summer Undergraduate Research Fellowship Program*, SURF, a 10-week training program that combines research experiences with related professional development activities. GlycoMIP researchers engage in a broad range of research activities related to carbohydrates, with emphasis on their material properties. Such work includes molecular modeling, oligosaccharide synthesis, and characterization of glycomaterials by techniques such as liquid chromatography, mass spectrometry, rheometry, and spectroscopy. One of only four NSF Materials Innovation Platforms (MIPs) in the country, the facility serves as a national resource for glycomaterial research, development, and training. GlycoMIP SURF students work directly with faculty, post-docs and graduate students in the GlycoMIP user facility, gaining hands-on experience with a wide array of techniques and instrumentation. Their work contributes directly to active research projects within the facility.

KAUST REU

Peter Vikesland

The King Abdullah University of Science and Technology (KAUST) REU program supports the research activities of fourteen Saudi Arabian nationals who are currently attending universities and colleges in the United States. During the summer of 2021, seven students are taking part in person and seven are taking part virtually.

MULTICULTURAL ACADEMIC OPPORTUNITIES PROGRAM (MAOP)

Monica Hunter (MAOP Director), Taylor Swan (MAOP Assistant Director), Amy Ingram (MAOP SRI Coordinator), and Ozioma Chinaka (MAOP SRI Program Assistant).

The MAOP Undergraduate Summer Research Internship (SRI) started in Summer 1993, and since then has been a transformative experience for hundreds of students. The purpose of the program is to provide undergraduates from diverse backgrounds an opportunity to conduct research on campus and to educate participants about graduate education. Students from a wide variety of academic disciplines spend ten weeks during the summer (late May - late July/early August) working closely with a faculty mentor in a mentor/protege relationship to design, conduct and present a scholarly research presentation.

Since many SRI participants eventually enroll in graduate school at Virginia Tech or elsewhere, this program has been an especially effective way to invest in and prepare a talented, diverse group of students for enrollment in graduate programs. Previous participants have been very successful in obtaining graduate degrees and in adding to the diversity of their institutions and within their professional fields.

MOLVI

Dr. Jamie Smyth

NEUTRINO REU

Dr. Camillo Mariani (Department of Physics) and Betty Wilkins (Department of Physics)

Our physics faculty is engaged in a broad spectrum of research within neutrino physics, including electron/neutrino scattering experiments, the search for sterile neutrinos, phenomenology studies, long baseline optimization for DUNE and the study of neutrino spectrum from nuclear reactors and supernovae neutrino experiments and theory.

In this rich intellectual environment, the REU students will have the opportunity to pursue independent and productive activities, guided by an established team of faculty members together with assistant professors and postdocs.

TRANSLATIONAL OBESITY UNDERGRADUATE RESEARCH SCHOLARS (TOUR)Drs. Deborah Good and Samantha Harden (Department of Human Nutrition, Foods, and Exercise)

The Translational Obesity Undergraduate Research Scholars (TOUR-Scholars) is an NIH Funded research-intensive summer experience, which prepares students for graduate and medical education in translation obesity research.

Ten undergraduate students representing Virginia Tech and three other universities were chosen to participate in the 2021 summer program and are working with 10 different mentors at Virginia Tech, FBRI, and VTCRI.

In addition to research, students participated in professional development around inclusivity, communication, and career training, including trips to TechLabs as well as VTCSOM and VTCRI in Roanoke.

VIRGINIA TECH RESEARCH AND EXTENSION EXPERIENTIAL LEARNING PROGRAM: SECURING OUR FOOD (VT-REEL)

Drs. Sasha Marine (Biochemistry), Glenda Gillaspy (Biochemistry) and W. Hunter Frame (SPES)

Virginia Tech's Research and Extension Experiential Learning (VT-REEL) program on Securing Our Food is a research-intensive 10-week summer experience, which engages undergraduate students in translational plant science research via a combination of hands-on laboratory and field-based experiences. Traditionally, VT-REEL fellows spend the first half of the program on-campus, working in molecular plant science labs, and spend the second half of the program at Agricultural Research and Extension Centers (AREC), working in applied plant science labs.

Eight undergraduate students from diverse academic institutions across the United States were chosen to participate in the 2021 summer program. Because of the ongoing pandemic, each VT-REEL fellow conducted a plant science project under the guidance of either an on-campus or an AREC faculty mentor. Students participating in the program also completed weekly scientific workshops and OUR's online Undergraduate Research Training series. VT-REEL fellows were provided with research stipends, housing and meal plans. Funding was obtained through the USDA-NIFA. This program will continue through 2025.

VT SCHOOL OF NEUROSCIENCE JAMES & LILLIAN GAY NEUROSCIENCE SUMMER UNDERGRADUATE RESEARCH FELLOWSHIP (NEUROSURF)

Dr. Sarah Clinton (School of Neuroscience)

The VT School of Neuroscience offers a vibrant research environment with faculty covering almost all areas of contemporary neuroscience. Expertise of our faculty spans a variety experimental approaches, ranging from molecular and cellular neuroscience, neurochemistry, pharmacology, behavioral neuroscience, and brain imaging. The competitive summer fellowship program provides VT undergraduate students with 10-week full-time research experience in a neuroscience laboratory, which allows them to contribute to research projects under the direction and leadership of a faculty mentor and gain valuable experience in data presentation at the end of the summer.

UK IRES (COE)

Nicole Sanderlin

INFORMATIONAL BOOTHS

We invite you to talk with representatives from several graduate programs, from across Virginia Tech’s Blacksburg, Roanoke, and National Capital region campuses.

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TRANSLATIONAL BIOLOGY, MEDICINE AND HEALTH

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Abstracts

Zaina Alabandi
Columbia University/Neuroscience and Behavior

Rules of contact inhibition locomotion for cells suspended on widely spaced nanofiber networks

Cell movement coordination is a fundamental element of wound healing, metastasis, and more. Contact inhibition of locomotion (CIL) is a phenomenon crucial to coordination and many developmental functions, in which two approaching cells make contact, then proceed to repolarize and move away from the site of contact. Most studies attempting to identify the rules of CIL have cells on flat surfaces; these settings are unrepresentative of in vivo conditions where cells are found suspended on fibers in a 3D matrix. To observe CIL in an environment that mimics the extracellular matrix, we suspend cells on nanofiber networks and examine how they react when they encounter one another. In CIL studies done in 2D settings, approaching cells often follow the expected rule of CIL and repolarized to move away from each other. However, in a 3D setting, we have seen that cells suspended on a single fiber walk past each other, while those suspended on multiple fibers end up moving as pairs, both opposing the repolarization rule. Additionally, we have seen that cells, response to making contact with one another changes depending on the number of fibers they are suspended on. Here, we look at cells moving and interacting along nanofibers in networks with wide spacing. Once we gain a more accurate understanding of the rules of CIL in a 3D matrix, we will have a clearer picture of how CIL works in vivo, which is valuable information for future studies on wound healing or cancer metastasis.

Mentor(s): Amrinder Nain (Mechanical Engineering, Virginia Tech)

Abdulaziz Alali
Kaust/Chemistry

The Application of Amorphous Solid Dispersions in the Delivery of Polypeptide Drugs

Polypeptide drugs have a great range of possible application that other types of drugs cannot provide; however, polypeptide drugs have several obstacles standing in the way of a reliable administration to patients. These include but are not limited to the susceptibility for polypeptides to be digested if it is administered orally, low solubility, and the health risk of injecting a foreign polypeptide directly into the blood. A possible solution to this problem is amorphous solid dispersions. In this project we synthesized a cellulose-based polymer to act as a possible polymer for a hypothetical polypeptide drug. The polymer in question was synthesized with hydroxypropyl celluloses starting material due to its higher solubility in water. The HPC was first oxidized and then merged with L-tyrosine, an amino acid, that can act as the connecting point for a polypeptide. Finally, a simple polypeptide will be used as stand-in for a hypothetical polypeptide drug. The HPC-tyrosine polymer's viability as carrier polymer for polypeptide will be tested by adding the polymer and the simple polypeptide together and then leaving the combination in a water solution with human body-PH level to track the dispersion of the simple polypeptide. Based on pervious work done by faculty in this university that conclude that cellulose derivative are good stabilizers for amorphous solid dispersions, we expect the polymer to be a viable choice as carrier for polypeptides.

Mentor(s): Kevin Edgar (Sustainable Biomaterials, Virginia Tech)
Yang Zhou (Sustainable Biomaterials, Virginia Tech)

Arwa Albaltan
UCLA/Mechanical Engineering

Optimization and localization method for tension controlled soft robotic actuation in biomimetic bat robot

Bats have the ability to use echolocation to navigate through complex environments and obtain fast reflexes to ensure their survival. The way bats are able to encode sensory inputs is by the combination of their noseleaves (emitters) and pinna (receptors) for signaling and sensing sound frequencies. The geometry and flexibility of the horseshoe's bat pinna allow the necessary deformations of the ear and its fast movements in order to achieve a self-generated doppler shift. With a nonlinear actuator placed at five different locations, giving the pinna five degrees of freedom the movement mimicking the muscular actuation in bats. In this project, the placement of the tension-based actuators will be investigated to optimize the variety of possible motion patterns given by the five actuators on each pinna. The placement was decided based on the velocity gradient on different regions of the ear and the placements of the muscles on the horseshoe bat pinna. A simulation using Fusion 360 software was used to test and alter the deformations resulting from the tension-based actuators, placements and forces. The biomimicry the bat's spatial sensitivity pattern for the reception of the biosonar signals can enable man-made sonar systems that could be used in autonomous soft robotic systems.

Mentor(s): Rolf Mueller (Mechanical Engineering Department, Virginia Tech)

Loay Alem
UCLA

Lithium extraction from seawater using electrolysis

Lithium is an important element for electronics. The importances comes from lithium,Äôs natural characteristics such as its low redox potential, and low density. There is a growth in lithium demand due to the worldwide movement to electrical vehicles, renewable energies, portable electrical devices, etc. Furthermore, Lithium resources on land are decreasing and are expected to be depleted by 2080. However, data has shown that the ocean contains 5000 multiples of lithium land reservoirs. Therefore, due to the possibility of an infinite lithium reservoir, many ideas have been experimented on to extract lithium from seawater, such as electrolysis, adsorption, and electrodialysis. Many of the systems mentioned, however, can be costly to scale, energy inefficient, or have a very slow lithium production rate. This study analyzes a promising 5 step continuous electrical pumping membrane electrolysis system, created by a research group from KAUST that improves on the caveats mentioned. This study analyzes the KAUST system to discover areas of improvement and challenges the system brings.

Mentor(s): Lei Zuo (Energy Harvesting and Mechatronics Research Laboratory, Virginia Tech)

Abdulelah Alkhamis
University of California, Los Angeles/2023

KGSP REU

Ocean-wave Powered Batch Reverse Osmosis System

Batch-mode Reverse Osmosis (RO) is a water desalination process in which feed water is circulated multiple times through the filtering membrane. Batch RO system requires a constant high-pressure input which consumes high amounts of energy. Therefore, previous research has focused on renewable energy to power desalination systems. Ocean wave energy has a higher power density of 10-20 kW per cubic meter than either wind or solar, which is up to 10 to 20 times. However, ocean wave energy is not put into commercial use yet due to the low frequency and oscillating velocity. Studies have investigated combing ocean wave energy and seawater desalination to solve the water crisis in coastal regions. However, the freshwater recovery ratio from the integrated system is not promising. In this project, we investigate the performance of batch-mode Reverse Osmosis (RO) desalination system under wave input conditions. On one hand, the pressure accumulator can stabilize the system pressure since the wave induced pressure is time-varying. On the other hand, the circulation pump can recycle the high-pressure brine to significantly increase the recovery ratio of the system. It is anticipated that this design requires less energy and operates faster than regular batch-mode RO systems.

Mentor(s): Lei Zuo (Department of Mechanical Engineering, Virginia Tech)
Xian Wu (Department of Mechanical Engineering, Virginia Tech)

Zainab Almuallim
University of Pittsburg/Bioengineering

Enhancing High-Speed Imaging of Bat Flight

Compared to birds and flying insects, bats have a more complex articulated multibody structure of their wings. Bats fly with non-steady dynamic motion patterns that help them capture their prey and navigate obstacles. It also makes tracking and studying their flight kinematics challenging. This research focuses on bats' flight and biosonar behavior from the perspectives of biophysics and bioinspired engineering. In 2018, a study by Windes et al. constructed an angular tunnel with 21 action cameras on the walls and six lights mounted in the upper corners to investigate the fluid phenomena of a flapping membrane. The method pursued in this study consist of a tunnel, 50 high-speed cameras, and 40 LED lights to get a more comprehensive detailed look on the construction of bat wings and bat flying pattern. Moreover, to attain the perfect lighting conditions, the brightness is manipulated in a smaller version of the tunnel that consists of five high-speed cameras and eight LED lights. The cameras are synchronized and arranged on the tunnel walls from different viewing angles to the bat model. In order to track the points of interest on the wingtip, tail, and claws, all images and videos will be later processed and analyzed using the deep learning method to reconstruct the model by subtracting the background and improving the quality of the model.

Mentor(s): Rolf Mueller (Mechanical Engineering, Virginia Tech)
Yihao Hu (Ph.D. Student, Virginia Tech)

Mustafa Almutawa
University of Massachusetts Amherst/Computer Science

KAUST-REU

Numerical Investigation of Ambient and Snow Parameters on the Tire Traction Coefficient Using Response Surface Methodology

To be branded with the three-peak mountain snowflake (3PMSF) symbol, which indicates that the tire can withstand severe snow usage, a tire must go through specific testing standards in snow. During the testing, several variables are recorded, some of which are kept fixed whereas others vary. This research numerically investigates the relationship between a set of input (independent) variables and an output variable. The input variables are the CTI index, ambient temperature, and surface temperature, while the output variable is the traction coefficient of a tire. Using computational tools and a dataset of tire testing, various data sensitivity models have been implemented to gain insight into how the different factors affect tire traction on snow. The models were trained using two MATLAB apps: regression learner and curve fitting. Rigorous validation of the meta-models is still to be achieved, and a response surface methodology (RSM) is suggested for better modeling. After validation, the objective is to potentially enhance tire testing standards by understanding what factors have a greater impact on the traction coefficient of a tire. Insignificant variables need to be given less attention while increased attention should be directed towards more impactful variables, as well as varying some of the previously constant variables during testing. Density of snow, inflation pressure, and normal load are some variables that are kept constant but could have an influence on traction. In the longer term, the results of this study can also contribute to the design of improved tire prototypes and testing methodologies.

Mentor(s): Costin Untaroiu (Department of Biomedical Engineering and Mechanics, Virginia Tech)

Julian Alonso
Virginia Tech/Biology

MAOP

Comparison of Effectiveness of Pathasure ELISA testing kit and PCR testing for the Diagnostics of Calf Diarrhea

Diarrhea is the most common disease of young calves and can have devastating economic consequences due to its mortality level. Diarrhea can be caused by Salmonella, Rotavirus, Coronavirus, E. coli K-99, and Cryptosporidium. The prevalence of these agents was tested using the Pathasure ELISA kit and bacterial culture of 32 samples from calves with diarrhea and the results were compared with polymerase chain reaction (PCR) testing as the "gold standard" diagnostic test to calculate sensitivity and specificity and to discover if the Pathasure ELISA kit is a feasible investment for the Virginia Tech Animal Laboratory Services (ViTALS). Fecal samples were collected from calves with diarrhea in southwest Virginia aged between 1 and 33 days, stored at -80oC, and aliquoted for ELISA, PCR, and Salmonella culture. Salmonella culture entailed plating samples on selective media and in enrichment broths throughout a 3-day process. Colonies suspicious for Salmonella were identified using MALDI-TOF mass spectrometry. Aliquots of feces were sent to Iowa State Veterinary Diagnostic Laboratory to be tested for all agents by PCR. Rotavirus had a 20% sensitivity, while Coronavirus had 0%. No samples were positive for Salmonella and E. coli by PCR, so the sensitivity for those organisms could not be determined. All agents had a specificity of at least 90% except for Cryptosporidium, which had a 58% specificity with 100% sensitivity. Overall, the Pathasure ELISA kit was not seen as a feasible investment for ViTALS because of the low sensitivity of the assay to detect multiple calf diarrhea pathogens.

Mentor(s): Tessa LeCuyer (Clinical Microbiology, College of Veterinary Medicine, Virginia Tech)

Yazeed Alroogi
Northwestern University/Biomedical Engineering

Bacteria biofilms as living Surface-Enhanced Raman Spectroscopy labels for virus (bacteriophage) detection

Surface-Enhanced Raman Spectroscopy (SERS) utilizes nanostructures to enhance the raman scattering of molecules, which acts as a fingerprint to identify different molecules. Such a technique can be used to monitor desired living environments to identify the processes and interactions that occur to better understand said environments. One such environment is bacteria biofilms, an organized collection of bacteria cells that forms as a survival mechanism. These biofilms can be used as organic labels for SERS to detect bacteriophages. We hypothesize that the introduction of viruses to the biofilm environment can selectively perturb its formation by altering metabolic pathways or lysing the bacterial cells. Thus, we are trying to detect bacteriophages by comparing biochemical information given by SERS spectra of biofilms with and without the virus at multiple different stages of development. Since the label-free SERS spectra of bacterial biofilms produces highly complicated signals, Principal Component Analysis will be used for data reduction and Linear Discriminant Analysis will be used for data classification. We expect that the results of SERS spectra and the following statistical analyses can give us a better understanding of how bacteriophages affect the biochemical process of bacterial biofilms, as well as a method of identification of virus-infected biofilms. Additionally, we hope that such an approach can be applied to the detection of human viruses using mammalian cells as organic SERS labels in the future.

Mentor(s): Wei Zhou (Electrical and Computer Engineering, Virginia Tech)

Asear Alruhaili
Purdue University/Material Engineering

Photothermal inactivation of bacteria using graphene oxide embedded bacterial nanocellulose membranes

The purpose of this research is to investigate the Photothermal inactivation of bacteria by graphene oxide embedded bacterial nanocellulose membranes using photothermal disinfection experiments and Raman spectroscopy. The global spread of pathogenic bacteria is considered a great threat to water quality. Rapid identification and efficient inactivation of pathogenic bacteria remains a critical challenge to overcome if we are to prevent infectious diseases and protect public health. In this study, we did a one-step biosynthesis of a bilayer structured hydrogel composite of graphene oxide (GO) and bacterial nanocellulose (BNC) for photothermal water treatment applications. A gram-negative bacteria, Pseudomonas syringae (P. syringae) and a gram-positive bacteria, Bacillus subtilis (B. subtilis) were grown in 50 % heavy water (D_2O) for Raman stable isotope labeling (Raman-D_2O). The isotope labeled bacteria showed distinct peaks in their Raman spectrum, which can be attributed to the carbon-deuterium (C-D) stretching vibrations. For future, experiments, the photothermal inactivation of bacteria will be quantified by observing the changes in the C-D signal of bacteria, before and after their exposure to artificial sun lights. In the preliminary inactivation experiments, bacterial culture-based colony counting showed significant decrease in bacterial colonies, suggesting inactivation of bacterial cells by photothermal inactivation. This simple approach shows the potential for the application of graphene oxide embedded cellulose nanomaterials for environmental applications.

Mentor(s): Peter Vikesland (Civil Engineering, Virginia Tech)
Asifur Rahman (ECE, Virginia Tech)

Raghad Alsalman
Columbia University/Chemical Engineering

Spatiotemporal monitoring of biochemical changes during biofilm maturation via SERS

Surface-Enhanced Raman Spectroscopy (SERS) is a sensitive, non-invasive detection technique that enhances the Raman scattering by factors of 1010 to 1011 using plasmonic nanostructures, such as gold and silver, as substrates. SERS is used in the identification and monitoring of low concentrations of various molecules and living organisms. One example of such use is biofilms, a communal mechanism of living for most microorganisms that is present almost everywhere. Studying the biochemical processes involved in the development of biofilms; such as the extracellular polymeric substance (EPS) formation, purine metabolites release, and quorum sensing process; is essential to human health and in understanding the interactions between biofilms and diseases. Such processes are spatially monitored over time via label-free SERS, providing highly complicated signals from molecular ensembles in the SERS hotspots. The biochemical information embedded in the complex data is then analyzed using two methods: Principal Component Method (PCA) for data reduction and Linear Discriminant Analysis (LDA) for classification. These findings could assist with future utilization of biofilms as labels in conducting further research on other living organisms.

Mentor(s): Wei Zhou (ECE, Virginia Tech)
Aditya Garg (Grad student mentor, Virginia Tech)

Lucas Angles
Vassar College/Neuroscience and Behavior

Measuring post-movement beta rebound in the motor cortex with optically pumped magnetometry

Magnetoencephalography (MEG) is frequently used to non-invasively monitor brain electrophysiology and get real-time measurements of cortical activity. Since MEG captures small extracranial magnetic fields produced by coordinated neuron firing, data collection is orders of magnitude faster than indirect techniques such as BOLD fMRI and PET. However, due to movement limitations, as well as high acquisition and operating costs of the cryogenic system, the technology is scarce. In recent years, Optically-pumped magnetometers (OPMs) allow MEG studies to run at low costs and be movement forgiving, but the technology remains nascent and more studies are required to fully evaluate its efficacy. Here, we constructed a wearable OPM-MEG system andtested its capability to accurately record data. In this study, we measured rebound of beta synchronization following movement due to its thorough analysis in previous literature. We found that OPMs detected increases in beta oscillation immediately preceding and succeeding movement at a sampling frequency of 2,000 Hz. Furthermore, we found increased contralateral hemispheric activation of beta rebound, providing further evidence for OPM-MEG to record with accuracy. Our results demonstrate how OPM-MEG can be utilized as a cost-effective method for sub-second functional neuroimaging. We anticipate this apparatus to be a starting point for more fine-tuned systems. For example, combining sensor position and orientation data would allow us to crossreference sensor recordings with fMRI structural scans and source localize cortical activity with significant precision. With a higher sensor density, OPM-MEG may exceed cryogenic MEG in spatial accuracy and revolutionize the field of neuroimaging.

Mentor(s): Read Montague (Physics, Virginia Tech)

Ahmed Balubaid
Rose-Hulman Institute of Technology/Mechanical Engineering

Pedestrian on Wheelchair Safety During Vehicle Crashes

The goal of this project is to study and understand how a pedestrian on a wheelchair is affected in a vehicle-to-pedestrian impact. This is done by simulating the crash with different pre-impact conditions such as vehicle speed and pedestrian posture. The post-impact pedestrian model is then analyzed to see how different conditions influence resulted injuries.

The first step in the simulation process is to prepare a wheelchair model to be used in the simulation. A wheelchair CAD model is broken down into finite elements using Hypermesh. Then, the finite element model is assigned material properties and joints are created to connect the model pieces together using LS Dyna. Afterwards, the model is tested and validated based on experimental data. Once the wheelchair model is ready, a human model is added on top of the wheelchair and the vehicle-to-pedestrian impact simulation can be implemented.

The purpose of this study is to make recommendations based on simulations with different vehicle designs such as bumper stiffness and location, and to provide design suggestions that can increase the safety of pedestrians.

Mentor(s): Costin Untaroiu (Department of Biomedical Engineering and Mechanics, Virginia Tech)
Daniel Grindle (VT/VTTI-Student)

Mahder Belew
Hollins University

Synthesis and Characterization of Dirhenium Compounds That Contain dppm, dppmMe and dppmCN

The ultimate aim of this project is to prepare complexes of the type cis-Re2(O2CCH3)2X2(PP)2 (PP = dppmMe, dppmCN) in order to help us assign a downfield resonance associated with two symmetry-related methylene hydrogens in the H-1 NMR spectrum of cis-Re2(O2CCH3)2Cl2(dppm)2.
Qualdruply-bonded dirhenium (III) complexes Re2(O2CCH3)X4(H2O)2 (X = Cl, Br) react with Ph2PCH2PPh2 (dppm), Ph2PCH(CH3)PPh2 (dppmMe), or Ph2PCH(CN)PPh2 (dppmCN) to give reduced complexes Re2(O2CCH3)X4(PP)2 and Re2X4(PP)2 (PP = dppm, dppmMe, dppmCN). We have observed that thermolysis of Re2(O2CCH3)X4(PP)2 in refluxing ethanol also leads to the formation of Re2X4(PP)2. All products synthesized were characterized by cyclic voltammetry and infrared spectroscopy.
We are planning to further investigate the characteristics of the compounds we synthesized by NMR spectroscopy and single-crystal X-ray diffraction.

Mentor(s): Daniel Derringer (Chemistry Department, Hollins University)

Josephine Beyer
Virginia Tech/Nanomedicine

Elucidating Molecular Interactions of the Endosomal Adaptor Protein TOM1 using Microscale Thermophoresis: Josephine Beyer, Tiffany Roach, Daniel Capelluto

The adaptor protein TOM1 plays a major role in protein turnover. TOM1 associates to endosomal ubiquitinated protein receptors, recognition that is required for their further transportation to the lysosomes, where they are degraded. In many reported cases, TOM1 requires binding to the adaptor protein TOLLIP for protein receptor transportation. TOM1 is composed of the N-terminal VHS domain, followed by a central GAT domain, and a C-terminal domain. Both VHS and GAT domains bind ubiquitin, a protein that is covalently bound to protein receptors when marked for their degradation. Infections with the pathogen Shigella flexneri induce host cells to overproduce the membrane phosphoinositide phosphatidylinositol 5-phosphate (PI5P) at signaling endosomes. In this scenario, TOM1 moves to signaling endosomes through recognition of PI5P, impairing protein turnover and, simultaneously, increasing cell survival. Association of TOM1 to PI5P is mediated by its VHS domain. The goal of this project is to quantify the binding events between TOM1 and its domains to both ubiquitin and membrane lipids using microscale thermophoresis (MST). This technique uses an IR-laser induced fluorescence to produce a temperature gradient that can be used to determine molecular events of protein-ligand interactions. With MST, we were able to measure high affinity interaction of TOM1 with TOLLIP, consistent with prior isothermal titration calorimetry data collected in our lab. Interactions of TOM1 and its domains with ubiquitin and PI5P are currently in progress. Additional future studies include a recently reported naturally occurring mutant TOM1 G307D, which causes autoimmunity, to elucidate what molecular interaction is altered due to this mutation.

Mentor(s): Daniel Capelluto (Biological Sciences, Virginia Tech)
Tiffany Roach (Ph.D. candidate, Virginia Tech)

Michaella Bono
Virginia Tech/Experimental Neuroscience

The Brainstem Cholinergic System and Parkinson's Disease

Parkinson's disease (PD) is a complex behavioral disorder characterized by a number of impairments in motor control. Previous research has shown that a major contributor to these impairments is the degeneration of dopamine cells that project to the striatum. Cells in the pedunculopontine nucleus and lateral dorsal tegmentum of the brainstem produce the neurotransmitter acetylcholine (ACh) and also show signs of degeneration in PD, however, we understand comparatively little about how damage to the brainstem cholinergic system may contribute to PD. A major target of brainstem cholinergic cells is the intralaminar thalamus, a structure which provides excitatory input to the striatum and can potently modulate motor control. We hypothesize that brainstem cholinergic inputs to the intralaminar thalamus play an important role in thalamic-striatal interactions, and thereby motor control. To test this hypothesis, we have designed a set of studies to detail brainstem cholinergic modulation of the intralaminar thalamus in freely moving mice. Specifically, we are using virally-mediated gene transfer to express a genetically encoded ACh (Exp 1) sensor, or a neural activity indicator in axon terminals of cholinergic cells (Exp 2) in the intralaminar thalamus. We then use fiber-photometry to characterize sub-second changes in thalamic ACh activity. Our preliminary recording data indicate a surprising inverse relationship between thalamic ACh release and locomotor output in the intralaminar thalamus. Future experiments will test the prediction that pauses in thalamic ACh release reduce locomotor output, and chronic deprivation of cholinergic drive leads to impairments in movement initiation similar to PD.

Mentor(s): Matt Howe (Neuroscience, Virginia Tech)

Nicole Botha
Virginia Tech/Human, Nutrition, Foods, and Exercise

How to Increase Engagement for Online Programs: Exercise Intervention Dissemination Tactics in Cooperative Extension

Physical activity is critical for the prevention and management of obesity. The Physical Activity Guidelines (PAG) for Americans provide recommendations for the adult population which reduce disease risk. Evidence-based programs encouraging these recommendations are important to implement for public health; as only 23.2% of Americans meets the PAG. A gap in literature remains at the end of the translational spectrum in how and why we deliver health behavior interventions. Dissemination and implementation science (DIS) is a promising field of study; recognizing how many health behavior interventions exist but are rarely studied in community-based settings. In this project, dissemination methods were employed to increase the use, delivery, and assessment of evidence-based physical activity programs for Cooperative Extension agents. Multiple DIS methods were undertaken to improve program uptake. First, a program website was adapted to increase its ease and function. Updates were based on feedback from an advisory board and google analytics will be used to determine site traffic and agent knowledge of resources. Second, a guide was designed to ensure efficient and appropriate use of social media sites to promote programs. Agent feedback will determine the effectiveness of the guide. Third, recruitment strategies were developed to increase the representativeness of open-access physical activity materials (e.g., in terms of body size, race, age, and ability). Challenges faced include the research to practice gap and the agents; varying levels of understanding, in terms of online navigation and social media use. DIS research ensures effective exercise interventions can be distributed to the target populations.

