Clemson University
HONORS COLLEGE

EUREKA 2.0

UNDERGRADUATE RESEARCH

2020

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Welcome to the 2020 EUREKA! Poster Forum

EUREKA! (Experiences in Undergraduate Research, Exploration and Knowledge Advancement) is a unique endeavor to immerse incoming Clemson University Honors College students into the academic world of Clemson University. From June 29th through August 8th, the 2020 EUREKA! program participants performed research in an even more unique way than the previous fourteen years of the program's existence. Due to the 2020 worldwide COVID-19 pandemic, EUREKA! 2.0 was born and all facets of the program, including the research experience, were performed remotely from home through video conferencing and other online means. Although completely an online program, participants were able to become acquainted with each other, campus resources, and some of the university's best faculty and administrators.

Created in 2006, the new **"Experiences in Undergraduate Research, Exploration and Knowledge Advancement!" (EUREKA!)** program was based on an idea conceived by Stephen Wainscott, former Director of the Clemson University Honors College, and further developed by a committee of the following members:

Dwight Camper, Professor of Entomology, Soil, and Plant Science;
Dana Irvin, Assistant Director of the Clemson University Honors College;
Pam Mack, Associate Professor of History;
James McCubbin, Professor and Chair of Psychology;
Mary Miller, Special Assistant to the Provost;
Gary Powell, Professor Emeritus of Genetics and Biochemistry;
Steve Wainscott, Director of the Clemson University Honors College;
Sean Williams, Associate Chair and Professor of English;
and Bill Pennington, Professor of Chemistry.

During the second summer session of 2020 the fifteenth group of EUREKANS!, consisting of thirty-three incoming Honors freshmen representing eight different states, and three current Honors students, serving as counselors, were joined together for a five-week period of research, scholarship, and discovery. As the world faced the COVID-19 pandemic and the Clemson campus was closed, EUREKA! was transformed into EUREKA! 2.0, an entirely online research program. Students worked on individual projects under the direction of faculty mentors in fields ranging from natural to physical sciences and engineering. In addition to their research activities the participants attended web-based workshops and seminars on various topics designed to orient them to academic life on campus and provide them with the basic skills needed to perform research in a broad range of areas.

In addition to the educational rewards of active participation in undergraduate research, the students got to know the campus resources and interacted with many faculty, staff, administrators, and other students. They developed networks of supportive mentors and colleagues that will serve them well in their academic careers. Many of our program participants continue their projects throughout their undergraduate years. We hope that their enthusiasm for research will encourage their peers to follow their lead to build an exciting and productive environment for undergraduate research, scholarship and discovery at Clemson University.

2020 EUREKA! Students

Participant	Hometown	Major	Faculty Mentor	Page
Raleigh Adams	Easley, SC	Political Science	Dr. Sophie Jörg	6
Sam Buckley	Rock Hill, SC	General Engineering	Dr. Liangjiang Wang	7
Simon Ciprari	Atlanta, GA	Biochemistry	Dr. Mark Blenner	8
Taylor Corcoran	Seneca, SC	General Engineering	Dr. Yongqiang Wang	9
Sarah Barclay Cribb	Spartanburg, SC	General Engineering	Dr. Qiushi Chen	10
Liz Dillard	Inman, SC	Microbiology	Dr. Hong Luo	11
Annalise Enger	Fort Mill, SC	General Engineering	Dr. Hong Luo	12
Nick Foehl	Malvern, PA	Biological Sciences	Dr. Sruthi Narayanan	13
Will Franklin	Carlisle Barracks, PA	General Engineering	Dr. Ethan Kung	14
Tyler Golbus	Irmo, SC	Biological Sciences	Dr. Ethan Kung	15
Mariana Holladay	Arlington, VA	Engineering (general)	Dr. Mark Blenner	16
Laura Jeniski	Ridgefield, CT	General Engineering	Dr. Rachel Getman	17
Vaishnavi Kanduri	Summerville, SC	Bioengineering	Dr. Mark Blenner	18
Emma Katovich	Palatine, IL	General Engineering	Dr. Sophie Jörg	19
Sydney Keffer	Greenville, SC	Health Science (Preprofessional Health Studies)	Dr. Michael Sehorn	20
Tori Luongo	Oxford, GA	Mathematical Sciences	Dr. Hong Luo	21
Omika Merchant	Simpsonville, SC	Biological Sciences	Dr. Xia Jing	22
Caroline Michaelson	Crystal Lake, IL	Food Science and Human Nutrition	Dr. Michael Sehorn	23

Participant	**Hometown**	**Major**	**Faculty Mentor**	**Page**
Matt Monaghan	Central, SC	Biochemistry	Dr. Ethan Kung	**24**
Victoria Murphey	Austin, TX	Biological Sciences	Dr. Michael Sehorn	**25**
Matt Mytych	Virginia Beach, VA	General Engineering	Dr. Liangjiang Wang	**26**
Andrew O'Rourke	Herndon, VA	General Engineering	Dr. Bing Li	**27**
Krishna Patel	Fort Mill, SC	Biochemistry	Dr. Liangjiang Wang	**28**
Elizabeth Peacock	Spartanburg, SC	Health Science (Preprofessional Health Studies)	Dr. Rachel Getman	**29**
Dante Piscitiello	Lakeville, MN	General Engineering	Dr. Qiushi Chen	**30**
Shrika Ravichandran	Greenville, SC	Health Science (Preprofessional Health Studies)	Dr. Hong Luo	**31**
Kaustubha Reddy	Greenville, SC	Psychology	Dr. Sharon Bewick	**32**
Jason Saadeh	Simpsonville, SC	General Engineering	Dr. Ethan Kung	**33**
Emma Simon	Boalsburg, PA	General Engineering	Dr. Patrick Hiesl	**34**
Noah Tavarez	Sumter, SC	Computer Science	Dr. Yongqiang Wang	**35**
Shreya Tellur	Simpsonville, SC	Biological Sciences	Dr. Xia Jing	**36**
Shreya Thammana	Greenville, SC	General Engineering	Dr. Ethan Kung	**37**
Kayleigh Trumbull	Chapin, SC	General Engineering	Dr. Jason McNeill	**38**
Nataly Wickstrom	Charleston, SC	Animal and Veterinary Science	Dr. Bing Li	**39**
Jackson Wiley	Woodruff, SC	General Engineering	Dr. Qiushi Chen	**40**
Thomas Zakrzwski	Piedmont, SC	General Engineering	Dr. Yongqiang Wang	**41**

Constructing a Virtual Environment for Collaboration Studies

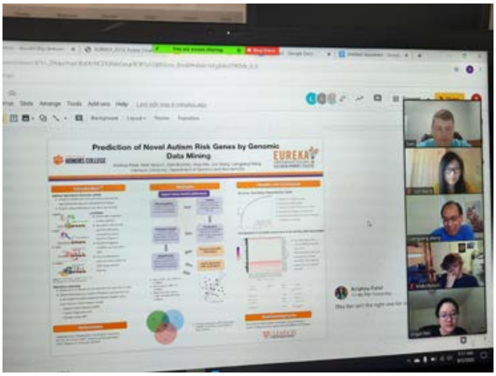
Raleigh Adams, Emma Katovich, Alex Adkins, and Dr. Sophie Jörg
School of Computing, Clemson University

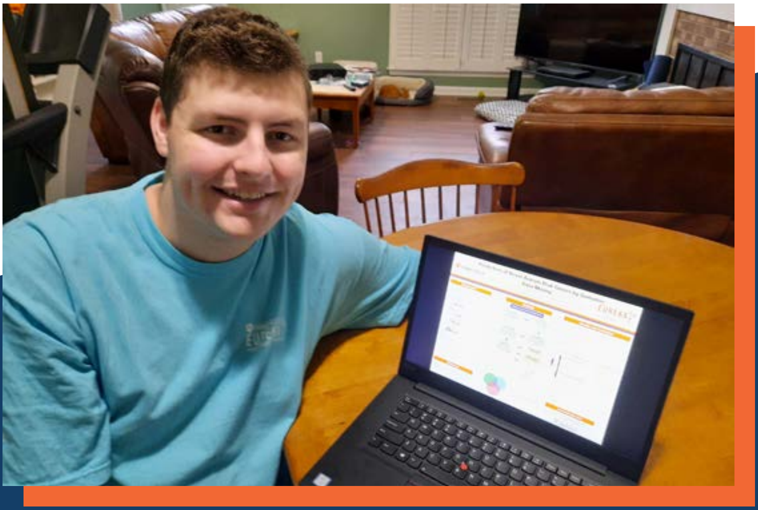
Virtual environments can be used to test a variety of scenarios that cannot be tested in the real world. The objective of this research project was to create a working virtual environment using the game engine Unity, that can be used to replicate NASA's Survival on the Moon test. In this test, team members are asked to rank fifteen survival items based on how important they believe them to be for reaching the mother ship. Their answers are then compared to the NASA ranking to evaluate their problem solving and teamwork skills. Our environment can be used to investigate teamwork between individuals and how different variables, such as different levels of control over the environment, presentation within it, or the challenge they are posed might affect the team's success.

