Research Reports from Undergraduate Students

Receiving Support from the Shackouls Honors College

Via the Honors Summer Undergraduate Fellowship Program

October 31, 2012

Program Director:

Dr. Seth F. Oppenheimer

Name: Bivens, Brooke
Major: Biochemistry
Faculty Advisor: Mark Welch, & Andy Perkins
Co-Arthur: Sree Pramod

Project Title: *Genome Microsatellite Analyzer: A comprehensive software package for analyzing microsatellite distributions in organismal genomes*

The goal of this project is to develop an integrated bioinformatic pipeline that is not error prone in order to study the distributions of microsatellites in related species of sunflower to test hypotheses regarding the role of microsatellites as agents of rapid evolutionary change. By determining which classes of these microsatellites are retained, which retain purity, and which are most variable for length across species, I will be able to perform multispecies comparisons. While the raw data necessary for this study is available in readily accessible sequence databases, extracting the information for testing these hypotheses is difficult. Collecting and analyzing this data requires running multiple files through several software packages. With each step, the manipulation of data files could result in error. In order to eliminate this error and increase the efficiency of the analysis process, I am using the Python programming language to develop a comprehensive bioinformatics pipeline and conduct analyses on transcribed microsatellites using nucleic acid sequence databases.

Currently, this pipeline requires one input file to extract from a user-specified range tandemly repeated sections of genomes and calculates the length of these sections, reporting them back to the user as well as finding and reporting where exactly these sections both begin and end, successfully incorporating both Tandem Repeats Finder (TRF)[2], SciRoKo[3], and ESTScan[4]. TRF and SciRoKo allow the user to specify the parameters required for identifying repetitive sequences such as microsatellites and report the location, length, repeat type, and purity of these sequences to the user. ESTScan is a BLAST based tool that identifies where likely start and stop codons are located, allowing researchers to determine in which domain (5' UTR, Coding, or 3' UTR) specific microsatellites are located. This pipeline also incorporates statistical subroutines in order to generate visual representations of the data through the R programming language[5] as shown in Figures 1-3, allowing for researchers to readily assess the distribution of microsatellites in a given sequence database or species.

To generate the integrated bioinformatic pipeline, TRF, SciRoko, and ESTScan have been combined with individual pieces of Python code that perform specific functions. These software fragments were melded together into a single menu driven software package that is being transformed into a web based utility or a graphic user interface (GUI). The software package will be hosted on a website that will be developed utilizing HTML and CGI scripting. Analysis will then be conducted on sunflower sequences in the lab via the pipeline in order to test our theory of microsatellites being agents of rapid evolutionary change.

At present, the pipeline is properly integrated with Tandem Repeats Finder, SciRoKo, and ESTScan. However, we are continuing to integrate more statistical analyses into the pipeline and the final web-based integration. Once completed, all of the individual pieces of the pipeline will be integrated, so that an output file is generated, and in the case of a web-based utility, emailed to the user of the software. I presented my work at the Summer Shackouls Undergraduate Research Symposium and also more recently, at the Southeastern Population Ecology and Evolutionary Genetics (SEPEEG) Conference in Pendleton, South Carolina on October 12-14, 2012. I received travel funds from the Department of Biological Sciences in order to make this trip.

Microsatellite DNA and its effects on adaptive evolution have only begun to be explored. Because of the number of microsatellites within or near genes that regulate essential cellular physiological processes, it is postulated that these microsatellites may play a functional role. It has been suggested that microsatellites act as "tuning knobs" causing incremental increases or decreases in microsatellite lengths which can have incremental effects on phenotypes by influencing gene expression, or protein function. If microsatellites can act as tuning knobs, it suggests that rates of adaptive evolution are being grossly underestimated. We hope to test this hypothesis that these microsatellites are agents of rapid evolution by examining what classes of microsatellites are most likely to increase/decrease the amount of proteins that a gene produces by determining which have the highest retention, purity, and variation in length across species. We base our theory that these microsatellites

may be agents of rapid evolution on the fact that the microsatellites in question have a high mutation rates. If these microsatellites are in fact agents of rapid evolution, this ability to switch forms rapidly suggests that populations may be able to adapt and evolve to changes in their environment far faster than previously believed.

Being able to streamline this process of collecting data will aid researchers in the long-term goal of discovering whether or not microsatellites are agents of rapid evolution. At present, individual transcriptomes are being considered one at a time. This software package will allow for comparisons across related species. This pipeline ultimately slashes the need for many different software packages to perform microsatellite analysis, making the generating of data easier to understand and more manageable. This will also cut down on user error due to mishaps during the transfer of information from database to database, making finding this data both more efficient and less frustrating for users.