Mentor(s): Samantha Harden (Human, Nutrition, Foods, and Exercise, Virginia Tech)
Morgan Gregg (Graduate Student, Virginia Tech)
Anna Dysart (Graduate Student)

Caitlin Bowman
Virginia Tech/Human Nutrition, Foods, and Exercise

TOUR

Feasibility of using Inertial Measurement Units to study fall risk during daily living: A pilot study on the effects of obesity

An estimated 42% of adults in the United States are obese[1]. Obesity is associated with an increased risk of falls, and laboratory studies have implicated less effective kinematic responses to common balance perturbations such as tripping and slipping[2,3]. However, little is known about these responses outside of the laboratory. Therefore, the purpose of this study was to develop a protocol to assess kinematic responses to balance perturbations during daily life using wearable inertial measurement units (IMU). This protocol will be used to measure the effectiveness of fall-prevention interventions, and to investigate the underlying causes for increased fall risk among individuals who are obese. 3 adults [female 47 yo, BMI=21.9 (Normal), WTH ratio=0.785 (low health risk); female 42 yo, BMI= 36.3 (Obese Class II), WTH ratio=0.928 (high health risk); male 74 yo, BMI=34.2 (Obese Class I), WTH ratio= 1.01 (high health risk)] passed medical screening. Subjects then received a take-home kit containing the IMUs (APDM Opal), voice recorder (Evistr Digital Voice Recorder), and pedometer (Omron HJ-321) and wore these devices for 8 hours on 5 consecutive days in their regular daily-life settings. Subjects were interviewed to assess feasibility of the methods and potential for improvement. Quantitative analysis of data from IMUs is currently on-going to compare between lean and obese subjects to identify differences that may contribute to the increased risk among the obese. A better understanding of how obesity increases fall risk can help guide clinical fall interventions for this population.

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Mentor(s): Michael Madigan (Grado Department of Industrial and Systems Engineering, Virginia Tech)

Megan Brown
Hollins University/Chemistry
Nurpur Sehgal
Hollins University/Chemistry

Let, go fishing : Catching cysteine containing proteins in cytoplasmic pools!

With Cysteine-containing proteins playing an important role in most biological processes, the detection and imaging of Cysteine proteins has been of great interest. Here, we present the synthesis and evaluation of two maleimide probes, Rhodamine and Biotin, designed for the detection of Cys-rich proteins. In this design, we postulate that maleimide protein, alkene substituent would react with the thiol group of the Cysteine to form a covalent bond at a certain pH in the presence of a reducing agent. From this bond, we propose that we would not only be able to detect Cys-rich proteins, but both qualitatively and quantitatively analyze the Cysteine concentrations. This methodology provides a way to identify the specific Cys-rich proteins and to further explore their roles and activities in related diseases.

Mentor(s): Dr. Son Nguyen (Chemistry, Hollins University)

Hannah Browne
Virginia Tech/Agricultural Economics

MAOP

Water infrastructure needs vs current funding proposals -- assessing the gaps

Among the funding possibilities, water quality improvement is important area to support, given that significant need of approximately 129 billion dollars of water quality challenges have been noted in the United States. As recently as 2019, the US was meeting less than half of estimated total water infrastructure capital needs, resulting in a critical water infrastructure gap that negatively affects human health and economic development. The current state funding needs are being discussed for water quality infrastructure is between 39.9 and 59 billion. We find this number is between 3% to roughly one quarter of the total requested funding of 205 billion.

We then consider different scenarios to prioritize available funds, evaluating which places would benefit or lose funding based on population vs type of need. This research illustrates the importance of considering not just funding is allocated, but also the process for allocating funding can have considerable implications on which regions and people end up seeing the benefits of planned and potential infrastructure upgrades. These scenarios would result in New York and California, the most populous states, would benefit the most across all scenarios such as total documented needs, type of funding requested, the sociodemographic characteristics.

States whose funding would vary the most include Florida and American Samoa. This research illustrates the importance of considering not just how much funding is allocated, but the process for allocating funding can have considerable implications on which regions end up seeing the benefits of these funds.

Mentor(s): Elinor Benami (Agriculture and Life Sciences, Virginia Tech)

Julia Brynes
Virginia Tech/Computational and Systems Neuroscience

Exploration of brain areas activated by visual and auditory imagery through intracranial electrodes

The neural dynamics related to visual and auditory imagination are relatively unknown, and there is especially little information about neural dynamics in subcortical structures. The brain areas used during tasks requiring visual or auditory imagination were studied on an intracranial level through recordings via depth or grid electrodes in the brains of epileptic subjects. Subjects performed three tasks: an angle discrimination task and two visual imagery tasks, one of which also incorporated auditory imagery. In the first task, the Angle Discrimination Task (ADT), subjects were shown an analog clock face and were asked to determine if the time created a specified angle. In the second task, the Clock Imagery Task (CIT), subjects were given two times auditorily and instructed to visualize which time would create the greater angle on an analog clock. The video imagery task consisted of the subjects watching a video consisting of both audio and visual components and then at random either (1) being shown just the visual component and told to imagine the audio, (2) being given just the audio component and told to imagine the video, or (3) being shown neither component and told to imagine both the audio and visual aspects. By comparing the different neural dynamics in these tasks, we hope to better understand the brain regions and communication processes involved during mental imagery. We hope to apply this insight about awake mental imagery to the imagery generation process that occurs during REM sleep, the sleep stage in which vivid dreams occur.

Mentor(s): Sujith Vijayan (School of Neuroscience, Virginia Tech)

Vincent Bui
Virginia Tech/Clinical Neuroscience

In silico analyses of a new PIK3 peptide inhibitor

Glioblastoma is the most aggressive form of brain cancer with an abysmal 5-year survival rate of only 6.8%. Phosphoinositide 3-kinase (PI3K) has been a major research focus due to its essential role in glioblastoma growth and survival; however, targeting PI3K has failed to achieve promising clinical outcomes. This challenge pertains to the divergent role of the four PI3K catalytic subunits of glioblastoma. Recent research from our laboratory has shown that PIK3CB/p110Œ≤, but not other subunits, plays an essential role in glioblastoma. Selectide-18, a mimetic peptide that targets an 18-residue motif (Œ≤18) unique to PIK3CB/p110Œ≤, blocks the growth of glioblastoma cells in vitro/-in vivo and outperforms existing PI3K drugs; however, the function of Selectide-18 remains elusive. Understanding the mode of action of this peptide drug is important for its conversion into a clinically applicable treatment. We hypothesized that the 3D conformation of Selectide-18 determines its function and that changes to key residues would result in a loss of function. To test our hypotheses, we performed in silico analyses using computational programming. Our data revealed that specific amino acids, such as Q14, played significant roles in the physical conformation and binding affinity of Selectide-18. As we mutated these residues, we witnessed a loss of function of the drug. Future steps include testing Q14 in vitro to determine if our hypotheses hold true in cells. In conclusion, our findings show that the 3D conformation of Selectide-18 determines its function and that changes to key residues, specifically Q14, result in a loss of function.

Mentor(s): Zhi Sheng (Department of Internal Medicine at VTC, Fralin Biomedical Research Institute, Virginia Tech)

Aymeric Busidan
Virginia Tech/Biochemistry

Directed evolution of the Amino Acid Permease gens from Arabidopsis as a mean to understand the molecular basis of their amino acid transport specificity

The Amino Acid Permease proteins are thoroughly characterized amino acid transporters in plants that show different, sometimes opposite, amino acid specificities. For instance, AAP3 and AAP5 transport positively charged amino acid while the other AAPs do not. The goal of this project was to identify the molecular basis of this selectivity. The chosen approach consists in subjecting the proteins to directed evolution in yeast, and identifying residues that would change amino acid specificity of an AAP protein so that its profile resembles that of another AAP. For this purpose, the OrthoRep system was used, in which the gene encoding the AAP of interested is expressed in yeast on the P1 plasmid, replicated by an error-prone polymerase. The first step of the project was to produce the biological material necessary for the system: (1) identifying which Arabidopsis AAPs were the suitable for growth selection of yeast, and (2) engineering the 22Œî10Œ± strain, that lacks endogenous amino acid transporters, to render it able to replicate the P1 plasmid. I first optimized the growth medium to select for the functional properties of the AAP proteins in yeast. By comparing the growth of 22Œî10Œ± cells expressing the eight Arabidopsis AAPs on these selective media, I then identified AAP2, AAP3 and AAP5 as the AAPs with the most different amino acid specificities. These three genes were then cloned by recombination into the P1 plasmid within the F102 yeast strain. In parallel, I deleted the HIS3 gene from 22Œî10Œ±, a necessary step for its fusion with the F102-AAP strain. The achievement of these two goals enables me to move to the next step, i.e. the directed evolution per se.

Mentor(s): Guillaume Pilot (School of Plant and Environmental Sciences, Virginia Tech)

Lillian Byer
Davidson College/Neuroscience

Distribution of ipsilateral-projecting retinal ganglion cells in mouse retina

Retinal ganglion cells (RGCs) project their axons to the brain to transmit visual signals. Based on their projection to the same (ipsilateral) or opposite (contralateral) side of the brain, RGCs can be divided into ipsilateral RGCs (ipsiRGCs) and contralateral RGCs (contraRGCs). ipsiRGCs localize in ventrotemporal (VT) crescent and contraRGCs are situated in the dorsonasal (DN) area of the retina. Although the mapping of these two types of RGCs has been known for several decades, the number and distributed area of ipsiRGCs in the whole retina area during development is unclear. Here we used the Sert (Et33)-cre-tdT genetic mouse line and whole-mount immunohistochemistry to figure out the change in number and proportion of ipsiRGCs during mouse development. Surprisingly, we found both ipsilateral and contralateral RGCs present within overlapping domains of the VT crescent. This suggests that information within the binocular visual field may be conveyed by four distinct channels to the brain for fine-tuned stereopsis. We confirmed this result in retinal cross-sections which also allowed us to immunostain for other subtypes of RGCs. These studies revealed that ipsiRGCs consist of subtypes of alphaRGCs and intrinsically photosensitive RGCs (ipRGCs), which express the photopigment melanopsin. Through this work, we hope to better understand the development of eye-specific retinal projections and improve our understanding of how such eye-specific RGCs parse visual information to create binocular vision.

Mentor(s): Michael Fox (Biological Sciences, Virginia Tech)

Julia Byrnes
Virginia Tech/Computational and Systems Neuroscience

Exploration of brain areas activated by visual and auditory imagery through intracranial electrodes

The pathway and brain areas activated by visual and auditory imagination are relatively unknown due to the limitation of scalp electrodes. Through the recordings of depth or grid electrodes in the brains of epileptic subjects, the areas of the brain used during tasks requiring visual or auditory imagination were studied on an intracranial level. The subjects underwent three tasks: an angle discrimination task and two visual imagery task with one incorporating auditory imagery as well. In the first task, Angle Discrimination Task (ADT), the subjects were shown an analog clock face and had to determine if the time created the specified angle asked for. For the second task, Clock Imagery Task (CIT), the subjects were given two times auditorily and instructed to visualize which time on an analog clock would have the greater angle. The video imagery task consisted of the subjects watching a video with both audio and visual components and then at random were either shown just the visual component and told to imagine the audio, given just the audio component and told to imagine the video, or were shown neither component and told to imagine both the audio and visual aspects. By comparing these different states of imagery and similar tasks intracranially in humans, we may be able to more accurately describe the brain regions involved and how they communicate with one another during imagery. This insight gained on visualization while awake we hope to apply to the visualization process used during REM sleep or dreaming.

Mentor(s): Sujith Vijayan (School of Neuroscience, Virginia Tech)

Alejandra Caceres

Virginia Tech/Computer Engineering - Networking & Cybersecurity

Development and validation of portable samplers to measure atmospheric gases

The earth's atmosphere contains thousands of different gases with varying impacts on people and ecosystems. It is essential to measure their spatial and temporal changes to better understand the changing atmosphere and environment. A custom portable, autonomous sample was developed and validated that will help us better measure the composition of atmospheric gases. Each sampler concentrates gases on an absorbent tube, with flow measured by a miniature flow meter and pulled by a variable speed pump controlled by a microcontroller. Samplers are housed in a 2.5in x 5.5in x 5.5in a waterproof box including a battery that can be charged through an outlet or a solar panel undisturbed sampling in remote locations. Samples are taken to the lab to be analyzed by a gas chromatography-mass spectrometry desorption system to identify and quantify components. Thirteen samplers were built and validated using controlled sample experiments, where multiple samples were collected in a small room in which fragrances had been released. The results show that the indoor atmosphere is a complex mixture of many gases. This provides a qualitatively similar understanding of the atmosphere, the sampler's measurement differed in concentration by less than 10% while the variability for others was higher. Future experiments will seek to understand these differences. These samplers will be deployed at the end of summer to an orchard being treated for agriculture pests to measure the concentration and efficacy of the applied treatment. Future deployments plan to broadly advance our knowledge about the composition of the atmosphere.

Mentor(s): Gabriel Isaacman-VanWertz (Department of Civil & Environmental Engineering)

Andry Cantarero
Frostburg State University/Health Science

Deletion of SARM1 s protective against SER199 Tau hippocampal accumulation at 6 months after repeated diffuse TBI

Traumatic brain injury (TBI) affects 1.7 million people annually and is a major cause of death and disability. Mounting evidence from clinical and pre-clinical studies demonstrated that post-traumatic tauopathy is a common long-term consequence of TBI. In the healthy brain, tau is a soluble natively unfolded protein crucial for axonal integrity. Yet, TBI induces hyperphosphorylation of tau forming an insoluble proteoform (cis-pTau), which accumulates in the brain, causing gradual Wallerian-like neurodegeneration. The accumulation starts in the axonal compartments of the neurons, leading to production of neurofibrillary tangles (NFTs). The NFTs are the hallmark of neurological disease. The Wallerian-like axonal degeneration is programmed by sterile alpha and TIR domain-containing protein 1 (SARM1). Previous studies suggested that SARM1 deletion is protective against axonal degeneration early but not more than 2 months post injury of mild TBI. Yet, it remains unclear how repeated TBI affects cis-p Tau accumulation in long term and whether SARM1 gene deletion is protective. In our study, we induced repeated mild TBI (mTBI) in 12-16 weeks old mice. We measured the mean fluorescence of cis-ptau in the subregions of the hippocampus in SARM1KO and wild-type C57BL6 mice at 6 months time point after rdTBI. Preliminary data suggest that cis-pTau immunofluorescence is reduced in SARM1 KO mice when compared to WT mice at 6 months after mTBI. In conclusion, our data suggest that that lack of SARM1 prevents cis-pTau accumulation at late time points after mTBI.

Mentor(s): Stefanie Robel (Assistant Professor, Fralin Biomedical Research Institute at VTC Assistant Professor, School of Neuroscience, College of Science Assistant Professor, Deparments of surgery and basic science education, School of Medicine)
Oleksii Shandra (Ph.D.)

Victorjose Catalan
Virginia Polytechnic Institute and State University/Wildlife Conservation

Scoping Anuran Research: Trends of Missing Traits in Anuran Physiological Research

Anurans (frogs and toads) represent a diverse group of amphibians facing challenges to their habitat due to climate change. As cold-blooded animals , anurans are susceptible to changes in temperature. Rising temperatures lead to declines in freshwaters and increased spread of disease. To determine the vulnerability of anurans to climate change, we conducted a literary search of physiological traits of 20 species in the southeastern United States. Our goal is to build a database upon which to create mechanistic niche models to assess temperature sensitivity. However, we found that most anurans lacked data in certain traits. Thus, I addressed the question: which physiological traits and genera are most understudied with anuran research. We used The Ecology and Behavior of Amphibians by Kentwood D. Wells along with scholarly search engines (Google Scholar and Web of Science) to collect trait data. Based on this initial search, species within the genus Pseudacris were understudied and basking, emergence, and foraging temperature were the most lacking in data across genera. I hypothesized that these trends would continue. We conducted further analysis by selecting 5 anurans, one from each genus studied, and highlighted traits studied, study location, sex, and age class. Basking temperature is the most underrepresented trait within anuran research and the genus with the least recorded instances was Dryophytes. Missing trait data means we cannot account for anuran behavior in our models. These behaviors are one way anurans can cope with changes in their local climate and are important for determining their vulnerability.

Mentor(s): Traci Dubose (Department of Biological Sciences, Virginia Polytechnic Institute and State University)

Nicole Chapman
Virginia Tech/Biological Systems Engineering

Time Series Analysis of Water Quality Parameters

The Learning Enhanced Watershed Assessment System (LEWAS) uses a sonde equipped with sensors to collect fine-resolution water quality (pH, dissolved oxygen, water temperature, specific conductance, turbidity, oxidation-reduction potential, and salinity), water quantity, and weather data from Stroubles Creek, upstream of the Duck Pond. The Online Watershed Learning System (OWLS) allows access to the real-time and historical data collected by the LEWAS sensors for water sustainability research and education. Data organization, preprocessing, and visualization of seven water quality parameters will be conducted from 2016-2021. Results obtained from the initial data analysis along with supporting information from literature on the impact of urbanization on water quality parameters will be used to select one parameter that is sensitive to urban development and demonstrates relative consistency. A causal analysis will be performed to provide possible explanation for detected changes in the selected water quality parameter with the concurrent land use changes and development in the Stroubles Creek watershed. Land use information will be gathered from national and local resources (e.g. National Land Cover database and the Town of Blacksburg GIS website). Parameter data that meets the requirement mentioned will be further preprocessed, which can include data imputation and resampling to reduce noisy data points. A predictive model (e.g. ARMA, ARIMA, SARIMA) will be created that will predict future values of the chosen water quality parameter. The predictive model aims to be an educational tool, providing a baseline upon which to compare notable deviations and evaluate stream health, especially after land use changes.

Mentor(s): Kang Xia (School of Plant and Environmental Science, Virginia Tech)

Spencer Chase
Virginia Tech/Experimental Neuroscience

Auditory Sleep Interventions for Improving Motor Learning in Parkinson's Disease: Phase I

Studies indicate individuals diagnosed with Parkinson's Disease (PD) experience abnormalities in brain wave activity when compared to healthy individuals. Such aberrant behavior impacts many facets of the patient's overall health. This includes their ability to achieve satisfactory sleep and brain activity during sleep itself. The impact PD has on sleep is problematic because sleep is an important component in memory consolidation. Additionally, slow wave sleep (SWS) has been shown to counteract both beta-amyloid and alpha-synuclein accumulation. These are pathological proteins believed to be linked with PD manifestation and progression. Moreover, auditory stimulation has been shown to improve SWS and performance on motor tasks. Consequently, successful auditory sleep intervention could lead to improvements in both sleep and motor learning for PD patients. To determine its viability and effectiveness, this investigation was separated into two phases. The objective of phase one was to identify abnormal brain dynamics during sleep related to PD and how such dynamics correlate to deficits in sleep-mediated motor learning. Data was collected by having participants perform a finger tapping task (FTT) before sleep and as soon as they awoke to measure sleep-mediated learning, and by monitoring brain activity as the participant slept. Brain dynamics were examined throughout the entirety of the experiment via electroencephalography (EEG). Initial calculations reveal either a slight positive trend or no change in FTT performance, as well as a reduction in SWS. Although still preliminary, current data is in line with the idea disrupted sleep may lead to impairments in sleep-mediated motor learning.

Mentor(s): Sujith Vijayan (School of Neuroscience, Virginia Tech)

Minyoung Choi
Virginia Tech/Biology

Influence of Acanthamoeba castellanii on the copper inactivation of environmental strains of Legionella pneumophila in simulated premise plumbing

Legionella pneumophila is an opportunistic pathogen responsible for the disease group Legionellosis. It has previously been shown that copper has a biocidal effect on L. pneumophila in premise plumbing. Among L. pneumophila serotypes, serogroup 1 (SG1) has been consistently found to be the most common serogroup recovered from clinical samples. However, little is known about the environmental conditions that can amplify or attenuate disease-associated strains as well as the microbial ecology of L. pneumophila and its host amoebae. The objective was to determine the differences in copper resistance between three environmental strains of L. pneumophila. These strains were inoculated with sterilized drinking water in conditions with the inclusion and exclusion of 5 mg/L of copper and amoeba (Acanthamoeba castellani). The inactivation rate of L. pneumophila was monitored through quantifying colony forming units for 24 hours. During this study, the strain QE (SG1) demonstrated the most susceptibility to copper after exposure. Surprisingly, none of the environmental isolates (F1, F55, and QE) showed substantial reductions in culturability. The lab strain 130B achieved a 6-log reduction. Interestingly, the presence of amoeba provided a protective effect against copper, leading to no detectable net cell death in conditions with copper. This particular study suggests that the amoeba provides some form of protection against copper. A greater level of recognition and understanding on how different serogroups pathogenicity and virulence changes based on the levels of copper and amoeba present in the environment could potentially advance strategies on how to control Legionella pneumophila in water systems.

Mentor(s): Amy Pruden (Civil and Environmental Engineering, Virginia Tech)
Marc Edwards (Civil and Environmental Engineering, Virginia Tech)

Jay-U Chung
Middlebury College/Physics

Investigating the Radiopurity of Lithium Molybdate for Improved Bolometers at CUPID

Detecting neutrinoless double beta decay (DBD), a hypothesized reaction with a lifetime above 10^25-10^26 years, remains an important problem for its implications for the Standard Model and the matter-antimatter asymmetry problem. The Cryogenic Underground Observatory for Rare Events (CUORE) is the largest experiment using bolometers to search for neutrinoless DBD. Critical to CUORE, search for these rare events is the use of radiopure materials that will minimize background events. We therefore analyze the radioactive spectrum of lithium molybdate (LMO) crystals containing molybdenum-100, a new DBD source for the upcoming CUORE Upgrade with Particle Identification (CUPID) project. In particular, we aim to characterize high energy events in LMO from cosmogenic activation; such events could be a problematic source of background for CUPID. To capture the radioactive spectrum of our 1 kg sample of LMO, we used a high purity germanium detector to perform gamma-ray spectroscopy. We find no statistically significant evidence for excess events above the 3034 keV level. However, we observe significant activity from potassium-40 and estimate that the sample contains 2.02 micrograms. With the simulation tool Geant4, we hope to characterize our detector, efficiency. This will allow us to more precisely estimate the level of potassium-40 impurity in our sample and to conclude if anomalous features in the high energy spectrum of LMO exist.

Mentor(s): Thomas O'Donnell (Department of Physics, Virginia Tech)

Lindsay Clay
Virginia Tech/Neuroscience

Reactivation of Herpes Simplex Virus from Neurotrophic Factor Deprivation in Neurons

Herpes simplex virus 1 and 2 (HSV-1 and HSV-2) cause symptoms of the common cold sore, genital herpes, ocular disease and in some cases, HSV encephalitis. HSV has the ability to establish latency within infected neurons, where the virus persists as a lifelong infection that can reactivate to cause recurrent disease. Neurotrophic factors are molecules necessary for neuron survival and growth. Neurotrophic factors also are important in maintaining HSV latency. When neurons that are latently infected with HSV are deprived of neurotrophic factors, reactivation occurs, viral reproduction resumes, and the host develops new sores or sheds virus in biological secretions. Cortisol is a primary stress hormone that regulates various responses in the body and high levels of stress hormones also cause HSV to reactivate to cause recurrent disease. In this study, we measure HSV gene expression in HSV latently-infected neurons that were treated with cortisol or deprived of neurotrophic factors to determine if the viral gene expression profiles were different after each of these reactivation stimuli.

Mentor(s): Andrea Bertke (Population Health Sciences, Virginia Tech)

Carolyn Clinton
Virginia Tech/Cognitive and Behavioral Neuroscience

Focused Ultrasound Neuromodulation in a Rodent Model of Depression

There is currently an unmet need to develop new neuromodulatory treatments for depression that are more effective and/or have fewer side effects than current options. Transcranial focused ultrasound (FUS) offers a non-invasive neuromodulation approach that holds promise as a novel treatment for depression. In a collaborative study between the Clinton lab and the Vlaisavljevich Lab, my project investigates the antidepressant efficacy of FUS neuromodulation of the hippocampus in a rodent model relevant to depression. We exposed adult male rats predisposed to elevated levels of anxiety and depression-like behavior to FUS (or control condition) once a day for 14 days (n=12/group). We subjected them to a series of behavioral tests to assess depression- and anxiety-related behaviors. We found that FUS modulation of the hippocampus elicited antidepressant effects, with FUS-treated rats showing less depression-like behavior compared to controls. A separate phase of the study harvested brain tissue after FUS exposure to examine brain activity patterns via immunohistochemical staining for the immediate early gene produce Fos. Using immunofluorescence, we aim to identify cells in the hippocampus that were activated by FUS exposure. We hypothesize that FUS-exposed rodents will display enhanced Fos activation within inhibitory GABAergic cells in the targeted hippocampus. The overall goal of this work is to better understand how FUS treatment impacts the brain to elicit antidepressant effects.

Mentor(s): Sarah Clinton (Neuroscience, Virginia Tech)

Quinn Conrad
Virginia Tech/Clinical Nueroscience

Central Mechanism of Gastrin Induced Satiety in Broiler Chicks

Gastrin, a 36 amino acid hormone and neurotransmitter, is released following stomach distension and is associated with food intake. Although gastrin suppresses appetite, the mechanism mediating this response is unknown. Therefore, we designed a study to elucidate the hypothalamic and myelencephalic mechanisms of gastrin induced satiety using chickens as models. In Experiment 1, those chicks that received intracerebroventricular (ICV) injection of 0.4 or 0.8 nmol gastrin had reduced food intake up to 90 and 180 minutes, respectively, following the injection. Additionally, water intake was reduced for the entire 180 minute observation period. In Experiment 2, we measured c-Fos immunoreactivity in several hypothalamic and brain stem areas that are associated with appetite following ICV gastrin. The abundant presence of protein c-Fos indicates recent increased neuronal activation. Those chicks that received ICV gastrin had increased c-Fos immunoreactivity within the arcuate nucleus of the hypothalamus (ARC) as well as the area postrema (AP) and nucleus of the solitary tract (NTS) of the brainstem. For Experiment 3, we have collected whole hypothalamus samples, and for Experiment 4 we have collected ARC, AP, and NTS samples, and plan to measure mRNA concentrations of key appetite-associated neurotransmitters. This will tell us what other neurotransmitters participate in gastrin-induced satiety. In Experiment 5, behaviors have been recorded and will be measured to understand their contribution to gastrin-induced satiety. Our study is designed to elucidate the central mechanism of gastrin-induced satiety and may provide a new perspective for the pharmacological reversal of anorexia and obesity.

Mentor(s): Mark Cline (Department of Animal and Poultry Science, Virginia Tech)
Elizabeth Gilbert (Department of Animal and Poultry Science, Virginia Tech)

Brice Crum
Virginia Tech/Biology

Quantifying the antimicrobial properties of urushiol

activists in the larger movement for Black lives remain unaddressed or fundamentally misunderstood. This project focuses on Black resistance to state-sanctioned violence and the causes for misrepresentation and co-optation. My research question: To what extent has the commodification, exploitation, and misrepresentation of Black resistance in the contemporary era quelled activism and political goals in relation to ending state violence in the United States? Aims to add to the current existing scholarly work that suggests U.S. political institutions continue to fail in reducing police violence. My methodologies included case analysis and surveying. The survey was advertised amongst organizers, academics, and social justice-oriented students. Using multiple-choice and open-ended questions, I learned what they believe to be significant political goals of the movement for Black lives, impacts of commodification, and whether current proposed legislation adequately addresses police violence. Early results showed 75% of respondents partially or strongly disagreed that if adopted, the George Floyd Justice in Policing Act adequately addresses police violence. Commodification, misrepresentation, and exploitation threaten to undermine activism and advance the political goals like defunding the police, needed to reduce and end state violence.

Mentor(s): John Jelesko (School of Plant and Environmental Sciences, Virginia Tech)

Fallon Curry
Virginia Tech/Clinical Neuroscience

Upregulation of MCU Alters the Size and Synaptic Localization Patterns of Mitochondria

CA2 is a unique structural and molecular region of the hippocampus involved in social memory. CA2 is plasticity-resistant compared to neighboring regions, specifically at synapses in its proximal dendrites. In order to provide a foundation for understanding the distinct plasticity mechanisms in area CA2 that support social memory, we compared the transcriptome of CA2 neurons to the transcriptomes of neighboring areas CA1 and CA3. Our data revealed that CA2 neurons are enriched for mitochondria-associated transcripts, specifically those involved in mitochondrial calcium handling and bioenergetics. In particular, CA2 neurons express high levels of components of the mitochondrial calcium uniporter (MCU) complex. We found that MCU labels mitochondria selectively in distal CA2 dendrites, and MCU-labeled mitochondria are larger in distal dendrites than in proximal dendrites. We hypothesize that the localization of large MCU-enriched mitochondria is not an inherent property of CA2, but rather that MCU expression drives mitochondria localization to more active synapses. To test our hypothesis, we used adeno-associated viral vectors to overexpress MCU in neighboring CA1, a region low in MCU expression with more active proximal synapses compared to distal synapses. By measuring the number and the area of mitochondria, we expect to find larger MCU-labeled mitochondria in proximal CA1 dendrites in mice overexpressing MCU compared with control mice expressing GFP. This would suggest that MCU-enriched mitochondria localize in areas with more active synapses, possibly contributing to unique plasticity found in proximal and distal dendrites of CA1 and CA2, respectively, underlying CA2's function in social memory.