Prediction of Novel Autism Risk Genes by Genomic Data Mining

Sam Buckley, Krishna Patel, Matt Mytych, Anqi Wei, Jun Wang, and Dr. Liangjiang Wang
Department of Genetics and Biochemistry, Clemson University

Autism Spectrum Disorders (ASD) refer to a group of neurodevelopmental disorders characterized by cognitive and behavioral delays. Many of the underlying causes of ASD delve into the molecular level, including both protein-coding and non-coding genes. Long non-coding RNAs (lncRNAs) are a group of non-coding RNAs that have no protein coding capacity, but have been linked to ASD. Traditional methods for identifying and validating ASD risk genes is time-consuming and costly, thus a machine learning model is necessary. In this study, we built machine learning models to predict and prioritize candidate lncRNAs associated with ASD. Three different models were trained using brain gene expression data collected from BrainSpan. Performance of the Support Vector Machine (SVM) model was compared to other classifiers, such as Logistic Regression (LR) and Random Forest (RF). From all three models, 564 lncRNAs and 6,093 protein-coding genes were predicted to be high-confidence ASD risk candidate genes. Developing a model to predict and prioritize autism-associated genes is one step closer to understanding the pathogenesis of ASD and to potentially find ways for treatment.

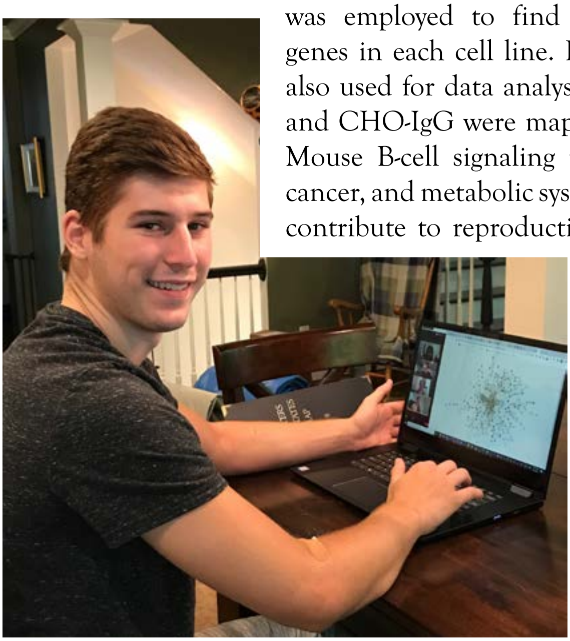


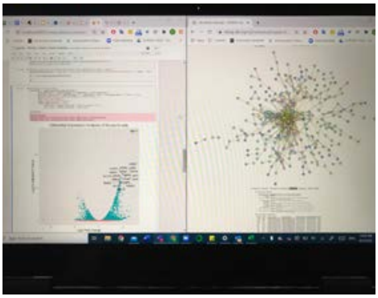


Comparative Analysis of CHO Cell Therapeutic Production to Native Cell Lines

**Simon Ciprari, Vaishnavi Kanduri, Mariana Holladay, Dyllan Rives,
and Dr. Mark Blenner
Department of Chemical and Biomolecular Engineering, Clemson University**

Chinese Hamster Ovary (CHO) cell lines are utilized to produce therapeutics, but selection methods for these cell lines are time-consuming and expensive. Finding cost-efficient ways to increase the efficacy of CHO cell lines is crucial to ensure the quality and availability of novel treatments. Genetic markers identified in native cell lines could optimize cell lines and decrease selection time. Our research aims to compare immature Follicle B (FoB) cells to mature bone marrow plasma cells (BMPC) acquired from mice to characterize genes that aid antibody production. Identified genetic markers in the BMPC are further compared to Immunoglobulin G (IgG) producing CHO cells to determine similarities and differences. The CHO-IgG cell line was compared to a wild type cell line to account for the variations in production. Differential expression analysis, using the DESeq2 software package, was employed to find upregulated and downregulated genes in each cell line. Heatmaps and volcano plots were also used for data analysis. Gene pathways of BMPC cells and CHO-IgG were mapped using the STRING program. Mouse B-cell signaling pathways contribute to immune, cancer, and metabolic systems. CHO cell signaling pathways contribute to reproduction and cancer systems. Both are generally involved in metabolic, apoptosis, and immune systems.

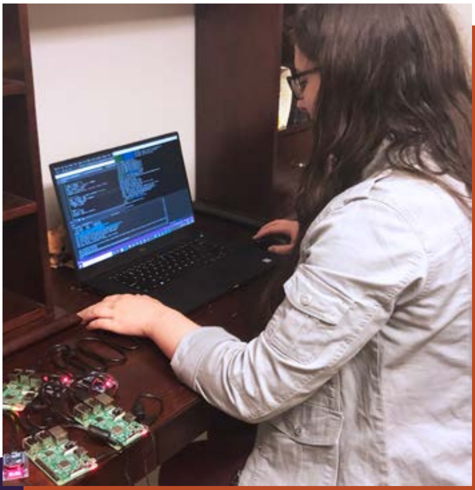




Achieving Decentralized Robotic Heading Synchronization Via Pulse-Coupled Oscillators

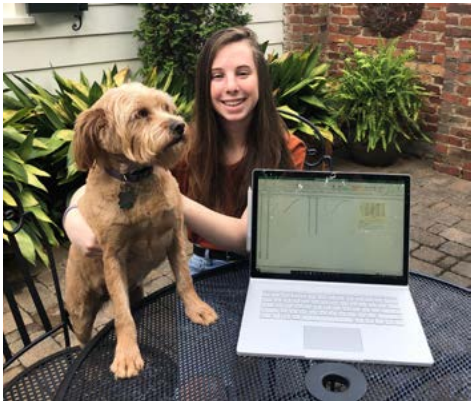
Taylor Corcoran, Noah Tavarez, Thomas Zakrzwski, Timothy Anglea, and Dr. Yongqiang Wang
Department of Electrical and Computer Engineering, Clemson University

Synchronization occurs when multiple parts of a system or network work together at the same time to complete a task. In centralized synchronization, robots send regular bursts of data to the rest of the wireless network, such as heading, position and sensor data, so the other robots can adjust to match. However, this method of synchronization has many problems regarding privacy and large data transfers, which complicates communication within the network. The goal of our project is to solve these problems by achieving decentralized synchronization between robotic systems with pulse-coupled oscillators (PCOs), which simplifies communication between robotic systems, reduces energy consumption, and reduces the chance of data loss and corruption. We compare four algorithms for PCO synchronization to determine which one is most effective and then use this information to implement a PCO protocol for synchronizing robotic heading.

