Undergraduate Research & Creative Achievements Forum

July 30, 2015
Abstracts in this book describe the research projects and scholarly and creative activities of 140 students in summer internship programs held at the University of Missouri.

Participating MU Departments & Divisions by Mentor Department

Art
Animal Sciences
Biochemistry
Bioengineering
Biological Sciences
Chemistry
Civil Engineering
Computer Science
Electrical and Computer Engineering
Endocrinology
Mathematics

Mechanical and Aerospace Engineering
Medical Pharmacology and Physiology
Molecular Microbiology and Immunology
Nutrition and Exercise Physiology
Obstetrics, Gynecology and Women’s Health
Pathology and Anatomical Sciences
Physics and Astronomy
Plant Sciences
Psychological Sciences

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IMSD-EXPRESS Coordinator Brian Booton
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Student Assistants Joey Fening, Briana Lynch, Kayla Symonds, and Jessica Welsh
Participating MU Departments & Divisions

The Summer 2015 Undergraduate Research & Creative Achievements Forum represents the 26th year of summer research intern presentations at the University of Missouri. Student interns displaying their research projects at the Forum are supported by one of 10 formal summer programs or are funded individually through their faculty mentor or other on-going programs. Undergraduates hail from 43 institutions of higher education, and their faculty mentors come from more than 20 academic units at MU.

Life Sciences Undergraduate Research Opportunity (LS UROP)

The University of Missouri funds the Summer 2015 LS UROP Undergraduate Research Internships. MU students conducted an independent project in the life sciences under the guidance of an MU faculty member to experience research first-hand and prepare for research, teaching and scientific careers. Students attended evening seminars and small group sessions to discuss issues related to scientific research, including ethics, career paths, emerging research areas, and opportunities for post-baccalaureate study. Students conducting plant biology research may be funded by the Monsanto Undergraduate Research Fellowship fund.

Program Director Dr. Linda Blockus, Undergraduate Research
Administrative Assistant Pam Cooper, Undergraduate Research

2015-2016 LS UROP Selection Committee

Dr. Lori Eggert, Biological Sciences
Dr. Sharyn Freyermuth, Biochemistry
Dr. Kevin Fritsche, Nutritional Sciences
Dr. Walter Gassmann, Plant Sciences
Dr. C. Michael Greenlief, Chemistry
Dr. Mark Hannink, Biochemistry
Dr. Casey Holliday, Path. & Anatomical Sciences
Dr. Mark Kirk, Biological Sciences

Dr. Joel Maruniak, Biological Sciences
Dr. Kevin Middleton, Path. & Anatomical Sciences
Dr. Melissa Mitchum, Plant Sciences
Dr. Charles Nilon, Fisheries & Wildlife Sciences
Dr. Brenda Peculis, Biochemistry
Dr. Rocio Rivera, Animal Sciences
Dr. Jim Spain, Animal Sciences

National Institute of Health – Initiative for Maximizing Student Diversity

The Initiative for Maximizing Student Diversity (IMSD) is designed to enhance the experience of a diverse group of students at MU through research opportunities, workshops, and mentoring. This purpose of this program is to encourage underrepresented minority students to earn a doctoral degree and pursue research career in a field related to biomedical research. IMSD-EXPRESS Fellows complete an independent research project.

Principal Investigator Dr. Mark Hannink, Biochemistry
Co-Principal Investigator Dr. Linda Blockus, Undergraduate Research
Program Coordinator Brian Booton, Undergraduate Research
Summer Research Internship Program in Cell & Molecular Biology

The Summer Research Internship Program in Cell and Molecular Biology Program prepares undergraduates for graduate study in cell & molecular biology research with faculty mentors who are members of the NIGMS Training Grant at MU. Undergraduate students conduct research on a cell and molecular biology project with faculty mentors from a wide array of departments and colleges at MU. Interns learn about graduate school life, advanced library and computing skills and effective ways to present their work. This program funded by the Life Sciences Fellowship program and a T32 training grant from NIH and administered through the MU Office of Undergraduate Research.

Principal Investigator  Dr. Mark Hannink, Biochemistry

Summer Research Internship in Medical Sciences

The Office of Research at the University of Missouri School of Medicine offers a summer research program for undergraduates enrolled at other institutions. The objective of the program is to recruit underrepresented minorities to the medical school with the goal of improving diversity and inclusion in the clinical medicine workforce. In addition to their research work, students participate in a full series of evening workshops and small group seminars. Weekly Medical Sciences Undergraduate Seminars are held to provide information specific to medical research and clinical education pathways and careers. This program funded by the MU School of Medicine and administered in partnership with the MU Office of Undergraduate Research.

Hugh E. & Sarah D. Stephenson Dean, School of Medicine  Patrice “Patrick” Delafontaine, MD
Senior Associate Dean for Diversity and Inclusion  Warren Lockette, MD
Senior Associate Dean of Research  Jamal Ibdah, MD, PhD
Associate Dean for Research  Jerry C. Parker, PhD
Program Coordinator  Debbie Taylor

National Science Foundation - Research Experience for Undergraduates (Educating for the Grand Challenges at the Intersection of Biocomplexity and High-Performance Computing)

Computation, and especially parallel computation, will be vital to science and engineering in the future, as increasing data volumes from instruments such as next-generation DNA sequencers overwhelm current laboratory techniques and software tools. This program seeks to link the computational and biological domains by placing pairs of undergraduates, one from computer science and one from the life sciences, into research laboratories in order to use high performance computing approaches to solve big data problems in biology. Now in its second year, our program has 12 students from seven institutions. This program is administered through the MU Office of Undergraduate Research.

Principal Investigator  Dr. Gavin Conant, Animal Sciences
National Science Foundation - Research Experience for Undergraduates (Neuroscience)

The Computational Neuroscience REU Program provides opportunities for undergraduates from outside MU to experience cutting edge research in neuroscience at University of Missouri. All research projects include a computational component, and students attend the 1-credit course ‘Computational Neuroscience’. The students also avail of the educational and social programming provided by the MU Office of Undergraduate Research. The faculty participating in the program span three colleges.

Principal Investigator  Dr. Satish S. Nair, Electrical & Computer Engineering
Co-Principal Investigator  Dr. David Schulz, Biological Sciences
Graduate Coordinator  Feng Feng

National Science Foundation - Research Experience for Undergraduates (Physics: Materials and Modeling)

This is the second year of an NSF-sponsored Research Experience for Undergraduates in physics at the University of Missouri. The nine-week program, hosted by the MU Department of Physics & Astronomy, engages students in high quality research on topics on a wide range of materials, such as biological molecules, nanoparticles, star dust, and alternative fuels. The program draws from a national pool of applicants, as well as students from partner institutions that serve underrepresented students. In addition to working on research projects (which is the primary aim of the program), participants also attend science and academic life seminars organized by the Office of Undergraduate Research and a weekly small group seminar on physics topics.

Principal Investigator  Dr. Sashi Satpathy, Physics & Astronomy
Co-Principal Investigator  Dr. Karen King, Physics & Astronomy

National Science Foundation - Research Experience for Undergraduates (Consumer Networking Technologies)

The REU projects will investigate some important issues related to software-defined networking, social media computing, social health networking for eldercare, body-area sensing and emotion recognition, and network performance optimization. As broadband services and mobile devices proliferate, consumers are migrating towards advanced social, information-intensive, and personalized services. The fast pace of growth, improvement to quality of life, and significant economic contribution of networked consumer systems have been receiving increasing attention. Technical challenges in this field include quality of service, network and device heterogeneity, network performance, mobility, device intelligence, security and privacy, and user experience and knowledge, etc. In this REU Site, students will participate and develop new skills in ongoing funded research projects of the faculty mentors by investigating, implementing, and testing viable solutions to technical challenges in consumer networking technologies.

Principal Investigator  Dr. Yi Shang, Computer Science
Co-Principal Investigator  Dr. Wenjun (Kevin) Zeng, Computer Science
National Science Foundation - PRISM Mathematics in Life Sciences Program

The increasing centrality of mathematics in life sciences research and thinking is obvious to anyone who has observed the field over the last few decades. Algorithmic annotation and analysis of massive amounts of sequence data has become a routine tool in all aspects of biology, including ecology and evolution, cancer research, neurobiology, agronomy, plant sciences, and other sub-disciplines too legion to enumerate. Over the same era, chemistry and physics, which have historically already been mathematics-intensive sciences, are increasingly being integrated into life sciences. Yet the mathematics training of American life science students does not generally prepare them well to exploit the opportunity that this interdisciplinary synergy offers. A consortium of science and mathematics researchers at the University of Missouri have established the Mathematics in Life Sciences Program to integrate mathematics more intimately into undergraduate science studies. Funding for this program is from a National Science Foundation PRISM grant awarded in 2009.

Principal Investigator
Dr. Dix Pettey, Mathematics

Co-Principal Investigators
Dr. George Smith, Biological Sciences
Dr. Rainer Glaser, Chemistry
Dr. Francis Schmidt, Biochemistry
Dr. Jeni Hart, Educational Leadership & Policy Analysis

Students Participating in the Undergraduate Research & Creative Achievements Forum
July 30, 2015

Life Sciences Undergraduate Research Opportunity Program (LS UROP)

University of Missouri

Benton Berigan Rachel Rozin
Sarah Biehn Michael Savio
Matthew Chisholm* Benjamin Shumate*
Alex Clarke* Anthony Shumate*
Caroline Dunn Stephanie Stupps
Sera Holland* Taylor Wagner*
Daniel Kranz Alex Willienbrink
Conner Rogan

*Funded by Monsanto Undergraduate Research Fellowship
NIH Initiative for Maximizing Student Diversity-EXPRESS

University of Missouri

Keisha Avery  Cynthia Koehler
Reginald Edwards  Tykeemi Manor
Kennady Gee  Anthony Onuzuruike
Romanus Hutchins  Amir K. Richardson
Nicholas Jackson

MU Summer Research Internship Program in Cell & Molecular Biology

Ambreka Benons  Medgar Evers College
John Harris  Minnesota State University
Karolina Marquez-Gil  Grinnell College
Fabienne Mondelus  Medgar Evers College

Summer Research Internship in Medical Sciences

Alex Akinrinmade  University of the Western Cape
Usisipho Feleni  University of the Western Cape
Mayra Garcia Hernandez  Truman State University
J. Kyle Kirkland  Michigan State University
Timothy Klein  University of Western Cape
Keenau Pearce  University of Western Cape
Sadara Taylor  Southern Illinois University - Carbondale
Franklin Woode  Princeton University

NSF Research Experience for Undergraduates (Biocomplexity and High-Performance Computing)

Julia Brose  University of Missouri
Katie Burch  Truman State University
Justin Deters  Truman State University
Wade Dismukes  University of Missouri
Micah Fletcher  University of Missouri
Ying Lin  Vanderbilt University
John Long  Columbia University
Taylor Maurer  Kenyon College
Eric Penton  Rockhurst University
Devin Petersohn  University of Missouri
Aniqa Rahman  Grinnell College
Jack Schoelz  Truman State University
NSF Research Experience for Undergraduates
(Neuroscience)

Joseph Del Rosario  Arizona State University
Sonia Dermer  College of William & Mary
Gabrielle Dohman  University of Notre Dame
Ashley Douglass  Purdue University - Calumet
David Goodman  Drake University
Steven Groff  University of Indiana - Purdue Fort Wayne
Allison Halt  Washington College
Frederick Henry  Truman State University
Elliot Lee  University of Waterloo
Kayla Miguel  University of Miami
Abigail Mutamba  University of Colorado Denver
Alexander Wood  Washington State University

NSF Research Experience for Undergraduates
(Physics: Materials and Modeling)

John Barron  Southern Illinois University - Carbondale
Matthew Brown  Hastings College
Marques Gulley  Lincoln University
Hannah Huhman  University of Missouri - Kansas City
Zoë Lemon  University of Missouri - Kansas City
Todd Lombardi  St. Mary’s University
Jacob Mieso  San Jose State University
Joshua Steffen  Iowa State University
Kevin Wang  University of Illinois at Urbana-Champaign
Renna Yi  William Jewell College

NSF Research Experience for Undergraduates
(Consumer Networking Technologies)

Olivia Apperson  University of Missouri
Vladimir Georgiev  Southeast Missouri State University
Stephen Jones  Berry College
Jay Kelner  Truman State University
Mark Lewis  Grinnell College
Taylor Rydahl  University of Wisconsin at Oshkosh
Andrew Smith  Southeast Missouri State University
Allen Stage  Humboldt State University
Mark Vassell  University of Missouri
Andrew Woods  Columbia College
Additional Students

Mahliyah Adkins-Threats  
*Truman State University*  
NSF Grant to P. McSteen

Laura Cipriano Crapina  
*St. Michael’s College*  
NSF Plant Genome Grant to D. Braun

Brett Heischmidt  
*University of Missouri*  
United States Department of Energy, Office of Science, Award (No. DE-FG02-00ER45818) to S. Satpathy

Mitchell Battles  
*University of Missouri*  
College of Engineering  
Undergraduate Research Program

Nicholas Cole  
*University of Missouri*

Joshua Kelly  
*Barry University*

Julie Bays  
*Truman State University*  
University of Missouri  
Department of Biochemistry

Dhruveesh Dave  
*University of Missouri*  
NSF Grant to H. Appel

Kara Klemp  
*Mizzou Advantage Grant to S. Nagel*

Katie Burkhardt  
*University of Missouri*  
College of Engineering  
Undergraduate Research Program

Creighton DeYoung  
*University of Missouri*  
NIH Grant (R01A1074389) to D. Burke

Andrew Ludwig  
*University of Missouri*  
United Soybeans and Missouri Soybean Alliance

Benjamin Cairns  
*University of Missouri*

Anita Donner  
*University of Missouri*  
NIH Initiative for Maximizing Student Diversity-EXPRESS

Abuzar Mahmood  
*University of Missouri*  
Grant to L. Pulakat

Shaoyang Chen  
*University of Missouri*

Laura Evans  
*University of Missouri*  
College of Engineering  
Undergraduate Research Program

Nicole Odom  
*University of Missouri*  
NSF Grant to H. Appel

Jeff Chininis  
*University of Missouri*  
University of Missouri System  
Intellectual Property Fast Track Funding Program

William Galvin  
*University of Missouri*  
Elemental Enzymes

Drew Olson  
*William Woods University*  
University of Missouri  
Department of Biochemistry
Additional Students continued

**Megan Osbahr**
*University of Missouri*

**Ana Paula Perin**
*University of Idaho*
Science without Borders (Brazil)

**Andrew Polk**
*University of Missouri*
College of Engineering
Undergraduate Research Program

**Imran Rashid**
*University of Missouri*
University of Missouri
Department of Pathology and Anatomical Sciences; National Institute for Arthritis and Musculoskeletal Diseases

**Seth Rewerts**
*University of Missouri*

**Chris Ricciardi**
*St. Michael’s College*
NSF Plant Genome Grant to D. Braun

**Laura Rottman**
*University of Missouri*
NSF IOS Grant to R. Cocroft

**Jacob Rusteberg**
*University of Missouri*

**Mason Schellenberg**
*University of Missouri*
3M Faculty Award to H. Hunt

**Michael Schoelz**
*University of Missouri*
United States Department of Transportation

**Adam Schoelz**
*University of Arkansas*
NSF Grant (CCF-1421765) to M. Becchi

**Connor Wolenski**
*University of Missouri*

**Yia Yang**
*University of Missouri*
Freshman Research in Plant Sciences

**Casey Yocks**
*University of Missouri*
Freshman Research in Plant Sciences

**Meiqi Yuan**
*University of Missouri*

**Dennis Zhu**
*University of Missouri*
ASPB Summer Undergraduate Research Fellowship to D. Zhu

**Adam Vojta**
*University of Missouri*
College of Engineering
Undergraduate Research Program

**Emma Tomes**
*University of Missouri*
NIH Grant (R01AI074389) to D. Burke

**Andrew Polk**
*University of Missouri*
College of Engineering
Undergraduate Research Program

**Haoqi Wang**
*University of Missouri*
College of Engineering
Undergraduate Research Program

**Thomas Welby**
*University of Missouri*
College of Engineering
Undergraduate Research Program
Characterization and mapping of the Suppressor of sessile spikelet 3 (Sos3) mutant in maize
Mahliyah Adkins-Threats, Shelbie Wooten, and Paula McSteen

Corn and rice are two of the most important cereals in world, playing major roles in industry and in food production. In both species, spikelets (small branches) on the inflorescences (reproductive branches) produce the seeds that feed millions. The difference between corn and rice arises in the spikelet number: maize produces paired spikelets while rice produces single spikelets. The Suppressor of sessile spikelet 3 (Sos3) mutant of maize produces single instead of paired spikelets, causing defects in the development of male inflorescences (tassels) and female inflorescences (ears). Sos3 mutants are phenotypically characterized by fewer tassel branches and fewer kernels on the ears. Characterization of mutant phenotypes through histology and scanning electron microscopy (SEM) allows the function of the gene to be deduced by showing the consequence of the mutation compared to the normal functioning gene. After investigating phenotypes, the mutant can be mapped to determine the location and identity of the gene that is mutated. Sos3 is linked to molecular markers on chromosome 1 (bin 6). In order to fine map the mutant, tissue from mutant plants was collected, DNA was extracted, and polymerase chain reaction (PCR) was performed with over 300 samples using known markers to test for recombination. The rates of recombination were used to determine the distance of the gene from the known markers. The location of the gene has been narrowed down to the region between the markers umc1988 and umc2025 on chromosome 1. The identification of the gene responsible for the Sos3 mutation in maize may provide insight into spikelet production not only in maize, but also in other cereals like rice. Understanding the conversion from paired to single spikelets could potentially double the yield in single spikelet rice, feeding even more.
Faculty Mentor: Dr. Zezong Gu, Pathology and Anatomical Sciences
Funding Source: Summer Research Internship in Medical Sciences

**Dietary elderberry mitigate cerebral ischemia-induced neuron damage**
Alex O. Akinrinmade and Zezong Gu

Abstract withheld at the request of the faculty mentor for proprietary purposes.
When working with critical-care patients, doctors and nurses need augmented reality based technologies to stay updated on the status of patients and care levels. This need is even more critical in a natural disaster scenario where a large volume of patients with varying states of injuries need to be treated through effective co-ordination of limited medical staff and supplies. In this project, we have developed an Intelligent Dashboard viz., “Panacea Glass” that provides the augmented reality benefits with minimal human communication through the integration of a standardized Incident Command System (ICS) application with Internet of Things (IoT) such as heads-up displays, virtual beacons, and wireless mesh network elements. The situational awareness and effective co-ordination is provided by our Panacea Glass through a resource density-graph optimization algorithm that allows: (a) orchestration of video feeds between the Incident Commander and First Responders at the disaster scene, and (b) dynamic tracking and replenishment of medical supply levels. The algorithm handles the prioritization of personnel and medical supplies between responder stations, and importantly recommends actionable intelligence to the Incident Commander for major actions such as for e.g., how many ambulances and which station to route them. We describe our implementation of the Panacea Glass that features a ‘Responder Theater Dashboard’ with WebRTC-based heads-up display video feed collaboration and QR-code based virtual beacon messaging to track patient care status in real-time. We conduct a usability evaluation and an incident simulation study following a template of a ‘Task Force 1 Rescue’. Our results show how our Panacea Glass allows the Incident Commander to deploy personnel and resources at the right locations more efficiently and reduces triage time, mitigates risk of over-triage/under-triage, and ultimately increases the number of successful rescue events.
Faculty Mentor: Dr. Heather Hunt, Bioengineering
Funding Source: NIH-Initiative for Maximizing Student Diversity-EXPRESS

Protein adsorption of pure-silica zeolite MFI thin films
Keisha Avery, Heather Williams, John Lewis, Matthew T. Bernards, and Heather K. Hunt

Abstract withheld at the request of the faculty mentor for proprietary purposes.
The effect of declining flower density on the foraging behavior of alpine bumble bees
Carlie Barham and Candace Galen

Worldwide, flower abundances are declining, contributing to reductions in bumble bee populations, particularly of long-tongued specialist bumble bees. These global changes may influence the evolution of foraging strategies in bumble bee species. A simple model based on optimal foraging theory predicts that reductions in flower density will lead to niche expansion in foragers. Application of this model indicates that short-tongued, generalist bumble bees are favored when resources are low. I specifically analyzed foraging on alpine clover, a historically critical resource for alpine bumble bees, over similar floral densities within five plots along the Bristlecone Ridge of Pennsylvania Mountain. Bumble species observed were B. balteatus, B. sylvicola, B. melanopygus, and B. mixtus. The model’s predictions depend on two basic parameters: flight speed and handling time. I measured variance in these parameters and in the degree of foraging generalization along environmental gradients in alpine ecosystems. My data will address the generality of the model and help pinpoint environmental features that affect its applicability.

Models that address a broader range of parameter estimates can provide more valid predictions about natural systems. My study will evaluate sensitivity of two parameters in a simple pollinator foraging model to variation in the environmental conditions in which host plant selection occurs. Ultimately, this knowledge should increase our understanding of how environmental conditions buffer or magnify costs and benefits of specialization.
Can graphene change the way you drive? Study of graphene nanoplatelets as a hydrogen adsorbent
John Barron, Elmar Dohnke, Andrew Gillespie, David Stalla, Mark Sweany, and Peter Pfeifer

Hydrogen and methane gas have both been recognized as possible substitutes for the currently used fossil fuels as energy sources for vehicles. In order to store larger quantities of gas, it needs to be pressurized, which requires large amounts of energy and will ultimately result in the need for thicker and heavier tank walls. This would result in heavier storage tanks and less free space within the vehicle. In order to improve upon the energy density of the gas, researchers have made use of adsorbent materials (e.g. activated carbons or metal organic frameworks), which have attractive potentials to pull the gas closer to their surfaces. By utilizing adsorption, gas storage tanks are able to store larger amounts of gas molecules at lower pressures inside the tank.

The purpose of these experiments was to determine the adsorptive properties of graphene nanoplatelets, an allotrope of carbon, with hydrogen gas. Samples of graphene which vary in surface area and particle size were subjected to high pressure, and the hydrogen uptake was measured at various temperatures. The results of these measurements allowed us to calculate the amount of excess gas adsorbed by the material. By comparing the gas adsorption at different temperatures, we were able to determine the amount of heat produced from adsorption. From low-pressure nitrogen isotherms, we obtained the surface area of the material. These values are important in determining the applicability of this material as a commercial adsorbent in the future.

The values of these results and their comparison will be presented in the poster.