Mentor(s): Shannon Farris (Center for Neurobiology Research, Fralin Biomedical Research Institute at Virginia Tech Carilion, Roanoke, Virginia)

Jason Davidson
University of Texas at Dallas/Biochemistry

Molecular Dynamics Investigation of a G-Quadruplex in the KRAS Promoter Region

G-Quadruplexes (GQs) are noncanonical structures found in guanine rich regions of DNA and RNA. They are characterized by repeated guanine sequences and are often found in promoter regions, which implicates them in transcription and regulation of gene expression. GQs, therefore, are a promising target when attempting to modulate gene expression. Full investigation of these structures requires a detailed and atomistic understanding of the structural dynamics and kinetics, which can be provided with molecular dynamics (MD) simulations. In this study, we investigated the dominant conformation of a 32-nucleotide GQ found in the promoter region of the KRAS gene, which has been found to play a role in solid tumor formation. We employed the Drude polarizable force field to better represent non-bonded and electrostatic interactions, which play an important role in nucleic acid structure. The GQ was simulated in aqueous solution with a 150 mM concentration of potassium chloride (KCl). After simulating the system for 250 ns, analysis was performed, including Root-Mean-Squared-Deviation (RMSD), Root-Mean-Squared-Fluctuation (RMSF), and dipole moment analysis. The structure was found to maintain structural integrity, and there were several sites at which repeated ion binding was observed, which could be promising as ligand binding sites. Finally, the G13-G25 propeller loop was flexible, making it an area of interest for further studies of this structure.

Mentor(s): Justin Lemkul (Biochemistry, Virginia Tech)

Olivia Deane
Virginia Wesleyan University/Earth and Environmental Science

MAOP

A dendroclimatic comparison of sugar maple and pignut hickory

Dendroclimatology is the study of the relationship between tree rings and past climate; the width of a tree's annual ring reflects the climate. Conservation biologists need to identify which species are most sensitive to climate change so that resources can be directed towards ensuring their sustainability. In this study, two tree species were compared: sugar maple (Acer saccharum) and pignut hickory (Carya glabra). One goal of the study was to determine if maximum monthly temperatures affected the growth of the two species differently, as the geographical range of each species varies. Another goal was to identify temporal shifts in the dendroclimatic responses of either species. For the data, tree cores were collected, then the samples mounted, sanded, crossdated, and measured. To identify significant correlations between tree-ring widths and monthly maximum temperature, DENDROCLIM2002 was used to calculate moving intervals of correlation coefficients and test for temporal shifts in dendroclimatic relationships. Both sugar maple and pignut hickory showed significant correlation between maximum monthly temperature and annual growth but varied in the type of correlation. Sugar maple had a stable dendroclimatic response over time, whereas pignut hickory's dendroclimatic response varied. Based on the results, pignut hickory may be more sensitive to climate change than sugar maple.

Mentor(s): Carolyn Copenheaver (Forest Resources and Environmental Conservation, Virginia Tech)

Felicity deToll
Virginia Tech/Environmental Science

SURF

Similar carbon uptake rates among wetlands with different development histories

Wetlands are highly effective carbon sinks, which is why they are a focus of many protection and preservation efforts. When wetlands are destroyed, underlying soil carbon is exposed to oxygen and can be respired and released as carbon dioxide. Wetlands are active sites of carbon uptake through biological processes. It is still not well known how biological uptake of organic carbon varies across wetland types and which wetlands are more efficient at carbon uptake. To understand how more natural (less developed), restored, and constructed wetlands cycle, store, and emit carbon, we must better quantify dissolved organic carbon (DOC) uptake. We estimated DOC uptake rates via laboratory bioassay incubations using water collected from four wetlands in Blacksburg, VA (one constructed, two restored, and one natural). The more natural wetland had the lowest mean DOC uptake (0.087d-1), while the constructed wetland had the highest mean DOC uptake (0.157d-1). However, there were no significant differences in DOC uptake among wetlands (P-value = 0.4), likely driven by adding a controlled carbon source (sucrose) while microbial inoculations were wetland-specific. Ongoing work includes exploring interactions between nutrient concentrations and DOC uptake. We predict that adding phosphorus will enhance DOC uptake as it may accelerate carbon cycling by alleviating nutrient limitation. Measurements of DOC uptake in wetlands can be used to further understand how DOC plays a role in carbon cycling, as well as how anthropogenic influences (elevated nutrients) impact wetland carbon uptake.

Mentor(s): Erin Hotchkiss (Department of Biological Sciences, Virginia Tech)

Truman DeWalch
Virginia Tech/Aerospace Engineering

Space Domain Awareness at Virginia Tech

The overall goal of this project is to develop a system to maintain Space Domain Awareness (SDA), which involves remotely and autonomously controlling a 14-inch telescope to track spacecraft and other objects in Low Earth Orbit (LEO) as well as aircraft in the local airspace. The telescope, along with its associated support electronics and instrumentation, will be located in a fully remotely controllable telescope dome located on the roof of Research Building 1311, the home of the Hume Center for National Security and Technology, in the Corporate Research Center (CRC). The system is developed using the Python scripting language. In order to control the image focus remotely, the telescope uses an electronic Focus Motor. A completely custom software suite for maximum flexibility is being developed, which required reverse engineering the focus motor hardware interface and control protocol. To achieve this, data was intercepted from a commercial hand controller and decoded using a logic analyzer and a breakout board. The next step was to develop a custom Python program to communicate via serial connections using a custom circuit to emulate the hand controller logic levels and communication protocol. Once this was done successfully, the circuit and software were adapted to work over a Local Area Network (LAN) using an RS-232 chip, Serial to Ethernet converter, and network socket programming. This is one of many significant steps taken in recent months towards a goal of producing high quality images of objects in orbit, such as the International Space Station, by the end of the Summer 2021 semester.

Mentor(s): Zach Leffke (Virginia Tech)

Grace Dinges
Virginia Polytechnic Institute and State University/Clinical Neuroscience

MAOP

Synthesis of Hyperbranched Polymers via Metal-Free Self-Condensing Ring-Opening Metathesis Polymerization

Hyperbranched polymers (HPs) possess many desirable properties including abundant functional groups, low viscosity, and high solubility.^1 HPs may be synthesized by a self-condensing approach, which requires a single molecule containing both an initiator and monomer moiety called an "inimer". Our group has previously prepared an inimer to synthesize HPs via self-condensing ring-opening metathesis polymerization (SC-ROMP) with a ruthenium catalyst, but ruthenium and molybdenum catalysts are expensive and can cause metal contamination.^1,2 The overall purpose of this study is to create an inexpensive, metal-free approach to SC-ROMP. Two metal-free SC-ROMP inimers were planned to be synthesized from metal-free ROMP initiators and a ROMP monomer.^2 In general, the two methods will generate an inimer with both an initiating and propagating site. The resulting inimer will then undergo polymerization by activation with blue LED light and the addition of pyrylium salt.^2 The two methods theoretically only differ in the initiator used for inimer formation. 1H NMR confirmed the successful synthesis of the desired metal-free SC-ROMP initiator by Method 1 and the successful synthesis of the inimer by Method 2. In the future, we will work on the synthesis of the inimer for Method 1 and study the SC-ROMP for Methods 1 and 2.

Mentor(s): Michael Schulz (Chemistry, Virginia Tech)

Grace Dinges
Virginia Polytechnic Institute and State University/Clinical Neuroscience

MAOP

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Mentor(s): Michael Schulz (Chemistry, Virginia Tech)

Lia Dopp
Virginia Tech/Public Health

TOUR

Examining self-regulation as a target to improve health outcomes for pregnant women with obesity and their offspring

Pre-pregnancy obesity affects 29% of the United States population, impacting physical and mental health for mothers and babies, including mother-child attachment. Self-regulation, the ability to control one's thoughts and feelings, has been shown to be impaired in obesity. Few studies have investigated whether thought training techniques to enhance self-regulation can improve outcomes for pregnant women with obesity and their infants. We utilized two approaches to investigate the hypothesis that improved self-regulatory abilities would be associated with improved health behaviors, physical and mental health, and parental attachment. Self-regulation was measured through temporal discounting (TD), a marker of future valuation. We found that in a group of mothers (n=604) with a range of BMIs, steep TD (decreased future valuation) was associated with increased fat intake (r=0.356, p<0.001), increased fruit and vegetable intake (r=.329, p<0.001), impaired physical (r=.233, p<0.001) and mental health (r=.397, p<0.001), increased stress (r=.161, p<0.001), decreased effortful control (r=-.211, p<0.001), and lower parental attachment (r=-0.425, p<0.001). Additional analyses will examine the moderating effects of BMI on these outcomes. Four participants are enrolled in the ongoing clinical trial where they are randomly assigned to receive either: 1) Episodic Future Thinking (EFT), which acts to decrease TD; or 2) a control intervention. This research is showing promise that TD can be a target to improve self-regulatory abilities in mothers with obesity and their relationship with their children.

Mentor(s): Julia Basso (Department of Human Nutrition, Foods and Exercise, Virginia Tech)

Salima Driss
Hollins University/History

To Create Beloved Community: Engagement in Post-COVID Anti-Suspension Work

As students and staff return to school after a year of online learning due to the COVID pandemic, there must be conscious effort made to individually and compassionately respond to learning loss that has occurred. This project aims to respond to educational disparities by developing parameters for building a "beloved community" that addresses the learning loss suffered by one group of learners in particular: young people at risk of school discipline, directed by the words of scholar bell hooks: "Beloved community is formed not by the eradication of difference but by its affirmation, by each of us claiming the identities and cultural legacies that shape who we are and how we live in the world." I intend to assess Roanoke City's current suspension and expulsion processes and to seek to improve outcomes for both the District and its students. In doing so, I look to build on ongoing research into learning losses stemming from the COVID-19 pandemic by tracing how many of the disparities present among students who have fallen behind during the pandemic are also prevalent among students who have been subject to exclusionary discipline. Ultimately, this project will endeavor to propose strategies for creating a more equitable model for education, founded upon the principles of beloved community, for Roanoke's own community of learners.

Mentor(s): Courtney Chenette (Political Science/Hollins University)

Lucas DuMez
Virginia Polytechnic Institute and State University/Biology

Transgenesis and Regeneration in Cannabis

Cannabis is a valuable crop with an ever-growing market, especially in Virginia thanks to its recent US federal legalization. Until recently, restrictions caused laboratory research to fall behind. Developing and increasing the application of biotechnology in cannabis can facilitate the improvement of crop traits. However, cannabis is known to be recalcitrant in tissue culture which hinders the application of biotechnology in this important crop. Morphogenic factors have been shown to enhance regenerative capacity in other recalcitrant crop species. Therefore, the current study wants to use the WUSCHEL gene (WUS) to promote the regeneration of cannabis shoots; ultimately growing an adult plant from undifferentiated callus cells. To do this a transformation protocol was developed using Agrobacterium tumefaciens. Green Fluorescent Protein (GFP) was used to establish proof of concept. After GFP transformation was repeatedly replicated the research can now determine if inducible expression of the WUS gene in cannabis can be achieved. Use of microscopy and growth of callus on selection media concluded that transgenes were present, and the tissue was successfully transformed. This is a productive start to ultimately enhancing regenerative capacity from cannabis in tissue culture.

Mentor(s): Bastiaan Bargmann (Translational Plant Sciences, Virginia Tech)

Nicholas Dunn
Virginia Tech/Psychology

Impact of COVID-19 on High School Student GPA; Exploration of Factors that Predict Academic Performance

With school closures and the transition to remote learning, the immediate response to the COVID-19 pandemic significantly disrupted learning. Researchers have speculated that this disruption could intensify established educational inequalities and undermine academic performance for certain groups. One such group is students with attention-deficit hyperactivity disorder (ADHD), who on average have more academic difficulties and lower GPA than their peers. Research from spring 2020 stay-at-home orders supports this notion, with parents of students with ADHD reporting more remote learning difficulties than their peers on average. As such, the present study explored the impact of the COVID-19 pandemic on GPA for high school students (juniors and seniors in 2020-2021) and examined whether differences emerged based on ADHD status and biological sex. Participants were 238 adolescents (55.5% male, 49.6% with ADHD). GPA significantly decreased on average from the 2019-2020 (M=3.66, SD=0.43) to 2020-2021 (M=3.54, SD=0.57) school year, t=3.70, p<.001. Both ADHD status and biological sex significantly moderated change in GPA. Specifically, students with ADHD reported significantly decreased GPA (Mchange:-0.22, p=.001), while students without ADHD reported non-significant change (Mchange:-0.04, p=.154). Similarly, males experienced a significantly decreased GPA (Mchange:-0.19, p<.001), whereas female GPA did not change (Mchange:-0.03, p=.483). These findings suggest that additional academic support is required for students, particularly students with ADHD and males, to overcome lapsed academic performance and improve trajectories in the 2021-2022 academic year. This is critical given that adolescents with ADHD and male students are more likely to drop out of high school and not attend or finish college.

Mentor(s): Rosanna Breaux (Department of Psychology, Virginia Tech)

Christine Emeric-Martinez
Hollins University/International Studies

The Pursuit for the Protection of Cultural Property

After the destruction and loss of cultural property during World War II, the 1954 Hague Convention for the Protection of Cultural Property in the Event of Armed Conflict was established. Since the 1954 Hague Convention and the 1970 UNESCO Convention on the Means of Prohibiting and Preventing the Illicit Import, Export and Transfer of Ownership of Cultural Property, the world has experienced globalization, described as the acceleration of the integration of nations into the global system. It also contributes to the expansion of cultural ties. Although cultural ties have continued to develop, the policies surrounding the protection of cultural property have lagged. Today individual states have taken on the responsibility of creating and enforcing cultural property rights of not only residents of communities within their borders but those states that are negatively affected by the possession of others' cultural property a global issue that transcends state boundaries. The purpose of this qualitative study is to understand international policies concerning cultural heritage through the Getty Aphrodite. Through this research, the ethical and moral responsibilities that states have taken upon themselves is dissected through an analysis of the language used to establish cultural property policy.

Mentor(s): Ashleigh Breske (Hollins University)

Paige Eversole
State University of New York at Fredonia/Medical Technology

TOUR

Irreversible Electroporation and its Effect on Interferon Gamma and Programmed Death-Ligand 1 Expression in Human Pancreatic Cancer Cells

Pancreatic cancer has one of the lowest survival rates compared to other primary cancers. Irreversible electroporation (IRE) is a tumor ablation technique that uses ultra-short powerful electric pulses to initiate cell death in the tumor cells. In mouse models, an increase in interferon-gamma (IFNŒ≥) and programmed death-ligand 1 (PD-L1) was observed following IRE treatment of pancreatic cancer. While IFNŒ≥ is a hallmark for antitumor immunity, it can also induce an escape mechanism for the cancer cell via the PD-1/PD-L1 pathway. Therefore, we hypothesize that in human pancreatic cancer cells, IRE will induce IFNŒ≥ expression, which eventually induces PD-L1 expression.

A human pancreatic cancer cell line (Panc-1) was used to investigate the interaction of IFNŒ≥ and PD-L1. Following treatment of panc-1 cells with IRE at different electric fields, the cells were counted to determine cell viability. As the electric field voltage increased, there was a decrease in the number of live cells and increased dead cells. Following treatment, cell supernatant and protein extracts were collected at varying time points to determine IFNŒ≥ and PD-L1 expression for each voltage and timepoint.

Panc-1 cells were also treated with different cytokines such as TNF…ë, IL-4, IL-10, and IFNŒ≥, protein, and supernatant were collected 48 hours after treatment. Western blot will be performed to determine which cytokine treatment induces PD-L1 expression. The findings of this study will assist in determining if PD-L1 is dependent on IFNŒ≥ expression for the future design of an effective co-treatment.

Mentor(s): Irving Allen (Department of Biomedical Sciences and Pathobiology, VA-MD College of Veterinary Medicine)
Khan M. Imran (Graduate School, Translational Biology, Medicine, and Health, Virginia Tech)

Sam Farrokhpoor
Virginia Tech/Biochemistry

Molecular Dynamics Analysis of VEGF promoter G-Quadruplex Using Polarizable Simulations

G-quadruplexes (GQs) are non-canonical nucleic acid structures with distinct topologies that are formed in guanine-rich sequences in DNA and RNA. GQs often arise in the promoter regions of a wide variety of genes expressed in humans and other organisms.¬† Vascular endothelial growth factor (VEGF) is a human signaling protein that also acts as a regulator and contributor to tumor development. Since VEGF is often expressed in a large number of human tumors, the promoter GQ could serve as a drug target for small molecules in developing novel cancer therapeutics. To do so requires an understanding of the function of the VEGF promoter GQ, properties of ligand binding, and effectiveness as a target for cancer therapeutics. Here, we employed molecular dynamics simulations to understand the structure and dynamics of the VEGF GQ. Simulations were performed using the Drude-2017 polarizable force field. This force field models the charge fluctuations in the system and how they affect different properties of the GQ. Such simulations allow for the study of electrostatic interactions between the VEGF GQ and its surroundings, dipole-dipole interactions, ion binding, hydrogen bonding, and structural rigidity. Through these analytical tools we were able to observe bulk ion interactions leading to a slight deviation in the G-quadruplex structure compared to the original NMR structure. With further analysis, we will be able to explore other areas such as ion mapping, changes in hydrogen bonding, and any other structural deviation of the G-quadruplex in the simulation.

Mentor(s): Justin Lemkul (Biochemistry, Virginia Tech)

Mikhyle Fehlman
Penn State/Plant Sciences

Plant Sugar Feeding Habits of Mosquitoes in Residential Blacksburg

Plant sugars, like fructose, represent an important source of energy for mosquitoes, yet it remains an understudied field with a high potential for disease vector prevention. The purpose of this research was to determine what flowers mosquitoes from suburban areas feed on for sugar meals based on plant DNA found in captured mosquitoes. This study aims to contribute knowledge on invasive mosquitoes, in particular Ae. albopictus, and improve the design and use of traps taking advantage of mosquito plant feeding (e.g., attractive toxic sugar baits). Mosquitoes were trapped at ten suburban locations around Blacksburg where human-feeding mosquitoes are found in high numbers. After species identification, we ran an anthrone assay which detected for the presence of fructose, a plant sugar, in the mosquito crop. This was done to determine which mosquitoes had fed on plants and could contain plant DNA. We then performed DNA extraction on the fructose positive mosquitoes and used PCR to amplify the rbcL gene which is common in plants. Finally, we relied on Sanger Sequencing to determine the plant species the mosquitoes fed on. Our data showed that Ae. albopictus fed on both dicot and monocot plants, including genera from Asteraceae, Poaceae, and Fabaceae that are often included in suburban gardens. With this work, we hope to inform the public and authorities on plants mosquitoes feed on preferentially and which consequently help them thrive in the urban environment.

Mentor(s): Chloe Lahondere (Biochemistry, Virginia Tech)

Biruktawit Fekru
University of Virginia/Foreign Policy

Decolonization without independence: framing EU and AU relations through the context of colonialism

European colonialism of Africa is often discussed as a gruesome part of history that is often detached from the present. The main reason for this is the confinement of the impacts colonialism has had on African states only to the 75 years of brutal direct European ruling that started after the partition of Africa following the 1884 Berlin Conference. As this research shows, however, although many African states formally became independent in the 1950s and 1960s, European influence and the institutions that have kept African states at an unfair economic and political disadvantage have continued to persist beyond decolonization. This research aims to assess the ways Europe has continued to influence Africa and analyze how the unfair institutions that date back to colonialism have carried on to the current date. My research methodology is qualitative, in which I consulted different books, articles, research papers, and other literature to construct my research. The research shows that Europe has maintained and continues to maintain influence on Africa through hard power, like military forces, as well as economic pressures, like policy of conditionality that tie the disbursement of aid to the enactment of laws, provisions, trade agreements, etc, that are favorable towards the EU. Analyzing how these policies are used by the EU to maintain influence on Africa would offer insight into how the asymmetrical relationship between the AU and the EU came to be and what can be done to better equalize the power dynamic between the two.

Mentor(s): Yannis Stivachtis (Political Science, Virginia Tech)

Rebekah Fogarty
Virginia Tech/Biochemistry

Polarizable Molecular Dynamics Simulations of the G-Quadruplex Present in the mutant-VEGF Promoter Region

G-quadruplexes (GQs) are noncanonical structures that form in nucleic acid sequences that are rich in guanine. Sequences that allow for the formation of GQs are most commonly present in promoter regions, therefore, it is suggested that GQs may function as regulators of gene expression. A 22-nucleotide segment of the vascular endothelial growth factor (VEGF) promoter sequence is heavily enriched in guanine and has been observed to form a GQ under experimental conditions. Overexpression of this growth factor is implicated in various types of cancers, and recent developments have led to the GQ structure becoming a potential target for novel therapeutic agents. It is predicted that by stabilizing this GQ structure, the overexpression of the growth factor may be inhibited. To better understand how to effectively stabilize this structure via chemotherapeutic agents, we conducted molecular dynamics simulations of the VEGF Pu22-T12T13 mutant utilizing the Drude-2017 polarizable force field. The parameters within this force field allow for a more accurate simulation by accounting for proper electronic behavior. Early analysis showed that bulk K+ ions readily interact with the exposed tetrads and the 4-nucleotide loop region of the GQ. These binding occurrences resulted in observable differences from the initial ensemble, suggesting that ion interactions may impact the ability to maintain the overall structure of the GQ. Additionally, the loop region manifested a higher flexibility than the GQ core. Further analysis will be conducted to explore specific ion-binding activity and electrostatic properties throughout the duration of the simulations.¬†

Mentor(s): Justin Lemkul (Biochemistry, Virginia Tech)

Maegan Gabby
Virginia Tech/Biochemistry

Fralin SURF

High-throughput drug screen to identify new therapeutics to eradicate Borrelia burgdorferi, the causative agent of Lyme disease

Borrelia burgdorferi is the causative agent of Lyme disease, the most prevalent vector-borne illness in the United States, and affects upwards of 500,000 individuals each year. Current treatment for Lyme disease constitutes an aggressive antibiotic regimen that is largely nonspecific and is comparable to chemotherapy as it takes a large toll on patient health. Further, an estimated 10-20% of individuals experience Post-Treatment Lyme Disease Syndrome where they are still symptomatic even after undergoing treatment. We hypothesize that more effective therapeutics exist but have yet to be discovered due to a lack of high-throughput screening techniques. Here, we developed a high-throughput screening methodology and investigated 467 unique FDA-approved drugs to analyze their potential efficacy against eradicating B. burgdorferi in vitro. Colorimetric screening studies were conducted to identify top-performing compounds in their ability to eliminate live bacteria. In tandem, we have examined bacterial growth in our high-throughput drug screen by using HADA, a fluorescent tracer, that monitors peptidoglycan cell-wall biogenesis. In this way, we can rapidly identify inhibitors while understanding their mechanism of action. Future studies will determine the lowest inhibitory concentration for the top 10% of compounds, both in vitro and in vivo. Collectively, these results will elucidate improved drugs that have greater specificity and efficacy to treat Lyme disease while minimizing harmful patient side effects.

Mentor(s): Brandon Jutras (Biochemistry, Virginia Tech)

Sara Gallegos
Virginia Tech/Biochemistry

MAOP

Determining pterin methylase function in Methanogens

Methanogenesis is the biological production of methane gas from various small molecules to generate energy within anaerobic microorganisms known as methanogens. During this process, tetrahydromethanopterin (H4MPT) acts as a carrier coenzyme.This structure is similar to the compound tetrahydrofolate, however, 2 methyl groups are present at the C-7 and C-9 positions of the pterin. In this project, we are investigating the MA1114 and MA1486 enzymes, which are Radical SAM enzymes suggested to methylate the C-7 and C-9 positions to create H4MPT. The goal is to identify which enzyme is responsible for methylating these two positions, or alternatively, if they work in conjunction. Here, the enzymes were expressed separately within different strains of E. coli, namely the BL21Codon+ and BL21+PDB1818 strains. Studying these enzymes within E. coli is more accessible and efficient, as E. coli synthesizes folates and does not normally produce methylated pterins. It was found that only the MA1486 in BL21+PDB1818 strain expressed, while other strains didn't. Further, the E. coli cells expressing MA1486 appeared to produce a pterin methylated at the C-7 position. In conducting a plasmid design to coexpress both enzymes within pETDuel-1, it was found that the MA1114 gene was successfully cloned and current work is focused on cloning MA1486 into the same plasmid. Characterizing these radical SAM methylases is vital in understanding the enzymatic processes in producing methane gas in methanogens.

Mentor(s): Kylie Allen (Biochemistry, Virginia Tech)

Caitlyn Gathright
James Madison University/Biotechnology

MAOP

Creating an RNA standard curve for SARS-CoV-2 qPCR

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2; Coronaviridae) is a virus that causes severe respiratory illness in humans and animals. Since its emergence in 2019, SARS-CoV-2 has caused a pandemic of coronavirus disease 19 (COVID-19) that has led to millions of deaths. There is a dire need for research into infection and disease caused by SARS-CoV-2. Currently, our lab is using Syrian hamsters as a small animal model to study SARS-CoV-2 transmission and pathogenesis. In such studies, we will use quantitative reverse transcription PCR (qRT-PCR) to quantify the amount of viral RNA in hamster samples. However, we will first need to create a set of SARS-CoV-2 RNA standard curve values that will allow for absolute quantification of the viral RNA in our samples. Here, we aim to utilize a combination of PCR, bacterial transformation, and in vitro transcription techniques to create a set of SARS-CoV-2 RNA standards with known concentrations. After extracting RNA from the SARS-CoV-2 virus, the nucleocapsid (N) gene was reverse transcribed and amplified using RT-PCR. The N gene DNA was then cloned into a plasmid and transformed into bacteria that were subsequently grown on antibiotic selection plates. Bacterial colonies were then screened via colony PCR for the presence of plasmid containing the N gene. Future steps in this project include in vitro transcription of the N gene, quantifying this RNA, and testing with qPCR. With the completion of this project, we will have established an effective SARS-CoV-2 quantification method allowing for better analysis of SARS-CoV-2 infection and disease.

Mentor(s): Nisha Duggal (Biomedical Sciences and Pathobiology, Virginia Tech)

Simran Gill
Salem High School

Complement C3 is required for microglia and monocyte phagocytosis of inhibitory perisomatic synapses in Toxoplasma gondii infection

Worldwide, over 1 billion people are infected with the protozoan parasite, Toxoplasma gondii, a pathogen that can invade and chronically infect the brain. Numerous studies show that Toxoplasma infection increases the chance of developing neuropsychiatric disorders like seizures and schizophrenia. Our research seeks to elucidate the cell and molecular mechanisms underlying these neurobehavioral changes in Toxoplasma infection. Previously, we discovered that mice chronically infected with Toxoplasma develop seizures, which is partly due to the phagocytosis of inhibitory perisomatic synapses by microglia and infiltrating monocytes. How might microglia and monocytes recognize inhibitory synapses to be phagocytosed? One possible mechanism is the innate complement cascade, which is responsible for removing debris and pathogens from the brain. In the developing brain and in other types of neuro-inflammation, complement components C1q and C3 tag synapses for microglial phagocytosis. To directly assess the role of C1q and C3 in microglia- and monocyte-neuron interaction and their phagocytosis of inhibitory synapses in Toxoplasma infection, we used infected transgenic mice lacking these proteins and visualized microglia/monocytes by both immunostaining and transgenic reporter proteins. Our analyses revealed perisomatic synapse loss in chronically infected wildtype mice, consistent with previous results, and in C1q,Åª/,Åª mice. In contrast, we observed less synapse loss and neuronal ensheathment by microglia/monocytes in infected mice lacking C3. Together, this suggests C3 is required for both monocytes and microglia to ensheath neurons and remove inhibitory perisomatic synapses in chronic infection, highlighting a novel way where immune molecules regulate neuron-glia interactions in parasitic brain infection.

Mentor(s): Michael Fox (Department of Biological Sciences, Virginia Tech)

Airinés González Velázquez
University of Puerto Rico - Mayagüez/Industrial Microbiology

Regulation of GJA1-20k translation by IGF2 mRNA binding protein 1 regulates gap junction formation.