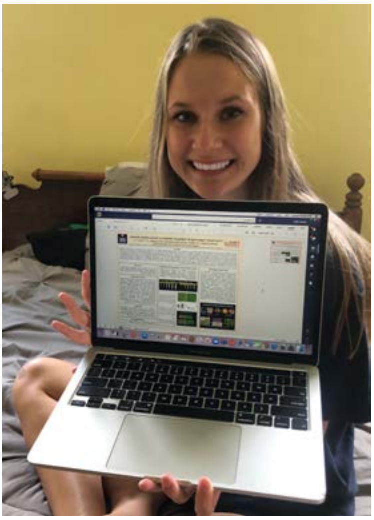


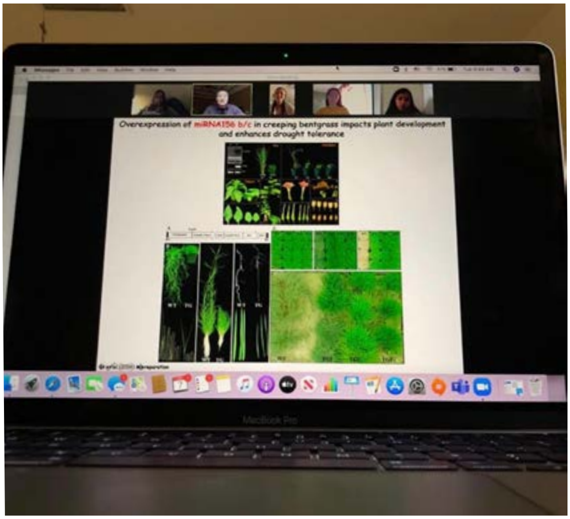
Understanding Lunar Regolith Simulants and Their Interactions with Drilling Tools for In Situ Resource Utilization

Sarah Barclay Cribb, Dante Piscitiello, Jackson Wiley, Zakia Tasnim, and Dr. Qiushi Chen
Glenn Department of Civil Engineering, Clemson University



NASA's upcoming Artemis program aims to return humans to the moon where they will drill Lunar regolith to gather materials for in-situ resource utilization, which will produce needed materials for Lunar exploration. The objective of this project is to use Lunar regolith simulants to understand the geotechnical, mineralogical, and chemical aspects of Lunar regolith and compile data on lunar regolith simulants into an organized database. An important geotechnical property of Lunar regolith is its particle-size distribution (PSD), and in this research, the PSDs of all existing Lunar regolith and regolith simulants are compiled. The research process involved digitizing images of PSD curves, taking the curve data, and modeling the curve in Excel. Researching Lunar regolith simulant databases and other scientific references was necessary to compile a mineral and chemical database of Lunar regolith simulants. The limitation of using terrestrial materials leads to a variety of chemical and mineral composition among different Lunar regolith simulants. Understanding the differences among these simulants and their intended purposes is essential to conducting accurate research on Lunar regolith. Existing Lunar drilling tools and numerical modeling tools are also explored and will be topics of future research.





Overexpression of miRNA156 b/c in creeping bentgrass impacts plant development and enhances drought tolerance

Crop Genetic Engineering for Enhanced Tolerance to Various Abiotic Stresses

Liz Dillard, Annalise Enger, Shrika Ravichandran, Tori Luongo, and Dr. Hong Luo
Department of Genetics and Biochemistry, Clemson University

Abiotic stresses, such as salt and drought, significantly affect plant development and are the major limiting factors on crop quality and productivity. Manipulation of genes involved in plant stress response facilitates plant mitigation of adverse environments. The objective of this project is to investigate the effects of specific genes on plant resistance to adverse environmental conditions. Several presentations and research papers were studied and discussed to gain knowledge on the processes of genetically engineering crops and on results of transgenic plants exhibiting improved stress responses controlled by different molecular mechanisms in past experiments. Specifically, to genetically improve perennial grasses for enhanced stress resistance, various candidate genes from rice were cloned and introduced into turfgrass cells. The genes were marked for testing to ensure they were being expressed in the regenerated transgenic turfgrass plants. The manipulated expression of rice genes in transgenic turfgrass affected plant development and led to enhanced plant resistance to multiple environmental stresses including salt, drought, heat, and nutrient deficiency. These data demonstrate the importance of biotechnology for enhancing agricultural production, especially when anticipating exponential growth in the world population as well as changes in climatic conditions.

Crop Genetic Engineering for Enhanced Tolerance to Various Abiotic Stresses

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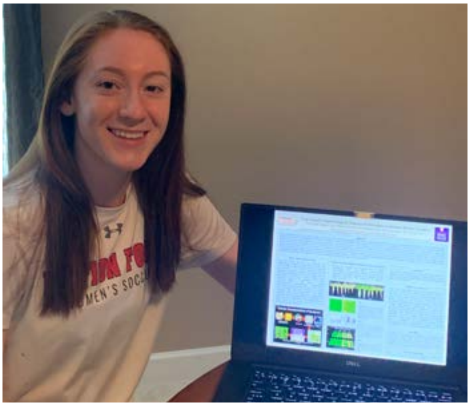
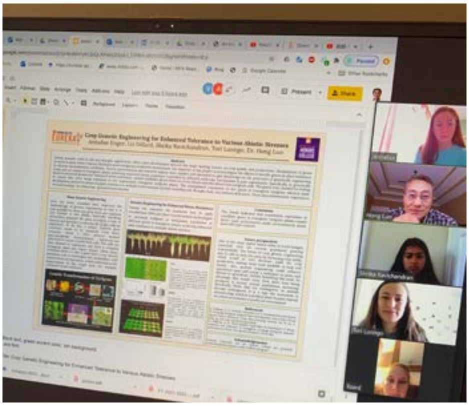
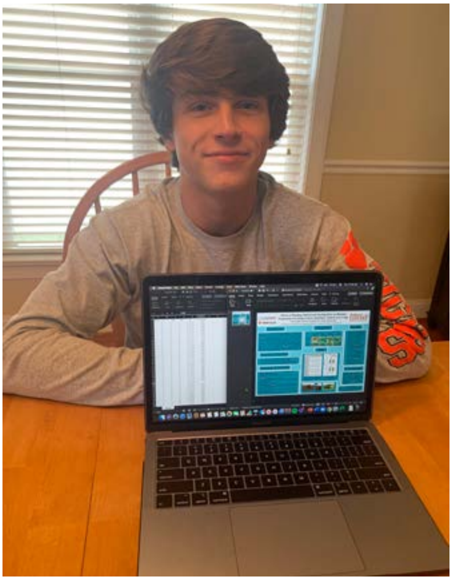




Effects of Planting Method and Seeding Rate On Biomass Production of Crimson Clover and Hairy Vetch Cover Crops

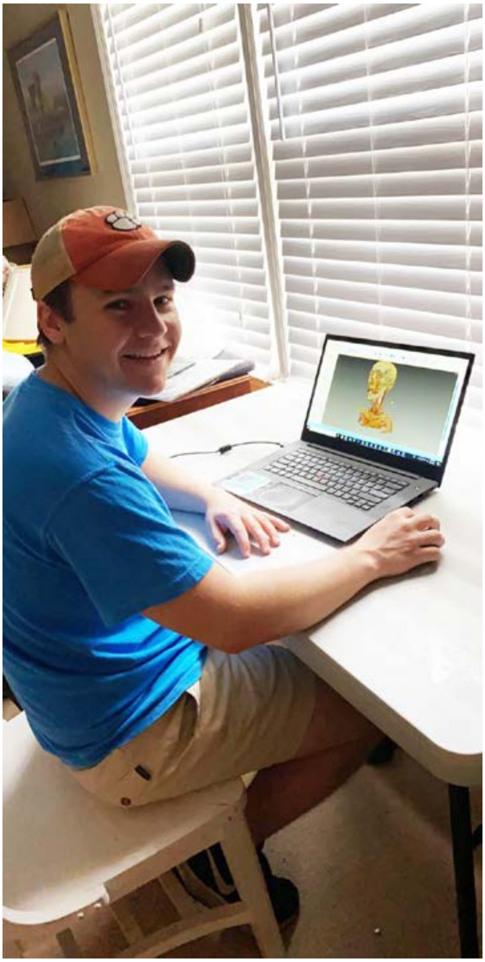


Nick Foehl, Ricardo St Aime, and Dr. Sruthi Narayanan
Department of Plant and Environmental Sciences, Clemson University

Cover crops are planted via broadcasting (seeds are widely dispersed throughout the field) or conedrilling (involves creating small furrows in the soil, ensuring accurate seed placement and depth). The objectives of this study were to evaluate cover crop biomass production under broadcasting and conedrilling and test how results vary for two different cover crops (crimson clover and hairy vetch), under two different seeding rates (optimal and high). Both cover crops were planted on 10/29/2019 at optimal (20 lb/acre) and high (30 lb/acre) seeding rates and harvested on 04/06/2020. When broadcasted, crimson clover and hairy vetch produced the same amount of biomass at both optimal and high seeding rates. With the use of conedrilling, crimson clover produced drastically more biomass than hairy vetch at both seeding rates. Furthermore, when conedrilled, crimson clover produced twice the amount of biomass than when broadcasted at both seeding rates. Biomass production did not differ between conedrilling and broadcasting for hairy vetch at both seeding rates. The results suggest that the effect of planting method on cover crop production is largely dependent upon the cover crop species, as crimson clover greatly responds to conedrilling, whereas hairy vetch does not, even under high seeding rates.