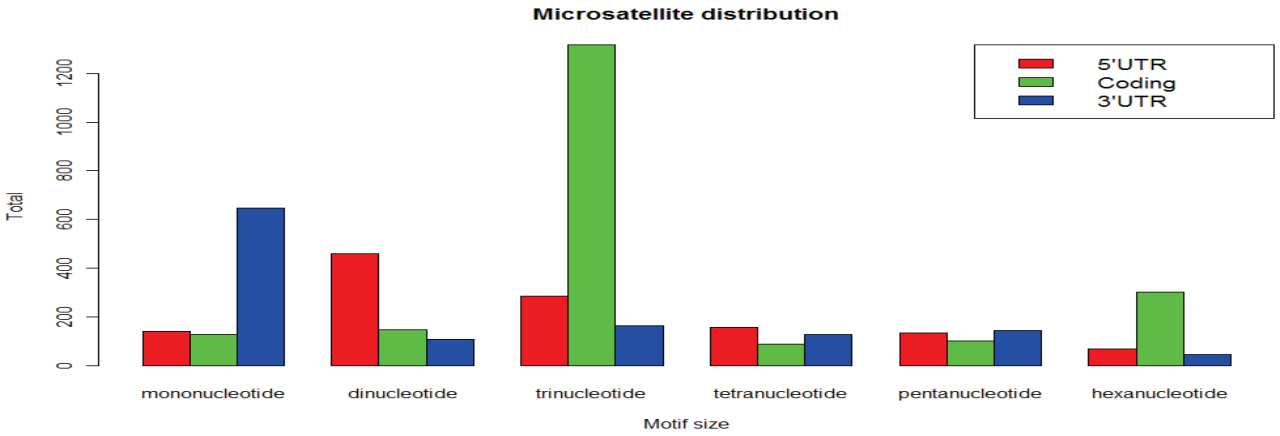


Figure 1 – Microsatellite Distributions by Motif Size[1]

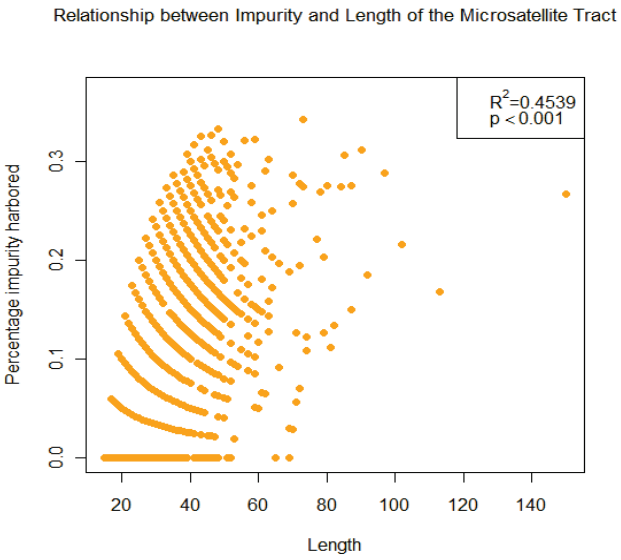


Figure 2 – Retained Impurity over Length[1]

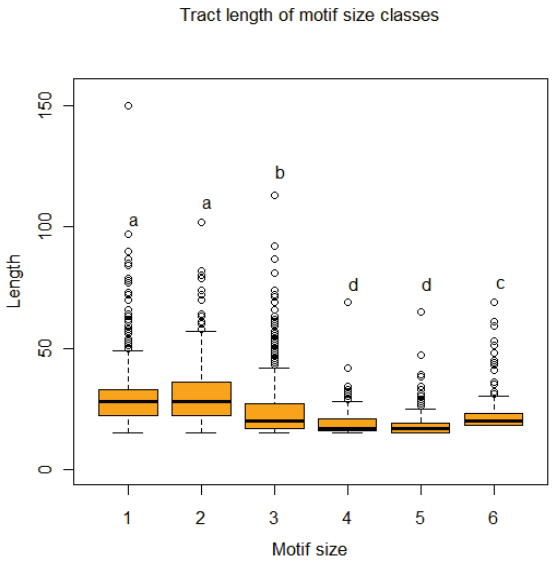


Figure 3 – Length over Motif Size[1]