This work was supported by the National Science Foundation award "Research Experience for Undergraduates in Materials and Modeling" (#1359430)
Automated image analysis is becoming increasingly useful and pertinent in a world where most individuals carry a smartphone with a built-in high resolution camera. One instance where this technology looks like it has a promising application is in plant phenotype and disease quantification. Researchers can, potentially, take their smartphone of choice out into the field with them; and without having to harm or destroy plant structures they can capture, analyze and quantify those plant structures using their smartphone. Other built-in functions such as GPS and wireless capabilities allow researchers to upload and save large amounts of data (including real-time coordinates) with speed and accuracy. In this poster, we present our mobile image processing and quantification pipeline used for plant phenotype analysis. We describe our plant phenotype database where collected and analyzed image data can be accessed. The database itself was constructed with MySQL. The images are stored in a separate web directory and linked to the database (far more efficient than direct upload). To access the database from the front end web application we utilized PHP, as it interacts nicely with SQL databases. The front end of the web application was developed using several languages and frameworks. PHP and JavaScript’s AJAX functions were useful for displaying information pulled off of the database. The actual web application visuals were created using a combination of jQuery, jQuery UI and Bootstrap frameworks. Our online, searchable plant image database also incorporates storage of meta-data, expert annotations and quantification results gathered from our mobile plant image analysis application.
Comparative inflammatory gene expression in duct-ligated salivary glands of wild type and P2X7 nucleotide receptor knockout mice
Julie E. Bays, Jean M. Camden, Lucas T. Woods, Laurie Erb, and Gary A. Weisman

Abstract withheld at the request of the faculty mentor for proprietary purposes.
Ambreka Benons
Queens, NY
CUNY - Medgar Evers College
Biology
Senior

Faculty Mentor: Dr. Bumsuk Hahm, Molecular Microbiology and Immunology, Surgery
Funding Source: NIGMS RISE Grant to Medgar Evers College; Summer Research Internship in Cell & Molecular Biology

S1P lyase promotes the type I IFN response
Ambreka Benons, Madhuvanthi Vijayan, and Bumsuk Hahm

Abstract withheld at the request of the faculty mentor for proprietary purposes.
Modulation of voltage-gated sodium channels by auxiliary proteins
Benton R. Berigan, Tyler G. Carron, Marco A. Navarro, and Lorin S. Milescu

Voltage-gated sodium (Nav) channels play a key role in the initiation and propagation of action potentials (APs) in mammalian neurons. Nav 1.2 and 1.6 subtypes are highly expressed in the axonal initial segment (AIS), the site where APs are generated. Fibroblast Growth Factor Homologous Factors (FHFs), members of the Fibroblast Growth Factor (FGF) family, are thought to co-localize and interact with Nav 1.2 and 1.6, competing with the intrinsic inactivation of the channel. This competition can potentially alter the availability of the Nav channels to generate APs, and thus can change the firing properties of the neuron. We are investigating the relationship between FHFs and Nav channels using immunohistochemistry, to determine their relative expression levels within the neuronal circuits responsible for generating respiratory rhythm in mammals. Our preliminary data confirm co-localization of FHFs and Nav, as determined by two-photon microscopy. In future studies, we will explore the functional relationship between FHFs and Nav channels.
Annotation of U8 snoRNA genes in the human genome
Sarah Biehn and Brenda Peculis

Abstract withheld at the request of the faculty mentor for proprietary purposes.
The effect of caterpillar herbivory on the induction of phenolic compounds in Arabidopsis thaliana MSL mechanoreceptor mutants

Samantha Breckenridge, Dhruveesh Dave, Clayton Coffman, Rex Cocroft, and Heidi Appel

To defend themselves against herbivores, plants produce chemicals that can deter feeding. Plants produce more of these chemicals when they detect that they are damaged. We asked whether plants use mechanoreceptor proteins to sense this damage. To test this, we used three genotypes containing mutations in the Arabidopsis thaliana mechanoreceptor family, MSL (MscS-like): the triple mutant msl4 msl5 msl6 (3X), the double mutant msl9 msl10 (2X) and the quintuple mutant msl4 msl5 msl6 msl9 msl10 (5x). We then challenged the plants with caterpillars in clip cages, using empty clip cages as controls. Forty-eight hours later, the concentration of phenolic compounds was measured in caged and uncaged leaves. Plants with caterpillar damage had higher levels of phenolics in the damaged leaves than in leaves from the plants that were not damaged. The extent to which the levels increased differed among the MSL genotypes and the type of phenolic.
Phylogeny of the tribe Brassiceae
Julia Brose, Jacob Washburn, and J. Chris Pires

The tribe Brassiceae (Brassicaceae) includes a multitude of diverse plants with economic and ecological importance. Many of these are consumed worldwide and some are used as fuels. For example, *Brassica oleracea*, includes cabbage, cauliflower, kale, broccoli, and other edible vegetables; while *Brassica napus* is used as oil (rapeseed or canola). Although the tribe Brassiceae has received considerable attention, its phylogenetic history remains poorly understood. To better understand the tribe’s evolutionary history, we inferred a more reliable phylogeny of twenty-five representative species. Genome survey sequencing (GSS) data was used to create a phylogeny based on almost all of the chloroplast coding regions (over 75 genes). Our improved phylogeny not only reveals the relationships between species within the tribe, but also gives insight into the evolution of traits.
Regional flora as electron reservoirs for the production of environmentally friendly gold nanoparticles
Matthew Brown, Hannah Huhman, Sagar Gupta, Chung-Ho Lin, Shibu Jose, and Kattesh Katti

Electrons, which are sources of energy, are abundantly available in our universe. However, tapping them as energy resource, without causing negative environmental footprint is a significant challenge. Our research project is aimed at utilizing the enormous reservoir of electrons available in a plethora of antioxidant-phytochemicals within herbs, shrubs, and perennials—all constituting regional flora. Toward this objective, we have explored the possibility of utilizing electron rich phytochemicals (called as antioxidants) available within flora native to the Missouri region for the synthesis of gold nanoparticles. We have chosen to focus on Swiss Mountain Pine, American Arborvitae, and Switchgrass. American Arborvitae and Switchgrass are both native to the Missouri region, while Swiss Mountain Pine is native to southern Europe, but flourishes within the Missouri region.

The electromagnetic absorbance of these nanoparticles is being tested with UV spectroscopy. The nanoparticles are being tested with Zetasizer, a system designed to characterize the electrokinetic potential and hydrodynamic size of the particles. The results of these tests show that the electrons from various phytochemicals present in these plant species can be injected into gold salt resulting in the production of gold nanoparticles. The nanoparticles created are small in size ranging from 1.058 nanometers to 16.33 nanometers, and have electrokinetic potentials between -13.7 mV and -26.4 mV.

Gold nanoparticles are used in a variety of applications, ranging from medical applications to future energy sources. They have shown great promise in the detection of a variety of cancers, as well as therapeutic treatment of these ailments. Gold nanoparticles have tremendous potential in the biofuels industry.

It is clearly advantageous to both research and industry to use nanoparticles synthesized in an environmentally friendly way, and through this research we have discovered the enormous potential of green nanotechnology to connect agricultural economy with the emerging nanotechnologies.

This work was supported by the National Science Foundation award "Research Experience for Undergraduates in Materials and Modeling" (#1359430)
Small viruses, big killers of bacteria
Courtney Buchanan, Hedieh Attai, George Smith, and Pamela Brown

Phage therapy is a host-specific alternative to antibiotics that may provide a naturally occurring way of killing plant pathogens. Agrobacterium tumefaciens is a bacterium that causes crown gall disease in flowering plants. I have tested 35 water and soil samples from a variety of environmental sources for lytic activity against A. tumefaciens. Thus far, I have isolated and purified one bacteriophage that forms large plaques on lawns of A. tumefaciens cells. We find that Agrophage (AP5) is lytic using growth curve analysis. The lytic properties and large plaques formed by AP5 are similar to phages AP2 and AP3 which were previously isolated in the Brown Lab. Growth curves of all three phages indicate that they start killing A. tumefaciens cells around the same time and have the same shape curve, supporting the possibility that the phages are related. As the multiplicity of infection decreases, AP5 seems to kill A. tumefaciens cells more rapidly. I am testing the specificity of phages AP2, AP3, and AP5. By spotting the phage on lawns of different strains of bacteria I was able to show that AP3 has a narrow host range. I am presently testing the specificity of phages AP2 and AP5. Restriction pattern fragment analysis of DNA from AP2, AP3, and AP5 determines that these three phages are closely related at the genomic level. In addition, transmission electron microscopy reveals similar morphologies of polyhedral heads for AP2, AP3 and AP5. Finally, we will use potato disk assay to test the effectiveness of using bacteriophage in preventing tumorigenesis. We expect that further characterization of phage AP2, AP3 and AP5 will give better insights into the use of bacteriophage as antagonists of A. tumefaciens.
Searching for the genes associated with the placentation of mammals
Katie Burch, Taylor Maurer, Yue Hao, and Gavin Conant

The genetic underpinnings of many significant evolutionary transitions, such as the origins of placentation, are poorly understood. Here, we attempt to identify the orthologous mammalian genes whose evolutionary origins coincide with the radiation of the placental mammals. Orthologs are homologous genes in different species that last diverged at a speciation event. These genes tend to conserve molecular and biological functions over time; as such, they are ideal for studying genetic evolution in addition to predicting gene function. In this study, the genomes of 38, primarily mammalian, species were compared against the human genome using a previously developed orthology assignment pipeline in order to determine the genes associated with the evolution of the placenta and internal mammalian development. This pipeline compares the gene sequences of two species with pre-determined sequence similarity parameters to identify genes with sequences similar enough to potentially be orthologs. These parameters include a word length for spawning potential matches, the pairwise percent identity of each pair, and their non-synonymous divergence. By adjusting these parameters in various trials we were able to identify a set of values — word length of 7, percent identity of 50%, and a $K_a$ threshold of 0.4 — that yielded the greatest number of orthologs for the comparison of relatively diverged genomes (e.g., humans and marsupials). We then mapped the orthologs to a phylogenetic tree and reconstructed the ancestral orthology states. Future work will include performing further orthology pipeline optimizations using the adjusted parameters on the remaining 27 species. We will then use a Gene Ontology analysis to infer molecular functions for the genes that appeared around the time of origin of the placental mammals. Further studies will involve conducting a multiple sequence analysis to infer instances of directional selection acting on genes at the time of the placental radiation. The long-term goal is to better illuminate the genetic origins of evolutionary innovations.
Faculty Mentor: Dr. Ferris Pfeiffer, Bioengineering  
Funding Source: College of Engineering Undergraduate Research Program

**Development of an *in silico* method for visualization of pelvic fractures and reconstruction**  
Kate Burkhardt, Lauren Cook, Brett Crist, and Ferris Pfeiffer

As of now current methods for evaluation of complex pelvic fractures are insufficient. The goal of this project is to develop a computational method for segmentation and manipulation of pelvic CT data. This will allow pelvic fractures to be visualized, and analyzed systematically. Therefore, computational methods via computer simulation are required in order to allow for a more complete 3D visualization for the patient anatomy. So far in this project I have been able to contribute to the development of computer algorithms for segmentation and manipulation of multiple CT datasets. I was able to achieve this with the implementation of FORTRAN code, which is how the CT data scans are manually manipulated. This method is successful, but not ideal. I hope eventually to develop an algorithm that automates the manipulation. I have completed three cases and am continuing to keep working on more. Within the next week I will be meeting with colleagues from the Department of Orthopedic Surgery to see where they would like the project progress from here. I am also expected to perform computational analysis in the form of finite element analysis. In addition to that I will design higher algorithms, perform data analysis of results including statistical analysis, generate a report of project findings upon completion, and contribute to manuscript generation and editing as a co-author.
Faculty Mentor: Hannah Reeves, Art
Student Research Partner: Courtney Buchanan (Dr. Pamela Brown, Biological Sciences)

De-coronation of the gall
Benjamin Cairns and Hannah Reeves

Students in the summer 3D Design Art class were paired up with an MU undergraduate researcher for their Wood Relief Project. After discussing the research project with their student partner, art students visited the research lab and obtained any visual support materials that the science researcher could offer. The student researcher’s project was the inspiration for the art student’s 24” x 24” wood relief art. The artwork attempts to conceptualize the research from a new perspective, abstracting and interpreting the ideas and impact of the research topic. Student art pieces will be displayed alongside the undergraduate research poster during the Forum.

Courtney Buchanan has been participating in research centered on bacteriophages—viruses that infect and replicate within bacteria—for this past term. In so doing, she and her colleagues are hoping to circumvent adverse effects of bacterial growths—such as crown gall disease—in agricultural products without the use of potentially harmful chemicals. Since the bacteria that affect plants constantly build immunities (like what occurs with antibiotics in animals), she and her fellow researchers regularly attempt to isolate new phages.

My overarching goal in this project was to visually represent integral aspects of this area of research. I created a relatively symmetrical image of two stem-like objects, one with a growth and one without. Since crown gall and similar diseases also affect trees, I chose to keep the woodgrain texture with a light stain so as to not distract from the plant-based medium. In the background, I attempted to mimic the dome-shaped reaction that occurs on potato slices, which the researchers infect with the bacteria and treat with the phage. Since the phage reduces the number of domes, or areas of “clearing,” there are fewer domes on the far right than in the middle, which was intended to appear similar to an untreated sample.

Mostly, this piece is composed of carved elements, featuring stems that were cut from large, carefully shaped wooden blocks and a similarly carved base. I feel I was especially successful until I stained the surface, which turned out darker than I’d hoped, as certain areas were more porous than the piece of wood I’d tested the stain on. Further, if I’d had the time, I also would have liked to touch up some areas with wood putty and coated the surface with polyurethane for a more glossy and cleanly finished appearance. Overall however, given the time constraint, I’m happy with the outcome.
Life within the cell - Collaboration work with science student
Shaoyang Chen and Hannah Reeves

Students in the summer 3D Design Art class were paired up with an MU undergraduate researcher for their Wood Relief Project. After discussing the research project with their student partner, art students visited the research lab and obtained any visual support materials that the science researcher could offer. The student researcher’s project was the inspiration for the art student’s 24” x 24” wood relief art. The artwork attempts to conceptualize the research from a new perspective, abstracting and interpreting the ideas and impact of the research topic. Student art pieces will be displayed alongside the undergraduate research poster during the Forum.

The scientist I work with studies the process of pathogen defense inside the plant body to prevent the decrease in agriculture output and loss of global harvest. On the surface of cell body, there are a number of receptors. Similar to how human bodies defend themselves from diseases, once the receptor detects something harmful to the plant, the cell body will automatically consume the receptors inside its body along with the harmful chemicals using Clathrin.

Personally, I’m a strong believer of natural evolution so I believe life originates from the ocean. So in my model, I painted the whole background in a dark navy color to represent the inside of the cell. To better present different part of the cell, like the surface and inside of the cell, I used different blue color to add more depth. In addition, I carved inside the board to add more dimensions to illustrate different layers inside the cell body. I also use the irregular orange shape to represent Clathrin. The yellow, question-mark shape thing represents the receptors on the plant body. The green and blue circles among receptors represent the cell body. On the left, I also made a green cylinder sticking outside to represent the plant that scientists use for research. Inspired by a picture that use fluorescence protein to show how this process works inside the cell body, I decided to set the base of this model with a dark blue color and add some little green dots all over the model. It is interesting to view the blow-up vision of this process while having those little green dots to remind us that such tiny things inside our cell body operate this process. In addition, instead constructing the cell body with a specific shape of circle, I want to construct the cell body with different shades of blue to bring out the oceanish feel to make the process seem more vibrant and liquid. Moreover, I carved inside to achieve the visual effect that the cell body is swallowing those “toxic” receptors inside. And this turns out to be my favorite part about the work.
Faculty Mentor: Dr. Heather Hunt, Bioengineering
Funding Source: University of Missouri System Intellectual Property Fast Track Funding Program

**Waveguide protocol fabrication**
Jeff Chininis, Paul Whiteside, and Heather Hunt

Abstract withheld at the request of the faculty mentor for proprietary purposes.
Efficient CRISPR/Cas9-mediated gene-knockout in soybean using hairy root transformation
Matthew Chisholm, Michelle Folta, and Zhanyuan Zhang

Genetic improvement of soybean yield and nutrition is highly desirable. There exist several transgenic approaches to modify soybean, however these approaches suffer from constraints. One major constraint is the consumer’s concern about genetically modified organisms (GMOs) which are costly and highly regulated by the government. The new gene-knockout system, CRISPR (clustered regularly interspersed short palindromic repeats), is capable of modifying plant genomes, and subsequently being removed from the modified genome through breeding. As a result, the modified plants can be considered non-GMOs. Jacobs et al. (2015) showed that the human codon-optimized Cas9 (CRISPR associated protein 9) was able to modify marker genes in the soybean genome. To further investigate the utility of the CRISPR/Cas9 in editing soybean endogenous genes, we are determining the effectiveness of the human codon-optimized Cas9 on knocking out three economically important genes. These genes are RS2, KTi3, and FAD2 which effect sugar, protein, and oil contents in soybean, respectively. To do this, we introduced CRISPR/Cas9 transgene to wild-type soybean genome using hairy root transformation. The hairy roots were collected and analyzed to determine the effectiveness of Cas9-mediated gene modification. In addition, possible enhancements to the hairy root transformation protocol were explored. The results from this research are expected to validate the effectiveness of the Cas9 on soybean gene-editing and to increase hairy root transformation efficiency.
Identification and characterization of the Carbohydrate partitioning defective1 mutant
Laura Cipriano Crapina, Benjamin Julius, Robert Baker, Mark Lubkowitz, and David Braun.

The high incidence of nucleotide sequence diversity as well as a highly sequenced genome promoted maize as a model organism for the genetic study of carbohydrate partitioning in plants. Carbohydrate partitioning is characterized as the process by which plants transport sugars, predominantly sucrose, synthesized in photosynthetic source tissues (e.g. leaves) to non-photosynthetic sink tissues (e.g. roots, flowers, fruits and seeds). Despite the essential nature of this process little is known about its genetic basis. Carbohydrate partitioning defective (cpd) mutants are incapable of transporting sugars properly from sources to sink tissues, which results in accumulation of carbohydrates in the leaves. Cpd1 is a semi-dominant mutant whose phenotype consists of chlorosis, accumulation of anthocyanins, and short stature plants. Mutants such as Cpd1 have been used to determine the genes involved in whole-plant carbohydrate partitioning. In order to clone the gene underlying the Cpd1 mutation, a positional cloning strategy is being used. A polymorphic mapping population was created and bulked segregant analysis (BSA) was conducted to determine the chromosomal region containing the mutation. Fine mapping is currently in progress. The knowledge gained through this project is essential to elucidate the metabolic pathways related to sugar transport as well as to guide possible genetic improvements of organisms that are key to food and fuel production, such as maize and sugar cane.
Role of clathrin-coated vesicle networks in plant growth and responses to bacterial flagellin
Alex Clarke, Erica LaMontagne, and Antje Heese

Abstract withheld at the request of the faculty mentor for proprietary purposes.
Diffusion-limited deposition using MBE for the development of compliant substrates
Nicholas Cole and Gregory Triplett

Advances in the computing and sensing world have been limited by the inability to create high-quality, low defect density, complex heterostructures. For years, semiconductor heterojunctions have been restricted to compounds with similar lattice constants to create necessary high-quality interfaces. This limitation has significantly narrowed possible material combinations and applications.

When trying to produce a structure of two materials with incompatible lattice constants, the traditional approach has been to gradually change the surface lattice constant by using a compositional gradient of multiple layers. The problem with this is that these layers increase the amount of defects in the sample and they propagate vertically to the material’s surface, significantly decreasing quality and performance. Through this research effort, we attempt to develop a method for creating abrupt heterojunctions between lattice-mismatched materials based on out-of-plane diffusion. If this approach can be refined, it would allow any semiconductor material to be grown on a number of substrates, offering tremendous design flexibility in material properties and cost, thus opening up a new realm of photonics and electronic devices.