Experimental and Computational Cardiovascular Research

Will Franklin, Tyler Golbus, Matt Monaghan, Jason Saadeh, Shreya Thammana, and Dr. Ethan Kung
Department of Mechanical Engineering and Department of Bioengineering, Clemson University



A buildup of plaque in the arteries can cause a potentially fatal disease called carotid stenosis, the narrowing of a major blood vessel that leads to the brain. The objective of this project is to create a model of the carotid bifurcation at the stenosis, simulate the patient's blood flow, and analyze the results to determine whether the patient's condition is severe enough to cause a stroke. By using CT scans from five patients and SimVascular software, segments of the carotid artery were created and lofted together to create an accurate representation of the shape and path of the carotid artery. To create a simulation, CT scans were opened in SimVascular, where the vessel was traced to make a model and create a mesh. Flow rate data was extracted from patient ultrasound doppler graphs, and data files were created with time and calculated volumetric flow rate data over one heartbeat. The data was translated into a spreadsheet, and the simulations were run, mimicking the human cardiovascular system by applying realistic pressures and flow boundary conditions to the 3D model. The results gained from these experiments provide detailed hemodynamic information that can help inform clinical diagnostics and treatment planning.

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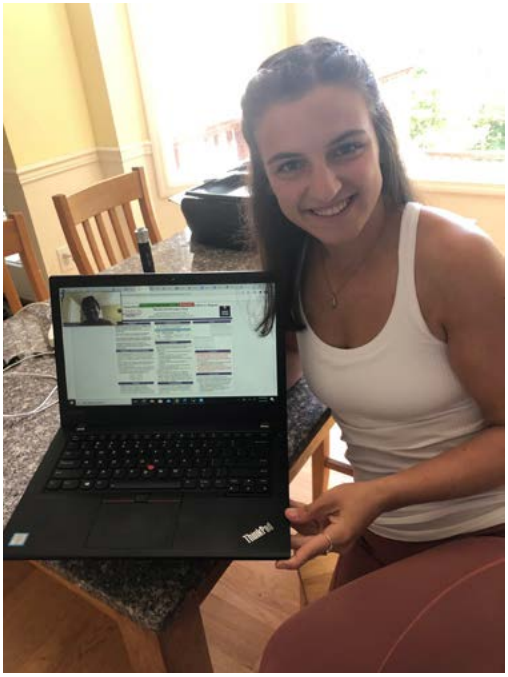
Comparative Analysis of CHO Cell Therapeutic Production to Native Cell Lines

**Mariana Holladay, Vaishnavi Kanduri, Simon Ciprari, Dyllan Rives,
and Dr. Mark Blenner**
Department of Chemical and Biomolecular Engineering, Clemson University

Chinese Hamster Ovary (CHO) cell lines are utilized to produce therapeutics, however, selection methods for these cell lines are time-consuming and expensive. Finding cost-efficient ways to increase the efficacy of CHO cell lines is crucial to ensure the quality and availability of novel treatments. Genetic markers identified in native cell lines could optimize cell lines and decrease selection time. Our research aims to compare immature Follicle B (FoB) cells to mature bone marrow plasma cells (BMPC) acquired from mice to characterize genes that allow for antibody production. Identified genetic markers in the BMPC are further compared to Immunoglobulin G (IgG) producing CHO cells to determine similarities and differences. The CHO-IgG cell line was compared to a wild type cell line to account for the variations in production. Differential expression analysis, using the DESeq2 software package, was employed to find upregulated and downregulated genes in each cell line. Heatmaps and volcano plots were also used for data analysis. Gene pathways of BMPC cells and CHO-IgG were mapped using the STRING program. Mouse B-cell signaling pathways contribute to immune, cancer, and metabolic systems. CHO cell signaling pathways contribute to reproduction and cancer systems. Both are generally involved in metabolic, apoptosis, immune systems.

Optimizing Computational Parameters for Calculations of Metal Ferrites

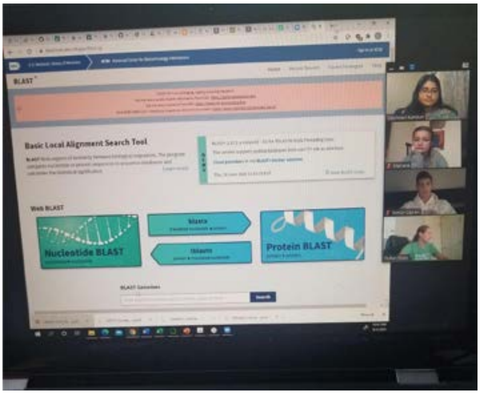
Laura Jeniski, Venkata Chaluvadi, and Dr. Rachel Getman
Chemical and Biomolecular Engineering, College of Engineering



Ferrites are iron oxide nanoparticles with substituted transition metals which are used in a variety of applications including computers, motors, and magnetic hyperthermia. The specific ferrite examined was M(x)Fe(3-x)O4 where M= Co and x = 1. Unfortunately, M(x)Fe(3-x)O4 where M= Ni, Cu, and Mn and x=1 could not be examined due to computational restraints. We used the VASP code to calculate the magnetizations and energies of the ferrite structures. In this experiment, the mixing flags (AMIX), space that projection operators use (LREAL), and method VASP uses to determine the initial charge density (ICHARG flag) were manipulated. Across the examined ferrites, the various ICHARG values, including no value, reflected no change in the magnetic moment, energy, or number of convergence steps. When changing the AMIX flags to the default setting, the energy increased by 4 eV and magnetic moment decreased by 10μB. When the LREAL flag was 'On', the energy increased by 10 eV thus destabilizing the compound. From this study, we concluded that the ICHARG flag should be commented out, LREAL should be set to True, and the AMIX flag should be the same as the control group to optimize the procedure.

Comparative Analysis of CHO Cell Therapeutic Production to Native Cell Lines

Vaishnavi Kanduri, Simon Ciprari, Mariana Holladay, Dyllan Rives, and Dr. Mark Blenner
Department of Chemical and Biomolecular Engineering: Clemson University



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Constructing a Virtual Lunar Environment for Interaction Experiments

Emma Katovich, Raleigh Adams, Alex Adkins, and Dr. Sophie Jörg
School of Computing, Clemson University

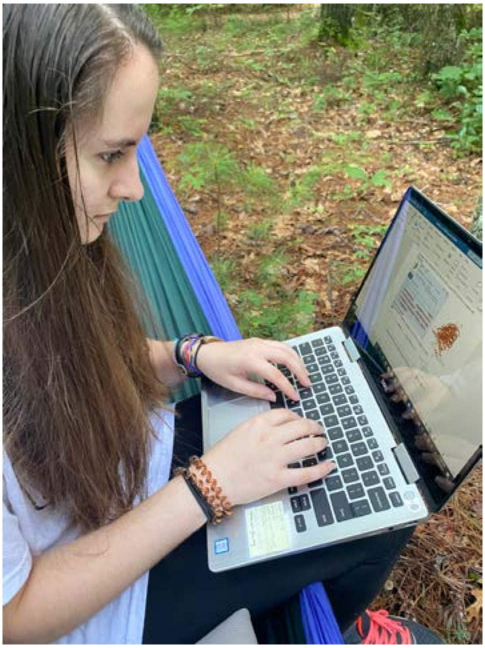
In 1999, NASA created an exercise titled "Survival on the Moon", which modeled a scenario of a member of a space crew stranded 200 miles from a designated rendezvous point due to mechanical difficulties. Much of the equipment was damaged, and there are only 15 items left to aid the member's survival. The exercise asked the member to rank the items, from 1 (most important) to 15 (least important), which determines how well the member would survive in the environment based on these rankings.