References

[1]Figures taken from Dr. Pramod's thesis – 2012

[2]Benson G.1999. Tandem repeat finder: a program to analyze DNA sequences. Nucleic Acids Research 27(2):573-580

[3]Kofler R, Schlötterer C, Lelley T. 2007. SciRoKo: A new tool for whole genome microsatellite search and investigation. Bioinformatics 23(13): p. 1683-1685

[4]Iseli C, Jongeneel CV and Bucher P. 1999. ESTScan: a program for detecting, evaluating, and reconstructing potential coding regions in EST sequences. Proc Int Conf Intell Syst Mol Biol.138-48
[5]R Development Core Team. 2012. R: A Language and Environment for Statistical Computing. R Foundation for Statistical Computing, Vienna, Austria. ISBN: 3-900051-07-0.url [http://www.R-project.org]

Name: Callahan, Kelly

Major: Biological Science
Faculty Mentor: Dr. Justin Thornton, Microbiology

***Project**: Expression of DNA-damage response genes in cells affected by pneumococcal pneumonia*

Programmed cell death, or apoptosis, is essential in the resolution of infection and damage caused by other cell stressors. When challenged with stress, the tumor suppressing protein p53 is responsible for regulating the expression of the Bcl-2 family of proteins, which contains a host of anti-apoptotic and pro- apoptotic proteins [1,3,4]. p53 can either inhibit apoptosis with proteins such as myeloid cell leukemia sequence 1 (Mcl-1) and B-cell lymphoma-extra large (Bcl-XL), allowing the cell time to repair damage, or it can initiate cell death by promoting the transcription and translation of proteins within the BH3-only family of Bcl-2s [2,4]. One BH3-only protein, p53 upregulated modulator of apoptosis (Puma), has been shown to be a potent inducer of programmed cell death [1,2]. Puma is localized to the mitochondria and works through interaction with the pro-apoptotic proteins Bak and Bax. When the cell is under stress or has incurred DNA damage from infection or other toxins, p53 is phosphorylated, and Puma and other downstream targets are transcribed to initiate the cascade towards apoptosis [1, 2].

During bacterial infections, apoptosis of damaged cells is necessary to help prevent further tissue injury [1]. Previous research hoped to characterize these apoptotic proteins in response to bacterial infection, using *Streptococcus pneumoniae,* a gram-positive bacterium and the leading cause of community- acquired pneumonia as the pathogen in question. When a pathogen is introduced into the body, immune cells phagocytize the bacterium, signaling the downregulation of anti-apoptotic proteins and the upregulation of pro-apoptotic proteins, such as Puma [1]. This Previous research has shown that Puma -/- mice are unable to clear pneumococcal infections and die more rapidly than mice in which the Puma protein was intact [1]. Through bone marrow transplantation, this same study showed that cellular immune defects and the inability to clear infections arise intrinsically from immune cells arising from the bone marrow. We are now seeking to unravel the mechanisms within the cell that cause the phosphorylation of p53, and thus the transcription and translation Puma during the apoptotic cascade.

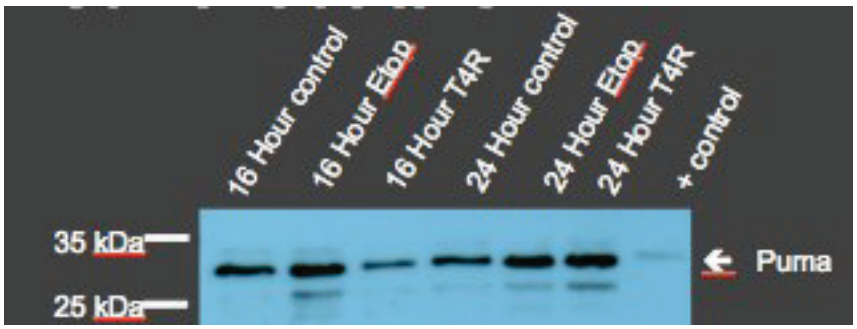
Of particular interest to us, immune cells, namely macrophages and neutrophils, sustain DNA damage from reactive oxygen species (ROS) in the process of clearing bacterial infections from tissues. We are investigating whether the cell itself is producing the damaging reactive oxygen or if the ROS comes from the pathogen, causing initiation of the apoptotic p53 cascade and induction of Puma. Two strains of *S. pneumoniae* have been used: an avirulent strain and a pyruvate oxidase mutant incapable of producing large quantities of hydrogen peroxide. These strains should allow us to see whether the ROS from the pneumococcus plays a role in the phosphorylation of p53 and the upregulation of Puma.