To determine the viability of our new approach, we selected the combination of InSb on a GaSb substrate (due to the very high 6.3% lattice mismatch). We produced several samples by repeating the deposition of a pure cation (i.e. indium) monolayer followed by a long anion (i.e. Sb) soak, allowing the atoms to diffuse through the top layer. These samples were created under various processing conditions using a solid-source molecular beam epitaxy reactor and were monitored during growth for qualitative surface roughening using reflection high-energy electron dispersion. Samples are analyzed using Raman spectroscopy, scanning electron microscopy, and energy-dispersive spectroscopy. Preliminary results indicate the formation of single crystalline InSb and InGaSb on GaSb substrates, thus demonstrating that this approach can be viable for novel device structures.
The effect of caterpillar herbivory on the induction of phenolic compounds in *Arabidopsis thaliana* mechanoreceptor mutants
Dhruveesh Dave, Samantha Breckenridge, Clayton Coffman, Rex Cocroft, and Heidi Appel

To defend themselves against herbivores, plants produce chemicals that can deter feeding. Plants produce more of these chemicals when they detect that they are damaged. We asked whether plants use mechanoreceptor proteins to sense this damage. To test this, we used three genotypes containing mutations in the *Arabidopsis thaliana* mechanoreceptor family, MSL (MscS-like): the triple mutant *msl4 msl5 msl6* (3X), the double mutant *msl9 msl10* (2X) and the quintuple mutant *msl4 msl5 msl6 msl9 msl10* (5X). We then challenged the plants with caterpillars in clip cages, using empty clip cages as controls. Forty-eight hours later, the concentration of phenolic compounds was measured in caged and uncaged leaves. Plants with caterpillar damage had higher levels of phenolics in the damaged leaves than in leaves from the plants that were not damaged. The extent to which the levels increased differed among the MSL genotypes and the type of phenolic.
Nitrate resistance in *Desulfovibrio vulgaris* Hildenborough

Leslie Day, Kara De León, Hannah Korte, Sam Fels, and Judy Wall

The sulfate-reducing bacteria are nearly ubiquitously distributed soil anaerobes that are particularly troubling for the petroleum industry causing "souring" of oil and corrosion of pipelines. In oil fields, nitrate has been used as an inhibitor of the activities of these bacteria. We are using *Desulfovibrio vulgaris* Hildenborough (DvH), a model strain for these bacteria, to explore the mechanism of nitrate sensitivity and spontaneously developed resistance. Previous work in our laboratory showed that DvH “adapted” to the presence of nitrate and retained resistance, suggesting a genetic change (*i.e.* mutation). To determine the naturally occurring mutations that result in nitrate resistance, six nitrate-resistant DvH cultures and one control were resequenced. We analyzed the data for significant single nucleotide polymorphisms (SNPs) and identified one in the predicted promoter region of DVU0251 and one within the gene itself. We hypothesize that these SNPs alter the function or expression of DVU0251 leading to nitrate resistance. To test this, I have created a deletion of the gene by marker replacement (MR), replacing DVU0251 with an antibiotic resistance cassette. Subsequently, I am creating a markerless deletion (MLD) which will remove the antibiotic resistance cassette. In the presence of nitrate, the ∆DVU0251 strain had a faster growth rate than the DvH parent strain, JW710. This result was congruent with DVU0251 being involved in nitrate sensitivity. The MLD construct will confirm that nitrate resistance is conferred by the deletion of DVU0251 and not by any polar effects of the antibiotic cassette. Future work includes testing the SNPs identified by sequencing to explore the mechanism for nitrate-resistance development.
Quantitative proteomic analysis reveals potential actions of Sutherlandia and elderberry on ischemic brain in mice
Joseph Del Rosario, Hailong Song, Hui Zhou, Zhe Qu, Jiankun Cui, Agnes Simonyi, Shanyan Chen, Victoria A. Engel, Jilong Li, Jianlin Cheng, Michael Greenlief, Shuwei Li, Andrew L. Thomas, Kevin L. Fritsche, William R. Folk, Dennis B. Lubahn, Grace Y. Sun, and Zezong Gu

Abstract withheld at the request of the faculty mentor for proprietary purposes.
Sonia Dermer  
Williamsburg, VA  
College of William and Mary  
Neuroscience  
Junior

Faculty Mentor: Dr. David Schulz, Biological Sciences  
Funding Source: NSF Research Experience for Undergraduates in Neuroscience

**A-type potassium currents in bursting activity of cardiac motor neurons in the crab *Cancer borealis***

Sonia Dermer, Brian J. Lane, Pranit Samarth, and David J Schulz

It is fundamentally important that neurons giving rise to motor function provide the appropriate level of excitatory drive in order to produce the necessary response of the muscles. The neural circuit in the heart of the crab *Cancer borealis*, for example, must consistently be producing heart beats, despite any external environmental changes or internal physiological changes that the organism may experience throughout its life. This simple network, known as the cardiac ganglion (CG), is a central pattern generator composed of 9 cells: four pacemaker cells that give excitatory input to five large motor neurons, whose bursting results in heart muscle contractions. Each of these neurons has a distinct balance of several ionic currents that work together to give rise to that neuron’s output. In this experiment, we studied the role of the A-type potassium current ($I_A$) in CG motor neurons. In model simulations of the CG, $I_A$ activates an outward current during initial depolarization, and quickly inactivates. Following the dissection and pinning of the CG in physiological saline, the A-type potassium channels were blocked in the three anterior motor neurons, and the resulting fictive motor output was measured *in vitro*. While each network had varying responses, consistent patterns observed include the network having a longer burst duration, and motor neurons spiking earlier and more frequently in each burst. We interpret these results to confirm current CG models of $I_A$ affecting only the generation of the burst through the aid of inhibiting the initial depolarization, thought to prevent over-excitability. The difference in resulting electrical activity between CGs is believed to be the result of the initial varying intrinsic properties between networks and individual neurons.
Parallel discovery of transcription factor motifs through the use of hash tables
Justin Deters, John Long, and Michela Becchi

Transcription factor binding sites, which occur in the base pairs just before the transcription start site of a gene, determine when and where a gene is to be expressed within the organism. Genes sharing transcription factor binding sites are regulated by the same factors and generally act in biologically related processes. Previous work has focused on searching for particular motifs in functionally related genes. We seek to find similar motifs by comparing genes directly across dozens of genomes. We accomplish this goal in a multiphase computation. First, the transcription sites are extracted. Second, each gene's regulatory region is compared to every other regulatory region. Finally, the genes are grouped into a weighted graph. These phases are then parallelized to decrease computation time.

In the first phase, we use hash tables by extracting upstream base pairs from each gene, and insert and sort them into buckets. Sorting allows us to compare two buckets in $O(n+m)$ rather than $O(n*m)$ time. Hashing provides a deterministic method of inserting an element into a table in near constant time. Next, we compare the hash tables of the genes and assign similarity weights between every pair of genes. The building of the hash tables and pairwise comparisons are completely independent, making them good candidates for parallelization. The final phase takes the gene weights and constructs connected components among the genes. We assume that the connected components represent co-regulated genes. We find that hash insertion takes much less time than our queries when using hash tables in this way. Hash tables also benefit from small sizes due to the trade-off between traversal time and bucket length. We also found significant improvement in computation time compared to our serial implementation. This technique may help us find genes of similar function and understand the gene regulatory network.
For the 35 million people living with HIV, there exists no vaccine and resistance remains a concern. Our research is aimed toward engineering nucleic acids—aptamers—to bind and inhibit the reverse transcriptase enzyme (RT) of HIV responsible for replication. Previously, plasmid delivery systems have been used to express aptamers intracellularly; our approach utilizes a lentiviral delivery system to deliver anti-HIV RT aptamers into target cells. This approach allows targeting of specific cells where HIV replicates, and serves as a gene therapy tool to introduce aptamers into animal models via transduction of CD34+ hematopoetic stem cells. Before use in cell culture and animal models, the vector system must be optimized. Since we use an HIV vector to deliver an anti-HIV therapeutic, self-targeting of the vector itself by the aptamer is anticipated. Self-targeting will decrease aptamer accumulation in target cells. Therefore, we are testing different elements to ensure production of high titer vector with sufficient aptamer accumulation in target cells: diverse promoters, aptamer cassette orientation, and presence or absence of a Poly(A) tail. These elements are being tested to understand the effects on aptamer accumulation, self-targeting, and the titer of the lentiviral vector. We observed two aptamers and an arbitrary sequence which will not inhibit replication. The aptamer cassette was ligated into a lentiviral vector using restriction enzyme cloning. The clones were screened by PCR to identify vectors with correctly ligated aptamer cassettes. Transducing particles containing the aptamer cargo were then produced by co-transfecting producer cells with the lentiviral vector and helper plasmids. The virus will then be used to transduce target cells to deliver the aptamer. Transduced cells will be assayed to quantify level of aptamer accumulation and ability to inhibit HIV. Currently, we have identified positive clones and are now evaluating our optimized constructs.
Floral and Photosynthetic Evolution in the Cleomaceae: Is there a link to polyploidy?

Wade Dismukes, Patrick P. Edger, Hong An, M. Eric Schranz, Jocelyn Hall, and J. Chris Pires

Polyploid events, including whole genome duplication (WGD) and triplication (WGT), play a major role in the evolution of the flowering plants. The most recent WGD event found in the model plant Arabidopsis thaliana has been studied in the context of the evolutionary history of the Brassicaceae (the mustard family). Identifying when this WGD event happened and where it occurred on the family’s phylogeny has provided insight into the retention and loss of gene duplicates after polyploidy. Understanding the genome evolution of the flowering plants requires the placement of these polyploidy events. One such polyploid event, a WGT, has taken place in Tarenaya hassleriana (Spider flower) in the Cleomaceae, the sister family to the Brassicaceae. However, it is not yet known when or where this WGT occurred. To identify the timing and phylogenetic location of this WGT event, we sequenced the transcriptomes of nine species and used published transcriptomes and genomes for two other species of Cleomaceae. With these datasets, we will build gene trees and analyze synonymous substitution rates. Together, these results will allow us to (1) infer the first multi-locus nuclear gene phylogeny for these species of Cleomaceae, and (2) determine the location and age of the WGT event. Finally, we will analyze the WGT event and patterns of gene retention relative to novel traits that vary in the Cleomaceae, such as C4 photosynthesis, floral morphology, and secondary metabolites.
Faculty Mentor: Dr. David Schulz, Biological Sciences
Funding Source: NSF Research Experience for Undergraduates in Neuroscience

**Effects of temperature, axon diameter, and potassium conductances on conduction velocity of unmyelinated axons of the crustacean stomatogastric nervous system**

Gabrielle Dohmen, Clare Diester, Brian Lane, and David Schulz

Conduction velocity is an important aspect of neural network output, as appropriate timing of action potentials across multiple units must be maintained in order for appropriate output to be generated. Conduction velocity is ultimately regulated by both the physical properties of the axon and its environment, as well as the active conductances involved in action potential generation. Our goal was to better understand the impacts of abiotic factors such as temperature, as well as physical structure (axon diameter) and active signaling (K+ conductances) on conduction velocity. Our experiments were performed using the stomatogastric nervous system (STNS) of Cancer borealis (C. borealis). Because these invertebrate neurons are unmyelinated, this allows us to look solely at the properties of the axons themselves and not the interaction between axon and glia. We measured action potential timing of identified neuron subtypes at two different locations nerves of the same nerve using extracellular electrodes. From the action potential amplitude on the recording we made inferences about relative axon diameter, and then we manipulated either temperature or potassium conductances (using specific K+ channel blockers) to determine whether any of these parameters had an effect on conduction velocity. We then used these different parameter measurements and their effects on conduction velocity to update a mathematical model of conduction velocity in unmyelinated fibers.
The Role of the Rnf complex of *Desulfovibrio vulgaris* Hildenborough
Anita Donner, Thomas R. Juba, and Judy D. Wall

*Desulfovibrio vulgaris* Hildenborough (DvH), a prokaryote in the delta-proteobacteria class of sulfate reducing bacteria (SRB). These bacteria cause industrial problems from metabolic accumulation of corrosive sulfide and organic acids. These end products cause localized pitting of metals and oil souring. SRB use electrons from hydrogen and organic acids, such as lactate, to reduce sulfate. The cells generate an electrochemical gradient by proton translocation across the inner membrane to the periplasm. The resulting proton motive force drives synthesis of ATP via the ATPase, necessary for energy conservation. The Rnf complex, an ion-pumping ferredoxin: NADH oxidoreductase, may contribute to the electrochemical gradient. Previously reported, Rnf mutants in *Desulforvibrio alaskensis* G20(G20), have limited growth compared to wildtype, when hydrogen or formate are electron donors for sulfate reduction. Studying the role of Rnf in DvH we deleted genes *rnfAB*, creating JW5111 (an intermediate marker-replacement deletion mutant), and JW5112 (an in-frame markerless deletion mutant). The growth of the mutants, measured as optical density at 600nm(OD), was compared to wild type growth on three sulfate containing media with lactate, formate, or hydrogen as the electron donor, with and without yeast extract. On sulfate media containing lactate, growth of deletion mutants and wild type were similar with and without yeast extract; however, with hydrogen as the electron donor, growth of the mutants was limited without yeast extract. In contrast when grown with formate, there is an initial lag, but the mutants have a similar final OD to wildtype. Hydrogen or formate as an electron donor does not allow substrate level phosphorylation, requiring Rnf to pump ions, possibly explaining the lag in growth. Similar to the previous reports in G20, this supports a similar role for Rnf in DvH.
Observing spontaneous refreshing as a strategy for recall using the EEG

Ashley N. Douglass, Frederick L. Henry, Evie M. Vergauwe, Mason H. Price, Nelson Cowan, and Jeffrey D. Johnson

Learning is limited in many ways by short term memory, so attempting to understand how information is maintained in short term memory could provide insight on how to teach our children who have notoriously short attention spans, or even shed light on the mechanisms that govern the process of forgetting. In this experiment we tested the method used to maintain information in short term memory. Adult subjects were asked to recall four letters on each trial. Between successive letters there were four distractor trials (spatial fit judgments), so there were 16 distractors in all on a trial. An electroencephalogram (EEG) was used to test whether the subjects spontaneously thought about the letters between the distractor tasks in order to keep them in mind (a process called refreshing). Spontaneous refreshing is a process that is intended to explain the nearly perfect linear relationship found between the free time allowed between distractors and number of items correctly recalled. We will be able to identify refreshing if the computer can correctly classify the complex EEG data and differentiate between the typical output waves it receives from the subjects when thinking about letters versus spatial distractors. Since the data are still being analyzed, it is unclear if spontaneous refreshing occurs when subjects are trying to remember letters between periods of distraction.
Investigating the effectiveness of attenuated *Salmonella enterica* serovar Typhimurium as a vector for cancer therapy drugs on canine cell lines

Caroline Dunn, Robert Kazmierczak, Alison Fea, and Abraham Eisenstark

A large number of cancer therapy drugs have been developed. However, many drugs are non-specific and attack and kill healthy cells in addition to cancerous cells. To solve this problem, we are developing a chemotherapeutic-carrying cancer-targeting vector, nontoxic *Salmonella enterica* serovar Typhimurium (Salmonella), which preferentially targets and colonizes cancerous cells over healthy cells and in solid tumors, further infiltrates and colonizes the tumor mass. There, the Salmonella strain deposits the drugs throughout the tumor. This therapeutic Salmonella strain is engineered to carry nanoparticulate chemotherapeutic payloads such as paclitaxel. Trials with attenuated, tumor-targeting Salmonella have been completed in mouse models and the strain is now being tested in cancerous lymphoma canine cell lines. To show cytotoxic effect on canine cells, canine B cell lymphomas are grown in the lab then incubated with our therapeutic Salmonella strain for varying lengths of time. All three canine lymphoma lines tested have shown substantial killing in two hours or less. Results suggest that non-adherent cells may be more susceptible to Salmonella treatment. To demonstrate Salmonella invasion of canine cells, the same therapeutic strain of Salmonella containing a constitutively expressed fluorescent protein is incubated for varying lengths of time with the lines to see how frequently the salmonella invades the canine cells. Next the cell lines will need to be tested with varying concentrations of Salmonella to determine chemotherapeutic dosage delivery potential. Testing new types of canine cancer such as breast cancer and prostate cancer will determine which canine cancers are the most susceptible to this treatment. New information on Salmonella’s effects on cancerous canine cell lines will enable us to begin clinical testing of our therapeutic Salmonella in the veterinary clinic, and eventually in human treatments.
Nerve conduction velocity, or the rate at which an electrochemical impulse propagates down a neural pathway, is crucial for an animal’s survival. With slow nerve conduction, the response of the animal is slower, which can prove problematic, as shown by people with neurodegenerative diseases (CMT, ALS, etc.) Ways of improving this conduction velocity within axons are by optimizing: the axon diameter, the myelin thickness around the axon, or the internode length between Nodes of Ranvier. There are carboxyterminal tails on neurofilament medium (NF-M) and neurofilament heavy (NF-H) subunits that, according to the Cleveland lab in 2003, affect the rate at which radial growth occurred and the final size of the axons. My project is to see if these tail domains affect the internode lengths present in axons. I hypothesize that internodal length will be reduced without the carboxyl terminal tails because of the positive correlation between fiber diameter and internode length shown by the Young lab in 1948. To test this hypothesis, the internode length in wild-type mice will be compared to mice with truncated C-terminus tail domains. I utilize mice of the following genotypes for my study: WT controls, NF-MtailΔ, NF-HtailΔ, and NF-(M/H)tailΔ. These mice are raised until 6 months of age before extracting the fifth lumbar motor root from the spine of the animal. Using this root, individual motor axons are isolated, and internode length was measured. Results for the NF-MtailΔ show that the internode length of WT controls and NF-MtailΔ animals are not significantly different, indicating that the neurofilament medium C-terminus may be reducing internode length, but does not determine internode length.
Biomechanical evaluation of posterior cruciate ligament transection and repair in the human knee
Laura Evans, Andrew J. Polk, James L. Cook, Pat Smith, James P. Stannard, Mauricio Kfuri, Matthew Mooberry, and Ferris M. Pfeiffer

Isolated injury of the Posterior Cruciate Ligament (PCL), and compound multi-ligament injuries involving the PCL contribute to a large number of clinical orthopedic trauma cases. It is well known that these injuries contribute to anterior-posterior instability of the knee, and if left untreated, can lead to early arthritis of the knee. Numerous surgical repair techniques currently exist to treat PCL injuries, however the relative efficacy of each technique is debated.

The objective of this project is to examine the biomechanical effects of isolated PCL injury on anterior-posterior (A-P) stability of the knee, and to evaluate the effectiveness of various surgical repair techniques in restoring stability. This project will provide clinicians with a better understanding of the biomechanical function of the PCL, and will lead to improved clinical treatment of PCL injuries. We hypothesized that an isolated PCL injury will significantly destabilize the human knee joint in the A-P direction, and that reconstruction of the injury using one of three repair techniques will restore function to within 80% of the intact state.

Based on the results of this study, we conclude that posterior cruciate ligament attachment significantly contributes to knee joint stability in A-P shear. We also conclude that the method used for PCL reconstruction can significantly affect stability of the surgically repaired human knee in A-P shear.
Enhancers are generally cis regulatory elements that promote the expression of nearby gene(s) either upstream or downstream from their position. Enhancers contain binding sites for sequencing specific transcription factors (TFs) and recruit coactivators and RNA polymerase II to the promoter of the target genes. Since the first enhancer discovery in humans, many more enhancers have been discovered in different organisms and it is estimated that over 1 million enhancers reside in the human genome. Thus, efforts to globally identify enhancers have focused on the histone marks including H3K4me1 and H3K27ac. There has been tremendous development of technology and methodology to study the role of enhancers in gene expression. Recent technological advances, particularly the combination of chromatin immunoprecipitation (ChIP) with high-throughput sequencing (ChIP-seq), precisely investigate the genome-wide distribution of chromatin binding proteins and histone modifications in any sequenced genome. In particular, the method offers a clearer picture of the organization and functions of enhancer. This work focuses on the chromatin signatures involved in the genome-wide identification of enhancer elements in normal and malignant precursor B-cells and the characterization of their cell-type specific activities. DNA methylation and expression signatures define molecular subtypes of acute lymphoblastic leukemia. In cancer cells, enhancers become methylated and lose enhancer marks leading to the silencing of the neighbouring tumor-suppressor genes. Chromatin fixing and shearing optimization were performed. Preliminary nanodrop results revealed the amount of DNA present in precursor B-cells sample which is related to the broad absorption band at 260 nm. The absorption band is attributed to the $\pi-\pi^*$ transitions of the amine bases in DNA, which has an associated energy band gap ($E_g$) value of 4.7 eV. This, therefore, indicates the pure helix characteristics of extracted DNA. The integrity of the DNA was measured by electrofluorescence which revealed the average DNA base pairs relative to the ladder used as a reference. Other experiments include chromatin immunoprecipitation using H3K4me1 and H3K27ac followed by next generation sequencing of the DNA. This work represents the initial steps toward the optimization of the protocols necessary for identifying enhancers in acute lymphoblastic leukemia samples.
Comparing African “killer bee” and European honey bee genomes: Identifying structural variations that might affect behavior
Micah Fletcher, Jack Schoelz, J. Spencer Johnston, Darren E. Hagen, and Christine G. Elsik

Abstract withheld at the request of the faculty mentor for proprietary purposes.
Fibonacci: An in-depth look at the famed sequence and its impact on nature
Morgan Fryman and Dix Pettey

The Fibonacci sequence started as a theoretical solution to a rabbit population problem. It’s limit Phi however has since then been deemed “golden” in attributes and applied to a wide breadth of study. Our goal was to take scientific applications of Phi and check for validity. We focused on Fibonacci and Phi in botany. The main reason behind why we chose this specific area of study stems from a mistreating of this concept by elementary educators. Fibonacci numbers are attributed to helping kids become interested in mathematics by correlating the sequence to some physical properties in plants. We wanted to test whether there’s legitimacy to that claim.

Half of the first 10 integers are Fibonacci numbers. This posed the question whether the numbers of petals actually were a result of Fibonacci, or if those numbers occur because of the frequency of Fibonacci numbers in the first ten integers. We tested the main concepts of petal count and phyllotaxis (spiral and angle). High magnification was used to take pictures of spirals on flower heads. Petals of each flower were counted after. We targeted flowers with larger petal counts in an effort to reduce the effect of statistical probability. It was found that flowers with higher petal counts did not strongly favor Fibonacci numbers. After counting we examined the photographs and concluded that the spirals were not easily determined on the flower heads. In an effort to widen the scope of spiral possibilities, we looked at pineapple and pinecone spirals. From our very small sample size, it seems that pinecones most reliably favor Fibonacci spirals. Pineapples did not seem to favor the Fibonacci patter. To test angle phyllotaxis, the angles between leaves were measured. This was an area that seemed promising but will require a more botanical approach to truly understand.
Faculty Mentor: Dr. Brian Thompson, Life Science Business Incubator
Funding Source: Elemental Enzymes

Microbial degradation of alternative herbicides
William Galvin, Joy Bailey, and Brian Thompson

Abstract withheld at the request of the faculty mentor for proprietary purposes.
Identifying patterns among the structural, functional, and ecological underpinnings of cranial joints is imperative to understanding cranial biomechanics and evolution. Crocodylians such as the American alligator (*Alligator mississippiensis*) are capable of producing powerful bite forces which significantly load cranial joints. However, alligators also show marked changes in diet as they grow larger and it is unknown if joints change shape to accommodate the potentially larger loads they experience during ontogeny. Here we used 3D modeling and computational methods to determine joint surface areas, congruence, shape and pressures in two key craniomandibular joints in an ontogenetic sample of alligators. Because bite force increases with ontogeny, we expect joint surface area increases to cope with the increasing forces. We expect average pressures to stay similar throughout ontogeny. Surface areas and joint shapes collected from alligator CT data were complemented with previously-collected bite forces from the same individuals. Joint congruence and joint pressures were then calculated using basic geometric properties.

Although the surface areas of the jaw joints scale isometrically with skull length, the PMJ surface area scales with positive allometry. Jaw joint congruence and pressure remain constant throughout ontogeny suggesting they grow under biomechanical similarity whereas the PMJ is likely loaded more heavily in larger individuals. These findings indicate that although many aspects of alligator cranial shape and size develop in unison, the PMJ may not, offering important insight into ontogenetic changes in the biomechanical environment of the crocodylian skull. This is the first study that analyses scaling patterns of joint function in a reptile skull and data from this study will be incredibly valuable for further studies in the evolution of other crocodylians as well as dinosaurs, birds and other vertebrates.
Order of substrate binding in Xenorhabdus nematophila PvcB enzymatic pathway
Kennady Gee, Jing Zhu, and Peter Tipton

Abstract withheld at the request of the faculty mentor for proprietary purposes.
Moving Target Defense for resilient cloud management
Vladimir Georgiev, Allen Stage, Saptarshi Debroy, and Prasad Calyam

With the increasing cybersecurity threats, such as Denial of Service, Information Compromise to the cloud based services, intelligent defense counter-strategies are the need of the hour that do not significantly increase cloud management and administration costs. Moving Target Defense (MTD) based security mechanisms are gaining traction due to its potential to take proactive measures even before such cyberattacks are launched. However, the related research on MTD based cyber- defense strategies lacks effective preventive strategies as they incur significant management overhead resulting performance degradation to consumers of such cloud based services.