The goal of our project was to create a virtual scene of this lunar environment that could be modified to work as an experimental environment. Future work could determine how prepared the player would be in completing the exercise under different situations. The model was inspired by a lunar environment, and through the game engine Unity's terrain tools and C# scripts we were able to create a playable situation.

Identification of Cancer Mutations in MEIOK21 and HSF2BP

Sydney Keffer, Garrett Buzzard, and Dr. Michael Sehorn
Department of Genetics and Biochemistry, Clemson University

Homologous recombination (HR) is an essential mechanism of DNA repair where a template strand is used to mend double-stranded breaks (DSBs). If DSBs are left unrepaired, they often lead to cell death and a loss of genetic information. It is suspected that *MEIOK21/BRME1/c19orf57* interacts with *MEILB2/HSF2BP* to modulate localization of recombinases to DSB sites during HR. In my project, I found conserved DNA sequences, developed models of the secondary and tertiary protein structure, and analyzed cancer databases for the common amino acid missense mutations and primary cancers associated with meiotic genes *MEIOK21/BRME1/c19orf57* and *MEILB2/HSF2BP*. I further analyzed the *MEIOK21/BRME1/c19orf57* and separately, *MEILB2/HSF2BP* genes to determine the overlap in cancers that contained a missense mutation in these genes. The goal was to determine which amino acids when mutated formed cancer, so that we could later determine their functionality and role in their respective gene.



Crop Genetic Engineering for Enhanced Tolerance to Various Abiotic Stresses

Tori Luongo, Annalise Enger, Liz Dillard, Shrika Ravichandran, and Dr. Hong Luo
Department of Genetics and Biochemistry, Clemson University

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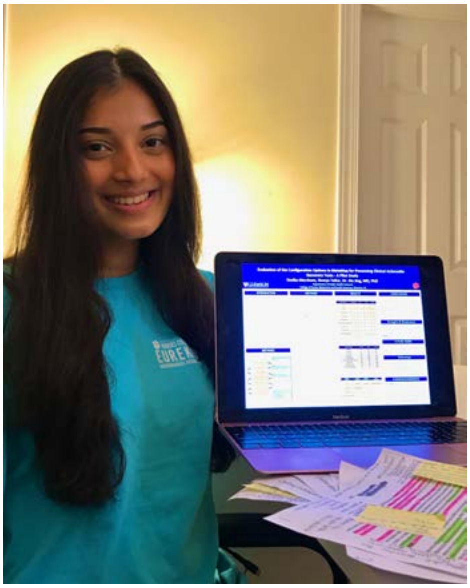
Evaluation of the Configuration Options in MetaMap for Processing Clinical Actionable Genomics Texts - A Pilot Study

Omika Merchant, Shreya Tellur, and Dr. Xia Jing
Department of Public Health Sciences, College of Social, Behavioral and Health Sciences, Clemson University



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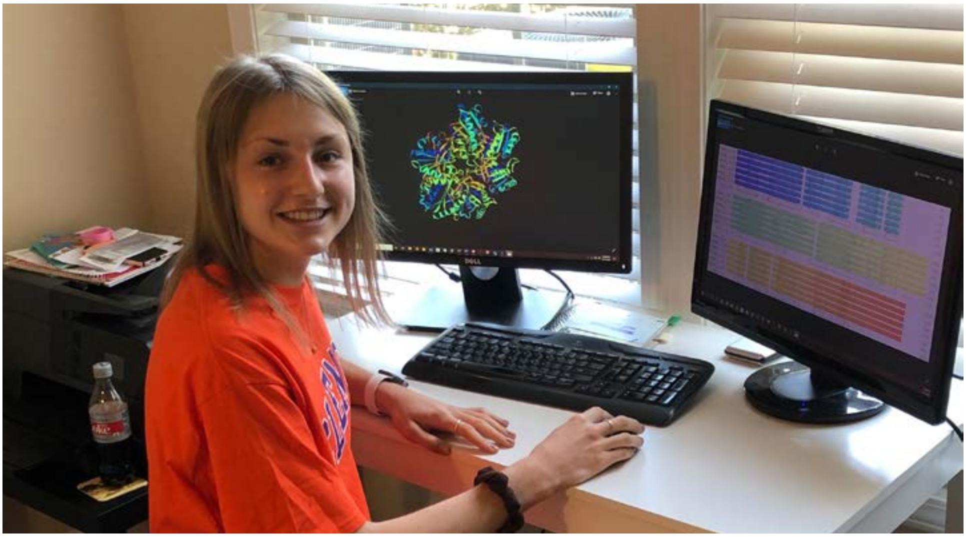

Characterization of the Shu SWS1-SWSAP1 Complex in DNA Repair

Caroline Michaelson, Garrett Buzzard, and Dr. Michael Sehorn
Department of Genetics and Biochemistry, Clemson University

Double-stranded breaks (DSBs) are one of the most severe forms of DNA damage and usually result from DNA lesions that arise from endogenous sources such as damaged replication forks and exogenous sources such as exposure to ionizing radiation. Homologous recombination (HR) is a mechanism used to repair DSBs that uses a homologous chromosome as a template for the repair process. Two proteins that are involved in HR are SWS1, a SWIM domain containing protein, and SWSAP1, a RAD51 paralog. SWS1 interacts with SWSAP1 to form a heterodimer named the Shu complex. This complex is involved in HR and serves to focus RAD51 onto DNA. Mutations in this complex hinder HR, giving rise to genomic instability and cancer in the organism. The purpose of this study was to analyze the structure of the proteins and identify residues responsible for their function.

Experimental and Computational Cardiovascular Research

Matt Monaghan, Will Franklin, Tyler Golbus, Jason Saadeh, Shreya Thammana, and Dr. Ethan Kung
Department of Mechanical Engineering and Department of Bioengineering, Clemson University

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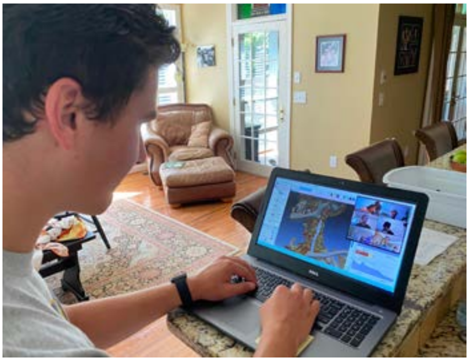