During each heartbeat, billions of individual cardiomyocytes must contract in synchrony which is achieved through electrical coupling via gap junctions. Gap junctions connect the cytoplasms of adjacent cells, allowing small molecules such as ions to pass from cell to cell. Alterations to gap junctions occur during stress, resulting in electrical disturbances leading to deadly arrhythmias. The gap junction protein connexin 43 (Cx43; gene GJA1) undergoes alternative translation initiation to yield a truncated isoform of Cx43 called GJA1-20k. GJA1-20k regulates Cx43 gap junction formation but the molecular processes governing GJA1-20k expression remain largely unknown. The RNA binding protein (RBP) IGF2 mRNA-binding protein 1 (IMP1) drives internal translation, but is unexplored in regulation of GJA1-20k expression. This led us to investigate how IMP1 impacts GJA1 mRNA. We hypothesize that IMP1 is a direct regulator of GJA1-20k expression. To verify this, we conducted western blot analysis on lung cancer cells exposed to BTYNB IMP1 inhibitor and, in a separate experiment, siRNA-mediated knockdown of IMP1. Results revealed a successful IMP1 inhibition/ knockdown accompanied by decreased expression of the GJA1-20k protein. Confocal immunofluorescence reveals remodeling of gap junctions in cells in which IMP1 has been ablated or inhibited. Finally, we identify IMP1/GJA1 mRNA complexes by super-resolution localization and fluorescence in situ RNA hybridization. These findings indicate that IMP1 is indeed a regulator of GJA1-20k internal translation. Future studies investigating how IMP1 is regulated and how it is altered in cardiomyopathies will help establish targeting IMP1 therapeutically to prevent arrhythmogenic gap junction remodeling in diseased hearts.

Mentor(s): James Smyth (FBRI/Biological Sciences, Virginia Tech)

Haley Grubbs
Virginia Tech/Civil Engineering

Short-term variations in nitrate can trigger lead solder corrosion problems

Nitrate concentrations in drinking water must be lower than 10 mg/L due to potential human health impacts and "blue baby syndrome". However, lower levels of sustained nitrate can sometimes be problematic for lead solder corrosion, as prior studies showed that slight elevations in nitrate from 1 mg/L to 2.5 mg/L could result in 119 times greater lead release in drinking water. Nitrate can fluctuate markedly in sources waters over decades, seasonally, diurnally and during storm runoff events, and these changes have been linked to cases of elevated lead release in drinking water. This study examined the nature of lead solder corrosion due to nitrate and screened for effective corrosion inhibitors in waters with variable nitrate. 90 simulated lead solder and copper pipe galvanic joints were exposed to 5 water conditions including: 1) normal source water control, and the same water spiked with 5 mg/L nitrate plus 2) no inhibitor, 3) orthophosphate, 4) zinc, and 5) zinc orthophosphate corrosion control. Water was changed on a Monday, Wednesday and Friday schedule and total lead was measured using inductively coupled plasma mass spectrometry (ICP-MS). Zinc orthophosphate decreased lead release from lead solder by 89% versus a control or orthophosphate alone (,âà 1440 vs 159 ppb) after 19 days, suggesting that it may be an effective treatment options for high nitrate waters.

Mentor(s): Marc Edwards (Civil and Environmental Engineering, Virginia Tech)

Rosalie Gude
Virginia Tech/Animal and Poultry Sciences

The Effect of Connexin43-based Gap Junctions on Endothelial Cell Branching and Pericyte Formation in Mice Retinas

Pericytes are cells that surround endothelial cells in vascular networks and are believed to be involved in the contractibility of capillaries by interacting with smooth muscle cells. Pericytes also contribute to the redistribution of immune cells throughout the body and to the removal of phagocytes from the capillary network. This assists with tissue regeneration as well as immune responses. Furthermore, pericytes are responsible for maintaining the microvascular elements of the blood brain barrier. Though there is much progress regarding the understanding of pericytes, many questions remain pertaining to their differentiation and development. Gaining knowledge of how pericytes develop will lead to more specific treatments for diseases that target the blood brain barrier such as Alzheimer's.

In a previous study, the Chappell lab observed direct cell-cell communication between endothelial cells and pericytes via Connexin43 (Cx43)-based gap junctions during vasculogenesis. However, when Cx43 was genetically removed in mice, pericytes continued to develop and endothelial cells continued to branch using alternative connexin isoforms. Leading to the hypothesis that Connexin43 is the preferred form of communication, but not required for communication to occur.

This experiment involved genetically removing Connexin43 in mice, to observe the extent of its effects on endothelial cell branching and pericyte formation in their retinas compared to wild type mice retinas. Imaging was performed using a Zeiss LSM880 Confocal, and statistical analysis was performed using ImageJ software. The results indicated that there was no significant impact on endothelial cell branching nor pericyte formation when Connexin43-based gap junctions were not present.

Mentor(s): John Chappell (Center for Vascular and Heart Research, Fralin Biomedical Research Institute, Virginia Tech)

DeAndre Guyton
University of North Carolina at Charlotte/Biology

TOUR

Racial Equity Audit to Develop Recommendations to Increase Accessibility of SNAP-Ed to People of Color

The Family Nutrition Program (FNP), the Virginia (VA) Supplemental Nutrition Assistance Program Education (SNAP-Ed) implementing agency, is a USDA-funded obesity prevention program targeting individuals and families receiving or who are eligible to receive Supplemental Nutrition Assistance Program (SNAP) benefits. The objective of this project is to audit t programming practices as well as staff perceptions to identify areas of strength and concern related to racial equity in VA SNAP-Ed. Focus group discussions were conducted in order to gain understanding of potential barriers to SNAP-Ed for people of color. An employee survey was distributed to program assistants (PAs) to assess staff perceptions of program equity. Common barriers for participants of color were not having FNP classes at community centers, not having more parent-children classes and the classes not being taught in the participants' native language. Results from the employee survey show that 96.4% of PAs working with adult participants said that FNP programming was somewhat or very welcoming to members of racial and ethnic minority groups. PA-suggested strategies for making programming more welcoming for people of color include having more diversity and inclusion training for PAs and creating more culturally relevant recipes for the participants. Recommendations for increasing the accessibility of SNAP-Ed programming for racially and ethnically-minoritized populations include having more classes in the native language of the participants, having materials reflect different cultures and include images that are reflective of members of racial and ethnic minority groups. Offering joint programming for parents and children would also increase accessibility.

Mentor(s): Sarah Misyak (Department of Human Nutrition, Foods, and Exercise, Virginia Tech)

Julia Hallworth
Virginia Tech/Civil and Environmental Engineering

Data Quality Assurance Plan for a Real-Time Water and Weather Monitoring System

The Learning Enhanced Watershed Assessment System (LEWAS) is an environmental monitoring lab that collects both real-time water and weather data. Water quality data is collected by a Hydrolab Multiparameter MS5 Sonde, water quantity data by a SonTek/YSI Argonaut-SW, and weather data by a Vaisala Weather Transmitter WXT520. Users can access this data on an interactive online educational platform called Online Watershed Learning System (OWLS). This research project aims to implement an optimal method to assure the quality of the data being displayed on the OWLS. To achieve this, a comprehensive data quality assurance plan will be developed and then implemented in the form of a case study on the LEWAS website. The developed data quality plan will stipulate using third-party independent sensors and resources to collect the same water quality, water quantity, and weather data to compare with the LEWAS sensors data. Different statistical methods, such as Root Mean Square Error and residual analysis, will be used for quantitative analysis of the collected data, and results will be observed using different visualization techniques. Moreover, this plan will include guidance and best practices on validation data collection, site maintenance, and sensor/instrument calibration according to standard schedules that are supported by a body of supporting literature and can meet the data quality needs of the LEWAS lab. The developed data quality assurance plan will also be utilized as a guide for the analysis and documentation of a few water quality and quantity incidents that happened over the summer of 2021.

Mentor(s): Kang Xia (School of Plant and Environmental Sciences, Virginia Tech)

Funded by the National Science Foundation-Research Experience for Teachers in Engineering and Computer Science program (Award Number 1609089)

Abraham Han
Virginia Tech/Human Nutrition, Foods and Exercise

Neural circuits for adolescent aggression induced by early life malnutrition

Pathological aggression in adolescents is a serious clinical and public health problem. Children who are malnourished in early life are more likely to be aggressive and antisocial throughout childhood and into their late teens. Yet, discrete neural circuits underlying adolescent aggression and their adaptation in response to early life malnutrition (ELM) has not been addressed. The lateral septum (LS) is thought to be a critical node for processing emotional information and behavioral stress responses. In particular, "septal rage" is a behavioral phenotype characterized by a dramatic increase in aggression after lesion of the LS, but less is known about the afferent inputs which regulate the LS activity to transduce ELM into pathological aggression. Our preliminary data show that juvenile mice exposed to ELM display escalated aggression upon encountering a conspecific mouse, whereas nutritional supplementation normalizes the behavior. We also found the LS is a significant target of the ventral tegmental area (VTA), a major source of dopamine (DA) neurons known to be affected by nutritional status in early life. Here, we will focus on the functional role of the DA system in the VTA-LS circuitry in developing adolescent aggression after ELM. The significance of this study is substantial because it represents the first steps towards understanding how ELM alters the activity of the VTA-LS circuit pathway associated with adolescent aggression. It will provide a framework for studying ELM-induced adolescent aggression in a circuit-specific manner, which is important for developing targeted therapies to treat psychiatric symptoms caused by early life malnutrition.

Mentor(s): Sora Shin (Human Nutrition, Foods and Exercise, Virginia Tech)

Zachary Hartman
Virginia Tech/Biochemistry

Investigating the Cell Wall Structure of Lyme Disease Bacteria

Lyme disease is the most common vector-borne illness in the United States, with over 450,000 individuals in the US diagnosed and treated yearly. Borrelia burgdorferi, a spirochete bacterium that utilizes hard-bodied ticks as a host, is the most common cause of this disease. A component of its cell wall, referred to as peptidoglycan (PG), has been implicated in Lyme disease symptoms, but very little analysis has been performed on its characteristics. The typical pattern for the structure of the PG cell-wall consists of glycan chains of alternating units N-acetylglucosamine (GlcNAc) and N-acetylmuramic acid (MurNAc), connected by a glycosidic bond. The MurNAc unit is also linked to a short peptide, which crosslinks with peptides from adjacent PG strands, forming a 3D bag, or sacculus, that encases the microbe. However, there is a structural deviation from this pattern observed in B. burgdorferi PG that may be related to Lyme disease. While several of these key PG structures have been identified, many have not been characterized. Here we describe the chemical and analytical methods used to characterize PG strands, referred to as muropeptides. Our main focus fell on that of the muropeptides found at the ends of PG chains, two of which have the same molecular formula but differ in their observed chemical properties. These two muropeptides were purified and analyzed in order to derive their chemical structures. The characterization of these and other muropeptides in B. burgdorferi could lead us to further knowledge on the mechanisms of Lyme disease and its treatment.

Mentor(s): Richard Helm (Department of Biochemistry, Virginia Tech)

Elena Hayday
University of Minnesota-Twin Cities/Neuroscience

Divergent roles of PI3K catalytic isoforms in melanoma

Melanoma accounts for only 1% of skin cancer diagnoses but the majority of skin cancer-related deaths due to the difficulty of treating invasive melanoma. Early-stage melanoma has a 99% 5-year survival rate, primarily due to the identification and selective targeting of hot-spot genetic mutations in BRAF, RAS, and NF1. However, the 5-year survival rate for regional and metastasized melanoma is 27%, indicating that these mutations are not the only driver of melanoma progression. Recent research has suggested that the PI3K signaling pathway is involved in promoting melanoma progression; however, it is unclear whether all four PI3K catalytic subunits play equally important or divergent roles in melanoma. Addressing this question is critical because treatment with pan-PI3K inhibitors often yields significant side effects. By analyzing the data from the TCGA melanoma datasets, we found that mRNA levels of PIK3CB and PIK3CD were significantly higher than the other two subunits. Further survival analyses revealed that high levels of PIK3CB, but not the other PI3K catalytic subunits, significantly correlated with poor prognosis in BRAF-V600E melanoma patients. This correlation was unique to the BRAF-V600E melanoma subtype. More importantly, metastatic melanoma patients with high levels of PIK3CB also exhibited worse prognosis. Consistent with results from the above clinical studies, PIK3CB inhibitors, but not PIK3CD inhibitors, resulted in a reduced viability in a BRAF-V600E cell line, UACC62. Our results collectively demonstrate that PI3K catalytic subunits play divergent roles in melanoma progression and, as such, selectively targeting PIK3CB represents a more feasible and effective approach than pan-PI3K inhibitors.

Mentor(s): Zhi Sheng (Fralin Biomedical Research Institute; Department of Internal Medicine, VT-Carilion, Virginia Tech)

Natalie Hedrick
Virginia Tech/Forestry

Dendroecological reconstructions of disturbance events in Table Mountain pine

Table Mountain pine (Pinus pungens) grows along the Appalachian Mountains on infertile, dry soils. In this study our objective was to reconstruct the disturbance events which impacted a population of Table Mountain pine growing on the top of Price Mountain near Blacksburg, Virginia. We used an increment borer to extract cores from the stems of 20 co-dominant Table Mountain pine trees. In the laboratory, we glued the cores on wooden holders and sanded with progressively finer sandpaper until we could see the xylem cells under a microscope. We crossdated the tree cores using narrow signature years and measured the annual tree-ring widths. We validated our visual crossdating with COFECHA, a statistical software. We used the radial growth averaging technique to identify canopy disturbances. A moderate release event was defined as 25% increase in growth sustained for 5 years, and major release was defined as 50% increase in growth sustained for 10 years. The variations in tree-ring width provided evidence of ice storm damage, canopy closure, and timber harvesting. A harvesting event in the late 1960s resulted in 55% of the sampled trees experiencing a moderate or major release in response to the increased growing space available post-logging. The results of this study demonstrated the successful application of dendrochronology to reconstruct a timeline of historical disturbance events in an Appalachian Mountain ecosystem.

Mentor(s): Carolyn Copenheaver (Forest Resources and Environmental Conservation, Virginia Tech)

Alison Henry
Virginia Tech/Biomedical Engineering

Wing's n Things: A study of cicada flight and snake landings

Cicadas have highly flexible wings due to a hinge in their fore wing created by numerous veins and the fusion of their fore/hind wing during flight. My work entailed motion analysis of the wings using flight data collected during Brood IX in 2020. In the experiment, three cameras were used to film the cicada's flight. In the analysis, first a calibration was created using both DLTdv8 and Fiji to sync the motion in the cameras together. Next, 13 points were manually tracked on the wing during it's wingbeat cycle in DLTdv8. These points are being used to train a machine learning-based tracking program (DeepLabCut) to track the same points in the remaining videos. These points will be used to test how wing bending influences the aerodynamics of the full stroke cycle.

Flying snakes are a main focus of the Socha Lab. I conducted an experiment to simulate these snakes landing on a branch from above using a falling chain. For the experiment, 3 drop heights, 5 PVC pipe diameters, and 19 horizontal locations of the pipes were used. Graphs were then created to compare these variables to the number of successful wraps the chain completed. Smaller diameter pipes were found to be more successful over a larger range of horizontal distances and higher drop heights resulted in a larger number of wraps around the pipe. Overall, the medium diameter pipe (1.5") resulted in the highest number of wraps for the largest horizontal range, regardless of drop height.

Mentor(s): Jake Socha (Department of Biomedical Engineering and Mechanics, Virginia Tech)

Ian Hicklin
Virginia Tech/Biochemistry

In Silico Exploration of Inhibitors of the Type IV Pilus Extension Protein PilB in Clostridioides difficile

On average, Clostridioides difficile causes 13,000 deaths due to antibiotic resistance in the United States. Type IV pili are virulence factors crucial for motility in many of the most dangerous antibiotic-resistant bacteria, such as C. difficile. For this reason, the pilus extension protein, PilB, is the target for an anti-virulence drug. In a prior experiment, to determine specific and effective inhibitors of PilB, the more easily expressible PilB from Chloracidobacterium thermophilum (CtPilB) was isolated and a high-throughput screening was performed, finding many inhibitors. Three promising candidates, quercetin, levodopa, and benserazide, had IC50s as low as 2 ¬µM in CtPilB. Computational methods can determine the effectiveness of these drugs more quickly, easily, and inexpensively than wet-lab approaches. In this experiment, homology models of CtPilB and CdPilB were created and key binding residues were identified by docking ATP. Additional docking of all screened inhibitors as well as a library of flavonoids like quercetin was performed and the free energy calculated for each. Free energy calculations could predict the relative IC50s of the three tested inhibitors. In addition, when the inhibitors were docked in CdPilB, they had similar positions and free energies compared to when docked in CtPilB, indicating these drugs could effectively inhibit CdPilB as well. One inhibitor, tilorone, had the greatest affinity for CdPilB of all tested inhibitors. While tilorone still needs to be tested for antibacterial properties to determine if it would be an effective anti-virulence drug, quercetin, levodopa, and benserazide would all act as anti-virulence drugs in C. difficile.

Mentor(s): Anne Brown (Biochemistry, Virginia Tech)
Dr. Zhaomin Yang (Department of Biological Sciences, Virginia Tech)

Grace Hight
Virginia Tech/Civil Engineering

Developing Test Methods and Water Quality Criteria for Mitigation of Cuprosolvency in Drinking Water

Gaps in implementation of the United States Environmental Protection Agency, Lead and Copper Rule may leave many residents at risk of elevated copper in their drinking water. This study aims to help utilities and residents experiencing copper concerns in drinking water by developing and validating a new jar test method for assessing cuprosolvency using copper particles. This method is a less-expensive and faster alternative to laboratory copper pipe testing. Literature and previous work suggests that increased pH tends to yield lower cuprosolvency, while increased orthophosphate dosages and alkalinities yield higher cuprosolvency. It is anticipated that the new test protocol will follow similar trends as previous pipe testing, but in a shorter time span. Furthermore, this study aims to utilize the new jar test protocol for the development of cuprosolvency decision tree criteria, taking into account the effects of pH, orthophosphate, and alkalinity on cuprosolvency. Utilities and residents can use these results to identify and address copper problems in their drinking water.

Mentor(s): Marc Edwards (CEE, Virginia Tech)
Rebecca Kriss (Ph.D. Candidate, Civil and Environmental Engineering, Virginia Tech)

Fadi Hindi
Virginia Tech/Biology

Comparison and Quantification of High Molecular Weight DNA Through Various DNA Extraction Kits

Short read sequencing disadvantages outweighs its uses. Short reads are constructed by short segments of DNA and require substantial computation to assemble and recover complete genomes. However, the mosaic nature of microbial genomes and fallibility of assembly algorithms causes information loss, missing regions, incorrect association of genes and uncertainty. By contrast, long read sequencing (LRS) has emerged as a powerful tool to resolve rich genomic contextual information without the need for assembly. However, recovery of high molecular weight DNA from diverse matrices is required to fully harness the technique, and there is currently a gap in knowledge on the appropriate extraction methods to gather strands long enough for LRS. LRS is key to finding how antibiotic resistance genes (ARGs) are transferred to create antibiotic resistance in the effluent of wastewater treatment plants (WWTPs). Here, we compared different DNA extraction kits (FastDNA Spin Kit for Soil, Monarch HMW DNA Extraction Kit for Tissue, Zymo Research Quick-DNA Magbead Kit and a novel experimental method, MicroGEM (2 methods)) on four different wastewater matrices including influent, effluent, filtered activated sludge, and weighed activated sludge from a local WWTP. After the data is extracted it's inputted into a software plugin in ImageJ known as DoNALD to determine the approximate fragment length distribution of recovered DNA based on gel band lines and relative intensity. This is cross referenced with Qubit concentrations along with NanoDrop Spectrophotometer ratios in order to determine the purity of HMW DNA. This anticipates the Zymo Kit to perform best for HMW extraction.

Mentor(s): Amy Pruden (Civil and Environmental Engineering, Virginia Tech)
Marc Edwards (Civil and Environmental Engineering, Virginia Tech)

Drew Hynes
Virginia Tech/Biological Sciences

The impacts of early life nutritional stress on the immune physiology of house finches.

Disturbances during early life development can have effects that last an individual's entire life. Thus, understanding these effects is crucial for anticipating long term fitness. Despite early life nutritional stress, some birds will grow to a similar mass as non-nutritionally stressed birds. This leads to the question: if not body mass, what does this nutritional deficit affect? We hypothesized that early life nutritional stress leads to a less developed and less reactive immune system. To evaluate this, we looked at both temperature response (fever) and corticosterone levels in house finches experimentally infected with Mycoplasma gallisepticum (MG), a common pathogen in this songbird species. Because we hypothesized that their immune systems would be less reactive, we predicted that nutritionally stressed house finches would show lower fever and lower corticosterone response to MG. To test these assumptions, we hand-reared 10 house finch nestlings, with controls (n=5) receiving ad lib food and nutritionally-stressed nestlings (n=5) receiving 70% of the food consumed by control nestlings. Once they reached the juvenile stage (approximately 60 days after hatching), we inoculated all captive-raised birds, along with 5 wild-raised house finches, with MG. These were compared alongside 4 wild-raised sham-inoculated controls. Eye surface temperatures were collected before and throughout the infection, and blood was sampled 5 days post-inoculation, during the peak of corticosterone secretion. As nutritional stress becomes more common due to shrinking habitats causing greater competition for food, it is important to understand how its effects could combine with emerging infectious diseases to threaten wild bird populations.

Mentor(s): Dana Hawley (Biological Sciences, Virginia Tech)

Rachel Inman
Virginia Tech/Smart and Sustainable Cities
Camryn Flores
Georgia Tech/Environmental Engineering
Nora Shanahan
Virginia Western Community College/Health SciencesEnvironmental Engineering
Hannah Kocen
Radford University/Geospatial Science

Public understanding of the downstream effects of bacterial stream impairments

Waterborne pathogens are a leading impairment of streams nationally, and this issue is often difficult to resolve. The primary causes of bacterial impairment vary depending on location: urban area impairments are often the result of stormwater runoff aggravated by impervious surfaces and aging infrastructure, while streams in rural communities can be impacted by agricultural influences, including manure spreading, cattle grazing, and the use of feedlots. Though public engagement is imperative to restoring stream health, it can be very difficult. Our group developed an infographic and a StoryMap utilizing publicly available data from the EPA and USGS to share with water-resource leaders in our local communities. Our goal was to educate the general public on how a stream can become bacterially impaired, the effects of impairment, and how our actions can affect communities that are downstream in a watershed. The design of this infographic was influenced by stakeholder feedback obtained through conversations with representatives from local government, nonprofit groups, and US agencies. After reviewing these interviews, we recommend providing clear, creative infographics, humorous social media postings, and news articles accessible to the general public. These resources should be tailored to the interests of each stakeholder group, as people of different backgrounds do not share the same perspectives on these issues. Raising public awareness on bacterial impairments in adjacent receiving waters will aid in the effort to achieve water sustainability for all through an increased understanding of the interconnectedness of our waterways.

Mentor(s): Leigh-Anne Krometis (Department of Biological Systems Engineering, Virginia Tech)
Cully Hession (Department of Biological Systems Engineering, Virginia Tech)
Brian Badgley (School of Plant and Environmental Sciences, Virginia Tech)
Erin Ling (Department of Biological Systems Engineering, Virginia Tech)

Gabriel Isaac
University of Tennessee, Knoxville/Biomedical Engineering

Episodic future thinking to promote self-regulation in prediabetes

As a response to the sharp rise in global prevalence of diabetes, a search has emerged for a robust behavioral marker that is both associated to maladaptive dietary habits (MDHs) and can serve as the basis for effective interventions. Delay discounting (DD); a measure that quantifies the degree to which earlier rewards are preferred to later ones; has been established as a marker of MDHs and now serves as the foundation for a proposed intervention termed Episodic Future Thinking (EFT). To assess EFT's capacity to remediate MDHs, this 3-phase study is examining the effects of EFT on dietary intake among individuals with prediabetes, using blood glucose (BG) levels to track and measure their consumption patterns. Participants wear continuous glucose monitors (CGMs) for an initial two-week baseline period followed by a second two-week phase of either the EFT intervention or a daily check-in (DCI) control condition. The collected data are then evaluated using an analysis of covariance to assess changes in BG variability from week 2 to week 4 for participants randomized to EFT or the DCI control condition. Preliminary covariance analysis has revealed that the EFT intervention produces a substantial decrease in BG variability, suggesting an increase in diet stability across time. Although these results are preliminary and subject to change, they corroborate the proposition of EFT as an effective intervention to remediate MDHs and may help to decrease the likelihood of developing diabetes.

Mentor(s): Warren Bickel (Professor of Psychology, Neuroscience, and Health Science, Virginia Tech - Professor of Psychiatry, Virginia Tech Carilion School of Medicine)

Kavya Iyer
Biochemistry

The Impact of Breastmilk-Derived Growth Factors on Infant Cognitive Development and Executive Function

Human milk has long been recommended as the ideal source of nutrition for infants, as this complex mixture contains essential nutritive components such as proteins, fats, and vitamins that all influence development of the growing child. Breastmilk is also rich in extra-nutritive components, including growth factors, which are biologically active molecules that play a substantial role in organ system development and maturation in the growing infant. Specifically, Insulin-like Growth Factor-1 (IGF-1) and Neuronal Growth Factor (NGF) have been found to play crucial roles in development of the intestinal system. While the Howell lab is studying the linkage between gut and brain development in infants, the effect of growth factor presence in milk on brain development has yet to be investigated. The goal of this project is to explore the relationships between IGF-1 and NGF in milk collected longitudinally on infant cognitive development and executive function assessed using the Minnesota Executive Functioning Scale (MEFS) for ten infants. Concentrations of these growth factors were determined using sandwich enzyme-linked immunosorbent assays (ELISAs) of collected milk samples from 0-18 months of age and trends were analyzed over the months of collection. Linear regression analysis yielded an insignificant relationship between the concentrations of NGF and IGF-1 and composite MEFS scores. Future studies will likely include increasing the sample size of breastmilk samples during a single analyses, utilizing fresh milk samples instead of frozen milk, and analyzing anatomical brain development of infants using infant MRI scans in relation to performance on these assessments.

Mentor(s): Brittany Howell (Center for Health Behaviors Research, Fralin Biomedical Research Institute, Virginia Tech)

Haley Jaffe
Virginia Tech/Animal and Poultry Sciences

MAOP

Functional role of Tfam in mitochondria in skeletal muscle

Research in mitochondria has significant implications in human genetic diseases such as Parkinson's Disease, Alzheimer's, and Mitochondrial DNA Depletion Syndromes 3 and 15. The objective of this study was to determine the role of mitochondrial transcription factor a (Tfam) in the mitochondria in skeletal muscle. To this end, we crossed a Tfam floxed mouse model with a skeletal muscle (HSA-MCM) specific Cre-inducible mouse line. We used Tfamfl/fl;HSA +/+ as the wild type (WT; n=2) and Tfamfl/fl;HSA Cre/+ as the knockout (KO; n=4). To induce Tfam KO, we injected these mice with the estrogen analogue tamoxifen to activate the cre-recombinase, which in turn, excised Tfam to generate the knockout mice. Ablation of Tfam caused mitochondrial DNA (mtDNA) to be unable to replenish or repair itself, as demonstrated by the finding that there was reduced mtDNA in the KO muscle compared to the WT. Three months after tamoxifen injections, these mice are subjected to an endurance run. We then collected the mitochondria from skeletal muscle and subjected them to an in vitro mitochondrial respiration analysis. We found that there was no statistical difference between genotypes in terms of mitochondrial respiration. In conclusion, we successfully ablated Tfam from mouse skeletal muscle and observed significant decrease in mtDNA copy number. Further analysis of muscle fiber morphology and contraction properties will reveal more phenotypical changes in response to Tfam KO.

Mentor(s): Tim Shi (Animal and Poultry Sciences, Virginia Tech)

Laily Jaghori
Virginia Tech/Microbiology

Analysis of an Amphipathic Helix in a Viral Replication Protein for Targeting Proteins to Endoplasmic Reticulum Membranes

Brome Mosaic Virus (BMV) is a positive-strand RNA virus that primarily affects cereal crops. The replication protein 1a in BMV is a key for viral replication. BMV 1a localizes in the perinuclear endoplasmic reticulum (nER) regions to assemble viral replication complexes in yeast and plant cells. It has been found that a 18 amino acid-long amphipathic helix (1a amino acids x-y), helix B, in 1a is sufficient to target 1a and other soluble proteins to the nER regions in yeast cells. In this project, I will identify key amino acids, which disrupt helix B's ability to target fluorescence protein, mCherry, to the nER membrane when they are mutated to alanine.

By performing overlap PCRs with the designed primers to introduce specific mutations, I have made plasmid constructs that will express helix B fused with an mCherry tag, which can be visualized using fluorescence microscopy for the localization of the helix-mCherry. I used GenBuilder to assemble and clone the gel-purified PCR products carrying the mutations into a suitable vector backbone. Following this, I transformed the products into E.coli, plating them on Ampicillin selection plates to screen for positive colonies. Plasmid was then extracted and confirmed by a restriction digestion with PstI and BamHI. The correct plasmids will be introduced into yeast cells and the localization of mC tagged helix B fragments without or with point mutations will be observed by using a fluorescence microscope. Any mC-tagged mutants that are not associated with the nER membrane contain the key amino acid .