In this paper, we propose MTD based proactive and reactive virtual machine (VM) migration strategies that significantly decrease cyberattack success rate without causing considerable performance degradations to the consumers. Our scheme not only identifies the optimal VM location to migrate the services without compromising the service performance, but also evaluates the optimal frequency of proactive migration that is not too frequent to cause service interruption and too seldom to be vulnerable. We evaluate the effectiveness and efficiency of the scheme both numerically and using a large-scale GENI testbed. The results show that the proactive scheme successfully migrates VMs with low attack success rate and performance degradation; whereas, the reactive scheme successfully migrates a VM under attack and the connected regular consumers except the attacker to safety without the attacker guessing.
Competition among model lateral amygdala principal cells during Pavlovian fear conditioning
David Goodman, Feng Feng, and Satish Nair

Computational modeling of a neural circuit involves several steps. These include (i) defining the biological problem, (ii) translating biological data to inputs, outputs and constraints for the model, and then (iii) the development of the model itself using appropriate computational software packages, and (iv) investigating various cases by a process of iteration involving tuning model parameters within biological ranges. To develop a research background in modeling from start to finish, my research involved two projects. The first of these involved steps (i) and (ii) of the process above using the lower urinary tract of the mouse micturition system in normal and spinal cord injured states. For learning steps (iii) and (iv), I focused on modeling Pavlovian fear learning in the rodent lateral amygdala since steps (i) and (ii) were already completed for this project.

Competition among principal neurons (PNs) is an important part of learning in mammalian brains, as it allows a given network to form stable sparse representations of distinct input patterns, allowing the neurons to be tuned for different areas of the input space. Our group has shown how competition might take place among PNs in the lateral amygdala to get recruited to the fear memory trace using one particular connectivity configuration. In this study we explore various connectivity configurations to study whether competition holds during memory formation in other regions of the brain. During associative fear conditioning, the dorsal lateral amygdala (LAd) forms a fear memory trace (Han et al., 2007) involving PNs that display persistent increases in CS responsiveness that is even resistant to extinction training (termed long-term plastic or LP PNs). We explored whether this competitive mechanism would be applicable for different network connectivity configurations and the features these configurations have in common.
Recent clinical studies have identified phosphoglucomutase 1 (PGM1) deficiency as an inherited metabolic disease. Disease presentation can range from fairly mild to life-threatening. Phenotypes of the selected patients include dilated cardiomyopathy, stunted growth, exercise intolerance, and heptopathy, indicating the central role the enzyme plays in glucose metabolism. Multiple missense mutations of PGM1 enzyme have been identified, and 13 of these were studied biochemically in our laboratory. The mutants fall into two biochemical phenotypes: those with apparent folding defects and those with compromised catalytic function. To gain a better understanding of how these mutants alter the efficiency of PGM1, we are characterizing their 3D structure of selected missense variants using X-ray crystallography. Crystals are grown from purified samples of the mutant proteins, and X-ray diffraction data collected for structure determination. The 3D structures of the mutants are compared with wild-type enzyme to better understand how the mutations may affect the function of the protein. To date, we have collected X-ray data sets for wild-type human PGM1 to 1.75 Å and for the D263Y and R503Q missense variants, to 2.1. and 2.6 Å, respectively. Refinement of these structures is underway. Studying PGM1 protein structure through X-ray crystallography may provide insight to develop new therapies and pharmaceutical chaperones to promote proper folding/stability in patients with this congenital error in metabolism.
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Funding Source: NSF Research Experience for Undergraduates in Neuroscience

Modeling of uninjured and injured lamprey reticuspinal neurons
Steven Groff and Andrew McClellan

Abstract withheld at the request of the faculty mentor for proprietary purposes.
Effects of cognitive tasks on cardiovascular functioning and stress perception

Allison K. Halt, Bri N. Herriott, Brad J. Ferguson, and David Beversdorf

Previous research has shown that propranolol, a beta-adrenergic antagonist, was found to improve cognitive flexibility and performance on difficult tasks (Campbell, H.L., Tivarus, M.E., Hillier, A., & Beversdorf, D.Q., 2008). Propranolol was also found to be able to reduce the negative effects of stress on problem solving ability (Alexander et al., 2007). Additionally, recent studies showed that meditation training, or paced breathing, can decrease physiologic effects of stress (Park, Y-J & Park, Y-B., 2012). Therefore, it may be possible that paced breathing can work in place of propranolol and increase performance on cognitive tasks while also reducing physiological stress caused by completing problem solving activities. However, there can be disconnect between physiological arousal, as measured by heart rate, and an individual’s perception of their stress level. The goal of this project is to find a non-pharmacological method to increase cognitive flexibility and better understand the relationship between perceived stress and physiological stress caused by cognitive tasks. Such cognitive tasks include semantic and letter fluency, alternate uses task, compound remote associates, and anagrams. We hypothesized that paced breathing—as compared to normal breathing—will decrease an individual’s cardiovascular response to stress, as measured by electrocardiogram (ECG) and blood pressure readings, decrease his/her stress perception following administration of cognitive tasks, and improve performance on difficult cognitive tasks. Obtaining this information can better our understanding of the relationship between stress perception and cardiovascular functioning. It can also provide us with a better understanding of stress associated with test-taking and problem-solving and provide a useful and easy to implement breathing technique to help reduce stress.
A study of GPU traversal on uncompressed DFAs
Mateusz Haruza and Michela Becchi

Finite automata are pattern matching structures that are used in networking and search applications. This expression matching capability needs to be especially efficient in biological applications which have extremely large genomic and other datasets. Automata come in two different forms including deterministic and non-deterministic. Both forms come with their pros and cons. NFAs (non-deterministic finite automata) can have multiple active states at a time which in large NFAs may result in a high number of these active states requiring a varying amount of memory to keep track of which is an important consideration when considering compute devices with limited memory such as the GPU. NFAs however can be converted to DFAs (deterministic finite automata) with only one active state at a time. This comes at a cost however because during the conversion a state explosion can occur causing the DFA to have a high memory cost which again is not optimal for certain processing devices such as the GPU with smaller global memory spaces. Also in order to exploit the GPU parallelism we need to be able to facilitate large amounts of DFAs and input streams.

In this study we look at uncompressed DFA traversal on the GPU. Uncompressed DFAs being known for having one outgoing transition per character per state. The code for this study is made to take in as input different amounts of trace and DFA files, as well as different packet sizes, device numbers, number of blocks, and number of threads. This allows for the study of varying memory size transfers with varying numbers of execution blocks on various types of GPUs which have different CUDA capabilities and number of streaming multiprocessors. From this we can see the behavior of the GPU on different size inputs with different compute resources. The purpose of the study being to learn how to effectively use the GPU to process regular expression matching using finite automata.
Free electron model of Dirac bands in graphene
Brett Heischmidt, Scott Kissinger, and Sashi Satpathy

Graphene, a planar structure with hexagonal arrangement of carbon atoms, has been of considerable current interest due to its linearly dispersive band structure, the so-called Dirac bands, and because of its potential for future applications in electronics and medicine. Here we present a novel method for finding the electronic structure of graphene, where we consider a free electron traveling along the one-dimensional lines joining the carbon atoms, obtaining the energy eigenvalues from the boundary conditions of the individual wave functions. The characteristic Dirac band structure is reproduced and the one-electron density of states is obtained. The method allows us to study the transport properties as well as the electronic structure under the application of a magnetic field in a physical and intuitive way.
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Faculty Mentors: Dr. Nelson Cowan and Dr. Jeffrey Johnson, Psychological Sciences
Funding Source: NSF Research Experience for Undergraduates in Neuroscience

Searching for spontaneous refreshing: Using EEG to decode the content of working memory
Frederick Lee Henry III, Ashley Douglass, Evie Vergauwe, Mason Price, Nelson Cowan, and Jeffrey Johnson

The human consciousness has many different aspects under study. One aspect that has seen particular scrutiny is working memory. Working memory is a cognitive system responsible for maintenance and processing of information. One can understand this through the Time Based Resource-Sharing (TBRS) theory. This theory proposes processing and maintenance share a common resource: attention. This shared resource focuses only on one function at a time. Consistent with this model, it has been observed that memory performance is inversely related to the proportion of time during which a concurrent processing task captures attention. Therefore, when attention is used for processing it is unavailable for the reactivation of memory traces of items to be remembered, through a process called refreshing. There exists, however, no direct evidence for the idea that people refresh. Behavioral studies have attempted to provide evidence but have yet to be successful. The present study aims to find direct evidence for spontaneous refreshing, that is, refreshing that occurs naturally without provocation. This was done making use of electroencephalogram (EEG) to obtain event-related potential (ERP) evidence. Pattern recognition techniques were used to identify the process of refreshing within the ERP results to examine whether, if given the opportunity, individuals spontaneously refresh between processing episodes. Machine learning was used to train software to recognize ERP patterns based on a learning phase in which the participant is presented with only one thing at a time (letters, or nonverbal distracting task items). Data are still being analyzed, though if participants performed as predicted a clearly recognizable pattern will be observed between processing episodes which corresponds to the instances where participants were certainly maintaining letters. If evidence for spontaneous refreshing is found the groundwork for further elaboration of the TBRS theory will be laid and an insight into better learning techniques will be achieved.
Surface functionalization of Whispering Gallery Mode microcavities for specific detection of detection of Helicobacter Hepaticus

James Hermansen, Mark Anderson, and Heather Hunt

The current standard for bacterial detection is culture testing. This method generally requires bulky equipment, specialized training, and takes a relatively long time to receive reliable results. This creates the demand for a bacterial testing method that is faster and more sensitive. Here, we present a Whispering Gallery Mode (WGM) optical microcavity-based sensor designed to be specific for the detection of Helicobacter Hepaticus. WGM optical microcavity sensors were chosen because they have been shown to detect Helicobacter Hepaticus at concentrations as low as $1 \times 10^4$ cells/mL and within 750 seconds using a non-specific sensor. Using silane coupling agents and grafting techniques, we have created a microsphere coated with Toll Like Receptor 2 (TLR2) for the specific detection of Helicobacter Hepaticus. The devices will be characterized via quantitative cavity analysis before and after functionalization, and optical and fluorescence microscopy. Control experiments on 2 um silica on (100) silicon wafers will be carried out in parallel, and will allow the surfaces to be characterized via ellipsometry, contact angle measurement, and profilometry to probe the thickness, hydrophobicity, and surface roughness of the generated coatings, respectively. The concentrations we plan to use for the sensing study are on the orders of $10^2$, $10^3$, $10^4$, $10^6$, and $10^7$ cells/mL. With this information we hope to lower our limit of detection below that of biological infection, $1 \times 10^3$ cells/ml, as well as present a new standard for specific bacterial infection.
Mechanisms for adaptive variations in locomotion: Turning maneuvers in the lamprey
Alicia Hoagenson and Andrew McClellan

Abstract withheld at the request of the faculty mentor for proprietary purposes.
Arbuscular mycorrhizal fungi (AMF) interact with over 80% of all land plant species and assist plants in absorption of nutrients and water. AMF increase the surface area over which plants absorb water as well as increase soil aggregation size, thus increasing soil water retention. AMF community composition and diversity influence plant productivity, however it is unclear whether AMF composition and diversity impact plant productivity and establishment through impacts on plant drought tolerance. AMF are dominant in grassland systems, where drought is predicted to become more frequent due to climate change. To determine the effect of AMF composition on drought tolerance and seedling establishment, we exposed native prairie grass *Schizachyrium scoparium* (little bluestem) seedlings to soil inocula collected from six calcareous prairies and six calcareous glades that we predict vary in AMF composition. As a control, we introduced half of the seedlings to sterile soil with non-mycorrhizal microbial wash from the same sites. Four plants from each treatment were grown in drought conditions (watered every 3-4 days), and four plants from each were watered daily. We predicted seedlings grown in drought conditions with AMF present would experience higher survival and growth rates than those exposed to drought without AMF. Because glade plant communities experience more severe drought conditions than prairies, we predicted glade AMF communities would better aid seedlings in drought tolerance. At this point, three weeks after the beginning of the experiment, soil sterilization, soil source identity, and drought exposure have no significant impacts on seedling growth or survival. In the drought treatment, initial seedling height has a stronger impact on seedling survival than the daily watering treatment, with larger seedlings showing higher survival rates. Final results from this experiment may help identify AMF communities that could be used to aid in grassland seedling establishment and drought tolerance.
Electrons, which are sources of energy, are abundantly available in our universe. However, tapping them as energy resource, without causing negative environmental footprint is a significant challenge. Our research project is aimed at utilizing the enormous reservoir of electrons available in a plethora of antioxidant-phytochemicals within herbs, shrubs, and perennials—all constituting regional flora. Toward this objective, we have explored the possibility of utilizing electron rich phytochemicals (called as antioxidants) available within flora native to the Missouri region for the synthesis of gold nanoparticles. We have chosen to focus on Swiss Mountain Pine, American Arborvitae, and Switchgrass. American Arborvitae and Switchgrass are both native to the Missouri region, while Swiss Mountain Pine is native to southern Europe, but flourishes within the Missouri region.

The electromagnetic absorbance of these nanoparticles is being tested with UV spectroscopy. The nanoparticles are being tested with Zetasizer, a system designed to characterize the electrokinetic potential and hydrodynamic size of the particles. The results of these tests show that the electrons from various phytochemicals present in these plant species can be injected into gold salt resulting in the production of gold nanoparticles. The nanoparticles created are small in size ranging from 1.058 nanometers to 16.33 nanometers, and have electrokinetic potentials between -13.7 mV and -26.4 mV.

Gold nanoparticles are used in a variety of applications, ranging from medical applications to future energy sources. They have shown great promise in the detection of a variety of cancers, as well as therapeutic treatment of these ailments. Gold nanoparticles have tremendous potential in the biofuels industry.

It is clearly advantageous to both research and industry to use nanoparticles synthesized in an environmentally friendly way, and through this research we have discovered the enormous potential of green nanotechnology to connect agricultural economy with the emerging nanotechnologies.

This work was supported by the National Science Foundation award "Research Experience for Undergraduates in Materials and Modeling" (#1359430)
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Investigating the self-healing property of the Airy beam
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The Airy beam is an accelerating beam that remains almost diffraction-free while its intensity features tend to transversely accelerate during propagation. The main lobe of the Airy beam can be recovered if it is blocked somewhere in space. This property is known as self-healing. Biomedical imaging methods such as deep tissue imaging and optical coherence tomography are potential applications that can utilize the Airy beam’s diffraction-free characterization. However, how the self-healing property impacts these applications is not clear. We hypothesize that there is an average distance that the self-healing property of the Airy beam can be observed in the turbid media. In our light scattering detection system a static object was placed in front of the beam so that it only covered the main lobe of the Airy beam, and, by doing so, we were able to see that the blocked main lobe was able to repair itself during the beam’s propagation. Our data suggests that the intensity ratio of the blocked main lobe and of the exposed side lobe increases as the beam propagates, and that there is a range in which the ration increases until the intensity of the main lobe and the intensity of the side lobe are the same. A better understanding of the range that the self-healing property of the Airy beam can be observed is a very important step toward real applications for this beam.
RNA binding: Understanding the properties behind RNA binding frequency
Nicholas Jackson, Matthew Martin, and Frank Schmidt

We are interested in the ways in which RNA can foreshadow contemporary living systems. The RNA world theory proposes that RNA, as a self-replicating catalyst, was a precursor to today’s genetic systems. RNA both stored genetic information and catalyzed the chemical reactions in primitive cells. Specifically, RNA can form a scale free network, which is characterized by a distribution function where there are a few “hub” RNA’s that interact with many partners. RNAs in the network are linked through these hubs. This kind of distribution is common to many biological systems. Our lab studies the structures of RNA binding as well as the properties that cause some hubs to have higher binding affinities than others. In order to measure the number of sequences that bind to the baits, we selected RNAs from a random library and ranked them by their relative reads per million (RPM). We used three well-characterized RNA loop motifs as baits and selected a population of RNAs that were able to bind each of these motifs, GAGA, UGAGAU, and UUCG. Deep sequencing of this population identified RNAs that were enriched during the binding experiment. In order to measure the amount of sequences that bind to the baits, we use the unit of measurement reads per million (RPM). Using sequences with different relative reads per Million (RPM) for each RNA bait, we tested for the strength of binding between RNA baits and the following sequences that bound to each hub. We thought that the higher the enrichment (relative reads per million) of RNA, the more likely a sequence is to bind to the baits. The previous experiments were used to determine which of the baits is a better binder. We hypothesized that GAGA would have better binding properties due to the frequency of appearance of GAGA in an RNA library. We hypothesized that the structure of GAGA and UUCG form stable tetraloops, which allow for more frequent binding than the less common hexaloop structure of UGAGAU. Deep sequencing identified the binding RNAs. The sequence templates used for binding the baits provide data that show the strength of binding. We want to demonstrate that selected RNAs will bind specifically to their baits. This observation would give detail into the forces behind formation of a scale free RNA network, supporting the RNA World theory.
What makes a neuron fast? The maximum firing rate depends on fine-tuned ionic conductance ratios
Elliot Jeon Lee, David J. Schulz, and Johannes Schul

The ability of a neuron to produce fast action potential rates is critical for the accurate encoding of fast stimuli in sensory systems. For example, in *Neoconocephalus* katydids, auditory neurons need to transmit pulse rates of 200-250 pulses/sec. We developed a biophysical neuron model in NEURON to explore the hypothesis that fast firing rates are made possible by fine-tuned ion channel conductance ratios. A BLAST search of a katydid transcriptome found voltage-gated sodium and potassium channels, which are typically important for AP generation. First we used a model with two ion channels, $I_{\text{Na}}$ and $I_{\text{Kd}}$. Varying the maximum conductance ($g_{\text{max}}$) of both channels independently revealed that continuous spiking occurred only for a $g_{\text{max, Na}}/g_{\text{max, Kd}}$ ratio range of 2.5–38. Within this ratio, lowering values of $g_{\text{max, Na}}$ and $g_{\text{max, Kd}}$ resulted in increased firing rates. At a given $g_{\text{max, Na}}$, reducing $g_{\text{max, Kd}}$ led to faster firing rates. Next, we added the Shaker channel. We kept $g_{\text{max, Na}}$ constant and varied $g_{\text{max, Kd}}$ and $g_{\text{max, Shaker}}$. Reducing $g_{\text{max, Kd}}$ and increasing $g_{\text{max, Shaker}}$ resulted in even faster firing rates, at the cost of narrowing the conductance ratio range in which multiple continuous spiking occurred. At a $g_{\text{max, Na}}$ value of 0.2 S/cm², a $g_{\text{max, Shaker}}$ value of 0.1 S/cm² allowed spiking in the absence of $I_{\text{Kd}}$ and generated the highest observed firing rate at 112 Hz. The results of the experiments conclusively showed that achieving high firing rates require fine-tuned ratios of low absolute ion channel conductances, Kd slows down firing rates, and that Kd can be replaced by Shaker to produce the fastest firing rates possible. The study supports our original hypothesis and allows greater understanding for the ionic channel and conductance mechanisms that allow neurons to generate high maximum firing rates.
A microassay system to investigate malignant tumor cell proliferation
Gabrielle Johnson, Stephanie L. K. Bowers, and George E. Davis

It is known that tumors arise from cells that are dividing uncontrollably. It is not clear whether the growth of malignant tumor cells is dependent on endogenous growth factors and signals versus their dependence on exogenous growth factors. To investigate such questions, we have set up an assay system using HT1080 fibrosarcoma cells that have been grown in two dimensions under serum-free conditions. In the assay we add growth factors exogenously in singles or in combination with one another. Interestingly, HT1080 cells can grow under these serum free conditions even without the presence of growth factors in vitro. We hypothesize that the addition of combinations of growth factors will increase growth of the HT1080 cells to a significant level, and these experiments are currently ongoing. If we are able to identify exogenous growth factors that spark an increase in growth then we can use siRNA knockdowns to see if our cells make these growth factors endogenously and if these same growth factors are functionally important. If we are able to find endogenous growth factors then we will be able to try and block the receptors that the growth factors bind to, thus stopping growth of the cell. Ultimately, if we are able to stop tumor growth we will try and transfer this system in vivo using a quail model for human tumor growth. This work might identify new approaches for cancer treatment.
Survey of social network structures
Stephen Jones, Mark Lewis, Kristopherson Culmer, and Wenjun Zeng

In today's society, online social networks (OSN) are one of the primary means by which people communicate, consume, and disseminate information about news, current events, etc. OSNs present themselves in many forms for expressed, differing, purposes; some as purely social networking sites like Facebook, content sharing networks like Twitter, and collaboration networks like DBLP. Intuitively, one might think because these OSNs serve different purposes that they will also be structurally different.