Characterization of DNA Mutated Repair Genes, SSB1 and SSB2

Victoria Murphey, Garrett Buzzard, and Dr. Michael Sehorn
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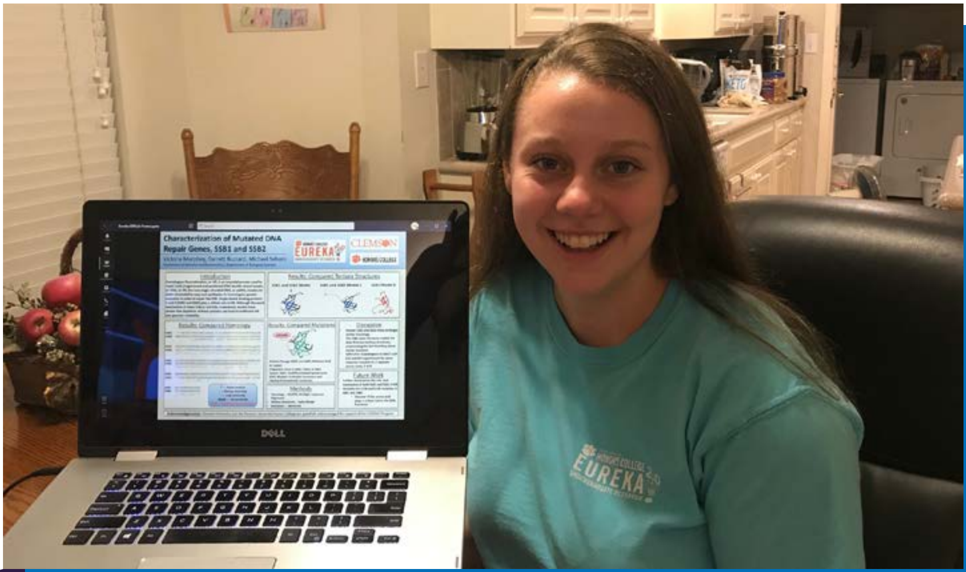
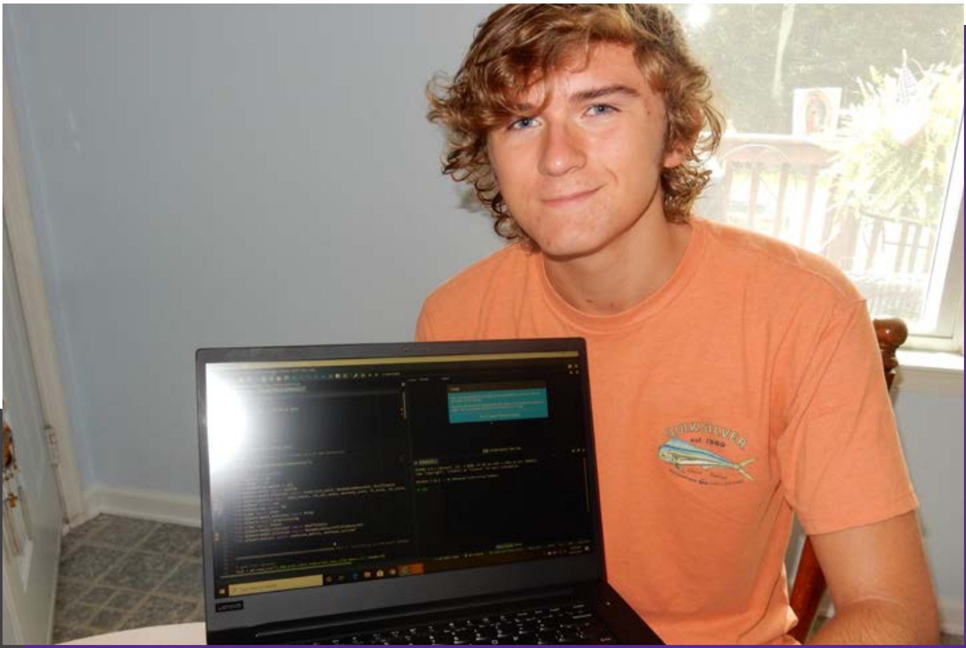
Homologous recombination (HR) is an essential process used to repair both programmed and accidental DNA double-strand breaks (DSBs). Single-strand binding proteins 1 and 2 (SSB1 and SSB2) play a critical role in HR. Although the exact mechanism of these SSBs is not fully understood, studies have shown that depletion of these proteins can lead to inefficient HR and genomic instability. Here we present evidence that SSB1 and SSB2 share similar functions, homology, secondary structures, and tertiary structures. Furthermore, we have found evidence that two pairs of residues in these SSBs show similar patterns of mutations. Through a CLUSTAL multiple sequence alignment, we found that mutations in SSB1 had the same mutations in the corresponding amino acids in SSB2. Using the same method, we also found that SSB1 had different mutations in corresponding amino acids found in SSB2. This suggests that these sites of interest could potentially be essential to the SSB functions and help us to characterize the role that these SSBs play in HR.



Prediction of Novel Autism Risk Genes by Genomic Data Mining

Matt Mytych, Krishna Patel, Sam Buckley, Anqi Wei, Jun Wang, and Dr. Liangjiang Wang
Department of Genetics and Biochemistry, Clemson University

Autism Spectrum Disorders (ASD) refer to a group of neurodevelopmental disorders characterized by cognitive and behavioral delays. Many of the underlying causes of ASD delve into the molecular level, including both protein-coding and non-coding genes. Long non-coding RNAs (lncRNAs) are a group of non-coding RNAs that have no protein coding capacity but have been linked to ASD. Traditional methods for identifying and validating ASD risk genes is time-consuming and costly, thus a machine learning model is necessary. In this study, we built machine learning models to predict and prioritize candidate lncRNAs associated with ASD. A Support Vector Machine (SVM) model was trained using brain gene expression data collected from the BrainSpan. Performance of the SVM model was compared to other classifiers, such as Logistic Regression (LR) and Random Forest (RF). From all three models, 564 lncRNAs were predicted to be high-confidence ASD risk candidate genes. Developing a model to predict and prioritize autism-associated lncRNAs is one step closer to understanding the pathogenesis of ASD and to potentially find ways for treatment.



Autonomous Wheelchair and Assistive Mobility Research using Computer Vision and AI

Andrew O’Rourke, Nataly Wickstrom, Ziyue Feng, and Dr. Bing Li
Department of Automotive Engineering, Clemson University

The visually impaired are limited in resources that allow them to be independent in their daily lives. Specifically in restaurants, the visually impaired face problems with reading a menu, visually confirming if the served food has been served to-order and navigating between objects on the table. Computer vision and AI can be used to address these problems. The goal of this research was to investigate the technology of computer vision and machine learning and to utilize its capabilities to assist the visually impaired. Our objectives were to explore the fundamental machine learning features and capabilities so that we could create a deep learning neural network capable of classifying images of foods, evaluate its performance, and improve upon it to increase its accuracy past 90%. In addition, we wanted to understand the hardware and how our model could be deployed through a device. We investigated self-defined neural networks that yielded low accuracy and shifted to transfer learning with pre-trained network models which were able to accurately classify images in our custom dataset to around 92%.

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Study of Ethene Hydrogenation with a Cobalt Oxocluster Catalyst Using Density Functional Theory

Elizabeth Peacock, Hafeera Shabbir, and Dr. Rachel Getman
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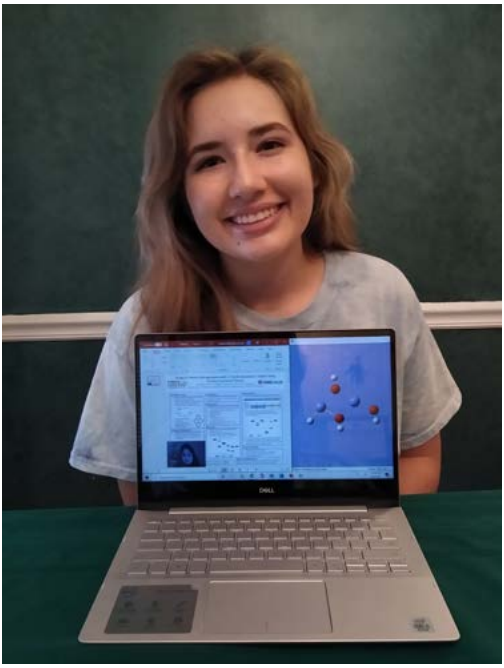
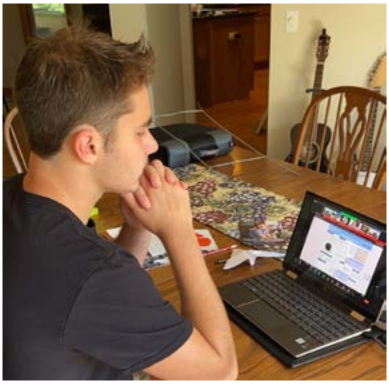


Increased supply of shale gas is driving the need to discover efficient catalysts for conversion of natural gas to liquids for use as fuel and chemicals to optimize energy consumption. De/hydrogenation reactions are essential to gas to liquid conversions. In this work we investigate the energetics of a Co2+ catalyst supported on a Metal Organic Framework (MOF) NU-1000 for ethene hydrogenation. A small metal-oxo cluster (~10 atoms) model is evaluated and compared to a large cluster (~70 atoms) model. Density Functional Theory (DFT) is used for calculating the energies of intermediates from a previously proposed reaction mechanism for Co2+ on NU-1000. The code Gaussian-09 with M06-L functional and basis sets Def2-SVP (H, C, O) and Def2-TZVPP (Co) are selected. Three spin states (triplet, quintet, and septet) are evaluated for the small cluster model and compared to the corresponding large cluster model. Our results indicate a stronger correlation in the relative change in Gibbs free energies for higher spin states than the lower spin states for the 2 models considered.