Mentor(s): Xiaofeng Wang (Translational Plant Sciences, Virginia Tech)

Srinidhi Jayakumar
Virginia Tech/Psychology

How Child Functioning Influences Parent Mental Health: Predictions from Spring 2020 Stay-at-Home Orders to Fall 2020

During the COVID-19 pandemic, parental stress has increased tremendously. Such stress is particularly high among parents of children with mental health problems, working parents, and mothers. Given this backdrop, the present study sought to examine the association between spring 2020 youth emotional, behavioral, and academic problems, and parent mental health during fall 2020, controlling for number of hours worked, spring 2020 parent mental health symptoms, and parent gender. Participants were 60 working parents (78.3% female; 91.7% White; 13.3% Latinx) who completed online surveys during spring 2020 stay-at-home orders and again in fall 2020 upon the return to school/in-person work. Parents reported on their mental health (depression, anxiety, stress) and their children's emotional (anxiety/depression), behavioral (inattention, hyperactivity/impulsivity, oppositionality/defiance), and academic difficulties. Parent mental health symptomatology did not change from spring to fall 2020; children’s behavior problems significantly decreased from spring to fall 2020 (t=2.67, p=.01), but emotional and academic problems remained consistent. Child behavioral (Íûµ=.37, p=.01) and emotional (Íûµ=.58, p<.001) problems significantly predicted higher levels of parent depression, anxiety, and stress during fall 2020. Parent gender was also a significant predictor of mental health, with mothers having higher symptomatology than fathers (Íûµ=.21, p=.04). Results suggest that child mental health during the pandemic is negatively influencing parent mental health. Results add to growing research highlighting the importance of supporting at-risk populations during the COVID-19 pandemic, especially working mothers with children who have emotional and behavioral difficulties.

Mentor(s): Rosanna Breaux (Psychology, Virginia Tech)

Neutrino REU

Zachary Jerzyk
St. Norbert College, De Pere, WI/Physics
Adam Dirican
University of Maryland, College Park/Physics

Evaluating fitting models of the missing energy contribution of Ar and Ti nuclear shell orbitals using the E12-14-012 (e,e’p) scattering experiment at Jefferson Lab

The Deep Underground Neutrino Experiment (DUNE) seeks to probe CP-symmetry violation via the oscillation rates of the neutrino and antineutrino, detect supernovae neutrinos, and potentially invalidate several grand unification theories by making the first observation of proton decay. DUNE will be the world's largest long-baseline neutrino experiment, using a liquid argon time-projection chamber (LAr-TPC) style detector. However, little work has been done on electron-nucleus scattering for isospin nonsymmetric atoms, let alone neutrino-nucleus scattering for the argon-40 specific to DUNE. In Jefferson Lab Hall A's experiment E12-14-012, the (e, e'p) scattering cross sections of argon (N=22) and titanium (Z=22) were measured against a detailed Monte Carlo (MC) simulation. Various kinematical cuts were performed on the experimental data and Monte Carlo for signal identification. Using CERN's Minuit package in ROOT, minimization was performed on each orbital's cross-section as a function of missing energy against either a Gaussian (symmetric) or Maxwell-Boltzmann (nonsymmetric) distribution and dependence or independence of the function on the mean energy. Goodness of fit was calculated using a œá2 function that compared experimental data against the MC. Nuclear theory constraints provided the basis for the initial fit models of argon and titanium from which model variants were chosen. After removing poor models from analysis due to large reduced-œá2 values or non-physical parameters, several fit models showed good agreement. We determined that the minimization process did not introduce a statistically significant systematic error due to the choice of fit models.

Mentor(s): Camillo Mariani (Department of Physics, Virginia Tech)

Leiah Johnson
Hollins University/Environmental Science

Population Dyanmics of Designated Atlantic Sturgeon Population Segments

The life history of the Atlantic sturgeon is poorly understood, specifically regarding its age and growth since the population's crash in the late 1890s to early 1900s. However, these traits are critical to understanding population demography and recovery potential. It is known that Atlantic sturgeon populations in the north, like Maine, live substantially longer than southern populations, like in the Carolinas which are sexually mature at a younger age than their northern counterparts. Previous research has estimated maximum ages for the Atlantic sturgeon to be as high as 60 years- like many human populations - but not much data has been done to distinguish the dynamics of different Atlantic sturgeon populations, given variation in age and growth. Previous research has used the von Bertlanffy growth models to show the relationship between the age and length of fish. We used data from published literature to predict the length values starting where length is zero for our growth models that describe length as a function of age of the Atlantic sturgeon in seven major rivers from Quebec to Florida. We used published data on the relationship between length, mass, and fecundity to predict the recovery potential of each population, given their specific growth and maturation patterns. We found that many of the populations we were studying either had entirely older populations that were not reproducing fast enough before entering functional extinction or were producing at levels slower than needed for actual recovery.

Mentor(s): Holly Kindsvater (Fish and Wildlife Conservation, Virginia Tech)

Chantal Johnson-Schuster
Virginia Tech/Animal and Poultry Sciences

MAOP

Analysis of the glycolytic pathways in genetically selected fast-growing broilers

Over the last century, population growth, urbanization, and rising incomes have elicited the global demand for poultry meat at an unprecedented rate. Due to the genetic selection, there has been substantial improvement in the growth of the pectoralis major (PM) muscle. As livestock species become more growth efficient, the skeletal muscle has concurrently become more glycolytic in metabolism. However, the driving force behind the more glycolytic phenotype in skeletal muscle remains elusive. Since phosphofructokinase-1 (PFK-1)-mediated reaction is the rate-limiting step of glycolysis and thus is one of the most important regulatory enzymes in the pathway, we first investigated the protein expression of PFK-1 in skeletal muscle. Samples from PM and quadriceps femoris (QF), representative of glycolytic and oxidative muscles respectively, were obtained from broilers (n=7). To quantify PFK-1 abundance in skeletal muscle, we separated the muscle proteins on the SDS-PAGE, transferred proteins to a nitrocellulose membrane, and blotted the membrane with a PFK-1 antibody. Our results showed that PFK-1 expression at the protein level was significantly higher in PM muscle than that in QF muscle. Future analysis including PFK-1 activity, pyruvate dehydrogenase lipoamide kinase isozyme 4 (PDK-4) abundance, and the involvement of the pentose phosphate pathway will shed light on the metabolic profiles of these two muscles in the broilers.

Mentor(s): Dr. Tim H. Shi (APSC, Virginia Tech)

Meghana Kamineni
Virginia Tech/Medicinal Chemistry

Computational Analysis of Brome Mosaic Virus Replication Protein 1a to Determie Potential Docking Sites, Mutations, and Membrane Association Region Structure

Brome Mosaic Virus (BMV), a positive-strand RNA virus, drastically reduces the yield of cereal plants through mottling, necrosis, and stunting. BMV is a member of the alphavirus-like superfamily in the Bromoviridae family, all of which share homologous domains and consequently similar replication strategies. The interaction between Protein 1a, which is encoded by BMV, and the peripheral ER membrane forms invaginations on the membrane surface which contain viral replication complexes (VRCs). Helices A and B are amphipathic Œ±-helices located in the capping domain of 1a, that are linked to perinuclear ER membrane association and VRC formation. Little is known about the impact and importance of these helices on membrane association. A potential structure of protein 1a was derived using a structural prediction program that utilizes a deep neural network. 20 docking sites of protein 1a were identified, and protein-RNA docked was performed to identify the most probable binding sites and RNA poses. Lastly, mutant structures of protein 1a were analyzed to identify two potential mutations, G109A and G907A, that can inhibit protein 1a's ability to replicate RNA. The results identify a probable structure of protein 1a, docking sites, and mutations that can inhibit the protein's ability to localize to the perinuclear ER and form VRCs. Simulation studies are ongoing to determine structural stability and interaction mechanisms of helices A and B with membranes. These findings reveal information about the structure and function of protein 1a which helps understand the mechanism through which BMV affects cereal plants and reduces crop yield.

Mentor(s): Anne Brown (Biochemistry, Virginia Tech)
Xiaofeng Wang, (Virginia Tech School of Plant and Environmental Sciences)

Ronak Kanodia
University of Florida/Neuroscience

Loss of Pericyte-specific Connexin 43 Impacts Early Vessel Morphology

Pericytes (PCs) are cells within the microvasculature that wrap around the endothelial cells (ECs) of the blood vessel wall. Various roles have been reported for PCs, including blood vessel stability, blood flow regulation, and blood-brain barrier maintenance, among others. How ECs and PCs communicate to coordinate such interactions is unclear. Gap junctions, such as Connexin 43 (Cx43), create channels that connect various cell types, allowing the rapid flow of ions and other small molecules between adjacent cells. Recent evidence suggests PC-EC communication via Cx43 during development. In a prior study, the role of PC-specific Cx43 in blood vessel morphology in the adult (10-week) was investigated via confocal microscopy, and no significant differences versus controls were observed. Here, we examined the role of developing (p7) mouse retinas via confocal microscopy. Using a conditional PC-specific Cx43 knockout mouse model (NG2:Cre/+;Cx43:lox/lox), we quantified blood vessel branching points and PC density. We found that the p7 partial knockout of Cx43 in PC yielded lower overall PC density, whereas the complete Cx43 knockout led to decreased blood vessel branching. These findings indicate that, while PC-specific Cx43 is not required for vessel development, there may exist early-stage vessel abnormalities that stabilize by the adult stage. While further studies are needed, this work provides initial insights into Cx43-mediated communication between PCs and ECs, and the impact on functional vasculature.

Mentor(s): John Chappell (Basic Science Education Dept., Virginia Tech Carilion School of Medicine; Biomedical Engineering and Mechanics Dept., Virginia Tech)

Heather Kashin
Virginia Tech/Human Nutrition, Foods, and Exercise

TOUR

Conducting an Accountability Evaluation for the Scaling Up Nutrition Movement's Global Business Network to Support the 2021 United Nations Food Systems Summit Agenda

Background: In 2010, the United Nations (UN) and other food system actors established the Scaling Up Nutrition (SUN) Movement to address malnutrition in all forms in low-income countries. To achieve its goals, the SUN Movement has four Networks (i.e., UN, Donor, Business, and Civil Society). This study conducted an accountability evaluation to examine commitments and actions for 25 Scaling Up Nutrition Global Business Network (SBN) member companies over 11 years.

Methods: A scoping review was conducted to develop a profile for the 25 SBN members. The National Academy of Medicine's LEAD (locate, evaluate, assemble evidence to inform decisions) framework was used to identify and organize evidence from 2010-2021. Evidence was used to evaluate the SBN members and assign a progress score (i.e., none, limited, some, or extensive) toward five steps in an accountability framework (i.e., empowered body, take, share, hold to and respond to the account) to reduce malnutrition and achieve relevant Sustainable Development Goals (SDGs).

Results: SBN members represented five business sectors. Some progress was made to appoint an empowered body to set goals and metrics; no progress for taking the account; some progress for sharing the account; no progress to hold SBN members to account (enforcement); and some progress to respond to the account (strengthen accountability structures).

Conclusions: Improvements could be made for each LEAD accountability framework step especially step 2 (taking the account) and step 4 (holding to account). The UN Secretary General could ensure greater accountability for the SBN to achieve the 2030 agenda.

Mentor(s): Vivica Kraak (Human Nutrition, Foods, and Exercise, Virginia Tech)

Sydney Kehoe
College of William and Mary/Neuroscience

Physiological data collection for resting state and task-based fMRI

The collection of physiological data such as cardiac and respiratory activity and galvanic skin response (GSR) is a valuable method of research. It has the ability to capture data that self-reporting and behavioral analysis can not in a variety of studies examining addiction, mood disorders, etc. This is especially key in tasks that take place in complex technology such as MRIs and fMRIs, where movement must be limited and physiological activity can actually create noise within the data. We asked whether physiological data could model correlations in changing brain states as well as whether it could be used to clean the scans of fMRI data to a substantial degree. Two different experiments were run, one in a task-based rt-fMRI where substance dependent individuals were shown images corresponding to "crave/don't crave" stimuli to see if there were any significant physiological correlations. The other experiment was run in a resting state rt-fMRI that was used to determine if there was a difference between brain activity with and without the physiological corrections. Analyzing the physiological data from the substance abuse study indicated a GSR stress response that was significantly higher for "crave" than "don't crave", while we expect that there will be a significant difference in the fMRI data with physiological corrections. These findings could be useful to emphasize the importance of physiological data collection as well as its possible contribution to helping modulate brain states.

Mentor(s): Stephen LaConte (Biomedical Engineering and Mechanics Department, Virginia Tech)

Rebecca Kelly
Virginia Tech/Biology

Investigation of interactions between flagellotropic bacteriophages and their hosts

Bacteriophages (phages) are viruses that infect bacteria and are the most abundant biological entities on earth. Phages are very host-specific, often only infecting a few strains within a species. This specificity is advantageous for treating bacterial infections, which is referred to as phage therapy. Phage therapy is currently being studied and has been used successfully as an alternative to antibiotics, especially as bacterial antibiotic resistance is increasing. In this study, we investigated the interaction between two phages and their pathogenic host bacteria, bacteriophage Chi, and the newly discovered bacteriophage Milano, which infect Salmonella enterica and the plant pathogen Agrobacterium tumefaciens, respectively. Many bacteria, including S. enterica and A. tumefaciens, use flagella for motility, which is directly correlated with virulence. Bacteriophage Chi is flagellotropic, meaning it requires a rotating flagellar filament to be present in its host for infection. One goal of this study was to determine the possible flagellotropic nature of phage Milano. To test this, multiple A. tumefaciens strains expressing different sets of flagellar filament genes were examined for phage susceptibility via spot assays. Through this effort, we determined that Milano is flagellotropic. Additionally, the host range of bacteriophage Chi was studied by testing different Salmonella strains for susceptibility using spot assays, plaque assays, and swim plate phage drop assays. From this, we determined that certain strains of Salmonella act as hosts for Chi, while others are resistant. This study broadens the current knowledge regarding two flagellotropic phages, which can help impact advancements in phage therapy.

Mentor(s): Birgit Scharf (Biological Sciences, Virgina Tech)

Steven Kenah
Virginia Tech

Auxin Biosensor for Metabolic Engineering Applications

Yeast naturally produce auxin, an indole derived plant hormone that controls plant growth and development. However, the extent to which yeast can modify plant growth is unclear, as well as which metabolic pathways are used by yeast to produce auxin since the metabolic pathways are complicated and complex. Therefore, in order to understand how yeast produces auxin and its effects on plant growth, an advanced and efficient tool is needed in order to detect and quantify auxin within yeast. A deep understanding of auxin, interactions within the auxin signaling pathway will allow scientists to disrupt fungal pathogens, enhance plant development, and screen libraries of yeast strains to identify the best fit for use in agricultural applications and biotechnology.

Mentor(s): Clay Wright (Biological Systems Engineering, Virginia Tech)
Patarasuda Chaisupa (Ph.D. candidate, Biological Systems Engineering, Virginia Tech)

Shayla King
Hollins University/Environmental Studies
Zoe Jordan
Hollins University/Biology
Breanne Sharp
Hollins University/Biology

Anthropogenic Noise Pollution Effects on Systems

Human generated noise is a pervasive and often ignored by-product of urbanization and development. However, short-term exposure to noise pollution raises blood pressure in humans and long-term has been associated with cardiovascular disease as well as other human ailments (Farooqi et. al. 2020); and has impacts on animals including altering the physiology of caterpillars, impacting reproductive success in birds, and impacting hunting success in bats (see Kunc and Schmidtt, 2019). In addition, noise may alter plant communities and thus ecosystem services by impacting pollination and seed dispersal (Francis et. al. 2012). We established microcosms containing four annual flowering species and two species of common annelids and placed them in two locations separated by 300m. The first location was along a busy road bordering the Hollins University campus and the other along a matching internal campus road. On four occasions we videotaped pollination activity at both locations. In addition, human subjects (anticipated sample size N=50) have been recruited to spend 15 minutes in both locations separated by at least 24 hrs. The initial blood pressure of each participant will be taken before they are asked to sit and relax under a shade tent facing away from traffic. After 15 minutes, each subject's blood pressure is taken again, and they complete the PANAS survey. We plan to compare pollination activity, plant growth, growth of soil annelids, and human responses in these two environments. We expect to see higher growth rates, pollination rates, and more positive affect scores on the internal campus road.

Mentor(s): Renee Godard (Biology, Hollins University)

Alia Korot
Kenyon College/Neuroscience

Mild TBI Causes BBB Leakage and Rapidly Induces an Atypical Neuronal Phenotype

The blood-brain barrier (BBB) is critical to the protection of the brain. BBB disruption is known to cause neuronal dysfunction and is implicated in a number of neurological disorders. Mild diffuse traumatic brain injury (TBI)/concussion is known to cause disruption and leakage of the blood-brain barrier. However, if BBB leakage harms neurons after mTBI and by which mechanism is unknown. We have previously shown that mild TBI induces an atypical astrocyte response within minutes of injury that is characterized by widespread downregulated protein expression, and this response is caused by BBB dysfunction and contact with blood-borne proteins. Here, we assessed the response of neurons to exposure of blood-borne factors in a mouse model of mTBI. Within a few minutes after injury we found a significant downregulation and mislocalization in the neuronal splicing factor NeuN, but no change in the density of Nissl+ cells, a marker of the endoplasmic reticulum widely used to quantify neurons. This suggests that BBB leakage caused by mTBI rapidly induces NeuN downregulation without causing neuronal cell death. Exposure of neurons to blood-borne factors thus induces a similar phenotype as previously observed in atypical astrocytes. The mechanism of this effect alongside determination of functional consequences is the focus of future studies.

Mentor(s): Stefanie Robel (School of Neuroscience, Virginia Tech)

Madison LaRoche
Virginia Tech/Clinical Neuroscience

The Association Between Demographic Characteristics and Self-Reported Quality of Life Among Individuals in Recovery From Substance Use Disorders

In this study, using data collected from The International Quit & Recovery Registry, we examined the association between quality of life (QOL) and certain demographic characteristics (i.e., age, gender, annual income, marital status, education level) and substance use variables (i.e., smoking status, primary substance of addiction, and length of abstinence from the primary addiction). Additionally, we examined the ability of those variables to statistically predict the length of abstinence among the same sample. Multivariable linear regression analyses of 206 participants self-reporting to be in recovery indicated that multiple domains of QOL for individuals in recovery from substance use disorder were significantly associated with gender, age, and education level. Scores of QOL in three of the four domains: physical, psychological, and environmental were significantly higher among males compared to females. Additionally, those scores were significantly positively associated with education level. Age was also significantly associated with psychological QOL, with older ages reporting a higher QOL. There were no significant findings with reference to the social relationships domain. Additionally, in this study, a separate multivariable linear regression analysis indicated that length of abstinence from the participant's primary addiction was significantly associated with annual income and smoking status. This study identifies demographic characteristics and substance related variables that may be useful in adjusting treatment plans to improve QOL scores and/or abstinence among individuals in recovery from substance use disorders and may help identify individuals at higher risk of relapse that may require special treatment or unique interventions to overcome their addiction.

Mentor(s): Warren Bickel (Professor of Psychology, Neuroscience, and Health Sciences, Virginia Tech Professor of Psychiatry, Virginia Tech Carilion School of Medicine)

Sophia Link
University of Virginia/Biology

The Effect of Insect Herbivory on Yield and Defense Mechanisms in an Oilseed Plant

Crop breeding typically focuses on increasing product yield and quality, often in a controlled environment lacking natural herbivory. The absence of native pests reduces selective pressures on plant defense systems; the resulting low-defense plants force a continued reliance on aggressive pesticide use, which especially disadvantages organic growers. Thus, it is worthwhile to develop breeding programs that simultaneously optimize yield and defense. To that aim, this work determined the baseline relationship between plant yield and defense traits and the effect of insect herbivory on that relationship. We hypothesized that the presence of insect herbivores would significantly decrease plant yield. Additionally, due to resource-allocation trade-offs, a negative correlation between yield and defense traits was expected. Brassica rapa, a relative of the canola oil plant, and Trichoplusia ni, a generalist insect herbivore, were chosen as a suitable model system. Thirty families of full-sibling B. rapa were grown in a greenhouse. Each family contained 20 plants, 10 of which experienced three days of feeding damage by T. ni caterpillars. The seed oil content of B.rapa was determined as a well-defined yield measurement. In addition, seed count, silique count, and biomass data were collected to assess their validity as proxies for oil content. Leaf trichome count and herbivore success (mortality and pupal mass) served as defense measurements. The results of this work will help inform future experimental evolution studies that will assess yield-defense trade-offs in generations of selected high oil producers and explore the possibility of generating plants with high productivity and anti-herbivore defense.

Mentor(s): Dorothea Tholl (Biological Sciences, Virginia Tech)
Anne Jones (Department of Biological Sciences, Virginia Tech)
Susan Whitehead (Department of Biological Sciences, Virginia Tech)

Nicholas Logan
Virginia Tech/Health, Nutrition, Food, and Exercise

TOUR

Circadian Rhythm's Potential Role in Energy Pathways of Cancer Cells

Circadian rhythms are endogenous oscillators that control physiological, behavioral, and metabolic processes in organisms. Circadian rhythms are regulated by transcription-translational feedback loops of which Period 2 (PER2) is a key component. Period 2 controls the stability and activity of the tumor suppressor p53 in unstressed cells. Cancer cells use aerobic glycolysis as a means of producing energy for cell division rather than a more efficient oxidative phosphorylation pathway. The phenomenon known as the Warburg effect, shows p53 overexpressing different components of the glucose pathways within cancer cells. PER2 modulation of p53's activity begs the question of the effects of the circadian clock factor on energy uptake in cancer cells. The relationship between PER2 and glucose was analyzed by using a colorectal cancer cell line. HCT116 cells were knockout for TP53 or expressed p53 at normal levels. Each cell line was placed in media containing different concentrations of glucose. Gene expression levels for the GLUT receptors and PER2 were analyzed using RT-qPCR. A single factor ANOVA test was completed to determine statistical significance for each targeted gene between the cell lines, using TBP as a normalizing gene. The data indicate there is a potential relationship among PER2 expression, p53 activity and glucose levels that merit further investigation.

Mentor(s): Carla Finkielstein (Molecular Diagnostics Lab and Cancer Research Group, Virginia Tech)

Nuwayra Mahreen
University of Maryland, College Park/Public Health Science

MAOP

Assessing the genetic determinants responsible for in vivo phenotypic differences between Mayaro strains TRVL 4675 and TRVL 15537

Mayaro virus (MAYV) is an emerging pathogen that produces a clinically similar disease to other arthropod-borne viruses such as Zika, dengue, and chikungunya. MAYV has the potential to become an epidemic, thus there is a need to develop effective tools to study the virus. Previously, infectious clones of two strains of MAYV were developed and shown to be efficient replicates of their respective parental strains, TRVL 4675 and TRVL 15537. However, when compared to each other, TRVL 4675 presented as more virulent, pathogenic, and transmissible than TRVL 15537. While similar in genomic sequence, seven amino acid changes exist between them that may be responsible for the differing phenotypes. To identify the causal mutation(s), we utilized our infectious clones to generate a single-mutant of each amino acid change. Mammalian in vitro viral kinetic assays showed that the E1-T65A mutant had shifted replication profiles from TRVL 4675 to TRVL 15537, indicating a possible key mutation to further examine. Because both strains also replicate differently in mosquito cells, we infected Aedes aegypti (Aag2) with our mutants and it was determined that the E1-T65A mutant had shifted kinetics. These findings encourage further studies of the E1-T65A mutant. The replication of the E1-T65A mutant in Aag2 was not a complete replicate of TRVL 15537, suggesting that more than one amino acid change may be necessary to achieve these unique phenotypes. Therefore, the E1-T65A mutant will be used to generate double-mutants expressing the remaining 6 amino acid changes to re-analyze the in vitro kinetics.

Mentor(s): James Weger-Lucarelli (Department of Biomedical Sciences and Pathobiology, Virginia Tech)
Christina Chuong (Department of Biomedical Sciences and Pathobiology, College of Veterinary Medicine, Virginia Polytechnic Institute and State University)

Anna Makarov
Virginia Tech/Biological Sciences

Labeling Transcription Sites to Measure Transcription Dynamics

Genetically identical cells can show variability in gene expression, even in identical environments, which can cause phenotypic differences between cells and affect their fitness. Part of this variability is stochastic, known as gene expression "noise", and can be attributed to the random timing of biochemical reactions involved in gene expression. Noise is inevitable, and can never be fully repressed. However, we have found several genes with unexpectedly low RNA noise and are currently working to understand how the cell is able to minimize noise for these genes. My research focuses on understanding the contribution of transcription dynamics to the low noise of these genes. I have been working to combine a LacO/LacI-GFP transcription site labeling system with single molecule RNA fluorescence in situ hybridization. This will allow me to quantify the number of RNA molecules being transcribed at individual transcription sites and directly measure transcriptional noise. This data will allow us to gain a better understanding of gene expression noise, how it is regulated, where it originates, and overall provide more insight into the dynamics of gene transcription.

Mentor(s): Silke Hauf (Department of Biological Sciences, Virginia Tech)

Arya Malek
Virginia Tech/Biology (Biomed)

A Role or Pannexin-1 in Regulating Nitric Oxide in Endothelial Cells

Coronary microvascular disease (CMVD) is a condition in which the arterioles of the heart fail to dilate, reducing oxygen flow to the heart. Little is currently known about CMVD and there are few tools for diagnosis and treatment. Typically, blood vessels in the microcirculation relax in response to nitric oxide (NO), a molecule produced in vascular endothelial cells (EC). We know that NO is regulated by intracellular calcium (Ca2+) and have previously illustrated that Panx-1 can control intracellular Ca2+. Thus, we can infer Panx-1 may control NO concentration by increasing Ca2+ concentration in the cell. We hypothesize that Panx-1 channels function to increase Ca2+ concentration and thereby upregulate NO production for vasodilation. To determine if Panx-1 contributes to CMVD, endothelial cells (EC) which had their Panx-1 partially inhibited with siRNA were compared to the control EC. BCA analysis was performed to determine loading concentrations for western blotting. We calculated the concentrations of Panx-1 and Phospho-eNOS, in the control and siRNA treated EC with the western blotting (WB). The results from WB illustrated that siRNA treated EC for Panx-1 had a lower concentration of that protein than the control EC. We then tested if active phospho-eNOS was increased after acetylcholine (Ach; 1uM) was introduced into the siRNA treated and control EC. The WB illustrated no significant difference; in future studies, we will test a range of Ach concentrations (1uM-1mM) to optimize the protocol for eNOS activation. Further studies will be performed to fully interrogate the relationship between Panx-1 and CMVD.

Mentor(s): Scott Johnstone (Center for Vascular and Heart Research, Virginia Tech)
D. Ryan King (Center for Vascular and Heart Research, FBRI)

Jon Mallen
Brown University/Applied Mathematics - Biology

Isolating Steady-States In Simulated Gene Expression Data

Numerous gene regulatory networks (GRNs), in which a set of genes control the expression of each other, govern biological processes. A GRN is often modeled well as a Boolean Network (BN). The BoolODE approach, which converts a GRN specified by a BN into a system of ordinary differential equations (ODE) and adds noise terms to minimize stochastic effects, has proven an effective approach to numerically simulate expression data. We are interested in determining whether the data output by BoolODE exhibits levels of stable protein expression that correspond to the steady states of the BN. We have developed a novel framework to isolate viable steady states of a GRN, if present, by taking into account the asymptotic behavior of BoolODE-generated ODEs. By using large simulation times for BoolODE across a large number of cells, we skew the distribution of cells towards those with expression levels in close proximity to a steady state. Thresholding to binary values of 1 and 0, in which the gene is "ON" or "OFF", respectively, assigns all cells to be equivalent to a given binarized state. We then use noticeably large multiplicities to determine the identity of steady state(s). This framework of numerical thresholding produces steady states consistent with numerous literature-curated models, and is a promising approach to infer steady states from simulated single-cell expression data.

Mentor(s): T.M. Murali (Computer Science, Virginia Tech)

Michael Marciano
Virginia Tech/Pre-Veterinary Dairy Science

Shoeing in the Heartland

This is a presentation for the Jacklyn W. and William R. Jones, Jr. Experiential Learning Scholarship about my time spent at Heartland Horseshoeing School in Lamar, Missouri. During my 8 weeks there, I acquired 750 hours of experience shoeing horses, forging, studying anatomy, and learning pathology of the equine hoof in order to benefit me as a future veterinarian. Overall, I was able to improve significantly my ability to communicate with farriers and gain many skills that will help me in my career. I am very proud to be able to call myself a graduate of that fine institution.