Our research investigates this intuition to determine the similarity or dissimilarity of OSN structures. We obtained datasets for Facebook and DBLP from online repositories and wrote a crawler to obtain a Twitter dataset. We analyzed the datasets from node-centric and network-centric perspectives using standard network metrics for comparison. Though we are still analyzing the data, initial findings show there are structural differences and similarities present. Further analysis needs to done before any conclusions are made.
Micro-dystrophin can partially restore myosin heavy chain distribution in the canine model of Duchenne muscular dystrophy
Joshua Kelly, Greg Jenkins, Chady H. Hakim, and Dongsheng Duan

Abstract withheld at the request of the faculty mentor for proprietary purposes.
A robust architecture for wireless data collection in mobile ambulatory assessment systems
Jay Kelner, Andrew Smith, Chen Zhang, Nickolas Wergeles, and Yi Shang

This study investigated the use of periodic synchronizations as a way to make a client-server mobile ambulatory assessment system (mAAS) more robust and energy efficient. This mAAS and similar systems can be used to collect vast amounts of data, so it was important to use an architecture that can manage data collection and communication efficiently. This paper presents the design we implemented to meet such needs, as well as an analysis of how we improved upon the previous design. We also discuss the energy efficiency trade-offs of semi-realtime communication with a server using varying packet sizes and varying intervals.
Effects of cross sectional area on bone strength in three strains of mice
J. Kyle Kirkland, Sarah J. Peacock, Brittney R. Coats, and Kevin M. Middleton

Bone's main function is load bearing, primarily through the cortical portion of the bone. When bones are unevenly loaded, such as in exercise, the cortical portion of the bone models itself to maximize the efficiency of the load bearing. Previous work has shown significant differences in cross-sectional properties of across mouse strains. We tested the strength of three strains of mice with bones that genetically differed in their cortical structure; low bone mass (C57BL/6), high bone mass (C3H/H3), and mini-muscle phenotype (MM) mice. Mini-Muscle mice, characterized by having a 50% reduction in the mass of the triceps surae in comparison to controls and run on a running wheel on average 2.5 times more. We estimated Young’s modulus, ultimate strength, yield stress, modulus of toughness, and ultimate strain using a three-point bending and compared mean values for the three strains. We found that the Young’s modulus was consistent with our predictions with C3H holding the highest values in both of our testing measures followed by B6J and lastly with MM. Ultimate strength and strain were consistent with our hypothesis when calculated based on the maximum stress but inconsistent when calculated based off the stress at failure. Lastly, modulus of toughness was the exact opposite of what was predicted. Based on these findings bone in C3H mice is consistently stiffer and has the greatest strength. Bone in C3H mice absorbs the greatest amount of energy up until the maximum stress point. While, bone in C57 mice absorbs the greatest amount of energy up until the failure point. Our results are consistent with findings of high mineralization in C3H mice and suggest that mineralization in MM mice may be similar to C57. Differences in loading response between C57 and MM may result from altered cross-sectional geometry.
KB Commons: A multi 'OMICS' integrative database framework
Timothy Klein, Thainan Bystronski Remboski, JiaoJiao Wang, and Trupti Joshi

The development of high-throughput technologies has significantly increased the amount OMICS data currently available for several organisms. These data are frequently scattered across different databases and studied independently. The independent analysis of OMICS data often does not portray an accurate account of processes occurring in a biological system. As result, there is a need for comprehensive web resources equipped with informatics tools that facilitate an integrative analysis approach to studying biological systems. SoyKB is a web-based resource developed to address the lack of integrative OMICS data analysis and has proven to be a great success with more than 400 registered users. It provides a bridge between soybean translational genomics and molecular breeding research. SoyKB contains large-scale data representing a range of soybean specific OMICS data including genomic, transcriptomic, proteomic and metabolomics. These OMICS data represent entities including genes, miRNA, SNP and metabolites.

In the current work we are expanding the SoyKB architecture to other organisms through the formation of “KB Commons” Knowledge Base framework. KB commons database aims to include data for additional biological models including Zea mays (maize) and Mus musculus (mouse). The database was populated with publicly available OMICS datasets representing a range of experimental conditions. An important feature of the KB Commons database is that users from the research community are able to upload data and share it with other members of the research community. Future KB Commons developments will include OMICS datasets for human data. KB Commons is a useful web-based tool that will serve as a publicly available and centralized resource for the comparative analysis of OMICS data.
Consequences of prenatal exposure to a mixture of fracking chemicals on folliculogenesis in mice
Kara C. Klemp, Chris D. Kassotis, Victoria D. Balise, Chaimaka J. Isiguzo, and Susan C. Nagel

The popularity of hydraulic fracturing (fracking) for natural gas and oil has been increasing in recent years, raising concerns about the process. Fracking is the act of forcefully opening fissures in the ground using high-pressure fluid in order to reach and extract natural gas and/or oil. There are approximately 1,000 known chemicals used in this process, including some known or suspected endocrine disrupting chemicals (EDCs), toxicants, and carcinogens. EDCs can cause adverse health effects through their ability to interfere with hormone action at low, environmentally relevant exposure levels. C57Bl/6 mice were time mated and exposed to a mixture of 23 hormonally active chemicals that are commonly used in fracking via their drinking water from gestation day 11 through birth. Six treatment groups were used: vehicle control (0.2% ethanol), positive control antagonist (50 mg/kg/day flutamide – anti-androgen), and 4 groups of the mixture with each chemical at 3, 30, 300, and 3000 mg/kg/day exposure. One unique female pup from each litter was collected at 21 and 85 days, ovaries were removed, fixed, paraffin embedded, sectioned, stained with hematoxylin and eosin, and follicle developmental stages were assessed. Our results suggest that developmental exposure to EDCs commonly present in fracking fluid and wastewater significantly affects mouse folliculogenesis at postnatal day (PND) 21. Two of our mixtures, Mix30 and 300, as well as flutamide, exhibited an increase in the percentage of more developmentally mature follicles, secondary and early antral. No significant differences in distribution of follicle stages were observed at PND85, though a trend was observed for increased atretic follicles in all treatment groups. Overall, our findings suggest that prenatal exposure to environmentally relevant concentrations of EDCs used in and produced by fracking can disrupt folliculogenesis and potentially accelerate pubertal development in female mice, which may lead to reproductive difficulties later in life.
Allelopathic properties of Virginia Rye exudate
Cynthia Koehler, Sam Delphin, Elizabeth Del Rosario, David Emerich, and Jason W. Cooley

Virginia Rye has been observed to prevent the growth of several species of moss and algae in both natural and controlled environments. Metabolic pathways of cyanobacteria can be manipulated through exposure to allelopathic substances. If the exudate from Virginia Rye is allelopathic, it could have significant implications for the study of light energy storage and harvesting. The aim of this project is twofold: to determine whether or not the Virginia Rye exudate is allelopathic towards the cyanobacterial models and to determine optimal concentrations most active in allelopathy so as to be able to use the exudate as a selective influence for studies of metabolic manipulation. Thus far, it has been found that the exudate significantly impedes growth at a concentration of 0.01 g/mL. Further studies will examine upper and lower limits of the concentration at which growth is impeded, as well as investigate the transcriptomic changes of the bacteria when they are exposed to exudates concentrations which both moderately and severely limit growth.
Clostridium botulinum is a Gram-positive, anaerobic bacterium that produces the highly potent neurotoxin, botulinum neurotoxin (BoNT). Through cleavage of a protein essential for docking synaptic vesicles to the presynaptic membrane, the toxin prevents neurotransmitter release at the neuromuscular junction, producing a flaccid paralysis known as botulism. Understanding the mechanism in which BoNT binds to and enters neurons is essential. One of the major variants of BoNT in pharmaceutical use is subtype BoNT/A1. A closely related subtype, BoNT/A2 has been shown to enter neurons with greater efficiency than BoNT/A1, resulting in enhanced toxicity. By generation of a mutated BoNT/A2A1 chimera protein, it was shown that BoNT/A1 and BoNT/A2 toxins have two different modes of binding to gangliosides-glycosphingolipids essential for the toxin’s binding and entry into neurons. BoNT/A1 binds ganglioside GT1b via hydrogen bonding and hydrophobic stacking interactions mediated by conserved residues located in the C terminal subunit of the binding domain. In comparison, binding of BoNT/A2 to GT1b appears to be stabilized by additional electrostatic interactions with residues in the N terminal subunit of the binding domain. The objective of this experiment was to determine which amino acid residue(s) in the N terminal subunit of the BoNT/A2 binding domain is responsible for greater affinity to ganglioside versus the N terminal subunit of BoNT/A1. Quick change site-directed mutagenesis was used to mutate six specific residues in BoNT/A1 binding domain to their respective BoNT/A2 counterparts. Using a solid phase binding assay, it was found that mutated BoNT/A1 bound to GT1b with greater affinity than wild type BoNT/A1, thus providing evidence that one or more of the six amino acids are responsible for the greater affinity of the BoNT/A2 N terminal subunit.
Using qualitative PCR to confirm gene expression changes between wild type and mutant Zebrafish embryos
Aishwarya Krishnan, Suman Gurung, and Anand Chandrasekhar

Several genes have demonstrated roles in motor neuron migration in the Zebrafish brain. For example, motor neuron migration is abolished in the embryos defective for the Vangl2 membrane protein. Using RNA sequencing, additional genes (sema6dl, lrrn1, sec24b, and itga6) were identified by comparing gene expression differences between wild type and the Vangl2 mutant. To validate the RNA sequencing data for these genes, I will perform qPCR to quantify differences in their expression between wild type and Vangl2 mutant embryos. Thus far, I have performed PCR with gene specific primers to distinguish between products derived from genomic DNA (contamination) and mRNA. I found that the RNA samples used for RNA sequencing have some genomic DNA contamination. To resolve this issue, the samples will be DNase I treated, and primers that span the exon-exon junction will be used. I will then be able to measure differences in gene specific mRNAs in the wild type and mutant samples using qPCR.
Anna Lauriello  
Columbia, MO

Faculty Mentor: Dr. Margaret Lange, Molecular Microbiology and Immunology; Dr. Donald H. Burke, Molecular Microbiology and Immunology, Biochemistry

Inhibition of HIV reverse transcriptase by aptamers through lentiviral vector delivery
Anna Lauriello, Creighton W. DeYoung, Esther Liu, Margaret J. Lange, and Donald H. Burke

For the 35 million people living with HIV, there exists no vaccine and resistance remains a concern. Our research is aimed toward engineering nucleic acids—aptamers—to bind and inhibit the reverse transcriptase enzyme (RT) of HIV responsible for replication. Previously, plasmid delivery systems have been used to express aptamers intracellularly; our approach utilizes a lentiviral delivery system to deliver anti-HIV RT aptamers into target cells. This approach allows targeting of specific cells where HIV replicates, and serves as a gene therapy tool to introduce aptamers into animal models via transduction of CD34+ hematopoetic stem cells. Before use in cell culture and animal models, the vector system must be optimized. Since we use an HIV vector to deliver an anti-HIV therapeutic, self-targeting of the vector itself by the aptamer is anticipated. Self-targeting will decrease aptamer accumulation in target cells. Therefore, we are testing different elements to ensure production of high titer vector with sufficient aptamer accumulation in target cells: diverse promoters, aptamer cassette orientation, and presence or absence of a Poly(A) tail. These elements are being tested to understand the effects on aptamer accumulation, self-targeting, and the titer of the lentiviral vector. We observed two aptamers and an arbitrary sequence which will not inhibit replication. The aptamer cassette was ligated into a lentiviral vector using restriction enzyme cloning. The clones were screened by PCR to identify vectors with correctly ligated aptamer cassettes. Transducing particles containing the aptamer cargo were then produced by co-transfecting producer cells with the lentiviral vector and helper plasmids. The virus will then be used to transduce target cells to deliver the aptamer. Transduced cells will be assayed to quantify level of aptamer accumulation and ability to inhibit HIV. Currently, we have identified positive clones and are now evaluating our optimized constructs.
Cellular membranes are ubiquitous in all known forms of life. They act as a selective barrier for what can enter the cell, such as specific ions, small molecules, and proteins. A good model for the cell membrane is a bilayer of lipid molecules, each consisting of a polar head group and two alkyl tails. For such a membrane to function, it must be well hydrated; that is, there must be a sufficient number of water molecules near its surface. Therefore, understanding how different lipid species interact with the interfacial water is of great importance. To elucidate the water-lipid interaction, we have investigated the effects of two different lipid species, which we denote by DMPG and DMPC, on the freezing and melting behavior of the hydration water. Neutron diffraction, which can be conducted at the University of Missouri Research Reactor (MURR), is one of the techniques that we use to study these phase transitions. The samples that we use for these experiments consist of a single bilayer-lipid membrane deposited onto a silicon substrate. By analyzing the intensity and scattering angle of the neutrons diffracted from the sample, we can investigate the structure of the solid water and its freezing/melting behavior. In particular, we would like to determine whether the interfacial water freezes into a crystalline or an amorphous structure. For both DMPG and DMPC membranes, preliminary results show evidence of a hexagonal crystalline ice structure (the most common form of ice). However, the temperature range over which hexagonal ice forms in the DMPG system is about twice as large as for the DMPC membranes. Furthermore, the maximum intensity of the Bragg peaks observed from the DMPG sample are about a factor of two smaller than for DMPC, suggesting that not all of the water in the DMPG system freezes into the hexagonal structure. Diffraction experiments planned for this summer are designed to confirm this preliminary finding.

This work was supported by the National Science Foundation award "Research Experience for Undergraduates in Materials and Modeling" (#1359430)
Survey of social network structures
Mark Lewis, Stephen Jones, Kristopherson Culmer, and Wenjun Zeng

In today's society, online social networks (OSN) are one of the primary means by which people communicate, consume, and disseminate information about news, current events, etc. OSNs present themselves in many forms for expressed, differing, purposes; some as purely social networking sites like Facebook, content sharing networks like Twitter, and collaboration networks like DBLP. Intuitively, one might think because these OSNs serve different purposes that they will also be structurally different.

Our research investigates this intuition to determine the similarity or dissimilarity of OSN structures. We obtained datasets for Facebook and DBLP from online repositories and wrote a crawler to obtain a Twitter dataset. We analyzed the datasets from node-centric and network-centric perspectives using standard network metrics for comparison. Though we are still analyzing the data, initial findings show there are structural differences and similarities present. Further analysis needs to be done before any conclusions are made.
Comparative analysis of nematode effector gene expression in soybean cyst nematode – soybean interactions
Ying Lin, Eric Penton, Michael Gardner, and Melissa Mitchum

Soybean cyst nematode (SCN) is a microscopic roundworm that lives in the soil and feeds on the roots of soybean. This nematode has the potential to reduce soybean yields by $1 billion annually, making it the most economically important soybean pathogen. Some soybean varieties carry genes that confer natural resistance against this nematode, but the widespread use of resistant soybean has selected for nematodes that have developed mechanisms to overcome soybean’s natural resistance. Therefore, the development of new management strategies against this parasite is necessary. In an effort to identify nematode genes important for infection, we used RNASeq to compare expression between per-parasitic juveniles and parasitic juveniles infecting either a resistant or susceptible soybean cultivar. A comparison of pre-parasitic to parasitic stages on either a resistant or a susceptible host identified 3,681 and 4,465 differentially expressed genes, respectively, as the nematodes infect and begin to feed from soybean roots. We bioinformatically mined the differentially expressed transcripts to identify those with a signal peptide and the lack of transmembrane domain in order to identify genes that might encode for effectors – proteins that are secreted into root cells to establish a parasitic interaction. From this analysis, we identified more than 550 nematode genes that encode for known or potential novel effectors. Interestingly, predicted effector genes are generally highly expressed in the susceptible interaction compared to the resistant interaction with very few exceptions. Among these exceptions was a class of effector – genes encoding for annexins. These genes appear to exhibit exon truncation, which is a form of alternative splicing, and may play an important role in SCN parasitism. The identification of effectors will not only increase our knowledge of nematode pathogenicity, but also provide potential targets to engineer nematode resistance.
For the 35 million people living with HIV, there exists no vaccine and resistance remains a concern. Our research is aimed toward engineering nucleic acids—aptamers—to bind and inhibit the reverse transcriptase enzyme (RT) of HIV responsible for replication. Previously, plasmid delivery systems have been used to express aptamers intracellularly; our approach utilizes a lentiviral delivery system to deliver anti-HIV RT aptamers into target cells. This approach allows targeting of specific cells where HIV replicates, and serves as a gene therapy tool to introduce aptamers into animal models via transduction of CD34+ hematopoetic stem cells. Before use in cell culture and animal models, the vector system must be optimized. Since we use an HIV vector to deliver an anti-HIV therapeutic, self-targeting of the vector itself by the aptamer is anticipated. Self-targeting will decrease aptamer accumulation in target cells. Therefore, we are testing different elements to ensure production of high titer vector with sufficient aptamer accumulation in target cells: diverse promoters, aptamer cassette orientation, and presence or absence of a Poly(A) tail. These elements are being tested to understand the effects on aptamer accumulation, self-targeting, and the titer of the lentiviral vector. We observed two aptamers and an arbitrary sequence which will not inhibit replication. The aptamer cassette was ligated into a lentiviral vector using restriction enzyme cloning. The clones were screened by PCR to identify vectors with correctly ligated aptamer cassettes. Transducing particles containing the aptamer cargo were then produced by co-transfecting producer cells with the lentiviral vector and helper plasmids. The virus will then be used to transduce target cells to deliver the aptamer. Transduced cells will be assayed to quantify level of aptamer accumulation and ability to inhibit HIV. Currently, we have identified positive clones and are now evaluating our optimized constructs.
Faculty Mentor: Dr. Donald H. Burke, Molecular Microbiology and Immunology; Biochemistry
Funding Source: NASA Exobiology Grant (NNX12AD66G) to D. Burke

RiboRegulation: RNA control through covalent modification
Melissa P. Lokugamage, Raghav R. Poudyal, Malak Benslimane, Mackenzie K. Callaway, and Donald H. Burke

The RNA World Hypothesis states that early life used RNA as both the genetic material and as catalyst for chemical reactions. This is unlike modern biology where DNA is the genetic material and proteins are the catalyst. In the RNA world, RNA could potentially have regulated other RNA creating pathways that are similar to our modern biology. We are studying covalent modifications catalyzed by RNA enzymes.

Our lab uses artificially selected RNA enzymes to modify a target functional RNAs to disrupt their function. Ribozyme K28min, which was selected for self-phosphorylation, has been engineered to recognize several functional RNA molecules. We have changed the internal guide sequence of the ribozyme to target molecules such as ATP aptamer, fluorescence “Mango” aptamer, and RzB4 hammerhead ribozyme. We have demonstrated that ATP aptamer loses its ATP binding function once it is thiophosphorylated. The fluorescence activity of the Mango Aptamer is turned off by K28min modification. The hammerhead ribozyme function is also modulated by K28 catalyzed modification. Our studies suggest that ribozyme catalyzed covalent modification can be a tool for regulating functional RNAs in synthetic biology. They also present a potential pathway used in the RNA World, furthering our understandings of the origins of life.
Verifying the FIR-radio relation in dusty starburst galaxies
Todd Lombardi and Haojing Yan

There is a tight correlation between radio flux and far-infrared (FIR) flux among galaxies with strong FIR emissions, which is thought to be due to strong star forming activities in such galaxies. The FIR-radio relation was discovered in nearby star-forming galaxies, and in this project we aim to verify this relation at higher redshifts. We used FIR data collected at the Herschel Space Observatory and radio data from the Very Large Array (VLA). As distance is needed in this calculation, we used the Sloan Digital Sky Survey (SDSS) to obtain the redshifts of the sources, from which we can calculate their distances. We confined our test to the SDSS stripe 82 region, in which we have constructed a sample of 168 objects. I will present the details of the results.

This work was supported by the National Science Foundation award "Research Experience for Undergraduates in Materials and Modeling" (#1359430)
Parallel discovery of transcription factor motifs through the use of hash tables
John Long, Justin Deters, and Michela Becchi

Transcription factor binding sites, which occur in the base pairs just before the transcription start site of a gene, determine when and where a gene is to be expressed within the organism. Genes sharing transcription factor binding sites are regulated by the same factors and generally act in biologically related processes. Previous work has focused on searching for particular motifs in functionally related genes. We seek to find similar motifs by comparing genes directly across dozens of genomes. We accomplish this goal in a multiphase computation. First, the transcription sites are extracted. Second, each gene's regulatory region is compared to every other regulatory region. Finally, the genes are grouped into a weighted graph. These phases are then parallelized to decrease computation time.

In the first phase, we use hash tables by extracting upstream base pairs from each gene, and insert and sort them into buckets. Sorting allows us to compare two buckets in $O(n+m)$ rather than $O(n*m)$ time. Hashing provides a deterministic method of inserting an element into a table in near constant time. Next, we compare the hash tables of the genes and assign similarity weights between every pair of genes. The building of the hash tables and pairwise comparisons are completely independent, making them good candidates for parallelization. The final phase takes the gene weights and constructs connected components among the genes. We assume that the connected components represent co-regulated genes. We find that hash insertion takes much less time than our queries when using hash tables in this way. Hash tables also benefit from small sizes due to the trade-off between traversal time and bucket length. We also found significant improvement in computation time compared to our serial implementation. This technique may help us find genes of similar function and understand the gene regulatory network.
Soybean cyst nematode, or SCN, is a parasitic roundworm that infects the roots of soybeans and causes over one billion dollars in yield losses each year. Host resistance is the primary management strategy adopted to combat this pathogen. In soybeans, serine hydroxymethyltransferase (SHMT) is required for resistance to SCN, but its function in the resistance pathway is poorly understood. The aim of this study is to better characterize the role of SHMT in resistance to SCN through the identification of interacting proteins. For this, SHMT cDNA from a resistant and a susceptible line of soybean were cloned as N-terminal hemagglutinin (HA) tag fusions in binary vectors under the control of the native promoter of SHMT. The constructs were transformed into *Agrobacterium rhizogenes* and used to generate transgenic soybean hairy roots expressing the SHMT HA-tagged proteins. Soybean cotyledons were infected with the agrobacterium then plated on growth media. Once roots developed, they were excised and propagated on growth media with antibiotics to select for the presence of the transgene. After two rounds of antibiotic resistance selection, transgenic roots were further tested for expression of the HA-tagged SHMT protein by western blotting. The selected roots have been inoculated with SCN to generate nematode-infected root tissues. These will be used in co-immunoprecipitation studies to isolate SHMT protein complexes. The interacting proteins will be identified by liquid chromatography-tandem mass spectrometry (LC-MS/MS). Identification of proteins that interact with SHMT and any differences in interacting partners between resistant and susceptible version of the protein will lead to a better understanding of the function of this enzyme in soybean resistance to SCN.
Nutrient stress response of cardiovascular cells to β-blockers, ARB and AT2R agonists
Abuzar Mahmood and Lakshmi Pulakat

Abstract withheld at the request of the faculty mentor for proprietary purposes.
Sphingosine kinase 2 is critical for suppression of virus-specific T cell proliferation and viral persistence
Tykeemi Manor, Curtis Pritzl, and Bumsuk Hahm

Abstract withheld at the request of the faculty mentor for proprietary purposes.
Faculty Mentor: Dr. Marc Johnson, Molecular Microbiology and Immunology  
Funding Source: Summer Research Internship in Cell & Molecular Biology

**Effect of Nef on HIV-1 Infectivity**  
Karolina Márquez-Gil, Yuleum Song, and Marc Johnson

Abstract withheld at the request of the faculty mentor for proprietary purposes.
Searching for the genes associated with the placentation of mammals
Taylor Maurer, Katie Burch, Yue Hao, and Gavin Conant

The genetic underpinnings of many significant evolutionary transitions, such as the origins of placentation, are poorly understood. Here, we attempt to identify the orthologous mammalian genes whose evolutionary origins coincide with the radiation of the placental mammals. Orthologs are homologous genes in different species that last diverged at a speciation event. These genes tend to conserve molecular and biological functions over time; as such, they are ideal for studying genetic evolution in addition to predicting gene function. In this study, the genomes of 38, primarily mammalian, species were compared against the human genome using a previously developed orthology assignment pipeline in order to determine the genes associated with the evolution of the placenta and internal mammalian development. This pipeline compares the gene sequences of two species with pre-determined sequence similarity parameters to identify genes with sequences similar enough to potentially be orthologs. These parameters include a word length for spawning potential matches, the pairwise percent identity of each pair, and their non-synonymous divergence. By adjusting these parameters in various trials we were able to identify a set of values — word length of 7, percent identity of 50%, and a $K_a$ threshold of 0.4 — that yielded the greatest number of orthologs for the comparison of relatively diverged genomes (e.g., humans and marsupials). We then mapped the orthologs to a phylogenetic tree and reconstructed the ancestral orthology states. Future work will include performing further orthology pipeline optimizations using the adjusted parameters on the remaining 27 species. We will then use a Gene Ontology analysis to infer molecular functions for the genes that appeared around the time of origin of the placental mammals. Further studies will involve conducting a multiple sequence analysis to infer instances of directional selection acting on genes at the time of the placental radiation. The long-term goal is to better illuminate the genetic origins of evolutionary innovations.
Dynamic charge transport in polymer-based transistors
Jacob Mieso, Amrit Laudari, and Suchi Guha

An organic field-effect transistor (OFET) is a transistor that uses an organic semiconducting material in its active layer. Using organic materials in designing transistors allows for their application in aspects where traditional transistors (those using silicon) may fail. They have become increasingly popular as interest has risen in low-cost, large-area and flexible electronics.