Understanding Lunar Regolith Simulants and Their Interactions with Drilling Tools for In Situ Resource Utilization

Dante Piscitiello, Sarah Barclay Cribb, Jackson Wiley, Zakia Tasnim, and Dr. Qiushi Chen
Glenn Department of Civil Engineering, Clemson University



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Crop Genetic Engineering for Enhanced Tolerance to Various Abiotic Stresses

Shrika Ravichandran, Annalise Enger, Liz Dillard, Tori Luongo, and Dr. Hong Luo
Department of Genetics and Biochemistry, Clemson University

What are flavodoxins?

Flavodoxins (Flds) are small soluble electron transfer flavoproteins that take part in various oxidation-reduction processes in prokaryotes and eukaryotes.

They are an alternative electron carrier flavoprotein under adverse environmental conditions.

Abiotic stresses, such as salt and drought, significantly affect plant development and are the major limiting factors on crop quality and productivity. Manipulation of genes involved in plant stress response facilitates plant mitigation of adverse environments. The objective of this project is to investigate the effects of specific genes on plant resistance to adverse environmental conditions. Several presentations and research papers were studied and discussed to gain knowledge on the processes of genetically engineering crops and on results of transgenic plants exhibiting improved stress responses controlled by different molecular mechanisms in past experiments. Specifically, to genetically improve perennial grasses for enhanced stress resistance, various candidate genes from rice were cloned and introduced into turfgrass cells. The genes were marked for testing to ensure they were being expressed in the regenerated transgenic turfgrass plants. The manipulated expression of rice genes in transgenic turfgrass affected plant development and led to enhanced plant resistance to multiple environmental stresses including salt, drought, heat, and nutrient deficiency. These data demonstrate the importance of biotechnology for enhancing agricultural production, especially when anticipating exponential growth in the world population as well as changes in climatic conditions.

Microbial Metapopulation Models

Kaustubha Reddy, Daniel A. Malagon, and Dr. Sharon Bewick
Department of Biological Sciences, Clemson University

A metapopulation consists of a group of spatially separated populations which interact through rare migration events. Metapopulations are most affected by rates of colonization and extinction by a species in a patch. The purpose of this study is to determine the effect on a metapopulation when turtles with a microbe traverse between local populations (ponds). To conduct this experiment, the software NetLogo is used to create agent-based models which simulates the microbial dispersion between 2 ponds with host turtles acting as dispersal mechanism. Observation of the results evinced that the more distant the ponds were from one another, the more difficult it was for the microbe to reach other ponds via turtle movement. This experiment substantiated that metapopulations are more stable and less likely to go extinct than single local populations.

Experimental and Computational Cardiovascular Research

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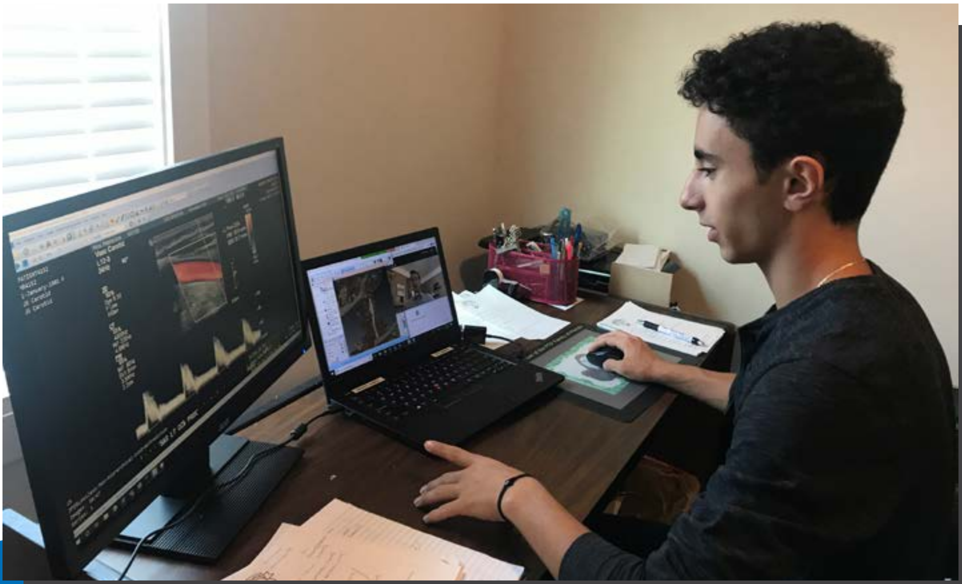

Fuel Consumption of Harvesting Equipment

<u>Emma Simon</u> and Dr. Patrick Hiesl
Department of Forestry and Environmental Conservation, Clemson University

Fuel consumption is a large cost factor to harvesting companies and varies from one company to another. When consumed, diesel fuel emits various greenhouse gases and lasting effects are felt by the environment. Minimal consumption benefits both the profits of the harvesting companies and the atmosphere. A literature review was completed to collect published fuel consumption data for different harvesting equipment operating in various forest stands around the world over the past 30 years. Reported information was collected regarding the stand, machine, productivity, and fuel consumption in each study. Values were then grouped based on harvesting equipment and figures were made to display the information visually. This data shows the range of fuel consumption for common harvesting equipment and can help inform multiple stakeholders about the variability of fuel consumption and associated cost. It was found that fuel consumption and cost vary within and between machine types. Currently, an article is being written for Land-Grant Press to inform local companies of the findings. There is a lack of information about fuel consumption to provide detailed geographic breakdowns and more research in this field would expand the current knowledge of the cost and carbon emissions of fuel consumption.

Achieving Decentralized Robotic Heading Synchronization Via Pulse-Coupled Oscillators

Noah Tavarez, Taylor Corcoran, Thomas Zakrzwski, Timothy Anglea, and Dr. Yongqiang Wang
Department of Electrical and Computer Engineering, Clemson University

Synchronization occurs when multiple parts of a system or network work together at the same time to complete a task. In centralized synchronization, robots send regular bursts of data to the rest of the wireless network, such as heading, position and sensor data, so the other robots can adjust to match. However, this method of synchronization has many problems regarding privacy and large data transfers, which complicates communication within the network. The goal of our project is to solve these problems by achieving decentralized synchronization between robotic systems with pulse-coupled oscillators (PCOs), which simplifies communication between robotic systems, reduces energy consumption, and reduces the chance of data loss and corruption. We compare four algorithms for PCO synchronization to determine which one is most effective and then use this information to implement a PCO protocol for synchronizing robotic heading.

Evaluation of the Configuration Options in MetaMap for Processing Clinical Actionable Genomics Texts - A Pilot Study

Shreya Tellur, Omika Merchant, and Dr. Xia Jing
Department of Public Health Sciences, College of Social, Behavioral and Health Sciences, Clemson University

Natural Language Processing (NLP) can facilitate information processing efficiently. One area is in precision medicine to extract clinically actionable genomics information automatically. UMLS, a biomedical terminology hub to aid interoperability between computers, is developed by the National Medical Library (NLM). MetaMap, is an NLP tool by NLM to identify UMLS concepts from biomedical texts. Although MetaMap has been used broadly, the options within MetaMap present a challenge to process a specific type of information (e.g., genomics). By using classic approaches in information retrieval, we manually evaluated parsed biomedical text by MetaMap by comparing output results to a given Golden Standard Text. The effort focused on the behavior option of MetaMap, which includes 17 items. To obtain a more objective judgment of output results, we developed metrics that classified results in exact, similar, and incorrect mappings. We then calculated the precision, recall, and F(□=0.33) measures of each of the 17 items. Based on the F measure, we deemed options as relevant (≥= 50%), too broad (40.0% - 49.9%), too specific (30.0% - 39.9%), or not relevant (≤=29.9%) to create a comprehensive table of configurations. Our results showed that 12 MetaMap items under the behavior option provided the most relevant results.