Mentor(s): Chris Gregory (Heartland Horseshoeing)

Justin Markov Madanick
Virginia Tech/Microbiology

Effects of Seasonality on the Eastern Oyster Microbiome Taxonomy

Shellfish such as the Eastern oyster (Crossostrea virginica) are an important agricultural commodity, and they are often cultivated via aquaculture. Aquaculture has become a viable and more sustainable alternative to traditional wild-caught harvesting. Unpublished research has demonstrated the resilience of the oyster's native microbiome against exogenous challenge by the human pathogen, Vibrio parahaemolyticus. However, the taxonomic makeup of the Eastern oyster's native microbiome and factors affecting it, including seasonality, are understudied. Research was conducted over a calendar year (i.e., winter, spring, summer, fall 2020, and winter 2021) to analyze the seasonal effects on the taxonomic diversity of the Eastern oyster microbiome. It was hypothesized a core group of bacterial species constitute the microbiome regardless of external factors including season, water temperature, and salinity. Each season, 18 Chesapeake Bay watershed oysters were collected from a local grocery store for microbiome composition analysis. Genomic DNA was extracted from the homogenized whole oyster tissues, and the bacterial 16S rRNA gene hypervariable V4 region was PCR-amplified using barcoded primers. Proper amplification was confirmed via gel electrophoresis, and the amplicons were then sequenced via Illumina MiSeq. Resulting sequences are currently being analyzed for taxonomic diversity using bioinformatics tools such as Quantitative Insights Into Microbial Ecology (QIIME2) and R, to establish the various bacterial species residing within the organisms' core microbiome. This study establishes a baseline understanding of the fluctuations and consistencies of the Eastern oyster's microbiome over a defined seasonal timeline. These findings are also relevant to host-pathogen interaction research and establishing improved aquaculture protocols.

Mentor(s): Ann Stevens (Biological Sciences, Virginia Tech)
David Kuhn (Food Sciences and Technology, Virginia Tech)
Ian S. Hines (Ph.D. candidate, Virginia Tech)

Jewel Mayo
Virginia Tech/Human Nutrition, Foods and Exercise

Micronutrient Intake and Physiological Outcomes in Masters and Collegiate

Purpose: Micronutrients can affect resting metabolic rate (RMR), maximal oxygen consumption (VO2max), bone mineral density (BMD), lean body mass (LBM), and other physiological processes. We examined the relationship between the aforementioned micronutrients and physiological outcomes in athletes. Methods: We conducted a cross-sectional study with Masters and Collegiate Athletes.We focused on micronutrient intakes of calcium, iron, magnesium, phosphorus, zinc, and how they correlated with RMR, VO2max, and body composition, and if differences existed among these variables between women and men. Dietary intake was measured using Block's 2005 Food Frequency Questionnaire (NutritionQuest, Berkeley, CA). Results: A total of 415 Masters and Collegiate Athletes (210 women, 205 men) participated (34.72±11.63 years [women: 36.39±11.29, men: 33.01±11.75 years]). Body mass index (BMI) for all athletes combined was 24.91±4.13 kg/m2 (women: 24.23±4.06, men: 25.62±4.09 kg/m2). For all athletes combined, magnesium (p=0.003), phosphorus (p=0.023), and zinc (p=0.041) were significantly correlated with RMR. Calcium (p=0.031), magnesium (p=0.002), phosphorus (p=0.004), and zinc (p=0.028) were significantly correlated with BMD. Calcium (p=0.014), magnesium (p=0.004), and phosphorus (p=0.0001) were significantly correlated with LBM. None of the micronutrients were significantly correlated with VO2max. We found significant correlations with iron and RMR (p=0.04) and iron and LBM (p=0.024) in men only. Conclusions: Magnesium and phosphorus were the common micronutrients correlated with RMR, BMD and LBM. Iron was significantly correlated with RMR and LBM in men only. Prospective research on micronutrient intakes on RMR, VO2max, BMD and LBM in athletes are needed to more definitively ascertain how they affect these physiological variables.

Mentor(s): Stella Volpe (Human Nutrition, Foods and Exercise, Virginia Tech)

Liam McMillan
Virginia Tech/Biology

An investigation of the chemoreceptor modification system in Sinorhizobium meliloti chemotaxis

Bacterial chemotaxis is the use of chemoreceptor proteins to guide bacteria along a chemical gradient. A chemoreceptor modification mechanism is crucial for this process to work. In Escherichia coli, a conserved pentapeptide at the C-terminus of chemoreceptors or Methyl-accepting Chemotaxis Proteins (MCPs) serves as a binding site for receptor-modifying proteins. In contrast, Sinorhizobium meliloti, a nitrogen-fixing soil bacterium that forms a symbiotic relationship with alfalfa plants, lacks this pentapeptide on half of its MCPs. Here, we used the amino acid sensor McpU, which lacks the pentapeptide motif, as a model to study the function of this motif. Traditional capillary assays were conducted to establish a dosage-response curve for taxis towards lysine and to measure lysine taxis of the wild type, a strain lacking mcpU, and a strain with a pentapeptide added to mcpU. Qualitative western blot analysis was conducted to determine the effect of the pentapeptide addition on McpU stability. The results showed that S. meliloti has the strongest chemotaxis response towards lysine at a concentration between 1 and 10 mM. Western blot assays revealed that the pentapeptide had a stabilizing effect on McpU. In future work, we will analyze the effect of the pentapeptide on McpU function by comparing lysine chemotaxis of wild type and mutant strains. The understanding of S. meliloti chemotaxis could have profound benefits to agriculture, as successful chemotaxis is crucial to the formation of a symbiotic relationship between S. meliloti and alfalfa. S. melioti's ability to fix nitrogen reduces the need for conventional fertilizers.

Mentor(s): Birgit Scharf (Biological Science, Virginia Tech)

Cassell McMillian
Virginia Tech/Biochemistry

Synthesis and Characterization of Dextran-b-PLA as Compatibilizing Agents in PLA/Starch Blends

Synthetic polymers from nonrenewable resources have proven to be useful materials because of their versatile properties and cheap production costs. Along with these useful properties comes their persistent environmental threats, prompting the need to transition to sustainable polymers. Biopolymers such as amylose and amylopectin from starch, and biodegradable polymers such as poly (lactic acid) (PLA) have been researched as alternatives, but their lack of useful properties compared to their synthetic counterparts limits their applications. One solution is the blending of biopolymers and biodegradable polymers which can result in a wider range of physiochemical properties, provided there is cooperative interaction between the two polymer components to overcome the unfavorable entropy of mixing. The blending of immiscible polymers causes phase separation leading to blends with poor mechanical properties. Block copolymer compatibilizers have been shown in the literature to reduce interfacial tension and phase separation in blends, resulting in enhanced mechanical properties superior to each individual component. In this work, we will synthesize and characterize novel block copolymers of dextran and PLA as compatibilizers for starch/PLA blends using a facile, efficient, and versatile condensation approach. We will then characterize the thermomechanical properties of compatibilized starch/PLA blends. We hypothesize that the dextran-b-PLA will be an ideal compatibilizer for PLA/starch or PLA/ starch ester blends due to the structural similarity between dextran and amylopectin branches. This blend would be inexpensive, sustainably sourced, and fully biodegradable, thereby reducing our reliance on non-renewable synthetic plastics.

Mentor(s): Kevin Edgar (Sustainable Biomaterials, Virginia Tech)
Rana Ashkar (Physics, Virginia Tech)

Jessica Melvin
Virginia Tech/Human Nutrition, Foods, and Exercise

TOUR

Neuronal Nhlh2 Expression in Muscle May Contribute to Energy Expenditure Pathways

Obesity is a worldwide epidemic affecting billions of people every year, with one-third of the United States population considered either overweight or obese. While many factors are involved in the development of obesity, the genetic component is still poorly understood. The transcription factor nescient-helix-loop-helix-2 (Nhlh2) has been implicated in cellular pathways that regulate energy metabolism, including exercise motivation and energy uptake; both of which are associated with obesity. To date, current research has not explored the role of Nhlh2 in tissues other than the hypothalamus. It is the goal of this study to determine the expression of this transcription factor in vitro in C2C12 mouse myoblast cells, and whether Nhlh2 regulates target genes such as Mc4r in muscle. A real-time qPCR analysis was performed, to compare RNA from undifferentiated cells to that of the differentiated cells, collected 2 hours post-treatment +/- leptin stimulation. Mc4r and Nhlh2 target genes were measured. Preliminary data indicates that leptin stimulation of differentiated as well as undifferentiated myoblasts increased Nhlh2 expression, with statistical analysis of the results still pending. MC4R expression, which was found in pig muscle, does not appear to be expressed in mouse C2C12 cells. The presence of Nhlh2 RNA in C2C12 cells has multiple implications for the transcription factor's role in muscle metabolism. As Nhlh2 serves as a transcription factor for many genes, the role of this protein in other areas of the melanocortin pathway should be explored.

Mentor(s): Deborah Good (Human Nutrition, Foods, and Exercise, Virginia Tech)
Dane Fausnacht (Animal and Poultry Sciences, Virginia Tech)

Antonia Mendrinos
Virginia Tech/Clinical Neuroscience, Biology

Adverse birth outcomes and proximity to poultry animal feeding operations on the Eastern Shore, Virginia

Previous research has associated exposure to poultry Animal Feeding Operations (AFOs) with various health effects; however, studies assessing adverse birth outcomes associated with proximity to poultry AFOs are limited. The Eastern Shore of Virginia has many poultry AFOs, which have grown in size and number and may be contributing to air pollution. The objective of this study is to investigate if maternal proximity to poultry AFOs is associated with adverse birth outcomes. This study includes birth outcome data collected from births occurring in VA from 2002-2015. The number of poultry AFOs within a 1 km, 2km, and 5 km buffer around each maternal residence address and within the maternal address zip code was calculated. Association between number of poultry AFOs within each buffer and adverse birth outcomes were determined, adjusting for available covariates (child sex, mother's reported race, age, ethnicity, education, tobacco use, method of payment, and previous births). The street-level analysis consisted of 5,768 birth records. The zip-code analysis included 7,306 birth records. We found a 54.5g (12.4,97.3) decrease in birth weight in the street-level analysis and a 47.8g (6.6,89.1) decrease in birth weight in the zip-code analysis. This study is suggestive of an association between living in close proximity to poultry AFOs and birthweight. As a next step, an inverse distance weighting model will be used to further refine the exposure metric.

Mentor(s): Julia Gohlke (Environmental Health, Virginia Tech)

Alicia Middleton
Rochester Institute of Technology/Physics

Building a Moving LED Device for Calibrating the NuLat Detector

The Neutrino Lattice Experiment (NuLat) is a neutrino detector consisting of 125 plastic scintillating cubes arranged in 5 x 5 x 5 lattice. NuLat uses photomultiplier tubes (PMTs), currently on three sides of the detector, to amplify signals from positron annihilation and neutron capture resulting from inverse beta decay, which are transmitted through the detector by a total internal reflection process. These signals can then be read and measured using the detector's data acquisition system and analyzed. This summer, we designed, assembled, and began testing an apparatus that will be used to calibrate the detector by sending a short signal from an LED into each cube on the faces of the detector without PMTs. The light from the LED will be transmitted through the detector and then caught and amplified by the PMTs on the faces of the detector directly across from and orthogonal to the face where we sent the signal. The device, which consists of three linear actuators run by stepper motors, is designed to be able to move an LED in two dimensions to the center of each cube on one face of the detector at a time. The stepper motors are controlled by Adafruit Stepper Motor HAT drivers on a Raspberry Pi computer and programmed using the CircuitPython programming language. Since the apparatus will be able to send an identical signal into each cube, it will ultimately allow for the calibration of the gains of the PMTs.

Mentor(s): Bruce Vogelaar (Department of Physics, Virginia Tech)

Albaraa Mirdad
Columbia University/Computer Science

KAUST REU

Development of an Algorithm for Detection and Tracking of Activated Neutrophils

Chemotherapy is the most common approach used for cancer treatment. However, there are limitations to the drug penetration through the tumor tissue to target cells far from the blood vessels. Therefore, bacteria-enabled drug delivery, wherein drug-loaded nanoparticles are interfaced with tumor-targeting bacteria offer a promising alternative to current approaches to cancer drug delivery. Bacteria such as attenuated strains of Salmonella Typhimurium have shown the ability to target and colonize tumor tissues. Understanding bacteria interaction with innate immune cells such as neutrophils which are the first line of defense against bacteria is critical to the successful development of bacteria-enabled drug delivery systems. Thus, this research aims to develop a method to detect and track neutrophils, response to live tumor targeting bacteria and bacteria-based drug delivery vectors through analysis of live-cell imaging data using machine learning. We prepared a training dataset by acquiring and labeling experimental neutrophil tracking data with MtrackJ, an imageJ plugin used to facilitate object tracking. The dataset was then fed into the YoloV5 object detection algorithm. The detected neutrophil data was then used by the Bayesian Tracking Algorithm to track the movement of each cell. During the remainder of this REU project, a machine learning model will be utilized to analyze time-lapse microscopy data of neutrophil under different stimulatory conditions (i.e., in response to bacteria and bacteria-based drug delivery vectors). Findings from this work will contribute to understanding the innate immune response to bacteria-based drug delivery systems and will facilitate the development of efficacious bacteria-based therapies.

Mentor(s): Bahareh Behkam (Department of Mechanical Engineering, Virginia Tech)
Ying Zhan (Ph.D. Candidate, Mechanical Engineering, Virginia Tech)
Ce Zhang (Biological Systems Engineering, Virginia Tech)

Erika Miyazaki
Blacksburg High/Biochemistry

Partial Agonism of Peroxisome proliferator-activated receptor γ (PPARγ) and Type II Diabetes: Redocking Natural Ligands from 2VSR Receptor

Type II diabetes (T2D) has become a more prevalent disease in society over the past few decades. In 2017, around 6.28% of the world's population were affected by T2D, and it is predicted that by 2030, T2D will be the seventh leading cause of death. Peroxisome proliferator-activated receptor γ (PPARγ) is a nuclear hormone receptor. PPARγ plays a significant role in T2D; it combats insulin insensitivity by regulating regulating inflammation, fatty acid storage, glucose metabolism, insulin sensitivity, vascular biology, and cancer. Since there are so many functions of PPARγ, using full agonists to target PPARγ for treatment can cause harmful side effects. This is why partial agonists are being further researched as alternative treatments for T2D.

Since PPARγ has a relatively large binding cavity, some partial agonists of it can only be activated if multiple ligands are present. This means that there are more possibilities for activating PPARγ. PDB 2VSR has three identical natural ligands, 9-Hydroxyoctadecadienoic acid (9-HODE), which cause partial agonism in PPARγ. It is important to research these possibilities by redocking the natural ligands found in PDB 2VSR and analyzing the protein ligand interaction to investigate the partial agonism of PPARγ. In this project, we identified the three identical 9-HODE ligands present in 2VSR and that they cause partial agonism in PPARγ.

Mentor(s): Anne Brown (Biochemistry, Virginia Tech)

Annie Morgan
Hollins University/Public Health

K-12 Student Learning Modalities and Mental Health during the COVID-19 Pandemic in Virginia

The purpose of this study is to explore students learning during the COVID-19 pandemic and mental health outcomes that different learning modalities may have on K-12 students given that some students are learning remotely or in-person, while others are doing hybrid. This project aims to answer these questions: what are the common classroom learning modalities for K-12 students during the pandemic; what is the historical trend of learning modalities during the pandemic; what are the primary themes as reflected in keywords/phrases prominent in educational and public health reports; what mental health issues are linked to particular modes of instruction?

The study utilizes content analysis methods to explore K-12 student learning modalities during COVID-19 and mental health outcomes in Virginia. Hypothesis coding of texts in education and public health reports will be done to identify key ideas and concepts to generate emerging themes. The focus has been to determine and clarify the existence and frequency of concepts in texts/reports, to assist in understanding what has been previously learned, and to provide valuable historical documentation and trends.

The anticipated results for this study are to contribute to the existing limited literature and identify potential areas of interest for future research in public health relating to the impact of COVID-19 on mental health with a focus on K-12 students within the context of learning modalities. This project is at the forefront of this area of study and has the potential to become one of the emerging preliminary sources of data for future studies.

Mentor(s): Abubakaar Jalloh (Department of Public Health at Hollins University)

Michelle Morris
Virginia Tech/Biomedical Engineering

Behavioral Characterization of Reward and Sensory Prediction Errors

Dopamine is an important neurotransmitter that plays a key role in learning, motivation, and attention. Reward prediction errors (RPEs) and state prediction errors (SPEs) are two metrics that characterize dopamine responses by the delivery of a reward and the type of reward, respectively. While both RPEs and SPEs have been identified and studied in previous literature, they have yet to be clearly separated from one another. Our study hopes to isolate RPEs and SPEs by introducing stimuli that are not tied to a reward but vary in time and type. To understand how a person's neurological response reacts to a change in state, dissociated with a reward, we developed a computer program to test this type-time relationship. Throughout this computer-simulated "journey", non-consequential events vary to create dissonance between predicted and occurring states. While this study is intended to utilize functional magnetic resonance imaging (fMRI) to characterize dopamine responses, current preliminary conclusions were drawn from purely behavioral results: namely, reaction time to "capture" a photo along the journey and to collect the reward. Using MATLAB and Microsoft Excel for analysis, we found no significant relationship (Œ± > 0.05) between mean reaction times when type or time of states is altered. However, there is much to explore still when adding fMRI and voltammetry data collection in future works.

Mentor(s): Read Montague (Biomedical Engineering and Mechanics, Virginia Tech)

James Mullet
Virginia Tech/Biological Sciences

mobileOGs-pl v. kyanite MGE Pipeline: tool for classifying bacterial mobile genetic elements

mobileOGs-db v. beatrix is a comprehensive manually annotated database of protein families (n=5,696) necessary to the life cycle of bacterial mobile genetic elements (MGEs). MGEs consist of many diverse elements that can transfer genetic material between or within various host genomes. Importantly, MGEs are key vehicles for horizontal gene transfer and are therefore crucial in spreading antibiotic resistance genes. mobileOGs-db allows for the recognition of many unique MGEs in an intuitive and easily interpretable way. This paper presents mobileOGs-pl v. kyanite, an MGE bioinformatics pipeline that attempts to isolate, identify, and characterize circular contigs consisting of MGEs from large datasets. mobileOGs-pl first identifies open reading frames in genomic fragments and then aligns full-length protein sequences with mobileOG-db. The aligned contigs are filtered, and the patterns of hits are evaluated to classify potential MGEs based on the number of hits to the database and the percent of hits from several distinct MGE categories. The pipeline was honed using control datasets of phage and plasmid sequences by evaluating various different alignment and filtering parameters. Finally, the tool provided putative classifications for a collection of wastewater metagenome-derived circular contigs of unknown classes. The results demonstrated that this pipeline classifies approximately 91.5% of plasmids and 98.7% of bacteriophages. This experiment illustrates that the MGE database and its associated v. kyanite pipeline are effective tools for detecting a wide array of MGEs.

Mentor(s): Amy Pruden (Civil and Environmental Engineering, Virginia Tech)
Mark Edwards (Civil and Environmental Engineering, Virginia Tech)

Natalie Murphy
Virginia Tech/Biochemistry

Spatial Variability of Microbial Metabolism in Mining-Impacted and Reference Streams

Headwater streams are geomorphically complex and biologically diverse. Mining legacies can impact stream form and function for decades, potentially changing the morphology, chemistry, and biological communities found in mining-impacted streams. While most streams have high rates of microbial carbon respiration, iron oxidizing bacteria commonly populate mining-impacted streams, adding metabolic activity of biogeochemical interest. This project tested the potential effects of mining legacies on microbial metabolism of different carbon substrates in streams. To characterize microbial functional diversity, water and sediment samples were collected at sites along a mining-impacted stream and reference stream near Blacksburg, Virginia. We also measured pH at each site. Water and diluted sediment samples from four sampling trips were added to EcoPlates containing 31 carbon substrates and a control in individual wells. Plates changed color from a metabolic tracer, and color change was quantified by absorbance. Across all sites (mining and reference) metabolic enzyme diversity, represented by a Shannon Diversity Index, was more positively related to microbial metabolism in water (R2 = 0.82) than sediment (R2 = 0.37) samples, suggesting different enzyme types dominate in the respective habitats. Microbial metabolism was not significantly different between the reference (med=0.0036 AU/h) and mining-impacted (med=0.0032 AU/h) stream. Additionally, no changes were detected in microbial metabolism in response to shifts in pH with time. Contrary to expectations, we found no significant differences in diversity and microbial metabolism between the mining-impacted and reference streams. Ongoing work seeks to compare environmental, hydrologic, and microbial functional variability across sites.

Mentor(s): Erin Hotchkiss (Biological Sciences, Virginia Tech)

Danya Nahas
Virginia Tech/Chemistry

Optimizing CO Oxidation Over Copper Single Atom Catalysts Supported by the Metal-Organic Framework, UiO-66

Metal-organic frameworks (MOFs) have been investigated previously as supports for heterogenous catalysts, owing to their permanent porosity and subsequent ultrahigh surface area, and tunability at both the nodes and linkers. MOFs are an inorganic-organic hybrid class of materials composed of metal oxide nodes connected by organic linkers. However, recent studies have shown the potential for the MOF to act not only as a support, but as a vital component for heterogeneous catalysis of gas phase reactions. For the work discussed here, the zirconium-based MOF, UiO-66, was synthesized with intentional missing linker defects, allowing for the coordination of single atoms of Cu. This material, Cu@UiO-66, was developed as a candidate for the destruction of chemical warfare agents (CWAs). Determining the ability of single atom metal-MOF based catalysts to oxidize small gas-phase compounds was assessed by using a simple and well-understood reaction, the oxidation of CO. Cu@UiO-66 was added to a packed bed ambient flow cell reactor with a feed gas composition of 1% CO, 10% O2, and 89% He at a total flow rate of 100 sccm. Under these conditions, a CO conversion of 4.5% was achieved. Previous literature suggests that CO conversion to CO2 over these materials should reach a steady-state conversion of around 57%, well above that found in the current study. Continued research shows that total flow rate, loading of sample, and feed gas composition, have a large effect on the rate of CO conversion to CO2.

Mentor(s): John Morris (Chemistry, Virginia Tech)

Yolanda Odufuwa
Beloit College/Political Science and Critical Identity Studies

Black Resistance In The Contemporary Era and Approaches to Ending State Violence

In 2013, Black activists Patrice Cullors, Alicia Garza, and Opal Tometi created the hashtag #BlackLivesMatter to call attention to state-sponsored violence and police brutality. The evolution of Black Lives Matter into a decentralized organization with multiple chapters across the country has advanced efforts in recent years to include the issue of state violence into popular political discourse. However, the implementation of demands from grassroots organizations and activists in the larger movement for Black lives remain unaddressed or fundamentally misunderstood. This project focuses on Black resistance to state-sanctioned violence and the causes for misrepresentation and co-optation. My research question: To what extent has the commodification, exploitation, and misrepresentation of Black resistance in the contemporary era quelled activism and political goals in relation to ending state violence in the United States? Aims to add to the current existing scholarly work that suggests U.S. political institutions continue to fail in reducing police violence. My methodologies included case analysis and surveying. The survey was advertised amongst organizers, academics, and social justice-oriented students. Using multiple-choice and open-ended questions, I learned what they believe to be significant political goals of the movement for Black lives, impacts of commodification, and whether current proposed legislation adequately addresses police violence. Early results showed 75% of respondents partially or strongly disagreed that if adopted, the George Floyd Justice in Policing Act adequately addresses police violence. Commodification, misrepresentation, and exploitation threaten to undermine activism and advance the political goals like defunding the police, needed to reduce and end state violence.

Mentor(s): Brandy Faulkner (Political Science, Virginia Tech)

Hana Olof
Hollins University/Biology

The Influence of Suspect Familiarity on Cross Race Effect

This project aims to investigate the cross-race effect (CRE) and its interaction with familiarity for eyewitnesses. Mistaken eyewitness identifications contributed to 69% of the more than 375 wrongful convictions in the United States, most of which are DNA exonerations (Innocence Project, 2021). From the DNA exoneration cases, 66.4% included African Americans as the falsely identified suspects (Wells, 2020). Such misidentifications are accounted to CRE, which occurs when individuals are better at recognizing other individuals of their own race compared to other races (Meissner & Brigham, 2001). The studies conducted on CRE so far have been on unfamiliar suspects. Although memory is generally worse for unfamiliar than familiar faces (Johnston & Edwards, 2009), there is some evidence indicating that individuals have more difficulty with remembering the source of their memory for familiar other race-faces (Horry & Wright, 2008; Pezdek & Stolzenberg, 2014). However, previous researchers did not use lineups and familiarity was not tightly controlled. Thus, the purpose of this study was to examine the effect of suspect familiarity on CRE using an eyewitness paradigm. Participants (N= 988) studied several other-race and same-race faces and then later tested using simultaneous lineups where the suspect was either Black or White, familiar (seen at the study) or unfamiliar (new) and guilty or innocent. Results obtained thus far show a CRE for familiar suspects but not for unfamiliar suspects. In addition, the confidence-accuracy relationship was harmed when a familiar Black suspect was present in a lineup, resulting in overconfidence.

Mentor(s): Alex Wooten (Psychology Department, Hollins University)

Mary Oster
Juniata College/Biochemistry

TOUR

Ultra Processed Foods and Eating Behavior Reinforcement

The increase in the number of individuals with obesity corresponds to increased access to ultra processed foods; currently, half of American food intake is estimated as coming from foods containing heavily refined ingredients. Data from the drugs of abuse literature shows drugs that reach the brain quickly have a higher potential for reinforcement and abuse. Post-ingestive signals communicating information about the nutritive values of foods are key in the reinforcement of eating behaviors. The consumption of foods made of refined and easily digested ingredients may release nutrients more rapidly than less refined foods leading to a more rapid brain response, a potential mechanism for their overconsumption and increased rewarding value. To understand how ultra processed foods manipulate these post-ingestive signals to influence future eating behaviors, a test of the differential nutrient release in ultra processed and minimally processed foods is needed. Carbohydrate oxidation, as a measure of nutrient release will be measured in future studies, using nutrient paired snack meals representing the two processing groups. Indirect calorimetry protocols are currently being piloted using both hood and whole room "flex" calorimeters which allow for measurement of carbohydrate oxidation in human volunteers.

Mentor(s): Alexandra DiFeliceantonio (HNFE, CHBR)
Mary Baugh (FBRI, Virginia Tech)

Annabelle Owens
Virginia Tech/Microbiology

Characterization and engineering of bacteriophages in microbial communities

Antibiotics are necessary life-saving drugs, but the increasing prevalence of antibiotic resistance is an issue of growing urgency. Therefore, it is imperative to investigate other mechanisms of countering pathogens. One potential approach is the attenuation of bacterial virulence factors. Recent work towards this goal has explored the use of temperate phage, which is able to lysogenize a bacterial host by inserting its genome within the bacterial chromosome. The use of this phage characteristic allows the introduction of new genes even in traditionally challenging environments such as the mammalian gut. This project aims to treat an enteric infection of Salmonella enterica serovar Typhimurium by engineering its temperate phage, P22, to specifically inhibit transcription of virulence genes using dCas9 and guide RNAs (gRNAs). The first step of this process is to identify nonessential genomic regions of P22 genome that can accommodate the insertion of genes coding for dCas9-gRNA complex without impairing phage function. P22 genomic regions termed B (from eaC to eaE) and C (from ninA to ninH), previously annotated as nonessential for lysogeny, were deleted. The lysogeny of these deletion strains were assessed both in vitro and in vivo. ŒîC expressed high lysogeny both in vitro and in vivo. However, ŒîB lysogeny was impaired in vitro. Currently, the double deletion strain P22 ŒîBC is being constructed and its lysogeny will be investigated in vitro and in vivo. If the P22 ŒîBC deletion strain proves to have a high percentage of lysogeny, the phage will be engineered to encode a dCas9-gRNAs complex.

Mentor(s): Bryan Hsu (Department of Biological Sciences, Virginia Tech)

Neel Patel
Virginia Tech/Computer Science
Amelia Whitehead
Virginia Tech/Computer Science
Madeline Shaklee
University of Massachusetts - Dartmouth/Biology

Using Clustering Algorithms to Identify Steady States in Gene Regulatory Networks

This project investigated Gene Regulatory Networks (GRNs), which are the set of interactions between genes that turn each other on and off. The project evaluated gene expression data to find steady states, i.e., periodic states in a GRN that the system does not leave once it reaches them. Developing ways to identify steady states of GRNs from simulated expression data is critical to further understanding gene expression and cellular function. Our specific goal is to examine if the simulated expression data obtained from BoolODE contains steady states that correspond to those of the GRN. The gene expression data came from BoolODE, a previously published method that models gene interactions with differential equations and simulates how much each gene is expressed at each time point. We used two clustering techniques to analyze the simulated gene expression data produced by BoolODE. The techniques search for clusters in the expression data which could represent the steady states of the GRN. The two techniques we used were k-means and DBSCAN. DBSCAN has the advantage of automatically detecting the number of clusters and discarding outliers. We pursued DBSCAN for its ability to cluster data of high dimensions and find the correct number of clusters without trying and evaluating several numbers of clusters. The result of this project is the successful application of the DBSCAN algorithm to obtain the correct number of steady states for five out of six simple toy networks and all four complex toy networks.