Field-effect mobility of the transistor can be determined using DC measurements. Although mobility is often considered static, in OFETs it is a dynamic characteristic that is dependent on electric field. In order to obtain an accurate determination of drift mobility, both time-domain and frequency-domain characterization of the OFETs must be made.

The OFETs studied were bottom gate transistors with a pentacene semiconducting layer, but were fabricated with different dielectrics. Polymer dielectrics were used in an effort to move towards devices which have the potential to be fabricated completely using printable technology. One such type of polymer was poly(methyl methacrylate) (PMMA). The other polymer used Cytop, a hydrophobic fluoropolymer. Water traps at the organic semiconductor/dielectric layer of the transistor decrease mobility, so Cytop’s strong hydrophobicity makes it an ideal dielectric.

The DC characteristics were measured using two sourcemeters, a Keithley 2400 and Keithley 236, which were configured to a program written in LabVIEW. The AC characteristics were measured by applying a square voltage signal to the gate and drain terminals from a Rigol DG4102 function generator, while measuring the output voltage at the source terminal with a Tektronix TDS1012B oscilloscope.

The DC mobility for the PMMA and Cytop devices were found to be $2.2 \times 10^{-2}\text{cm}^2/\text{V} \cdot \text{s}$ and $3.8 \times 10^{-2}\text{cm}^2/\text{V} \cdot \text{s}$, respectively. The larger mobility found in the Cytop device leads to the previously mentioned property that hydrophobic materials have increased mobility. Preliminary results of drift mobilities upon biasing the devices in a diode configuration and using an AC voltage will be presented at the Forum.

This work was supported by the National Science Foundation award "Research Experience for Undergraduates in Materials and Modeling" (#1359430)
Temperature sensitivity of fruit fly receptors
Kayla C Miguel, Autoosa Salari, Troy Zars, Lorin S Milescu, and Mirela Milescu

Abstract withheld at the request of the faculty mentor for proprietary purposes.
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Funding Source: Summer Research Internship in Cell & Molecular Biology

The genetic deletion of IL-13 receptor in mice yields enhanced neonatal vaccine responses
Fabienne Mondelus, Mindy M. Miller, and Habib Zaghouani

Abstract withheld at the request of the faculty mentor for proprietary purposes.
Are people slower to remember when distracted?
Abigail Mutamba, Evie Vergauwe, and Nelson Cowan

Working memory is responsible for maintaining (remembering) information while processing it. According to the time-based resource sharing (TBRS) theory, maintenance and processing compete for attention (Barrouillet & Camos, 2012). If one is processing information, one cannot focus on maintenance concurrently, and vice versa. We examined participants’ maintenance of a series of five letters while they performed a perceptual task in which line lengths were judged. According to the TBRS theory, letter information would decay while attention is absorbed by line-length judgments. Decaying letter information can be forgotten unless the periods between line-length judgments are used for refreshing the letters, to counteract decay. When processing of the lines captures attention for a large proportion of time (high cognitive load), decay causes loss of more letters from working memory. Lower cognitive loads allow more time for refreshing to counteract decay. Consistent with this idea, recall performance is inversely related to cognitive load (Barrouillet et al., 2007; Vergauwe et al., 2010, 2012). Our experiment sought direct evidence for the proposed link between cognitive load and memory strength. Participants saw a series of five to-be-remembered, red letters. Each to-be-remembered letter was followed by five stimuli: four lines to be judged longer or shorter than the space between two dots (a spatial fit task), and somewhere in this sequence, one black letter probe. Participants were to decide whether the letter probe corresponded with one of the to-be-remembered letters. The idea was to observe changes in memory strength as a function of the local cognitive load. Therefore, we studied response times to the black letter probes. Contrary to expectations, response times improved with higher cognitive load. This leads us to believe that either some unanticipated factor such as time pressure from higher cognitive loads played a role, or else refreshing may not occur in this situation.
Analysis of volatile organic compounds released by Arabidopsis in response to feeding vibrations
Nicole Odom, Chung-Ho Lin, Rex Cocroft, and Heidi Appel

Plants are attacked by a wide variety of herbivorous insects with adverse effects on their ability to survive and reproduce. As a result, plants are equipped with elaborate defense mechanisms that allow them to rapidly identify and respond to their insect attackers. They may make more – or different - chemical defenses in their leaves, some of which are released as volatiles. Plants normally synthesize a baseline of volatile chemicals including monoterpenoids, homoterpenes, sesquiterpenes, green leaf volatiles, and benzanoids. However, in response to insect herbivory, plants release more volatiles that differ in amount or composition from standard emissions. Since volatile chemical compositions vary with the plants and herbivorous insect species involved, these volatiles function as a defense mechanism by attracting predatory insects to the herbivore feeding site and inducting defense responses in adjacent plants.

Previous work in our lab has shown that Arabidopsis thaliana experiencing feeding by Pieris rapae caterpillars releases different volatile profiles than those of undamaged plants. Our lab also recently discovered that plants respond selectively to the vibrations caused by this caterpillar when feeding, even in the absence of the actual caterpillar. Plants experiencing the feeding vibrations produced more chemical defenses in their leaves when subsequently attacked.

In this experiment, I tested whether feeding vibrations caused by P. rapae can similarly elicit an increase in volatile release by A. thaliana. I captured and measured the amount and variety of compounds emitted using a volatile collection system and GC-MS.
Roles of a Dynamin-related protein and a receptor-like kinase in plant growth
Drew Olson, Michelle Leslie, and Antje Heese

Abstract withheld at the request of the faculty mentor for proprietary purposes.
Leptin, a satiety hormone produced by adipocytes, regulates body weight. Those who develop obesity or hyperglycemia become insensitive to leptin over time and tend to become hyperleptinemic (leptin levels are higher than normal). Maternal diet and obesity during pregnancy can affect the offspring’s propensity to develop metabolic diseases such as hypertension, diabetes, and obesity in adulthood, a phenomenon described as developmental programming. We reasoned that high maternal leptin concentration in obese and diabetic states may mediate some developmental programming effects during pregnancy. Bone can also be impacted by developmental programming. Ongoing studies in our laboratory indicate that adult males challenged with a high fat diet (HFD) change their femoral geometry to compensate for compromised material. However, adult males that had been exposed to high maternal leptin levels in utero do not respond to HFD by altering geometry, and may be protected from the effects of HFD on bone. The goal of the present study is to determine the effects of maternal hyperleptinemia on the composition of bone in adult offspring. To test this, we compared offspring of genetically hyperleptinemic mice to offspring of wildtype mice and compared offspring of mice infused with leptin to offspring of mice infused with saline. In order to measure the composition of bone, collagen, a structural protein that contributes to the quality and strength of bone, was measured indirectly with a hydroxyproline assay. In addition, advanced glycation end products (AGEs) were measured by using a fluorescence assay. AGEs are by-products of a hyperglycemic diet that impact collagen crosslinking and bone quality. Preliminary results suggest that maternal leptin levels do not impact offspring hydroxyproline and AGE content per gram of bone. However, a general trend for decreased AGE content was observed when offspring were challenged with a high fat diet, though this did not reach significance.
The Resistance
Megan Osbahr and Hannah Reeves

Students in the summer 3D Design Art class were paired up with an MU undergraduate researcher for their Wood Relief Project. After discussing the research project with their student partner, art students visited the research lab and obtained any visual support materials that the science researcher could offer. The student researcher's project was the inspiration for the art student's 24” x 24” wood relief art. The artwork attempts to conceptualize the research from a new perspective, abstracting and interpreting the ideas and impact of the research topic. Student art pieces will be displayed alongside the undergraduate research poster during the Forum.

Metabolic enzymes can reproduce within a biofilm. This biofilm expands and contracts to accommodate the enzymes within. The enzymes and biofilm can adapt to their environment, creating resistance to foreign invasion.

I have created movement and rhythm, as well as texture by using a stippling and crosshatching technique. This represents the expansion and contraction of the biofilm. The abstract shapes and lines appear to move and manipulate themselves. The abstract shapes are also free flowing and resemble the production of biofilm around the enzymes as well. However the contrast of the sharp lines and edges emulate a defense mechanism. I also created balance through the spacial usage of my shapes. A pyrography technique and 3D design create depth and several focal points throughout the piece. I purposefully made my birch rounds different sizes to mimic the reproduction of metabolic enzymes.

The frame of the piece is built from solid oak that I rubbed with oil to create a more natural color. In fact all pieces are rubbed with oil to create a natural color and detail within the wood. My birch rounds are wood glued to their frame and represent the metabolic enzymes. The abstract pieces protruding outward are made of pine and give more of a 3D representation of the biofilm, giving it a surrounding or enclosing feeling. The background image also represents biofilm and it was made using a pyrography technique.
Typha capensis — An electron rich resource for the synthesis of phytochemical-encapsulated gold nanoparticles through green nanotechnology

Keenau Pearce, Kavita Katti, Menka Khobchandani, Melissa May, Ralph Henkel, and Kattesh V. Katti.

Typha capensis, a widely used medicinal plant in South Africa, has been found to be a rich source of antioxidants, inhibiting both reactive oxygen species and reactive nitrogen species. The antioxidant capacity of such plant species serves as a reservoir of electrons to transport them into gold salt for the production of gold nanoparticles through green nanotechnology.

Our objective was to utilize the rich antioxidant capacity of Typha capensis for the synthesis of gold nanoparticles, encapsulated with cocktail of phytochemicals, for effective delivery as novel nanomedicines.

We have investigated the optimal synthetic protocols for the synthesis of gold nanoparticles from Typha capensis, without the use of any toxic chemical. Hereafter, these particles were characterized by measuring the Plasmon wavelength, hydrodynamic size and zeta-potential. Next, these particles were visualised using TEM, the average particle size distribution calculated, and the in vitro stability in various media tested.

Typha capensis produced gold nanoparticles in a single step reaction, playing a duel role of reducer and stabilizer. These gold nanoparticles produced fairly narrow peaks at 540 nm under both heated (50°C) and unheated conditions. These particles proved to be highly stable, showing no agglomeration over time. Furthermore, these gold nanoparticles showed no deterioration when washed by centrifugation or during in vitro stability studies. An average hydrodynamic size of 120.2 d.nm, including an average zeta-potential of -23.2 mv, was measured. Moreover, TEM demonstrated spherically shaped, un-agglomerated particles, with a calculated average particle size distribution of 27.9 nm.

Highly stable gold nanoparticles, encapsulated with a plethora of phytochemicals from Typha capensis, have been synthesized through a single step. The enormous potential of delivering phytochemicals from Typha capensis through gold nanoparticles for the treatment of various diseases is being tested in vivo.
Soybean cyst nematode (*Heterodera glycines*) causes more than $1 billion of damage annually to soybean production in the United States. The most predominant management practice is planting of resistant soybean cultivars, however nematode populations adapt to overcome the resistance and eventually reduce its effectiveness. In order to better understand the process of infection and virulence of this nematode, we examined gene expression changes in nematodes infecting a resistant (incompatible interaction) and susceptible (compatible interaction) soybean variety. We identified 4,465 and 3,681 differentially expressed transcripts in the compatible and incompatible interaction, respectively. We then compared the two sets of differentially expressed nematode transcripts and found 1,481 unique transcripts in the compatible interaction and 697 unique transcripts in the incompatible interaction. Further analysis identified differentially expressed transcripts encoding for putative effectors in each population. These were identified using bioinformatics tools that predict characteristics of effectors, such as the presence of a signal peptide and the lack of a transmembrane domain. The analysis discovered 663 (154 unique) and 571 (62 unique) predicted effectors in the compatible and incompatible interactions, respectively. Interestingly 14% of all differentially expressed transcripts were effectors, while only 7% of transcripts were differentially expressed compared to the whole transcriptome. Also, a vast majority of effector transcripts were upregulated in the susceptible soybean interaction. These results may reflect a delay in development of the nematode in the resistant soybean population, or an influence of host genotype on the expression of effector genes. A better understanding of the process of *H. glycines* infection in soybeans will aid in the identification of vulnerable points of disruption to engineer enhanced plant resistance.
Urease, found in plants, bacteria and fungi, is a nickel-dependent enzyme that catalyzes the hydrolysis of urea to ammonia and carbon dioxide. In addition, ureases from *Canavalia ensiformis* (jack bean) and *Glycine max* (soybean) display insecticidal activity, independent of their enzymatic activity. However, these ureases only present insecticidal action when insects that ingest them have digestive enzymes that are mainly cathepsins. These cathepsins “cleave out” a 10kDa entomotoxic sub-peptide from the 95 kDa urease subunit. Importantly, this isolated sub-peptide is toxic to normally tolerant insects that lack cathepsins. Recombinant sub-peptide, jaburetox, from Jack bean urease, is under control of the T7 promoter of pET23a, and inducible by IPTG (isopropyl thiogalactoside) in the BCL-21 strain of *E. coli*. The goal of this study was (i) to purify His-tagged jaburetox by Ni$^{+2}$ column chromatography and confirm its presence and purity by Western blot analysis, and (ii) to determine whether *Drosophila melanogaster* (lacking digestive cathepsins) is susceptible to the peptide. A third, longer-term goal, is to employ the peptide as a selection agent for resistant mutants to identify a genetic target. We have determined the best induction conditions for recombinant jaburetox, and identified antiserum (polyclonal) to soybean urease, that appears to recognize jaburetox epitopes. The purified peptide has been mixed with an artificial diet and fed to *Drosophila* eggs, on an eclosion medium. Hatched larvae normally develop to the pupal stage. We will record the number of pupae as well as the duration of pupation and adult emergence time. Updated results will be presented. If the peptide proves toxic, we will design experiments to recover resistant mutants to identify the peptide target(s).
As the cost of genome sequencing decreases, studies that were previously impossible are becoming more feasible. For population geneticists, however, sequencing every individual in a population is often cost prohibitive. Pooled sequencing is a commonly used, cheaper alternative to individual-level sequencing. However, accurately estimating the haplotype frequencies of a population from pooled sequence data remains a challenge. In order to address this problem, we have developed and refined an algorithm to estimate haplotype frequencies from pooled data. To experimentally validate our method, we used genomic data collected from pooled sets of recombinant inbred lines with a completely known haplotype structure. These lines were derived from a 50 generation controlled cross of 15 homozygous founder lines of *Drosophila melanogaster*. We validated the predictive accuracy of our haplotype estimator by comparing the haplotype frequency estimates obtained by our method with the known haplotype composition of the pool. We present a study in which the accuracy of the haplotype estimator is tested against variability in raw sequence coverage, SNP density, and the procedure of the algorithm. This algorithm, which can accurately estimate the haplotype frequency of a population from pooled sequence data, has the potential to significantly progress the field of genotype-phenotype mapping, a major goal of modern biology and bioinformatics.
Biomechanical evaluation of posterior cruciate ligament transection and repair in the human knee
Andrew Polk, Laura Evans, James L. Cook, Pat Smith, James P. Stannard, Mauricio Kfuri, Matthew Mooberry, and Ferris M. Pfeiffer

Isolated injury of the Posterior Cruciate Ligament (PCL), and compound multi-ligament injuries involving the PCL contribute to a large number of clinical orthopedic trauma cases. It is well known that these injuries contribute to anterior-posterior instability of the knee, and if left untreated, can lead to early arthritis of the knee. Numerous surgical repair techniques currently exist to treat PCL injuries, however the relative efficacy of each technique is debated.

The objective of this project is to examine the biomechanical effects of isolated PCL injury on anterior-posterior (A-P) stability of the knee, and to evaluate the effectiveness of various surgical repair techniques in restoring stability. This project will provide clinicians with a better understanding of the biomechanical function of the PCL, and will lead to improved clinical treatment of PCL injuries. We hypothesized that an isolated PCL injury will significantly destabilize the human knee joint in the A-P direction, and that reconstruction of the injury using one of three repair techniques will restore function to within 80% of the intact state.

Based on the results of this study, we conclude that posterior cruciate ligament attachment significantly contributes to knee joint stability in A-P shear. We also conclude that the method used for PCL reconstruction can significantly affect stability of the surgically repaired human knee in A-P shear.
Faculty Mentor: Dr. Elizabeth King, Biological Sciences  
Funding Source: NSF Research Experience for Undergraduates: Biocomplexity and High-Performance Computing  

**Estimating haplotype frequencies of *Drosophila melanogaster* from pooled sequence data**  
Aniqa Rahman, Devin Petersohn, and Elizabeth King  

As the cost of genome sequencing decreases, studies that were previously impossible are becoming more feasible. For population geneticists, however, sequencing every individual in a population is often cost prohibitive. Pooled sequencing is a commonly used, cheaper alternative to individual-level sequencing. However, accurately estimating the haplotype frequencies of a population from pooled sequence data remains a challenge. In order to address this problem, we have developed and refined an algorithm to estimate haplotype frequencies from pooled data. To experimentally validate our method, we used genomic data collected from pooled sets of recombinant inbred lines with a completely known haplotype structure. These lines were derived from a 50-generation controlled cross of 15 homozygous founder lines of *Drosophila melanogaster*. We validated the predictive accuracy of our haplotype estimator by comparing the haplotype frequency estimates obtained by our method with the known haplotype composition of the pool. We present a study in which the accuracy of the haplotype estimator is tested against variability in raw sequence coverage, SNP density, and the procedure of the algorithm. This algorithm, which can accurately estimate the haplotype frequency of a population from pooled sequence data, has the potential to significantly progress the field of genotype-phenotype mapping, a major goal of modern biology and bioinformatics.
Vertebrae provide strength to the spinal column, and conditions like Dowager’s hump result from vertebral compression fractures in the elderly population. Genetics is an important factor in determining bone strength, and exercise has been shown to increase bone strength. The genetic effects of exercise on bone can be difficult to study in humans, but strains of mice have been developed that are selected for high levels of voluntary exercise. These mice, which run over twice as much as controls, were compared to mice that were randomly bred in two groups: either wheel running or sedentary. This study focused on looking at the application of compressive loads to vertebrae of mice selected for exercise. We applied axial loads to vertebrae using a magnet that stabilized a vertebrae that had been glued to a metal disk. For caudal and lumbar vertebrae, we measured the morphology of the bone, compressive strength, axial stiffness, and energy to failure. The measurements are important for comparing the different lines of mice and their exercise regimen. We found greater compressive strength with running is selected mice as opposed to sedentary high runner mice and the reverse was found in the control lines. We also found that the energy to failure for lumbar vertebrae followed the same pattern as compressive strength, but this was not the case for caudal vertebrae. The compressive strength relationships found in caudal and lumbar vertebrae may be because the mice that were selected for exercise are more dependent on more intensive exercise to keep the spinal column strong whereas the control lines cannot handle the intense exercise as well so it decreases the compressive strength. The differences between the caudal and lumbar in regards to energy to failure may be because of the varying distributions of load due to the caudal being close to the sacrum and the lumbar being higher up the spinal column. More data on the effects of intense exercise on mice selected for exercise in comparison to the results of intense exercise on randomly bred mice can help gain a better understanding as to why exactly these patterns show.
Tunable characteristic temperature for mid-infrared Vertical Cavity Surface Emitting Lasers
Seth Rewerts and Gregory Triplett

The demand for mid-infrared Vertical Cavity Surface Emitting Lasers (VCSELs) has grown rapidly in recent years, due in part to their small size and low cost. With increased power and thermal stability, mid-IR VCSELs could have significant impact in many application areas, but especially in sensing. Possible applications include sensing organic compounds (such as methane), explosive ordinances, and environmental detection. Mid-IR VCSELs also have military applications when utilized for low-altitude radar or infrared countermeasures. However, challenges exist when using 2-4 µm lasers, involving improving power conversion efficiency.

Characteristic temperature is a metric useful for determining performance of laser diodes. Laser diodes with higher characteristic temperature have better performance and are more stable over a larger range of temperatures compared to those with lower characteristic temperature. This project aims to identify the characteristic temperature of a laser device designed to suppress Auger recombination (a carrier loss mechanism), and the effects of varying pulse width, frequency, and duty cycle to allow optimum thermal stability while maintaining high power density.