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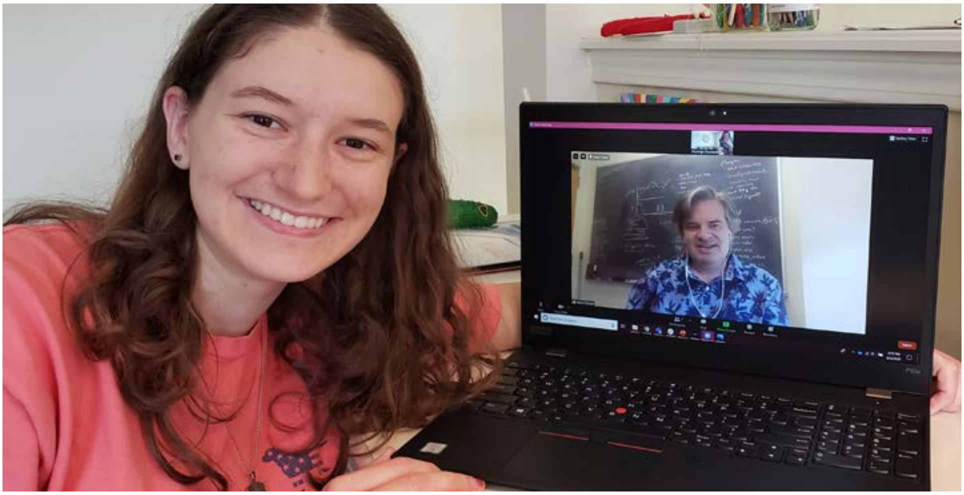


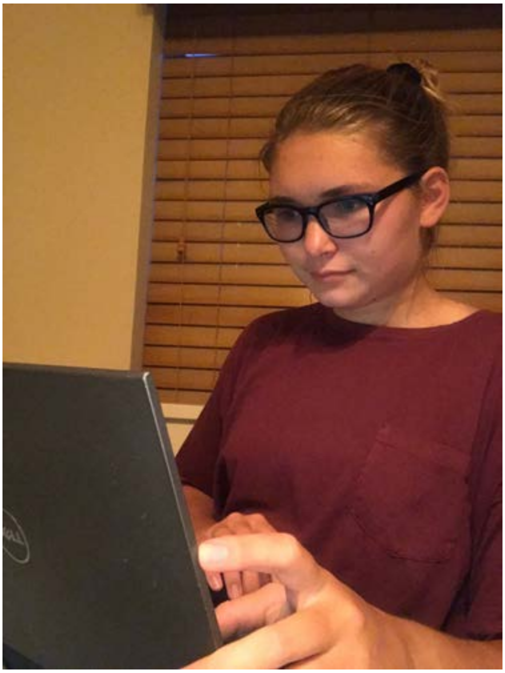
Molecular Dynamics Simulations of Nanoparticle Tethers for Super-resolution Microscopy

Kayleigh Trumbull and Dr. Jason McNeill
Department of Chemistry, Clemson University

Localization-based fluorescence microscopy techniques (e.g., PALM and STORM) can circumvent the diffraction limit, providing greatly improved resolution (20-50 nm, typically). These techniques rely on attachment of antibody-linked dyes to specific molecules on the specimen and using a combination of laser pulses to switch individual dyes between an on state and an off state, recording their positions to build up a super-resolution image. Ultra-fluorescent photoswitching nanoparticles provide a localization resolution of better than 1 nm. However, at this resolution, the several nanometer long assembly, consisting of an antibody tethered to a nanoparticle, can introduce artifacts in the image. In order to develop methods to correct these artifacts, we need an improved understanding of the nanoscale motion of nanoparticles tethered to a surface in solution. We performed molecular dynamics simulations of two different oligopeptides (deca-alanine and deca-serine) held fixed at one end. Mean square displacement analysis was used and the results were compared to the predictions of various modified Brownian motion models. Preliminary results indicate that repeated measurements of tethered nanoparticles could be used to estimate the "true" position of the underlying target molecule, permitting partial correction of the tether artifact and improving the effective resolution of the technique.

Visual Substitution for the Blind Using AI

Nataly Wickstrom, Andrew O'Rourke, Ziyue Feng, and Dr. Bing Li
Department of Automotive Engineering, Clemson University



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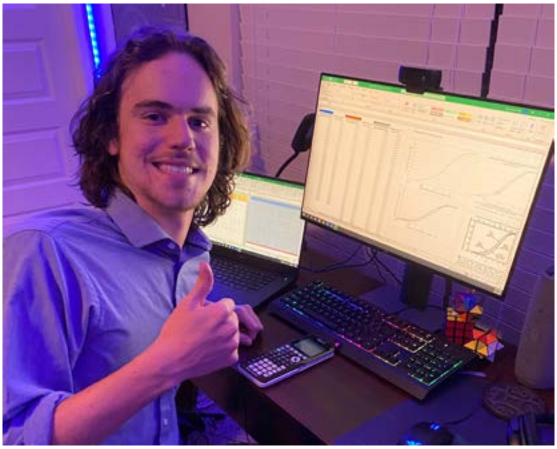

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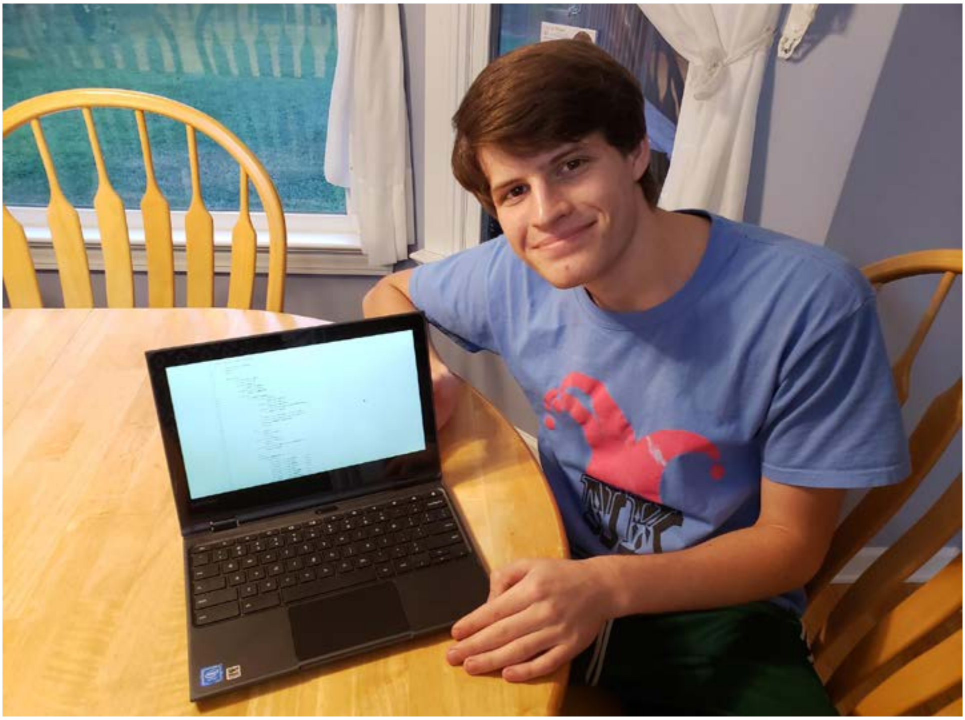

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EUREKA! 2.0 Contributors

While EUREKA! was conceived through the vision of Dr. Wainscott and the hard work of the committee and continues to thrive with the support of Provost Bob Jones, Dean John Griffin, and Honors College Executive Director, Dr. William Lasser, we are grateful for Dr. Bill Pennington, who guided the EUREKA! Program, serving as its Director from the program's inception in 2006 until 2017.

This year we are so appreciative of the dedicated Clemson Honors staff who worked together to provide a quality program for all of our EUREKA! 2.0 participants:

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Jacqueline Overton	Administrative Assistant
Rachael Wallace	EUREKA! Program Assistant
Jenny Wirtz	Finances

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