Mentor(s): T. M. Murali (Computer Science, Virginia Tech)

Shannon Pollock
Virginia Tech/Biochemistry

Evolutionary Precursors to Sulfate Reduction Enzymes in Methanogens: Constructs for Complex Isolation

Methanogenesis and sulfate reduction, two of the most ancient respiratory metabolisms of Earth, apparently cannot co-exist, as sulfite, an intermediate of sulfate reduction, impedes methanogenesis. However, homologs of sulfate activation and reduction genes are present in methanogens despite their inability to use sulfate as a sulfur source. Additionally, they evolved before the oxygenation of Earth, so they did not originally encounter sulfate. Therefore, these homologs likely provide a fundamental function that is unlinked to sulfate reduction in methanogens but eventually evolved to provide the sulfate reduction system elsewhere. Attempts to understand the function of these genes in a recombinant E. coli model have been inconclusive. A better approach would be to study the respective proteins isolated directly from a methanogen because it will cover the possibilities that these form complexes with other proteins and methanogen-specific cofactors. Accordingly, we are analyzing this system in Methanocaldococcus jannaschii (Mj) because this ancient methanogen lives in deep-sea hydrothermal vents, which are considered to be analogous to early Earth. Leveraging a genetic system developed recently in our laboratory, we have modified each targeted gene in Mj for producing the respective protein product with an N-terminal 3X-Flag-2X-Strep-tag, allowing facile isolation via tandem affinity purification (TAP). We will determine if the purified products contain partnering proteins and bound cofactors, and with this information, we will develop and test hypotheses about the functions of these putative sulfate reduction genes. More broadly, the results will provide insights into the evolution of life on Earth and potential life elsewhere.

Mentor(s): Biswarup Mukhopadhyay (Biochemistry, Virginia Tech)

Julia Post
Virginia Tech/Biological Systems Engineering
Peter O'Brien
University of Maine, Orono/Economics
Alayna Carter
Radford University/Biology
Rannd Bohnert
Radford University/Geospatial/Env

Stormwater Infrastructure Impacts on Water Quality in Urban Streams

Stormwater management, and the associated infrastructure, have critical implications for watershed health. Stormwater runoff can carry harmful pollutants from fertilizers, litter, trash, animal waste, and petroleum products into water bodies. Our objective was to identify how several varieties of stormwater management infrastructure impact water conductivity and total dissolved solids (TDS) in urban streams located in multiple basins across different ecoregions. Establishing baseline conductivity levels and TDS concentrations for water bodies is important because sudden changes in these indicators can indicate local pollution discharge. We directly measured conductivity and TDS over a period of several weeks, both upstream and downstream of four individual stormwater infrastructure types in four distinctly different watersheds. The types of stormwater infrastructure studied were retention ponds, culverts %26 buried streams, combined sewer overflow discharge points (CSO), and stormwater drainage pipes. Compiled data were analyzed to determine the severity with which different stormwater infrastructure types impact water conductivity and TDS, in particular during peak runoff events. On average, we observed that conductivity levels and TDS concentrations increased downstream of CSO outfalls and stormwater discharge pipes increased after heavy runoff events (e.g. post-heavy rainfall). In contrast, our results suggest that retention ponds reduce downstream conductivity and TDS levels during peak flow events, and these results were also observed downstream of buried stream segments. These results help to shed light on the ways in which differing approaches to stormwater management can influence the effect of stormwater runoff on watershed health.

Mentor(s): Cully Hession (Department of Biological Systems Engineering, Virginia Tech)
Leigh-Anne Krometis (Department of Biological Systems Engineering, Virginia Tech)
Brian Badgley (School of Plant and Environmental Sciences, Virginia Tech)
Erin Ling (Department of Biological Systems Engineering, Virginia Tech)

Nadia Qutob
Georgia Institute of Technology/Physics

Heavenly Rays Illuminate Our Darkest Of Matter: Understanding Particle Physics of Dark Matter Through Cosmic Ray Dark Matter Interactions

Despite being the most abundant form of matter in the cosmos, Dark Matter remains one of the galaxy's most perplexing enigmas. Both Dark Matter (DM) and Neutrinos present a tremendous gap in the standard model and thus our understanding of physics, therefore it may be possible that they may originate from the same source. As we have very little definitive proof about the physical properties of DM beyond gravitational impact, we should not necessarily assume that it possesses the same behavioral characteristics of normal matter. Particularly, the ratio of the rate at which DM protons and neutrons absorb energy deposited by charged particles such as Cosmic Rays may be different than that of normal matter and more similar to that of Neutrinos. Through theoretical calculations based on data gathered by the Xenon 1 Ton experiment and Bringmann and Pospelov's research, we can evaluate at what ratios of proton-neutron energy deposition from Cosmic Rays our current model for understanding DM breaks down. This factor may change the physics of how Dark Matter scatters within a physical detector and thus reshape our understanding of DM direct detection. Comprehending Dark Matter is an imperative step in understanding the physics of gravity and galaxies; hence devising a means of efficiently observing DM particles through direct detection is a crucial step to the progression of astrophysics as a whole.

Mentor(s): Ian Shoemaker (Physics, Virginia Tech)

Yusuf Rafiqzad
Virginia Tech/Clinical Neuroscience

BBB leakage causes an atypical neuronal phenotype after early mTBI

In the United States, around 1.7-3.8 million cases of traumatic brain injuries (TBI) occur each year, the majority of which are classified as mild TBI (mTBI). Currently, there is no treatment to prevent the cascade of events leading to post-concussive symptoms, making the understanding of the cellular mechanisms following TBI crucial. Previous studies in our lab have shown that blood-brain barrier (BBB) disruption after mTBI induces an atypical astrocyte phenotype, characterized by the downregulation of astrocytic proteins important for brain homeostasis, such as glutamate transporter-1 (Glt-1). Within the areas of atypical astrocytes, a downregulation of the neuronal marker NeuN was also present, suggesting that the blood-borne factors may induce a similar phenotype in neurons. To further investigate the phenotype of neurons present in areas of BBB leakage, we analyzed the expression of two distinct proteins in neurons, Parvalbumin (PV) and CamKII at early time points using an mTBI mouse model, immunohistochemistry, and confocal microscopy. A dysfunction in PV+ or CamKII+ neurons may create an imbalance of excitatory and inhibitory neurons, increasing susceptibility to neurological disorders. Upon analysis, a change in PV and CamKII expression between Sham and TBI mice was found, however some TBI mice showed little to no change in protein expression. The data suggests that an atypical neuronal phenotype is possible within areas of leakage however the impact of the blood-borne factors on neuronal functions needs to be further investigated.

Mentor(s): Stefanie Robel (School of Neuroscience, Virginia Tech)

Samantha Reitz
Radford University/Physics and Chemistry

Analyzing systematic trends in cosmic SFR evolution

New star formation rate (SFR) density measurements (from 2006 to current) were recorded into a database in order to study systematic trends in cosmic SFR evolution in Mathematica. Over 200 SFR densities were recorded along with other types of information provided by authors such as redshift, cosmological assumptions, extinction methods, types of indicators, standard calibration factors (metalicity and initial mass function, IMF), active galactic nuclei (AGNs) contamination, and statistical and systematic errors. We specifically made three different log plots to investigate the impacts of different types of indicators, extinction methods, and IMF. Then, the results were compared with Hopkin, and Beacom, SFR density database from 2006 to either prove or deny systematic shifts in SFR density measurements. Proving the robustness of SFR density measurements can support accurate predictions of the diffuse supernova neutrino background (DSNB), which in turn will help experimentalists to have a good target to build future experiments around.

Mentor(s): Shunsaku Horiuchi (Physics, Virginia Tech)

Divinity Richardson
Virginia Wesleyan University/Earth and Environmental Science

MAOP

Frost Ring Impact in Two Species of Pine

Jack pine (Pinus banksiana) and eastern white pine (Pinus strobus) are economically important timber species. Jack pine grows further north and often germinates after fire, while eastern white pine has a more southerly range and prefers cool, humid climates. Both species form frost rings when sub-freezing temperatures damage under-lignified xylem cells. The presence of frost rings reduces the strength of lumber. The objectives of this study were to: 1) Quantify the frequency of frost ring formation in jack pine and eastern white pine by calendar year and 2) Quantify the frequency of frost ring formation in jack pine and eastern white pine by tree age. As a secondary objective, we will be able to compare frost ring formation at northern latitudes (jack pine) with southern latitudes (eastern white pine). At each study site, we collected cores from 20 trees using an increment borer. In the laboratory, we sanded the cores so that we could see the cells and dated the annual rings under a microscope. Within each year, we recorded frost ring presence or absence. Both jack pine and eastern white pine formed frost rings, but the northern samples of jack pine had a substantially higher frequency of frost ring formation. Tree age was more important than calendar year in determining frost ring frequency, with younger trees having a higher frequency of frost rings. Given the relationship between frost rings and decreased wood strength, southern pines are more likely to have uniform strength properties.

Mentor(s): Carolyn Copenheaver (Forest Resources and Environmental Conservation, Virginia Tech)

Kelly Richardson
Virginia Tech/Engineering Science and Mechanics

Effect of anode and cathode luminous sensitivity on photomultiplier tube readings for use in the CHANDLER neutrino detector

In addition to their uses in scientific research, neutrino detectors can be used to monitor nuclear reactor contents from outside and without any prior knowledge of its contents. Building neutrino detectors for this purpose requires developing standards for each component. The MiniCHANDLER detector is designed to use 80 R6231-100 Hamamatsu photomultiplier tubes (PMTs), divided evenly across two faces. Since the PMTs are responsible for converting the light from the scintillators into electrical pulses, knowing how they operate in the detector individually and relative to each other is imperative to knowing how the detector will work as a whole. Hamamatsu provides the cathode luminous sensitivity (CLS) and anode luminous sensitivity (ALS) for each PMT; however, these were measured using a brighter source than the light produced in the scintillators from inverse beta decay. This study examines the correlation between ALS and average pulse height, as well as CLS and the standard deviation of the pulse height distribution using a light source more similar to the light in the detector. We did this by testing four PMTs at a time with different ALS and CLS over a range of voltages using an LED flasher designed to mimic the flashes seen in the scintillator. We found that we can use ALS to predict pulse height and CLS to predict RMS. Therefore, we can use ALS and CLS to set standards on what PMTs we should use in the final detector and calibrate the PMTs in the detector accordingly.

Mentor(s): Jonathan Link (Physics, Virginia Tech)

Kayla Richardson
Hollins University/Political Science

Catholic Social Thought and the Free Market

In this paper, we focus on finding the moral intersections between Catholic social thought and free market theory. While the Catholic Church does not endorse socialism, it does not accept the free market in its totality; our mission is not only to find where the Church, and the free market, morals collide, but to also determine what economic model the Church would like to see within society and if this model could work. To obtain this information, we examine various papal encyclicals, economic morals within the bible, writings on the social teachings of the church, and then proceed to investigate the thoughts of numerous economists and economic theories.

Mentor(s): Edward Lynch (Global Politics and Society, Hollins University)

Jah'Shawn Ross
North Carolina Central University/Physics

Designing Data Read Out Electronics for the CHANDLER Neutrino Detector

CHANDLER is a reactor neutrino detector technology with potential applications in nuclear security, nuclear instrumentation, and basic technology. In 2017 a prototype of CHANDLER named MiniCHANDLER was deployed at North Anna Nuclear Generating Station, where it demonstrated the detection of reactor neutrinos. Since this deployment, the CHANDLER collaboration has been working to make improvements. One of the many improvements that are being made to MiniCHANDLER is the readout electronics. The old electronics were based on a shaper circuit, single-ended input of the photomultiplier tubes (PMT) signals, and a digitizer with a 12-bit analog to digital converter (ADC). The old electronics were not able to effectively measure higher energy neutron proton recoils, there was cross-talk between neighboring channels, and high energy pulses would lead to a large oscillation of the baseline. In the new electronics, there is improved dynamic range and no cross-talk. The new electronics consist of a custom all-in-one base that will digitize and process the PMTs signals as well as provide the high voltage. This all-in-one base is based on a field programmable gate array, which allows coding capabilities that were not present in the previous electronics. This summer, to improve the trigger algorithm, a new running baseline code was made. This running baseline takes an average of previous ADC counts and accounts for baseline fluctuations. Having this new baseline potentially allows for a more precise online separation of neutrons and gammas in the FPGA. Once these electronics are fully assembled testing will take place.

Mentor(s): Jonathan Link (Department of Physics, Virginia Tech)

Nicholas Russell
Virginia Tech/Cognitive and Behavioral Neuroscience

Quantifying Endocannabinoid Levels in the Nucleus Accumbens Shell Using In Vivo Microdialysis

Endogenous cannabinoids, otherwise known as endocannabinoids (eCBs), have similar effects as cannabinoids found in recreational drugs like Tetrahydrocannabinol (THC) and Cannabidiol (CBD). These naturally occurring molecules are produced in the brain and bind to the same receptors: Cannabinoid receptor type 1 (CB1r) in the central nervous system and type 2 (CB2r) in the periphery. CB1r is a major inhibitory receptor in the brain, using retrograde signaling to prevent synaptic vesicle release. Since CB1r plays a role in numerous pathways in the brain including the reward pathway, understanding how eCB levels in the extracellular space are altered by drugs of abuse is critical. Despite their importance, not many papers have been published about eCB levels present in the extracellular space. Due to eCBs being present in very small concentrations in the extracellular space (in the attomole to femtomole range), previous methods took weeks to months to accurately measure eCB levels. Our aim is to shorten current methods while maintaining accuracy by matching to known, baseline levels. To measure eCBs in the extracellular space, we used in vivo microdialysis to collect dialysate samples by implanting probes into the brain region known as the Nucleus Accumbens (NAc) shell in mice. Samples were collected at 15-minute intervals for 6 hours. Endocannabinoids were extracted from the dialysate and then analyzed using liquid chromatography-mass spectrometry. By establishing a quicker method to measure eCB extracellular levels, more efficient studies can be conducted on how different drugs impact eCB extracellular levels.

Mentor(s): Matthew Buczynski (School of Neuroscience, Virginia Tech)

Helen Salko
Virginia Polytechnic Institute and State University/Water: Resources, Policy, and Management

Evaluating Zinc Orthophosphate's Ability to Control Lead Solder Corrosion in Corrosive Drinking Waters

In many U.S. source waters, chloride levels are increasing due to road salting practices and sulfate levels are declining due to federal regulations on sulfur emissions. Water utilities are thus seeing increases in chloride-to-sulfate mass ratios (CSMRs), which affects the corrosivity of water, and are struggling to control lead levels in drinking water systems--a serious economic and public health challenge. Lead-based solder in plumbing, a major source of lead in drinking water, is particularly susceptible to the CSMR. Zinc orthophosphate, a chemical corrosion inhibitor, has been able to reduce lead levels substantially in areas with high CSMRs like Brick, NJ but has failed in others. This study aims to determine the performance and longevity of the effectiveness of this inhibitor at reducing lead levels in highly corrosive water conditions.

This study tested 48 water conditions with three alkalinities (20, 60, and 180 mg/L CaCO3), 3 corrosion inhibitors (zinc, orthophosphate, and zinc orthophosphate), and 4 CSMRs (0.5, 1.5, 5, and 10). 144 jars containing simulated lead solder and copper pipe connections underwent electrochemical, lead release, pH, and metal weight loss measurements for over 133 days. Preliminary data shows that CSMR has a greater impact on lead release than alkalinity and zinc orthophosphate appears to be beneficial in high alkalinity waters, especially the CSMR=10 case where lead levels dropped from their peak at 1500 ppb to 810 ppb (46%) in 100 days. This work will help water utilities optimize their corrosion control even as water chemistries change.

Mentor(s): Marc Edwards (Environmental and Water Resources Engineering, Virginia Tech)

Samantha San
Virginia Tech/Biological Systems Engineering

SURF

Sensitive and visual detection of HIV-1 DNA using CRISPR-assisted lateral flow assay

Human immunodeficiency virus (HIV) causes acquired immunodeficiency syndrome (AIDS) which disrupts the body's immune response and can lead to death by opportunistic infection and cancer. Currently, there is no cure for HIV, but early diagnostics can reduce mortality rates and prevent further transmission. The current technologies to detect HIV rely on immunoassays and nucleic acid-based methods. These methods are also time-consuming and require costly instruments that are difficult to use. In this study, we developed a sensitive and accessible technique for the detection of synthetic HIV-1 DNA for point-of-care (POC) application. A lateral flow assay enhanced enzymatically using horseradish peroxidase (HRP) is constructed for more sensitive colorimetric detection. The cleavage of the crosslinker by the activated CRISPR-Cas12a complex represents a positive test result as the probes on the capture line and particles cannot hybridize. We expect to detect down to 1 nM of synthetic HIV-1 target DNA without amplification. The use of sample amplification techniques can lower the detection threshold of this method. The further development of this method can increase the accessibility of nucleic acid detection of HIV-1, improving the livelihoods of people infected.

Mentor(s): Juhong Chen (Virginia Tech)

Kendall Sanders
Hollins University/Sociology

The Socially Dead: an analysis of museums, identity, and the African diaspora

This article seeks to show how museums as an institution perpetuate the dehumanization of Black people throughout the African diaspora. I examine the ways exhibits are curated, along with who constructs them and what narratives are put on display. Repatriation is a controversial topic as the public realizes the importance of original ownership; though, many are more concerned with the allure of museums and private collections. Taking into account the current political state of Black peoples, I highlight the repatriation of African peoples and artifacts through theoretical frameworks such as Afro-pessimism and Critical Race Theory. I use Critical Race Theory to explain the institutionalization of racism in America and its parallels globally and Afro-Pessimism to explore the root of the mistreatment of Black people as a whole. I compare types of repatriation (people vs. artifacts and human remains). Further, I analyze museums that chose to tell the story of another culture (The Africa Museum of Tervuren, Belgium) compared to those who collaborated and allowed the culture of focus to control their narrative (Robben Island of the South Africa Museum). My research found that in instances of outside narrative control the source communities felt, as do I, that their history was trapped in a past that was unchanging while collaborative exhibits showed a complex understanding that fueled discussions and a critical understanding of the issues presented.

Mentor(s): Ashleigh Breske (Global Politics and Socities, Hollins University)

Kevin Sanford
University of California – Santa Cruz/Physics

Studies of Proton Structure from Photo- and Electro-Production of Light Vector Mesons

The analysis of light vector meson production by a high-energy electron or photon beam in a particle accelerator provides insight into the composition of the proton, further expanding the fundamental understanding of physics. The electro-production of light vector mesons off of protons happens when a high virtuality photon interacts with a quark, which can be studied to extract the Generalized Parton Distributions (GPDs). These functions provide access to the correlation between the longitudinal momenta of partons and their transverse position. They can be further interpreted to obtain multidimensional images of the proton. Vector mesons are particularly sensitive to the GPDs H and E and allow for flavor decomposition of the proton's GPDs. We implemented the rho vector meson ρ(770) in a generator used in simulations for Jefferson Laboratory (DEEPGen) and for EIC (DEEPSim). Our goal is to contribute to the development of future Hard Exclusive (light) Vector Meson experiments for Jefferson Laboratory and EIC. We will discuss the physical interest of measuring light vector mesons for accessing GPDs, then present our work with the event generator and our projections for future experiments.

Mentor(s): Marie Boër (Physics, Virginia Tech)

Shirin Sayani
Virginia Tech/Biochemistry

Nitrogen Dosage Response Study of Various Strawberry Cultivars: Preliminary Findings

Proper nitrogen dosage is a key component towards ensuring quality crop plant and fruit harvest. Currently, there is little known about nitrogen needs of the different strawberry varieties. As such, commercial growers in the south and mid-Atlantic region of the U.S. rely on findings from a single study that recommends 60 lb/acre of preplant nitrogen for the Chandler variety though they grow many other newer cultivars. The purpose of this study was to gather preliminary data on optimal preplant concentration of nitrogen fertilizer for various strawberry cultivars and advanced germplasm. In this non-replicated trial, strawberry plants were treated with five different nitrogen concentrations, 0, 30, 45, 60, and 75 lb/acre applied at the time of making beds. Five cultivars, Chandler, Camarosa, Festival, Merced, Ruby June, and three advanced germplasms, 146T54, 1240, and 143T35 were transplanted in early October. In the following spring season, an additional 7 lb/acre/week of nitrogen was applied through drip irrigation to a total of 55 lb nitrogen/acre. Fruits were harvested twice per week, categorized into marketable and non-marketable fruits, and weighed. During this period, fruit size, firmness, total soluble solids (TSS), and pH of fruit from each treatment and cultivar were also recorded once a week. Data collected reveals that the various cultivars differed in their response to the different nitrogen rates pertaining to factors such as size, firmness, pH, and TSS; however, the 60 lb and 75 lb rates seem to result in the highest marketable yield per plant.

Mentor(s): Jayesh Samtani (Hampton Roads Agricultural Research and Extension Center, School of Plant and Environmental Sciences, Virginia Tech)

Tyler Schroeder
College of William and Mary/Physics and Mathematics

Simulating the hard exclusive production of heavy mesons to access proton GPDs

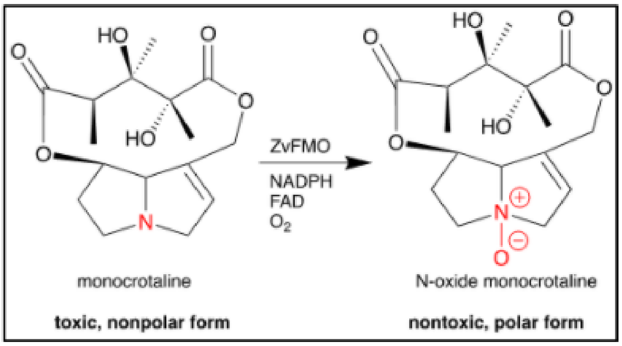
Heavy meson production is a key tool for accessing the inner dynamics of the proton. These production reactions involve the proton Generalized Parton Distributions (GPDs), which correlate the longitudinal momenta and their transverse distribution of the proton's composite partons. The hard exclusive production of Quarkonia (J/psi, Upsilon, etc.) is particularly interesting, as it accesses the gluon GPDs at the lowest order. We used ROOT to create a new flexible generator for the photoproduction, quasi-photoproduction, and electroproduction of vector mesons off a proton, with specific focus on the production of J/psi and Upsilon mesons. The output phase space is weighted by the reaction cross-section, creating a realistic graph of event count as a function of energy. We will discuss the relevance of measuring hard exclusive production of Quarkonia, present our work on the event generator, and discuss our projections for the upcoming Electron-Ion Collider (EIC).

Mentor(s): Marie Boër (Physics, Virginia Tech)

Starlina Shepard
Virginia Tech/Clinical Neuroscience

Identification of a Key Residue in the NADPH Binding site in a Flavin-Dependent Monooxygenase from Zonocerus variegatus (ZvFMO)

Zonocerus variegatus or the painted grasshopper is a major agricultural pest in Central and Western Africa because it has evolved a counterstrategy against the toxic pyrrolizidine alkaloids; plant toxins that act as chemical defense against herbivores. This new-found resistance amounts to several hundreds of millions of dollars in crop damage annually. The mechanism of resistance involves nitrogen oxidation, performed by the flavin-dependent monooxygenase, ZvFMO, which renders the pyrrolizidine alkaloids non-toxic. ZvFMO catalyzes the addition of one oxygen atom into a substrate with the help of the cofactors: nicotinamide adenine dinucleotide phosphate (NADPH) and flavin adenine dinucleotide (FAD). In this work, we have analyzed the involvement of a noncanonical lysine residue predicted to be involved in NADPH binding by using site-directed mutagenesis, steady-state, and rapid-rate kinetics. We successfully performed site-directed mutagenesis to substitute the lysine of interest to both arginine (K215R), and alanine (K215A). Additionally, we have recombinantly expressed and purified these mutants from *Escherichia coli* then compared the kinetic parameters for both mutants to the wild-type values. For the steady-state kinetics, we have determined the Km values and found that the K215R and K215A mutants have a lower affinity for the NADPH than the wild-type. Based on this analysis, we can confirm that this residue is important in the binding of NADPH. This work lays the groundwork for further biochemical characterization of a unique NADPH binding site, which will expand our knowledge on flavin-dependent monooxygenases as well as aiding in the design of inhibitors against ZvFMO.



Scheme 1: Reaction catalyzed by the enzyme ZvFMO.

Mentor(s): Pablo Sobrado (Biochemistry, Virginia Tech)

Benjamin Siedlarz
Virginia Tech/Nanomedicine

MOLVIS

Relevance of per2 in Tumor Suppression

The ability of Metazoan cells to identify, repair, and halt the replication of DNA damage is strongly correlated to the prevention of tumorigenesis. As a defense, cells employ rhythmic proteins such as per2 that indirectly regulate metabolism and progression through stress response reactions carried out by various post-translational events. Recent studies suggest that the cellular localization of per2 affects its function and thus its tumor suppressing capabilities. To better understand the relevance of per2 in DNA damage response, we examined the effect of various site-specific single nucleotide polymorphisms (SNPs) and insertion/deletion polymorphism (indels) on per2 localization in a non-cancerous embryonic mouse fibroblast cell line (NIH 3T3) via plasmid transfection with fluorescent microscopy. Following gamma radiation, transgene hper2 wt was seen to localize in the nucleus, while mutants with altered phosphorylation sites along the casein kinase I isoform epsilon (CSNK1E) and deletions in the Per-Arnt-Sim (PAS) binding domains exhibited perinuclear/cytosolic localization after the DNA damage stress response.

Mentor(s): Carla Finkielstein (Molecular Diagnostics Laboratory, VT Cancer research group, Virginia Tech)

Kyndall Sirmons
Florida A&M University/Biology/Pre-med

Production and properties of pure bacterial cellulose and surface-acetylated bacterial cellulose

Bacterial cellulose is an organic material that is produced by several species of bacteria, the most common being Komagataeibacter xylinus. The unique physical structure of bacterial cellulose gives it a greater water holding capacity and higher durability compared to plant cellulose. These properties in turn make bacterial cellulose an ideal candidate for application in the biomedical field. This project produces bacterial cellulose and then chemically modifies the surface of the bacterial cellulose through acetylation. This project seeks to determine the potential of surface-acetylated bacterial cellulose to be used as a material for a new antimicrobial wound dressing.
The bacterial cellulose is grown in Hestrin-Schramm media using petri dishes sized 100x15mm. The bacteria cultures are incubated at 28 degrees Celsius for 7 days. Once grown the cellulose is purified through a series of base and water washes. Then the surface of the pure bacterial cellulose is acetylated. The resulting material is then tested for antimicrobial properties using model non-pathogenic bacteria and for potential cytotoxicity using human skin cells.

Mentor(s): Maren Roman (Department of Sustainable Biomaterials, College of Natural Resources, Virginia Tech)
Timothy Bertucio (M.S. Candidate, Department of Sustainable Biomaterials, College of Natural Resources, Virginia Tech)

Emily Smith
Virginia Tech/Civil and Environmental Engineering

Copper Pipe Corrosion

High levels of dissolved copper in drinking water can result from corrosion of copper pipes and may cause aesthetic and health concerns. Water quality parameters such as pH and alkalinity have been shown to affect cuprosolvency. Contrary to the literature, preliminary results demonstrated higher cuprosolvency in copper pipe segments that contained water with low natural organic matter (NOM) at a pH of 8.1, compared the same conditions at a lower pH of 7.5. This study aims to recreate and further investigate these discrepancies with a novel cuprosolvency test protocol that uses copper particles as surrogates for copper pipe. Experiments will investigate the role of NOM in cuprosolvency using 0-2 mg/L NOM at both pH values to recreate the observed discrepancies and to facilitate comparison with previous pipe test results.

Future experiments will examine the role of sulfate in the observed discrepancies. It is hypothesized that malachite, a low solubility copper mineral, forms a protective pipe scale under the low NOM, low pH conditions tested, whereas brochantite, a more soluble copper sulfate mineral, forms in the waters with higher pH. Results of this study could demonstrate conditions where the presence of sulfate may prevent the formation of protective pipe scales. This study indicates that sulfate concentrations may warrant further consideration by residents and utilities when addressing copper problems in drinking water.

Mentor(s): Marc Edwards (Civil and Environmental Engineering, Virginia Tech)
Rebecca Kriss (Ph.D. Candidate, Civil and Environmental Engineering, Virginia Tech)

Daysha Smith
Virginia Tech/Human Development

Daily Activities and Cognition in U.S Older Adults

Purpose: A variety of everyday activities including physical exercise, cognitive engagement, and social interaction have been associated with better cognitive functioning during aging. Here we drew on the Health and Retirement Study, a nationally representative longitudinal data set of over 20,000 U.S. Older Adults, to examine which common activities may be associated with better executive function in old age.

Method: We drew our sample from 3,424 individuals who completed the Number Series Test in the 2013 wave of the Health and Retirement Study. We then ran a series of Linear Regressions using a set of 10 common activities spent hour/per week including: prayer/mediation, reading books, sports/exercise, yard work/gardening, volunteer work, playing cards/games/puzzles, singing/playing an instrument, arts and crafts, pet care, and taking care of grandchildren. We also included years of education, gender, age, and wealth in our model as covariates.