For this project, a 2µm laser bar is mounted on a non-oxidized copper stage using thermal paste. The stage is temperature-controlled by a two-stage thermoelectric cooler with a thermistor embedded to monitor temperature, allowing various temperatures to be maintained (293K to 343K). The laser bar is optically pumped using a high-power, single mode laser coupled through an optical fiber and focused through a set of lenses to reshape the beam into a rectangular stripe. Light from the laser bar is collected using collection optics, an optical fiber, lock-in amplifier, and infrared detector. Collected light is filtered, eliminating interference from the pump laser, allowing for more accurate measurement of light emitted by the laser bar. Results show as duty cycle decreases (from quasi-continuous to continuous), characteristic temperature improves dramatically.
The Carbohydrate partitioning defective2 mutant
Christopher Ricciardi, Robert F. Baker, Tanner Buschmann, Kristen A. Leach, Mark Lubkowitz, and David M. Braun

Abstract withheld at the request of the faculty mentor for proprietary purposes.
The nematode effector protein 30D08 may alter gene expression by targeting an auxiliary spliceosome component
Amir K. Richardson, Anju Verma, and Melissa G. Mitchum

The soybean cyst nematode (SCN), *Heterodera glycines*, is a sedentary, root-based endoparasite that is responsible for billions of dollars of damage to the soybean industry. SCN manipulates the root cells of a host plant to form a feeding site, known as a syncytium. The syncytium not only works as a command center for the nematode, but also saps nutrients from the plant, which causes a loss of yield for farmers with infected crops. In order to facilitate infection, SCN injects a collection of effector proteins into a target plant cell that have a variety of different functions, including cell wall digestion, immune system suppression, and plant protein mimicry. We previously determined that the novel effector protein known as 30D08 targets the plant protein SMU2, a homologue of the human RED protein family, an auxiliary splicing factor. Using RNA-seq, we identified 243 differentially expressed genes in wild type Arabidopsis plants expressing 30D08 under the control of the *SMU2* promoter. A high percentage of these genes were involved in cell wall modification, metabolism, host defense, and iron transport. In this study, we used qRT-PCR analysis to examine the relative expression of a subset of these differentially expressed genes in wild type, *smu2* mutant plants, and *smu2* mutant plants expressing *SMU2p:30D08*. Our analysis confirmed that the expression of several of these genes is regulated by SMU2. These data suggest that 30D08 may target the host protein SMU2 in order to differentially regulate genes important for syncytium maintenance and host immune suppression.
Plants have developed a variety of perception mechanisms to detect pathogens enabling them to survive and reproduce in challenging environments. Most pathogens are recognized at the cell surface by detection of common pathogenic structures such as fungal chitin or bacterial flagella causing the plant to produce an immune response called PTI. Pathogens have evolved proteins called effectors to disable these defenses. In response plants have evolved defense proteins to detect these pathogenic effectors and activate an immune response called effector-triggered immunity (ETI). SRFR1 is a plant protein that negatively regulates ETI, so srfr1 mutants exhibit increased immunity to certain effectors. Surprisingly, the srfr1 mutant was subsequently found to be more resistant to pests that are not thought to induce ETI, opening the possibility that SRFR1 has a broader role in determining a set-point of the plant immune system to a broad spectrum of biotic stresses.

To further explore possible pathways not related to ETI regulated by SRFR1, I infected wild type Arabidopsis plants and srfr1 mutants with wild type Pseudomonas syringae and three attenuated strains, one lacking two effectors, another lacking the ability to use effector proteins and the last missing a phytotoxic called coronatine that increases virulence. Two attenuated strains interrogate the PTI pathway and the coronatine mutant explores SRFR1's possible regulation of plant hormones important to immune responses. Plants were inoculated by forcing bacterial suspensions into leaves. Three days after infiltration bacterial replication was assessed within the leaves, a measure of plant susceptibility to bacterial pathogens. Although we predicted that the weakened bacteria would replicate less in the srfr1 mutants compared to the wild type, infection levels were similar across all bacteria mutants. These results suggest that SRFR1 regulates a novel aspect of the plant innate immune network that does not involve PTI or coronantine induced hormonal changes.
Faculty Mentor: Dr. Rex Cocroft, Biological Sciences
Funding Source: NSF IOS Grant to R. Cocroft

Is root growth of corn seedlings influenced by underground insect vibrations?
Laura Rottman, Jeremy Gibson, Kelly Hougland, Heidi Appel, and Rex Cocroft

Abstract withheld at the request of the faculty mentor for proprietary purposes.
Feeding biomechanics in the wild turkey, *Meleagris gallopavo*, and its significance for avian cranial evolution
Rachel Rozin, Ian Cost, and Casey Holliday

A critical component of the avian feeding apparatus is cranial kinesis: the mobility of bones within the skull due to intracranial joints. Key joints include the flat palatobasal joint between the pterygoid and the parabasisphenoid, the condylar otic joint between the quadrate and the braincase, and the saddle-shaped jaw joint that connects the mandible to the quadrate. However, underlying patterns between avian skull function and joint shape, and their significance for ecology and evolution remain largely unknown. Although the cranial musculoskeletal system responsible for cranial kinesis is modestly understood, the ecomorphological patterns of avian cranial joints is poorly known. Gallinaceous birds, including chickens, guineafowl and turkeys vary in size and have diverse diets but feed similarly and have similar skull shapes. Therefore, we expect their cranial joints will only differ relative to size and the forces loading them. To explore this relationship I developed a 3D model of a wild turkey (*Meleagris gallopavo*) and using computational modeling methods, I quantified joint shape, muscle forces and cranial forces to determine relationships between joint form and function in the complex 3D biomechanical environment of a bird skull. I then compared joint shape data with similarly derived data from chicken (*Gallus gallus*), guinea fowl (*Numida meleagris*) and the primitive Screamer duck (*Chauna torquata*). This is the first comparative analysis of muscle and joint function within the heads of birds. Data gathered from this study will provide valuable groundwork for further studies in the mechanics and evolution of cranial kinesis in other bird species as well as in their extinct dinosaur ancestors.
For this experiment, the impact that leakages pose upon a system in which the discharge pressure is used to drive hydraulic cylinders is being studied. This data is being used in order to validate a numerical model. In order to do this, a test set up, which mimics a steering system of a large mobile machine, was constructed with certain paths that can be controlled so that certain leakage situations can be replicated by opening valves and redirecting the pressurized flow back to the reservoir. One leakage situation that is being simulated is the leakage of the pump discharge flow directly back to the reservoir. This instance simulates a failure of the pump. Another instance is imposing a leakage in the hoses directly before the main load, which will be the hydraulic cylinders. This imposed leakage would be similar to a situation in which the hoses next to the load burst from the high pressure. During these situations, the performance response of the cylinders is expected to decrease due to the loss in pressure. This decrease in responsiveness will be measured and analyzed through taking measurements of the cylinder displacement versus time. In addition, there are expected to be changes in the volumetric efficiencies of the pump as well, however, those are yet to be determined. These changes will be measured by analyzing the discharge flow, pressure, swash plate angle, and the angular velocity of the pump itself. Analysis of the data will yield further information on this topic.
This project was conducted to test the effectiveness of an interactive, networked exercise video game as a method to reduce the risk of anterior cruciate ligament (ACL) injuries by utilizing proven prevention techniques as a control to the game. Specifically, we targeted female high school athletes for this project, a group that is known to be at a higher risk of ACL injury. To begin, we collected survey data from high school athletes regarding the types of games they played and platforms used. We categorized and analyzed these data to help determine, categorically, what types of games students were playing and popular platforms. Based on these data, we built a simple, networked, multiplayer game, controlled by a smartphone strapped to the leg, that we call Paddle. The game was designed and compiled using the Unity Game Engine, a software framework used to simplify the process of designing and creating video games. Doing so allowed us to quickly produce a version of Paddle for testing on mobile devices, specifically those that use either iOS or Android operating systems. This version allows us to both validate the movements being used to control the game as well as to test user receptiveness to this method of injury prevention. In the future, these preliminary data will be used to produce a networked exercise game that aims to be both highly appealing to the target audience and effective in preventing ACL injuries.
Faculty Mentor: Dr. Andrew McClellan, Biological Sciences
Funding Source: Life Sciences Undergraduate Research Opportunity Program

Axonal regeneration of ascending spinal neurons in the lamprey following spinal cord injury
Michael Savio and Andrew McClellan

Abstract withheld at the request of the faculty mentor for proprietary purposes.
Detected of *campylobacter jejuni* using whispering gallery mode optical biosensors in an aqueous environment

Mason Schellenberg and Heather Hunt

Abstract withheld at the request of the faculty mentor for proprietary purposes.
A deterministic finite state automaton (DFA) is a finite state machine that can either reject or accept a series of characters designated as input. The automata take a token from the input and, depending on its value, transition to another state. When the input sequence matches one of the patterns encoded in the DFA, the automaton will transition into an accepting state. These can be used for pattern matching using regular expressions, which have a number of applications. In this work, the emphasis is on increasing the speed of gene sequence analysis. Graphics Processing Units (GPUs) can be used to accelerate this computation. Previous work (Yu/Becchi 2013) detailed implementations of automata on GPUs focusing on large, real-world datasets and comparing various approaches of implementations of finite automata. Their design takes advantage of the highly parallel nature of GPUs allowing many calculations to be done simultaneously.

Here we will focus on decreasing runtime of one approach, the Uncompressed-DFA solution. This solution takes advantage of thread-level parallelism by having each thread run a DFA over an input stream, in a sequence of instructions executed on the GPU called a kernel. Each group of threads (or thread-block) will process a separate input stream. Thus, multiple input streams are run at once on several DFAs on the GPU. While this takes advantage of parallel hardware, runtime can be decreased by overlapping GPU computation and data transfers between CPU and GPU. To do this we use CUDA streams, which are software queues executed in parallel on the GPU. We tested our implementation with various input streams, as well as with a variable number of CUDA streams. 4 streams resulted in 15393.07 characters per second processed, versus 3864.43 with just one stream, nearly a 4x increase in throughput on the Tesla K40c GPU.
Comparing African "killer bee" and European honey bee genomes: Identifying structural variations that might affect behavior
Jack Schoelz, Micah Fletcher, Darren E. Hagen, J. Spencer Johnston, and Christine G. Elsik

Abstract withheld at the request of the faculty mentor for proprietary purposes.
Driving and bicycle simulators
Michael Schoelz, Benjamin Shetley, and Carlos Sun

The development of simulators is a valuable tool used in research and development within the discipline of transportation engineering. A simulator is a virtual replication of scenarios that facilitate a realistic experience of operating a vehicle without the danger or cost of creation of the original. The focus of this project is to develop the hardware for two simulators, a car and a bike. To accomplish this goal, we must balance the fidelity of the simulation and scenarios with cost and practicality restraints. Due to the open-ended nature of this project, many of the hardware needs were determined through trial and error and a consideration of simple solutions that would have the greatest impact on fidelity. For example, the bike simulator steering is digitally input using a laser attached to the bike and mounted on a rotating platform. Further, data-collecting sensors will be mounted non-intrusively and the rooms that house the simulators are prepared to provide a professional environment for the participants. Once the hardware for the simulators is fabricated and configured, scenarios can be developed to test the safety and practicality of a particular research design. Raw data from particular research designs will be collected via human trials of simulated scenarios with accompanying surveys. The initial research subject of the motor vehicle simulator is two different J-Turn designs. The bicycle simulator will test road marking options that trigger a signal change at an intersection as well as road markings for wayfinding. During human trials, the simulators will collect data on driver/rider performance, safety and relative preference from which the superior option will be determined. In both the hardware fabrication and scenario development, attention to detail in creating a believable simulation from which quality data may be collected is a nuanced process that prioritizes simple solutions that achieve the greatest improvement in fidelity.
Differentially methylated regions overlap with putative enhancers, providing therapeutic insight for relapse acute lymphoblastic leukemia

Emily Shank, Alex Stuckel, and Kristen Taylor

Acute Lymphoblastic Leukemia (ALL) is a hematopoietic stem cell derived cancer, predominantly found in children. ALL is characterized by the accumulation of precursor B-lymphocytes in the bone marrow. Approximately 10% of children who are treated for ALL relapse after complete remission 1 (CR1). Histone tails contain chemical modifications that result in an open chromatin formation. These histone modifications can affect how enhancer regions bind to transcription factors. If the enhancer regions are hypomethylated, they can form a loop with distant genes and recruit RNA polymerase II. Hypermethylation can prevent the enhancers from binding transcription factors. We generated DNA methylation profiles using MIRA-seq for matched samples at diagnosis and relapse in 10 pediatric ALL patients to identify differentially methylated regions (DMR) of the genome. ChIP-seq was used to locate putative enhancer marks from a B-cell line using ENCODE available data. Of the 70,747 DMRs, 45 regions became hypermethylated at relapse and 70,702 became hypomethylated at relapse. We compared overlapping enhancer regions to the DMRs and found 3 overlapping hypermethylated regions and 2,159 overlapping hypomethylated regions. We visualized overlapping enhancer regions with hypomethylated DMRs to find common transcription factors. A candidate tumor suppressor gene, IQSEC1 was found to have hypermethylation in its 5’ regulatory region overlapping with an enhancer region, potentially leading to apoptotic evasion in B-cells. The mechanism through which IQSEC1 participates in apoptosis has yet to be elucidated. Finding hypermethylated tumor suppressors and hypomethylated oncogenes, preventing from these genes from functioning correctly, can indicate biomarkers.
Faculty Mentor: Dr. Patrick Shiu, Biological Sciences
Funding Source: Life Sciences Undergraduate Research Opportunity Program

**Characterization of a silencing complex in *Neurospora crassa***
Benjamin S. Shanker, Logan M. Decker, Erin C. Boone, Hua Xiao, and Patrick K. T. Shiu

Abstract withheld at the request of the faculty mentor for proprietary purposes.
Driving and bicycle simulators
Benjamin Shetley, Michael Schoelz, and Carlos Sun

The development of simulators is a valuable tool used in research and development within the discipline of transportation engineering. A simulator is a virtual replication of scenarios that facilitate a realistic experience of operating a vehicle without the danger or cost of creation of the original. The focus of this project is to develop the hardware for two simulators, a car and a bike. To accomplish this goal, we must balance the fidelity of the simulation with cost and practicality restraints. Due to the open-ended nature of this project, many of the hardware needs were determined through trial and error and a consideration of simple solutions that would have the greatest impact on fidelity. For example, the bike simulator steering is digitally input using a laser mouse attached to the bike and mounted on a lazy Susan. Further, data-collecting sensors will be mounted non-intrusively and the rooms that house the simulators are prepared to provide a professional environment for the participants. Once the hardware for the simulators is fabricated and configured, scenarios can be developed to test the safety and practicality of a particular research design. Raw data from particular research designs will be collected via human trials of simulated scenarios with accompanying surveys. The initial research subject of the motor vehicle simulator is two different J-Turn designs while the bicycle simulator will test road marking options that trigger a signal change at an intersection as well as signage for wayfinding. During human trials, the simulators will collect data on driver/rider performance, safety and relative preference from which the superior option will be determined. In both the hardware fabrication and scenario development, attention to detail in creating a believable simulation from which quality data may be collected is a nuanced process that prioritizes simple solutions that achieve the greatest improvement in fidelity.
Evaluating RNA gene expression through fluorescent RNA constructs
Tanner Shull, Emma Tomes, Carolina Camargo, and Donald Burke

Abstract withheld at the request of the faculty mentor for proprietary purposes.
Exploring potential crosstalk between phototropins and the plant immune system in *Arabidopsis*

Anthony Shumate and Mannie Liscum

Light is an essential component of plant survival. Not only is it needed for photosynthesis, recent studies suggest that light is also necessary to effectively fend off pathogens, although the mechanism by which this occurs remains unknown. Several hypotheses have been developed to explain how light may influence this system. One explanation describes light as being necessary for the synthesis of antimicrobial molecules. Additional studies have demonstrated circadian regulation of defense machinery, though why light is still necessary for defense when entrainment of the circadian clock is disrupted is yet to be explained. Lastly, involvement of plant photoreceptors provides another possible mechanism for light-dependent regulation of pathogen defense. Our research examines the potential involvement of blue light photoreceptors, phototropin 1 (phot1) and phototropin 2 (phot2) in the defense of *Arabidopsis thaliana* against bacterial pathogen *Pseudomonas syringae*. The phototropins mediate several biological processes such as chloroplast movement, phototropism, and stomatal opening. In our studies, pathogenesis-related protein 2, a nonspecific antimicrobial protein, was used as a marker for immunological activity. With this marker, defense against *Pseudomonas* was monitored in *Arabidopsis* mutants missing several light-signaling components. Among the mutant lines tested was the phototropin double null mutant (*phot1-5phot2-1*). Time points prior to, and following infection were studied in order to identify possible phototropin involvement in early pathogen defense. This procedure was repeated using additional bacterial strains to test various defense signaling pathways. Our results showed that the *phot1-5phot2-1* mutant mounted a significantly weaker and delayed immune response against *Pseudomonas*, suggesting that the phototropins do play a role in plant immunity. Further studies aim to characterize the exact mechanism of the aforementioned results. In addition, we are also interested in exploring the possible effects an active defense may have on phototropin activity by measuring chloroplast movements, a well characterized phototropin-mediated response, during different stages of innate immunity.
A robust architecture for wireless data collection in mobile ambulatory assessment systems
Andrew Smith, Jay Kelner, Nick Wergeles, and Yi Shang

This study investigated the use of periodic synchronizations as a way to make a client-server mobile ambulatory assessment system (mAAS) more robust and energy efficient. This mAAS and similar systems can be used to collect vast amounts of data, so it was important to use an architecture that can manage data collection and communication efficiently. This paper presents the design we implemented to meet such needs, as well as an analysis of how we improved upon the previous design. We also discuss the energy efficiency trade-offs of semi-realtime communication with a server using varying packet sizes and varying intervals.
Faculty Mentors: Dr. Sheila Grant and Dave Grant, Bioengineering
Funding Source: College of Engineering Undergraduate Research Program

**Development of AuNPs conjugated to injectable tissue constructs**
Colten Snider, Dave Grant, and Sheila Grant

Abstract withheld at the request of the faculty mentor for proprietary purposes.
Faculty Mentor: Dr. Prasad Calyam, Computer Science
Funding Source: NSF Research Experience for Undergraduates in Consumer Networking Technologies

Moving Target Defense for resilient cloud management
Allen Stage, Vladimir Georgiev, Saptarshi Debroy, and Prasad Calyam

With the increasing cybersecurity threats, such as Denial of Service, Information Compromise to the cloud based services, intelligent defense counter-strategies are the need of the hour that do not significantly increase cloud management and administration costs. Moving Target Defense (MTD) based security mechanisms are gaining traction due to its potential to take proactive measures even before such cyberattacks are launched. However, the related research on MTD based cyber-defense strategies lacks effective preventive strategies as they incur significant management overhead resulting performance degradation to consumers of such cloud based services.

In this project, we propose MTD based proactive and reactive virtual machine (VM) migration strategies that significantly decrease cyberattack success rate without causing considerable performance degradations to the consumers. Our scheme not only identifies the optimal VM location to migrate the services without compromising the service performance, but also evaluates the optimal frequency of proactive migration that is not too frequent to cause service interruption and too seldom to be vulnerable. We evaluate the effectiveness and efficiency of the scheme both numerically and using a large-scale GENI testbed. The results show that the proactive scheme successfully migrates VMs with low attack success rate and performance degradation; whereas, the reactive scheme successfully migrates a VM under attack and the connected regular consumers except the attacker to safety without the attacker guessing.
Dust formation around asymptotic giant branch stars
Joshua Steffen and Angela Speck

The asymptotic giant branch (AGB) is the final stage of a low mass star's life and is characterized by intense mass loss. The material ejected from the AGB star forms a circumstellar dust shell around the star. At the end of the AGB phase, the circumstellar dust shell begins to drift away. The gases that accompany the dust become ionized by the stellar remnant, forming a planetary nebula. The dust will eventually become part of the interstellar medium and future stars. While this ending is not as spectacular as ending with a supernova, most of the carbon in the universe was produced by AGB stars.

Depending on the ratio of carbon to oxygen in the star, the dust will be composed of either carbon-rich compounds or oxygen-rich compounds. The focus of this research is the carbon-rich AGB stars. Given that the dust produced in these stars is carbon rich, this research may give insight on the carbon materials that are necessary for the development of organic life. The goal of this project was to determine properties of the circumstellar dust shell.

Radiative transfer modeling was used to study the characteristics of the circumstellar dust shell. The radiative transfer code used was DUSTY. With this program, theoretical models of star/dust spectroscopy can be made and compared to the measured spectroscopy of AGB stars and their dust shells. Using DUSTY, we have been able to determine the chemical composition, grain size distribution, temperature, density distribution and optical depth of the circumstellar dust shell around AGB stars.

This work was supported by the National Science Foundation award "Research Experience for Undergraduates in Materials and Modeling" (#1359430)
Fluorescence characterization of naturally occurring polyphenolic compounds
Jessica Stengel and Renee Jiji

Polyphenolic compounds are known to disaggregate plaques similar to the protein aggregates found in the brains of patients with Alzheimer disease. These plaques are comprised predominately of a single peptide, commonly referred to as A-Beta (Aβ). Polyphenols are abundant in fruits and vegetables and exhibit both anti-aggregate and antioxidant properties. Thus, they can potentially provide positive health outcomes for Alzheimer’s disease. Thioflavin T (ThT) fluorescence assays are a common method to assess the effect of polyphenols on Aβ aggregation. However, the intrinsic fluorescence from the polyphenols can interfere with the ThT assay. Using UV-visible and fluorescence spectroscopy, the polyphenolic compounds were assessed. It was found that ThT fluorescence could be measured in the presence of Nordihydroguaiaretic Acid and Rosmarinic Acid without interference. However, Resveratrol and Curcumin were found to interfere with ThT fluorescence.
Parvoviruses are small, linear, single-stranded DNA viruses that infect invertebrate and vertebrate hosts. They are non-enveloped viruses approximately 20-24 nm in diameter containing genomes 4-6 kb in length. Due to their compact genetic organization, they utilize alternative RNA processing strategies such as alternative splicing, alternative polyadenylation and alternative translation initiation to generate multiple proteins required for a productive life cycle in the host. This is an effective expression strategy that maximizes their coding capacity. Minute virus of canines (MVC) is a Bocaparvovirus that infects dogs and causes gastroenteritis, respiratory distress and infertility in adult female dogs. MVC encodes two non-structural proteins, NS1 and NP1, and two structural proteins, VP1 and VP2, all of which are essential for viral replication.

We focused on elucidating the gene expression strategies exploited by MVC to generate multiple isoforms of its essential NS1 proteins. NS1 is required for viral genome replication through its interaction with viral origins of replication. Previous work in the lab revealed that during MVC infection, three NS1 proteins of approximately 66kDa, 84kDa, and 100kDa were detected with NS1 antibodies developed against an epitope in the C-terminus of the protein. This was surprising because the open reading frame (ORF) of the major nonstructural protein NS1 was predicted to yield a full length protein with an estimated molecular weight of 88kDa. It has been shown that the smaller 66kDa protein was translated from an alternatively spliced transcript which resulted from the excision of two introns from the NS1 ORF. We are currently identifying and characterizing both the putative genomic cis-acting elements and ORFs required for the expression of MVC NS1 isoforms. Amongst other results, our experiments suggest that the 100kDa NS1 isoform represent the full length protein. In addition, we identified a new 50kDa NS1 isoform that is generated from a transcript that spliced the MCV first, second and third introns.
Aptamers and HIV: A story of evolution
Alexander D. Swain, Kyle J. Hill, Margaret J. Lange PhD, and Donald H. Burke

Approximately 35 million individuals are infected with Human Immunodeficiency Virus (HIV) globally. This far-reaching and chronic epidemic has spawned an intensive worldwide effort to understand how HIV develops, and to produce increasingly effective therapeutics, via gene therapy or vaccines, that target critical events in the virus’ life cycle. Novel nucleic acid-based compounds are being studied involving small RNA molecules, known as aptamers, which can selectively bind specific proteins, in this case, HIV proteins. A conserved retroviral target is Reverse Transcriptase (RT), an enzyme that converts HIV’s RNA genome into dsDNA, which subsequently integrates into the infected host’s genome. The Burke lab has developed anti-RT aptamer libraries via SELEX (Systematic Evolution of Ligands by Exponential Enrichment) that selectively bind and inhibit HIV-RT. Inhibition is achieved by the aptamer competitively binding the active site of RT, thereby preventing the genomic template from binding. However, the aptamers have not been optimized for packaging into developing virus to overcome stoichiometric constraints, and this is a key event for increased therapeutic functionality. We are currently exploring additional rounds of *in vivo* cellular SELEX to select for the enhanced packaging of the aptamer libraries into budding viruses. By co-expressing the aptamer libraries with the proviral plasmids, we can harvest the virus and isolate the aptamers using the cellular environment to perform the selection for us. Subsequently, by reverse transcribing into cDNA and re-cloning the aptamer into our expression plasmid, we will be selecting for aptamers that are enriched for packaging into the virus while maintaining the anti-RT functionalities. Ultimately, High Throughput Sequencing will reveal the sequences of thousands to millions of individual aptamers. This will allow us to identify the common motifs/sequences that have been conserved via selection, which we hope to implement to increase the functionality of aptamer therapeutics in HIV.
Acetazolamides effect on the accumulation of triglycerides in differentiated 3T3L1 adipocytes by inhibition of bicarbonate
Sadara Taylor and Warren Lockette

Abstract withheld at the request of the faculty mentor for proprietary purposes.
Lorisidae, how many are there really?

Chelsea Titus, Rachel Munds, and Lori Eggert

Their large doleful eyes, small stature, and fluid movement make primates of the family Lorisidae, especially the slow loris (Nycticebus), easily recognizable to the public. However, the remoteness of their habitat, nocturnal lifestyle, and the threat of the illegal pet trade make these creatures the least known and most endangered of all the primates. Analyses of facemask patterning have proven reliable in discerning species for the genus Nycticebus found in southeastern Asia. Even though facemask analyses are successful in elucidating Nycticebus species and other nocturnal primates (c.f. owl monkeys, galagos, mouse lemurs, etc.), it has not been done on the other primates of the family Lorisidae (Arctocebus, Loris, Perodicticus). Based on photographs and known locale of individuals of each species, we have analyzed facemask variation among all four genera of the Lorisidae primates to determine groups that cluster geographically as well as by facial mask variation. Facemask groups that map together strengthen the claim that they are distinct species from other facemask groups. Finally, a phylogenetic tree based on the candidate gene 12S has been generated. The phylogenetic tree allowed us to compare the patterns of evolution inferred using morphological and genetic data.
Evaluating RNA gene expression through fluorescent RNA constructs
Emma Tomes, Tanner Shull, Carolina Camargo, and Donald Burke

Abstract withheld at the request of the faculty mentor for proprietary purposes.
When working with critical-care patients, doctors and nurses need augmented reality based technologies to stay updated on the status of patients and care levels. This need is even more critical in a natural disaster scenario where a large volume of patients with varying states of injuries need to be treated through effective co-ordination of limited medical staff and supplies. In this project, we have developed an Intelligent Dashboard viz., “Panacea Glass” that provides the augmented reality benefits with minimal human communication through the integration of a standardized Incident Command System (ICS) application with Internet of Things (IoT) such as heads-up displays, virtual beacons, and wireless mesh network elements. The situational awareness and effective co-ordination is provided by our Panacea Glass through a resource density-graph optimization algorithm that allows: (a) orchestration of video feeds between the Incident Commander and First Responders at the disaster scene, and (b) dynamic tracking and replenishment of medical supply levels. The algorithm handles the prioritization of personnel and medical supplies between responder stations, and importantly recommends actionable intelligence to the Incident Commander for major actions such as for e.g., how many ambulances and which station to route them. We describe our implementation of the Panacea Glass that features a ‘Responder Theater Dashboard’ with WebRTC-based heads-up display video feed collaboration and QR-code based virtual beacon messaging to track patient care status in real-time. We conduct a usability evaluation and an incident simulation study following a template of a ‘Task Force 1 Rescue’. Our results show how our Panacea Glass allows the Incident Commander to deploy personnel and resources at the right locations more efficiently and reduces triage time, mitigates risk of over-triage/under-triage, and ultimately increases the number of successful rescue events.
Interfacing Whispering Gallery Mode optical microresonators with molecularly imprinted polymers
Adam L. Vojta, Gail Denise Hammond, and Heather K. Hunt

Abstract withheld at the request of the faculty mentor for proprietary purposes.
Faculty Mentor: Dr. Abraham Koo, Biochemistry
Funding Source: Life Sciences Undergraduate Research Opportunity Program

Biochemical study on initial steps of jasmonate biosynthesis
Taylor Wagner, Tong Zhang, and Abraham Koo

Abstract withheld at the request of the faculty mentor for proprietary purposes.
The fermentation of switchgrass for 2,3-butanediol by SSF method
Haoqi Wang, Zhu Chen, and Caixia Wan

2, 3-butanediol is of great interest to industries as platform chemicals and liquid fuels. Biomass feedstock with low cost is required for economically viable production of 2, 3-butanediol. Switchgrass, a high-yielding perennial grass with high carbohydrate content (31–37% hemicellulose and 29–45% cellulose), is a promising crop for bio-based chemicals production. The hydrolysates of pretreated switchgrass obtained from acid-catalyzed or enzyme-catalyzed hydrolysis contain a mixture of pentose and hexose (e.g., glucose, xylose, arabinose, mannose, etc.), which are useful and valuable feedstock for the fermentative production of value-added chemicals.

In this study, simultaneous saccharification and fermentation (SSF) was conducted for 2, 3-butanediol production using the pretreated switchgrass as carbon source. Many microorganisms can be used to ferment sugars into 2, 3-Butanediol, among which Klebsiella pneumonia and Klebsiella oxytoca are the ones frequently used. However, microorganism like Klebsiella sp. is regarded as a pathogenic microorganism not suitable for 2, 3-butanediol production. Bacillus licheniformis ATCC 14580 was used to produce 2, 3-butanediol at 50°C, SSF conditions, such as substrate loading and culture time, were optimized to maximize the conversion efficiency. The results indicated the pretreated switchgrass is a promising substrate for economical production 2, 3-butanediol through SSF.
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Developing a new method for RNA sequence-structure analysis  
Kevin Wang and Shi-Jie Chen

Ribonucleic acids (RNA) molecules are critical for cellular functions at the level of gene expression and regulation. Recent theoretical and experimental studies have suggested that an RNA sequence may form multiple alternative structures and reciprocally, one structure can be formed by multiple sequences. Inspired by the significant biological and therapeutic applications of the intriguing sequence-structure relationships of RNAs, I developed a clustering method for RNAs in both the sequence and the structure space. I analyzed sequence-structure data of mutants from a target RNA sequence. I was looking for groups of sequences that form the same 2-D structures. In particular, I was interested in finding “neutral nets” among these mutants, i.e., sets of sequences interconnected by single-point mutations that share the same structure. I used the X-Means clustering algorithm (a variation of K-Means), and a hierarchical clustering algorithm to group sequences according to the structure they form. I also analyzed the relationship between mutational stability, i.e., how many single-point mutations conserve the native structure of a sequence, and thermodynamic stability of the sequences. Defining the prototype sequence as the highly thermodynamically stable sequence with the maximum number of single-error mutants forming the same structure, I expect to find a distinct correlation between the Hamming distance from this prototype sequence and the free energies of the mutant sequences. The method that I developed would be applicable to a broad range of biologically and therapeutically significant problems such as understanding mechanisms of RNA cellular functions and rational design of RNA-based therapeutic strategies.

This work was supported by the National Science Foundation award "Research Experience for Undergraduates in Materials and Modeling" (#1359430)
Anaerobic co-digestion of edible and inedible food waste and sewage sludge
Thomas Welby, Bennett Harman, Amanda Prescott, Misha Kwasniewski, Christine Costello, and Caixia Wan

The goal of our study was to explore the feasibility of using anaerobic digestion to treat food waste. Given interest in reducing the edible fraction of food waste, the study used both edible and inedible fractions of food waste observed in Campus Dining. Inedible food waste consists of material that would not be eaten under normal circumstances, including banana peels, orange peels, egg shells, etc. Sludge from a Columbia waste water treatment plant was incorporated in order to improve the stability of the digestion. Three trials in duplicate were explored: (1) 50% of organic loading rate provided by sludge 50% inedible and edible food waste; (2) 50% sewage sludge with 50% inedible food waste; (3) 75% sewage sludge, 25% edible and inedible food waste. The reactors were maintained at a temperature of 97 degrees Fahrenheit with hydraulic retention time of 28 days. Every day the reactors were fed new material and old material was removed from the reactor for testing. The pH levels of the influent and effluent were measured to assure the reactor has the correct conditions to produce methane gas efficiently. Airtight bags were attached to the reactors to collect the gas produced. The volume and composition of the gas in the bags was recorded to calculate the potential energy produced from the reactors. The results of this study show that all three trials generate useful ranges of methane production. Future work will be focused on optimizing the mixing ratios for improved methane production.
Understanding subset glia functionality in *Drosophila melanogaster* through locomotion and calcium imaging

Alex Willenbrink and Bing Zhang

Glia are major brain cells with diverse structure and function, but they are not well understood. Our project focuses on the uncovering subset glia and their function in the fruit fly, *Drosophila melanogaster*. Through genetics, we isolate minute subsets of glia, express a mutant protein with expanded glutamine (polyQ, which causes ataxia and Huntington’s disease), and examine their effects on fly behavior. Out of ~400 different strains of flies, we have now identified a range of subset glia that can either decrease or increase the speed of walking.

Currently, my work is directed towards a better understanding of the molecular mechanisms associated with these subsets of glia and their regulation of neuronal circuits. One way to explain this is through calcium imaging. When calcium levels are high, an intracellular calcium sensor, GCaMP5, fluoresces when struck by excitation wavelengths. Similar to neurons, glia communicate through vesicle release of chemicals called gliotransmitters, initiated by a sudden increased intracellular calcium level. The calcium signal has the amazing ability to travel to neighboring glia in an oscillatory fashion coined a “calcium wave”. Recent research has shown that this communication is not restricted between glia but has the ability to extend to that of neurons, asserting an almost puppet-master role of glia in the nervous system. We show that PolyQ disrupts calcium waves, which we hypothesize are important for glial signaling. To further test this hypothesis we have introduced TRPA1, a heat-activated cation channel, in glia and allowed intracellular calcium levels to skyrocket by simply raising the temperature above 32°C. We show that flies expressing TRPA1 in the entirety of glia experience rapid paralysis upon exposure to restrictive temperatures. One major consequence of this manipulation is that the vibrant calcium waves are abolished. We are now screening for other molecules that can restore calcium waves in both PolyQ and TRPA1 flies. Because the basic structure and function of glia and neurons are conserved from flies to humans, we hope the insights revealed from our studies help understand human brains.
Influence of life history on genetic diversity in salamanders
Mary Madeline Willis, Jake Burkhard, Raymond D. Semlitsch, and Lori S. Eggert

Dispersal is a critical component of animal ecology that is poorly understood for most species, but is vital to our understanding of metapopulation dynamics. Factors that have been shown to influence dispersal include landscape and habitat variables, life history, and organism physiology and morphology. Previous studies conducted in our lab show that at Fort Leonard Wood two sympatric, fall-breeding salamanders, the marbled salamander and ringed salamander, have populations consisting of two and three genetic clusters, respectively. Another sympatric species, the spotted salamander is a spring breeder and displays only a single genetic cluster. We hypothesized that this difference in genetic clustering between these species can be directly attributed to the difference in breeding season. To test this hypothesis, we studied the genetic structure of the eastern newt (Notopthalmus viridescens), a co-occurring spring breeder. We used nuclear microsatellite loci to analyze 110 individuals from 11 ponds across the same landscape. Preliminary data analysis revealed a single genetic cluster for this species, which supports our hypothesis. Our results will better inform management strategies that seek to increase connectivity for amphibian populations that are increasingly fragmented due to anthropogenic effects.
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Noninvasive examination of stress in In$_x$Ga$_{1-x}$Sb epitaxial layers mismatched to GaSb
Connor Wolenski, Weinan Zhang, and Gregory Triplett

In$_x$Ga$_{1-x}$Sb is a promising semiconductor material for use in a variety of optoelectronic devices operating in the mid-infrared 2μm to 4μm region. Widespread uses for these devices include optical communication and remote sensing of atmospheric pollutants. Additionally, infrared lasers based on these types of materials are used for military applications such as low-altitude radar and infrared countermeasures. However, it is inherently difficult to produce high quality InGaSb because of the large lattice mismatch (up to 6.3%) that exists between the InGaSb material and the substrate on which it is deposited (GaSb).

In our experiments, undoped 100 nm In$_x$Ga$_{1-x}$Sb epitaxial layers with mole fractions varying from $x = 0.1$ to $x = 0.4$ were grown by molecular beam epitaxy (MBE) on GaSb (100) semi-insulating substrates. The samples were characterized ex situ through the use of scanning electron microscopy (SEM), energy dispersive spectroscopy (EDS), and Raman spectroscopy. Characterization results show that with increasing indium composition, the samples generally become increasingly strained due to the lattice mismatch of the In$_x$Ga$_{1-x}$Sb active layer and the GaSb substrate; however, some regions across the sample reveal immediate strain relief and material exhibiting a free standing lattice constant for In$_x$Ga$_{1-x}$Sb. Strain in the samples was modeled to approximate a numerical value of stress in the samples as a function of Raman shift. Additional models are developed in order to relate the critical layer thickness and indium composition in the samples that will open up new opportunities for monolithic design of In$_x$Ga$_{1-x}$Sb-based devices.
Coupling axonal models to live neurons: Real-time computation and visualization
Alexander Wood, Marco A. Navarro, and Lorin Milescu

Information in the brain is encoded and travels as action potentials, which are brief changes in neuronal membrane voltage. Action potentials are initiated in the axonal initial segment and travel down the axon towards synaptic terminals, but they also back-propagate towards the soma. This back-propagation has specific effects on the action potential shape, as measured at the soma. The shape and timing of the action potential reflect the underlying properties of the neuron, such as axonal geometry and electrical properties, sodium channel distribution and density, etc. To understand these properties, we use a combination of computational and experimental approaches, where a model of the axon is coupled to a live neuron, using dynamic clamp. The axon is modeled as a series of compartments populated with voltage-gated sodium and potassium channels, described by realistic Markov models. We are also developing tools to visualize the activity of the model in real-time.
Quantitative analysis of craniofacial characteristics in single-suture craniosynostosis
Franklin K. Woode, Joan T. Richardsmeier, Arshad R. Muzaffar, and Kristina Aldridge

Single-suture craniosynostosis (SSC) is a common condition in which the suture between two bones of the skull fuses prematurely, occurring in 1 in 1500 births. Altered growth patterns in the skull associated with suture fusion result in characteristic changes in the shape of the head and face, requiring invasive medical interventions during infancy. Despite the frequency of SSC, there are few quantitative assessments of these craniofacial shape differences to inform intervention strategies. In this study we seek to quantitatively assess the clinically described characteristic craniofacial shapes associated with the two most common forms of SSC, sagittal and metopic craniosynostosis. We use landmark data collected from three-dimensional reconstructions of MRIs from infants ages 8-80 weeks diagnosed with sagittal (n = 9) or metopic (n = 8) craniosynostosis and age-matched subjects unaffected by craniosynostosis (n = 10) using etdips® software. We use Euclidean Distance Matrix Analyses (EDMA®) to statistically compare head shapes among the three groups. As expected, cluster analyses show that head shape in both metopic and sagittal subjects differs significantly from that of the control subjects. In metopic subjects, results of EDMA form comparisons show significant alterations in relationships among upper- and mid-facial structures. These findings corroborate previous clinical descriptions of restricted growth of the fronto-orbital region; however, we do not find increased breadth of the posterior cranium as described for metopic craniosynostosis. Interestingly, results of EDMA form comparisons of sagittal subjects do not show a significant amount of the cranial elongation previously described. Instead, we see a significant anterior displacement of the vertex of the head. These findings suggest that clinical descriptions of sagittal and metopic craniosynostosis may misinterpret the patterns of dysmorphology. Future work with increased sample sizes will provide additional information to craniofacial care teams in considering best practices for intervention strategies in SSC.
Enhancement of the automated prediction pipeline of the alcohol craving study
Andrew Woods, Nickolas Wergeles, Can Li, and Yi Shang

The study of alcohol use and craving in the past has relied on mostly laboratory experiments and artificial environments that would induce the craving of alcohol. In some cases, physiological data was not recorded and if the data was recorded, they did not automate the analysis and prediction of alcohol use. This project is looking at data of individuals participating in the Alcohol Craving Study conducted by the University of Missouri Psychology and Computer Science Departments. The data is then analyzed to better understand the effects of drinking alcohol by using automated machine learning algorithms performed by a computer. Using these methods, the system develops models which can predict the moment when the user drinks or craves alcohol based on sensor and survey data collected from the user. The approach starts by analyzing and cleaning up the noise in the input data. Afterwards, the data is analyzed in both drinking and non-drinking episodes. A model is then developed that can differentiate between these episodes and automatically indicate a drinking episode or a craving incident. It will then notify the system, which will prompt a survey for the user to complete, in order understand why the user started drinking in the first place. The results of the system have not yet been thoroughly tested, but previous and current testing shows promising results, and further testing may yield similar if not better results.
Soybean is a unique plant that can provide both oil and protein. Soybean seeds contain about 40% protein and about 20% oil. In my project, I am screening a fast neutron mutant population of soybean to find mutant seeds with increased oil and/or protein content. I first made aliquots of 100 seeds from each mutant plant and then later use Near Infrared (NIR) spectroscopy to measure the oil and protein content in the seeds. In total, I measured the oil and protein content of seeds derived from 1,322 mutant plants. Based on these measurements, I identified several soybean mutants with altered production of seed oil and protein. The average oil content in the mutant soybeans is 19.4%, the average protein content is 35.6%, and the average oil+protein content is 55.5%. The highest oil plus protein content in one of the mutants is 57.9%, which is 2% higher than the un-mutated William 82 soybean cultivar. These mutants will be useful for the improvement of soybean seed quality.
Determining the composition of T Cep's stardust and implications for stellar evolution
Renna Yi and Angela Speck

Stardust is formed as mass is ejected from low-to-intermediate mass (LIM) stars during the Asymptotic Giant Branch (AGB) phase, late in the star’s life cycle. The ejection is caused by the stars’ pulsation, which levitates atoms high into the stellar atmosphere. At high altitude, the temperature is low enough for solids to form. And thus these LIMS develop a dust shell. Radiation pressure acts on the dust grains so that they are pushed away from the star, so that the dust shell evolves. Understanding the nature of stardust is important, as this dust contains matter from which all subsequent stars, planets, and potential life forms will be made. Moreover, the dust grains affect energy flow through the universe, and thus dust affect any environment in which it is found. In this study, we investigate the physical parameters of the dust shell around LIM star T Cep, currently in its AGB phase. T Cep is an oxygen-rich star and has an optically thin atmosphere, so by determining the surface composition and using the pressure/temperature space, we can gain insight into the dust formation mechanism. Each star has a characteristic light spectrum, whose shape depends on the central star temperature, the density of the dust shell, and the size distribution, shape, temperature, and chemical composition of the dust grains. We model T Cep’s spectrum using these parameters with the radiative transfer program DUSTY. The present study utilizes recently published optical constants, which should generate models more accurate than those previously derived from synthetic data. Our models indicate stellar temperatures lower than previously expected. Further results will be presented.

This work was supported by the National Science Foundation award "Research Experience for Undergraduates in Materials and Modeling" (#1359430)
Developing tools to investigate the role of TCP transcription factors in the plant immune response
Casey Yocks, Benjamin Spears, and Walter Gassmann

The plant defense response to pathogens is highly regulated. Several members of the TCP transcription factor family of Arabidopsis thaliana recently have been shown to be positive regulators of plant immunity, previously found mainly to regulate plant development. A group of TCPs interact with SRFR1, a negative defense regulator. A tcp8 tcp14 tcp15 triple mutant has a susceptible phenotype to pathogens and shows how highly redundant TCPs are. We aimed to develop genetic and protein biochemical tools to further investigate the role of TCPs in plant immune responses. Using restriction cloning we generated epitope-tagged genomic TCP14 and TCP15 constructs, which will be used to transform A. thaliana plants. These transgenics can be used to better evaluate the interactions of other proteins with TCPs and look at the specific genes they control. The transgenics will be validated through complementation of a tcp8 tcp14 tcp15 triple mutant, shown by decreased susceptibility in a bacterial growth assay. This tool can be used in various experiments to enhance our understanding of the role of TCPs in the plant immune response to pathogens.
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Faculty Mentor: Hannah Reeves, Art  
Student Research Partner: Sera Holland (Dr. Candace Galen, Biological Sciences)

Fungi: Protectors of life  
Meiqi Yuan and Hannah Reeves

_Students in the summer 3D Design Art class were paired up with an MU undergraduate researcher for their Wood Relief Project. After discussing the research project with their student partner, art students visited the research lab and obtained any visual support materials that the science researcher could offer. The student researcher's project was the inspiration for the art student's 24” x 24” wood relief art. The artwork attempts to conceptualize the research from a new perspective, abstracting and interpreting the ideas and impact of the research topic. Student art pieces will be displayed alongside the undergraduate research poster during the Forum._

My scientist Sera Holland works on a type of fungi, which can help plants survive, and I transfer this idea into a wood project. Basically, the fungi will attach on the root of the plants and hold water, so that the plants will get enough moisture and result in a better growth.

For this wood project, I enhance the idea of showing the natural beauty of wood. For the texture part, I kept everything natural, so we can still see the texture of wood logs clearly. Since the fungi are the key elements in this research, I used tiny wood logs to represent the fungi, which support the plants to survive, and attached them at the underneath the tree trunk. I built up the tree trunk or the plant part with several wood pieces. I painted the overall tone in green to emphasize the signs of life, and I tried to bring the natural color of tree trunk mixing brown with darker and lighter greens. The piece as a whole is well balanced, and indicates the beauty of nature.
Characterization of vegetative and reproductive defects in the maize tassel-less 4 mutant
Dennis Zhu and Paula McSteen

Abstract withheld at the request of the faculty mentor for proprietary purposes.