Summary of Results: Findings indicated that reading books, arts and crafts, playing cards/games/puzzles, and volunteer work were all significantly associated with better cognitive functioning, while taking care of grandchildren and pets were marginally associated with better cognitive functioning. Surprisingly, prayer and meditation were associated with lower performance on the Number Series Test. Thus, while some activities may have a straightforward positive association with better cognition during aging, others may have more nuance or indirect links. Future research should explore additional covariance and causal effects of these activities on cognition during aging.

Mentor(s): Benjamin Katz (Human Development and Family Sciences, Virginia Tech)

Sophia Sobrado
University of Virginia/Neuroscience
Norah Griggs
Blacksburg High School

Expression of circadian clock genes in mouse hepatocytes

The propensity for many physiological processes to occur in 24-hour cycles is attributed to the circadian clock. The circadian rhythm is seen in organisms across all domains of life and is responsible for regulating the sleep-wake cycle as well as many other physical and behavioral processes. The mammalian circadian rhythm is known to be driven by transcriptional-translational feedback loops consisting of core clock genes, and this machinery exists in all somatic cells. The aim of this project was to observe and compare the expression patterns of selected circadian core clock genes in AML12 and MMH-D3, mouse hepatocyte cell lines. These cell types were chosen because while the non-rhythmic nature of AML12 has been established, it remains unknown whether this is true for MMH-D3. RNA isolation and cDNA synthesis, followed by qPCR was conducted to quantify gene expression levels. We found that MMH-D3 has higher expression than AML12 of Per2 and Per2AS, two core clock genes. The expression of Per2 and Per2AS appeared rhythmic in MMH-D3 cells, although not at a statistically significant level. Overall, these studies provide important information regarding which cell types exhibit more robust rhythmic regulation of the circadian clock, although further experiments should be conducted to confirm these results. Establishing gene expression patterns as well as evidence of rhythmicity for MMH-D3 cells will benefit future projects when having to select cells for study.

Mentor(s): Shihoko Kojima (Department of Biological Sciences, Fralin Life Science Institute, Virginia Tech)

Bridget Spruill
Virginia Tech/Biology

MAOP

Molecular mechanism of Phafin2-mediated induction of autophagy

During cellular autophagy, a portion of the cytosol that contains aging organelles and long-lived proteins is taken up by a specialized organelle, the autophagosome. Autophagosomes fuse with lysosomes, where the autophagosome's contents get recycled into amino acids and metabolite degradation products. Phafin2 is a critical phosphatidylinositol 3-phosphate (PtdIns3P) binding protein that helps regulate lysosomal activity through the induction of autophagy. Phafin2 is composed of an N-terminal PH domain, a central FYVE domain, and a C-terminal polyD motif. The polyD motif contains a stretch of conserved aspartic acid residues of unknown function. Phafin2 binds to PtdIns3P through its PH or FYVE domains. Whereas the FYVE domain constitutively binds PtdIns3P, the binding of the PH domain to the lipid is autoinhibited by the polyD motif. The serine/threonine kinase AKT is a well described inhibitor of autophagy through binding of its PH domain to phosphatidylinositol 3,4,5-trisphosphate (PIP3). However, when Phafin2 is bound to lysosomal PtdIns3P, Akt is recruited to the site, consequently promoting autophagy. We propose that the Phafin2/AKT complex leads to changes in membrane shape that are important for the fusion of lysosomes with autophagosomes and consequently for the induction of autophagy. We aim to test how binding of Phafin2 to PtdIns3P monolayers cause changes in lipid packing by the use of Langmuir Trough technology. In addition, we are currently investigating if the AKT PH domain binding to PI3P is downregulated by the Phafin2 polyD motif of Phafin2 in order to block the AKT's autophagic inhibitory activity.

Mentor(s): Daniel Capelluto (Biological Sciences, Virginia Tech)

Ben Stallings
Virginia Tech/Biochemistry

The Characterization of a Potential Phosphatase Family in Plants

Phosphate (Pi) is a crucial macronutrient for plant growth and development. Plants must be able to control the amount of Pi that they take up because too much or too little can severely limit plant growth. To maintain Pi homeostasis, plants utilize prominent signaling molecules called Inositol Pyrophosphates (PP-InsPs). PP-InsPs can relay different messages in the plant, depending on the number of Pi groups they contain. The goal of our study is to characterize the enzymes hypothesized to remove Pi groups and alter plant Pi signaling from PP-InsPs containing 7 and 8 Pi groups. Lowering PP-InsPs signals the plant to increase Pi uptake from soil. There is a very strong understanding of how Pi groups are added onto PP-InsPs, but the enzymes responsible for removing Pi groups are still not well understood. We identified a potential pyrophosphatase and cloned this gene. We characterized the encoded enzyme by expressing and purifying recombinant protein, as well as through performing enzyme assays with different substrates. The long term goal is to determine the substrate specificity of the enzyme. In my project, I achieved optimization of recombinant gene expression, protein purification, and enzyme assay conditions. This in combination with molecular modeling and analysis of gene expression patterns in plant tissue brings light to the function of the hypothesized pyrophosphatase.

Mentor(s): Glenda Gillaspy (Biochemistry, Virginia Tech)
Janet Donahue (Technician, Virginia Tech)
Branch Craige (Post-doc, Virginia Tech)
Catherine Freed (Graduate student, Virginia Tech)
Caitlin Cridland (Graduate student, Virginia Tech)

Rose Stanphill
Virginia Tech/Aerospace Engineering

Diagnostics Development for Gaseous Detonation Velocity

A detonation is a type of combustion that propagates through a medium at supersonic speeds and drives a shock wave due to exothermic chemical reactions. The fundamental properties of a detonation, such as the combustion velocity, temperature, and pressure, are characteristic properties unique to specific detonable substances and energetic materials. Combustion velocity is an important parameter used to characterize the combustion characteristics of a material and is often compared against the theoretical detonation velocity to determine the likelihood that a deflagration or detonation has occurred. However, measuring the combustion velocity of gaseous hydrocarbon mixtures is challenging because of the extreme conditions of temperature and pressure associated with a detonation, as well as the extremely short time scales of interest, on the order of microseconds. The objective of this research is to develop two diagnostic approaches that take advantage of the ionized flame front, namely, ionization probes and Doppler radar. Ionization probes measure the arrival time of the flame as the combustion front completes a circuit. As the circuit is completed, the velocity was then calculated from time-of-arrival data obtained from an array of ionization probes. Similarly, because the plasma densities on the surface of the flame front are sufficiently ionized to reflect microwaves, continuous Doppler radar was implemented to resolve detonation velocity by measuring the frequency shift between the source and reflected waves as described by Doppler theory. Both measurement techniques were experimentally validated with a series of large-scale detonation experiments performed using 1, 4, and 6 cu ft of an acetylene-oxygen gas mixture at the Virginia Tech Shock Tube Research Facility. Theoretical predictions created in NASA CEA estimated a Chapman-Jouguet detonation velocity of 2566.8 m/s for this mixture, and the results obtained from the experiments were compared against each other to measure the accuracy and quality of both techniques.

Mentor(s): Eric Jacques (Civil Engineering, Virginia Tech)

Trevor Stephens
Virginia Tech/Water: Resources, Policy, and Management

Examining the potential for chlorine to inhibit galvanic corrosion of lead solder in drinking water

Chlorine is commonly applied to drinking water systems to control bacteria levels, but there is limited research on how chlorine affects lead release in drinking water infrastructure, particularly from lead solder. Previous research on lead pipe suggests that chlorine can inhibit lead corrosion by creating protective lead (IV) oxide scale and increasing the corrosion potential to that of gold, a corrosion resistant metal. This study aims to: 1) determine whether chlorine can electrically reverse the galvanic corrosion of lead solder by forming lead (IV) scale; and 2) provide recommendations for utilities struggling to control lead solder corrosion.

Two water conditions were tested, the first containing 40mg/l of free chlorine, and the other containing 40mg/l of total chlorine from chloramine, an alternative disinfectant thought to exacerbate corrosion in some cases. These waters were added to jars containing a simulated lead solder and copper plumbing connection. Current, voltage, and corrosion potential of the metals were recorded with a multimeter to examine corrosion progression. Visual observations were recorded for the jars, noting the color and turbidity of the water and scaling that had built up on the metals. Water was collected from these jars after every 24 hours Monday-Friday and then analyzed using inductively coupled plasma mass spectrometry (ICP-MS) to determine the total amount of lead present in each jar. Visual evidence of lead (IV) scaling and an increase in corrosion potential from -398.03 to -195.9.15 mV after 25 days in the chlorine waters suggests that corrosion reversal is occurring.

Mentor(s): Marc Edwards (Civil and Environmental Engineering, Virginia Tech)

Nola Story
Virginia Tech/Clinical Neuroscience

Effects of Pro-Inflammatory Microglia Activation on Behavior in Female Mice

Major Depressive Disorder (MDD) is a common mood disorder that affects males and females differently. Females are twice as likely compared to males to develop MDD. Males commonly describe anger, substance abuse, and risk-taking behaviors, while females describe irritability, fatigue, anhedonia, and sleep and appetite disturbances. Beyond these sex-specific symptoms, inflammation is a biological factor associated with MDD. Microglia are the immune cells of the brain and become activated in response to injury or stress. This project investigates the role of microglia activation in modulating behavior in female mice. To test whether microglia activation induces stress susceptibility, female mice received a single intraperitoneal injection of either LPS, a bacterial endotoxin commonly used to elicit microglia pro-inflammatory activation, or saline; followed by either three days of variable stress or no stress. The variable stress model consisted of three types of stressors: foot shock, tail suspension, and restraint tube; each stressor was administered for one hour. Following three days of variable stress, mice underwent a series of behavioral tests: Splash Test, Social Interaction, Novelty Suppressed Feeding, and Forced Swim Test. Interestingly, our behavioral test results suggest that in female mice, LPS combined with 3 days of variable stress promotes stress-resilience, while LPS without 3 days of variable stress results in depressive-like behaviors.

Mentor(s): Georgia Hodes (School of Neuroscience, Virginia Tech)

Emily Testa
Virginia Tech/Biochemistry

Polarizable Molecular Dynamics Simulations of a G-Quadruplex in the promoter region of the human KRAS gene

G-Quadruplexes (GQs) are noncanonical DNA and RNA structures that form stacked tetrads from guanine rich sequences. GQs play a major role in modulating gene expression and genomic stability due to their presence in promoters, telomeres, and origins of replication. Hence, it has been of great interest to study GQs in promoter regions of disease-related genes. One of the most mutated oncogenes, KRAS, has the ability to form a GQ in a nuclease hypersensitive element (NHE) within its promoter sequence. KRAS encodes for the protein K-Ras which plays an important role in cell division, cell differentiation, and apoptosis in cancer cells. Therefore, developing a greater understanding of the structure, dynamics and ion binding properties of this NHE region will open up implications to possible drug designing strategies. To investigate these properties, molecular dynamics simulations were performed on a NMR ensemble (PDB code 6suu) of the KRAS GQ. Here, we employed the Drude-2017 polarizable force field. Simulations showed a strong amount of ion binding between our GQ and bulk K+ ions, which may shed a light on properties useful for targeting by small molecules. Structural integrity and fluctuation were analyzed using RMSD and RMSF. Further analysis will be conducted to investigate hydrogen bonding, dipole moments and ion mapping.

Mentor(s): Justin Lemkul (Biochemistry, Virginia Tech)

Talmadge Tomlinson
Virginia Polytechnic Institute and State University/Fisheries Conservation

Spawning behavior of Blacknose dace (Rhinichthys atratulus) in Toms Creek in relation to temperature and potential nest association.

Blacknose dace have long been thought to be facultative nest associates of Bluehead chubs and Central stonerollers, mainly due to the observation of individuals on or around the Bluehead chub spawning mounds and Central stoneroller pits. To verify if this assumption is true in Toms Creek, Blacksburg, we began collection of larval Blacknose dace prior to the construction of pits and mounds and conducted electrofishing to determine timing of male spawning coloration. Collection began in late April and was done using 400 lumen flashlights and dip nets to collect larval samples in small eddies and pools after dark. All larvae sampled were euthanized in 95% ethanol and stored for genetic analysis. After onset of pit and mound spawning, we placed underwater cameras to detect the presence of Blacknose dace on mounds and pits. Egg samples from selected pits and mounds were then collected for genetic analysis. We extracted DNA from larvae and eggs and amplified using the DNeasy Blood and Tissue Kit (Qiagen). Additional genetic analysis is pending. Preliminary visual analysis of collected larvae indicate the presence of possible Blacknose dace and Mountain Redbelly dace which is another nest associate. Underwater videography showed Mountain Redbelly dace directly on pits and mounds often spawning, whereas few Blacknose dace were seen on pits and mounds but never spawning. Pending genetic analysis of eggs, our preliminary conclusion is that Blacknose dace are not nest associates, but instead spawn in open substrates. Early spawning Mountain Redbelly dace also calls for more investigation.

Mentor(s): Emmanuel Frimpong (Fisheries conservation, Virginia Tech)

Megan Toms
Virginia Tech/Biological Sciences

MAOP

Assessing Ligand Influence on the Dynamics and Structure of Sphingosine Kinase Isoforms Using Molecular Dynamics Simulations

Sphingosine kinase (SphK) is an enzyme that catalyzes the formation of sphingosine-1-phosphate (S1P). When S1P is elevated, it impacts and upregulates the occurrence of many different diseases including cancer. There are two different isoforms of sphingosine kinase, SphK1 and Sphk2. At this time, little is known about the binding conformations of sphingosine kinases to isoform specific ligands. This work examines the two different SphK isoform binding sites and structural morphologies with and without natural substrates including, sphingosine and ATP. Atomistic molecular dynamics (MD) simulations were used to determine the structural morphologies and examine the binding pocket with ATP and sphingosine bound to the kinase isoforms. Through the examination of SphK isoforms, the structural stability was calculated with ATP and sphingosine bond to the binding site as well as ATP alone in the binding site. Quantitative assessments of structures such as root mean-square deviation (RMSD), root mean-square fluctuation (RMSF), and solvent accessible surface area (SASA) were performed on both of the isoforms. Paired with dominant morphology percentages, the RMSD analysis showed that SphK2 systems were stable and can be used for structural analysis. Through RMSF it was determined that ATP and sphingosine influence the fluctuation of the elongated loop in SphK2 isoforms, which could indicate that this region has an important role in structural morphology changes. The SASA values show that there are no large conformational changes in the isoforms from the substrate binding. Based on the data collected the SphK2 homology model can be used as a tool for inhibitor design. With this data analyzing the SphK isoform binding patterns it can be used for further drug discovery.

Mentor(s): Anne Brown (Biochemistry, Virginia Tech)
Amanda Sharp (Virginia Tech)

Christine Trieu
Virginia Tech/Smart and Sustainable Cities
Matt Hall
Virginia Tech/Smart and Sustainable Cities
Izzy Hausrath
UC Santa Barbara/Environmental Studies
Liz Myers
Ohio University/Civil Engineering

Impacts of Human Watershed Alterations on Stream Temperature

Stream temperature is critical to the health of native aquatic organisms, as some species are sensitive to even small temperature variations. The goal of our research was to correlate variations in temperature with different human alterations of streams across the United States to help inform the general public during future development efforts. We examined four streams in three states that have been previously altered due to restoration, reinforced banks, rerouting, and damming. We hypothesized that, in more severely altered areas, the streams would have a higher temperature due to the removed or inhibited riparian or streamside vegetation. Water temperature data, as well as weather data (air temperature, barometric pressure, dew point, and heat stress index), were collected at an upstream and downstream site for each stream. These metrics, combined with qualitative observations such as cloud cover, riparian zone, and flow level, provided a fuller picture of how these streams changed with the human alteration. While actual temperature changes varied across sites, all locations had higher temperatures due to the alterations, while streams with more severe alterations had higher increases. To put the significance of temperature changes in our streams into context for our audience, we related the changes to the viability of sensitive native species that inhabit our study environments.

Mentor(s): Cully Hession (Biological Systems Engineering, Virginia Tech)
Leigh-Anne Krometis (Biological Systems Engineering, Virginia Tech)
Brian Badgley (Plant and Environmental Sciences, Virginia Tech)
Erin Ling (Biological Systems Engineering, Virginia Tech)

Caroline von Raesfeld
University of California, Los Angeles/Astrophysics

The use of Coherent-Elastic Neutrino-Nucleus Scattering to monitor Spent Nuclear Fuel

With a growing demand for a clean energy supply along with concerns over effective nuclear waste storage, it is imperative to be able to monitor highly radioactive waste in a safe and effective way. In this research we explore the applicability of Coherent-Elastic Neutrino-Nucleus Scattering (CEvNS) to monitor the content of spent nuclear fuel (SNF) from dry storage casks in comparison to Inverse Beta Decay (IBD). We use the electron antineutrino flux from SNF calculated in Brdar et al. to obtain event rates from both CEvNS and IBD events for a variety of isotopes such as 12C, 40Ar, 74Ge, and 184W. We demonstrate that at low nuclear recoil energies CEvNS events occur at magnitudes 2-3x larger than IBD events for a given detector mass, owing to the N^2 dependence of the CEvNS cross section and the fact that CEvNS has no neutrino energy threshold. We find that 10 kg Argon and Germanium detectors 3 meters from a fuel cask can detect over 100 events per year if a nuclear recoil threshold of 70 eV can be achieved. We then consider irreducible backgrounds from cosmic ray neutrons and demonstrate that with passive shielding of 2 m.w.e a S:N ratio of 10:1 can be achieved. Finally, a chi-squared analysis is carried out to determine the 1σ error on the measurement of fuel in the cask, to examine with what certainty the fuel content can be verified.

Mentor(s): Patrick Huber (Physics, Virginia Tech)

Zijun Wang
Blacksburg High/Biochemistry

Resistance to Ribosome-Targeting Antibiotics: Docking of Amicetin to the Binding Site of Blasticidin S in Thermus thermophilus

Antibiotics are used to treat numerous bacterial infections such as streptococcal pharyngitis, bacterial pneumonia, and tuberculosis by destroying the bacteria, preventing bacterial reproduction, or blocking protein synthesis. Ribosomes within the bacteria are the most common targets of antibiotics such as blasticidin S. Overuse or misuse of these antibiotics, however, combined with the lack of new drug development, has led to a rapid increase in antibiotic resistant bacteria. Over 2.8 million people in the US are infected with antibiotic resistant bacteria each year, resulting in at least 35,000 deaths. The lack of innovation for new antibiotics to combat resistance in bacteria continues to contribute to the surge of resistant strains. Blasticidin S, a powerful inhibitor of translation in both prokaryotic and eukaryotic cells, is one among many antibiotics that bacteria have acquired resistance against. This project aims to aid in the identification of the compound amicetin as a potential candidate in antibiotic development in place of blasticidin S through computational docking to the 70S ribosomal subunit of Thermus thermophilus. By exploring the binding of amicetin to T. thermophilus, we found that the binding site of amicetin overlaps significantly with that of blasticidin S. Amicetin was also found to be able to fit within the binding site of blasticidin S through volume measurements. In this project, we identified the binding site of amicetin in the 70S ribosomal subunit of T. thermophilus that can potentially be utilized for antibiotic drug development.

Mentor(s): Anne Brown (Biochemistry, Virginia Tech)

Andrew Wang
Blacksburg High/Biochemistry

Comparisons of host CD4 from multiple animals using multiple sequence alignments

CD4 is a glycoprotein that serves as a receptor in a T cell. HIV takes advantage of CD4 for infection. HIV contains a glycoprotein called gp120, which presents itself as a membrane spike and helps facilitate the entry into the host cells. The gp120 binds to CD4 and this interaction allows the virus to enter in the cell. This research focuses on how CD4 proteins from various animals differ from each other and how the difference may explain why HIV can infect apes such as humans and chimpanzees but can infect other animals. In this project, the following methods: Unipro UGENE, Immuno Medicine, ConSurf, and Microsoft Excel, were used to compare and analyze CD4 amino acid sequences and structure among a selection of animals. It can be concluded that chimpanzee CD4 is most similar (98.9% identical) and mouse CD4 is the least similar (13.3% identical) to human CD4. R59 (Arginine 59) makes a salt bridge within CD4 to stabilize its structure to interact with gp120 and plays a critical role in the interaction between CD4 and gp120. These results show that humans and chimpanzees are the only 2 animals with R59, but not other animals in the selection, suggesting that the presences of R59 may determine whether HIV is able to infect an animal. This can indicate that humans, chimpanzees, and possibly other apes are the animals that can be infected by HIV.

Mentor(s): Anne Brown (Biochemistry, Virginia Tech)

Jennie Weitzenhofer
Virginia Tech/Wildlife Conservation

Beary Active Cubs? - Quantifying American Black Bear Mother and Cub Behavioral Changes Surrounding Hibernation Emergence

American black bear (Ursus americanus) behaviors change surrounding hibernation. Understanding of hibernation patterns can lead to more effective wildlife management. However, it is challenging to study bear behavior in the wild. Thus, little work has been done to assess behavioral changes systematically associated with the onset of, and emergence from hibernation. Utilizing a unique dataset collected at Virginia Tech's Black Bear Research Center, we cataloged 37 behaviors and quantified the proportion of time mothers and cubs spent exhibiting behaviors from February to April 2016 via 24/7 video monitoring of wild bears that were temporarily held in captivity. As expected, we found that both mother and cubs exhibited mostly passive behaviors pre-emergence, at 0.96 and 1.0, respectively. Active behavior increased as bears emerged from the den, 43 days after birth, but passive behaviors were still high into April (0.91) for both mother and cubs. As the cubs gained weight, the proportion of active behaviors rose by 0.09 for both mother and cubs. We expect active behaviors to increase dramatically through April as we documented cubs beginning to engage in play behavior at that time. Ongoing analyses will isolate daily trends in behaviors (e.g. playing, fighting, climbing, etc.) and establish whether heavier cubs exhibit more dominance behavior towards siblings. This information is important to the Virginia Department of Wildlife Resources because it provides better understanding of emergence times and when bear activity levels increase, which is relevant to potential human-bear interactions.

Mentor(s): Marcella Kelly (Fish and Wildlife Conservation)

Tamer Whittle-Hage
Virginia Tech/Clinical Neuroscience

Blood Brain Barrier Disruption in a Mouse Model of Chronic Stress

Long-term variable stress is a major risk factor for developing emotional disorders like depression and anxiety. In a collaborative effort between the Clinton Lab and the Hodes Lab, my project examines how chronic stress disrupts the blood brain barrier, gut microbiome, and emotional behavior of male and female mice. We examined how stress impacts blood brain barrier integrity using Evans Blue stain. Male/female mice were exposed to 28 days of variable stress (daily exposure to either tail suspension, foot shock or restraint) or control conditions (n=6 per group). On the final stress (or control) day, mice were injected with Evans Blue and perfused to harvest brain tissue. Brains were sectioned, mounted, coverslipped, and imaged to analyze Evans Blue staining in brain areas that regulate emotional behavior (hippocampus and nucleus accumbens). We hypothesized that stressed animals would exhibit higher Evans Blue staining compared to control animals. Breakdown of the blood brain barrier following stress could allow for the influx of unwanted molecules into the brain, which could trigger disruption of emotional behavior-regulating brain circuits. We also processed fecal samples from stressed and control mice to evaluate potential differences in gut microbiome content. Next-generation sequencing was conducted and data is currently being analyzed to identify specific bacterial species that are disrupted by stress in male and/or female mice. We hypothesize that select microbiome abnormalities could contribute to stress-induced changes in brain and behavior, and may be relevant to biological changes that occur in humans that experience stress-related disorders like depression.

Mentor(s): Sarah Clinton (School of Neuroscience, Virginia Tech)
Keaton Unroe (Graduate Student, Virginia Tech)
Elizabeth Shupe (Graduate Student, Virginia Tech)

Shelby Williford
North Carolina State University/Plant Biology

Weeding out the Competition: Competitive Effects on Container-Grown Nursery Plants

Agriculture is the largest private industry in Virginia with nursery plant production as the highest earning plant commodity in terms of annual sales. A significant portion of nursery plants are produced in containers. However, unwanted pests impeding upon container-grown plants can degrade the quality of plants produced. This project was designed to observe the effects of weed competition on container-grown ornamentals. The research is comparing different species of common nursery ornamentals and weeds to examine the effects of weed competition across a broad scope. The ornamentals were Spiraea japonica, Coreopsis grandiflora, and Calamagrostis acutiflora. These plants were grown in four liter containers with treatments of zero, one, or three weeds of southern crabgrass (Digitaria ciliaris), eclipta (Eclipta prostrata), rice flatsedge (Cyperus iria), or doveweed (Murdannia nudiflora) per pot. Height and width measurements were taken for each ornamental and weed species at the time of planting and after five weeks. This allows us to compare the growth among species to see which weeds have the greatest impact on ornamental growth. Our anticipated results are that ornamentals grown with three southern crabgrass or eclipta plants will show the greatest decrease in ornamental growth due to the competitive nature of those weed species and their rapid growth observed during the project. The data collected from this project will aid in the development of weed management procedures to improve the growth of container-grown nursery plants.

Mentor(s): Jeffrey Derr (School of Plant and Environmental Sciences, Virginia Tech)

Bryce Wozniak
Virginia Tech/Biochemistry

Identification and characterization of the Fusobacterium nucleatum outer membrane bound proteins that drive host-microbe interactions

Fusobacterium nucleatum is a gram negative, anaerobic bacterium that is typically found in the oral microbiome. It's recently been shown that this bacterium plays a key role in progressing colorectal cancer by modifying inflammatory signaling pathways. Many outer membrane bound proteins have previously been characterized to aid in cell recognition, docking, and invasion. Fap2, one such protein, has been shown to bind to the Gal/GalNAc lectin, which is overexpressed on the surface of cancer cells, allowing this bacterium to bind and affect the signaling pathways present. We have identified many Fap2 paralogous genes that have previously been unknown and remain uncharacterized. The studies presented here use bacterial genetics to characterize the role these Fap2 paralogous genes may play in Fusobacterium nucleatum's virulence with the goal of better understanding this bacteria's role in colorectal cancer invasion and disease progression.

Mentor(s): Daniel Slade (Biochemistry, Virginia Tech)

Brynn Yaun
Virginia Polytechnic and State Institute/Biochemistry

Determining the timing of spore production of *Pseudogymnoascus destructans* isolates, a virulent pathogen of bats

Emerging wildlife pathogens can have devastating effects on host populations. *Pseudogymnoascus destructans*, the causative agent of white-nose syndrome (WNS), a fungal disease of bats, has resulted in mass mortality since it's introduction to North America in 2006. Species affected by WNS have experienced regional exterpations and many remaining populations have been reduced >90%. Transmission of P. destructans occurs through direct transfer among hosts and indirect transfer mediated through the environment. *P. destructans* produces conidia or asexual spores that can shed by infected bats into the environment where they can remain present for decades in the absence of bats. Here we seek to determine differences in spore production of two isolates of *P. destructans*. We selected an isolate collected from China where the disease is endemic, and an isolate from New York where severe population declines occurred. We first determined the appropriate filtering method to separate *P. destructans* conidia from other hyphal growth using glass wool. We then inoculated isolates onto Sabouraud dextrose agar and incubated at 9°C, a common roosting temperature of bats during hibernation. Six replicates per sample were harvested each day from the onset of the experiment, filtered through glass wool to isolate conidia, and quantified using a hemocytometer. The anticipated results from this work will provide valuable insight into the timing of peak propagule pressure and its implications for transmission.

Mentor(s): Joseph Hoyt (Biological Sciences, Virginia Tech)

Rianna Zacharias
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The Role of MCU in Regulating Mitochondrial Size and Synaptic Localization

Hippocampal area CA2 is involved in processing social memory, however, the underlying molecular mechanisms through which it performs this function are unknown. CA2 has a higher mitochondrial content and contains functionally distinct mitochondria from those found in the neighboring CA1. The mitochondrial calcium uniporter (MCU) is a transmembrane protein responsible for calcium uptake from the cytosol into the mitochondria, thereby serving as an important regulator for calcium homeostasis. In addition, mitochondria generate ATP to power cellular processes, including synaptic plasticity. Synapses in the stratum radiatum (SR) layer of CA2 are resistant to a form of plasticity called long-term potentiation, and this is due to robust calcium buffering and extrusion mechanisms, of which differences in MCU expression may be a contributing factor. However, CA2 neurons selectively localize MCU-enriched mitochondria in the stratum lacunosum-moleculare (SLM) layer, a more plastic region compared to SR. Furthermore, MCU-enriched mitochondria in SLM are larger than those in SR. Thus, we hypothesize that MCU-enrichment selectively localizes larger mitochondria to plastic regions and that MCU knockdown will result in smaller mitochondria localizing to the SLM layer of CA2. To test this, we performed immunohistochemistry for MCU in brain sections obtained from CA2-specific MCU knockdown mice. We then imaged and quantified mitochondrial area and fluorescence in the SR and SLM layers of CA2. The results of this study will allow us to elucidate the role of MCU in regulating mitochondrial size and localization and further characterize the mechanisms in CA2 that may be supporting the plasticity underlying social memory.

Mentor(s): Shannon Farris (Center for Neurobiology Research, Fralin Biomedical Research Institute, Virginia Tech)

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