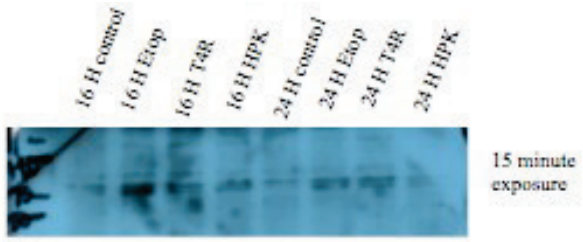
While Puma expression has been studied in neutrophils, little research has been done to characterize its role in macrophages. We are also attempting to characterize the regulation of the anti-apoptotic protein Mcl-1 in macrophages in response to pneumococcal infection. Some previous studies have shown that Mcl-1 is expressed at basal levels in macrophages at all times, and it is not essential in survival when presented with pro-inflammatory cytokines [3]. We will be exploring the expression or Mcl-1 in response *S. pneumoniae*.

Current Results: Using the J774.1 Mouse Macrophage cell line, cultures were infected for one hour with either an avirulent strain of *Streptococcus pneumoniae* , T4R, or with the ΔHPK strain, a pyruvate oxidase mutant. A positive control was treated with etoposide, a known DNA damaging agent, and one well was left untreated. Following infection, cells were lysed at various time points for analysis of Puma, Phosphorylated-p53, and Mcl-1 proteins.

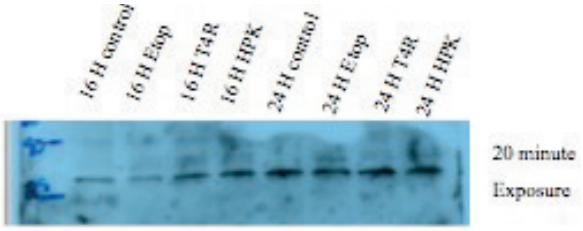
Using Western Blot analysis, we show that Puma is being downregulated 16 hours post-infection, and it is being upregulated 24 hours post-infection. We conducted qRT-PCR of these same time points, and Puma has shown up-regulation in T4R strains at 9 and 16 hours post-infection. These times will be repeated to confirm findings. Western Blots for the HPK-infected cells have been inconclusive thus far, but RT-PCR of th HPK-infected macrophages has shown an upregulation at 9, 16 and 24 hours post-infection, later than in T4R strains.

This suggests that bacterial reactive oxygen production plays a role in the induction of Puma and apoptosis. Phosphorylated-p53 has only been properly developed on one Western Blot thus far. The blot shows a doublet on all samples but the control, implying that p-53 is only phosphorylated in the presence of DNA damage. Western Blots of Mcl-1 in macrophages has been inconclusive.





1. Anti-Phospho-p53 rabbit in 5% milk 1:1000
2. Goat-anti-rabbit in 5% milk 1:1000



1. Anti-Mcl-1 rabbit in 5% milk 1:100
2. Goat-anti-rabbit in 5% milk 1:1000

Future Research:

We will continue to look for Puma at earlier time points, as Puma RNA in the T4R-infected macrophages appears to be transcribed earlier than in HPK-infected cells. 3,6, and 9-hour lysates will be prepared for both Western Blot and qRT-PCR analysis. Western Blots will be probed for Puma, phosphorylated-p53, and Mcl-1. qRT-PCR for Puma at 9, 12, 16 and 24-hour times will also be repeated to ensure the data from the initial PCR was accurate.

Although research shows that Mcl-1 expression in macrophages is not necessary for the survival of macrophages [4], we will continue to probe for Mcl-1 on Western Blots, as its expression during pneumococcal infection in macrophages has not yet been studied.

We will try once again to grow macrophage-like progenitor cells. The initial cultures were not differentiating properly, but L-cells were obtained and cultured to collect serum to help the progenitors grow and differentiate. If the differentiation works properly, the same experiments performed on the J774.1 macrophages will be performed on the progenitors.

References

1. Garrison SP, Thornton JA, Häcker H, Webby R, Rehg JE, et al. (2010) The p53- Target Gene *Puma* Drives Neutrophil-Mediated Protection against Lethal Bacterial Sepsis. PLoS Pathog 6(12): e1001240. doi:10.1371/journal.ppat.1001240

2. Dzhagalov, I., St. John, A., & He, Y. (2006). The antiapoptotic protein Mcl-1 is essential for the survival of neutrophils but not macrophages. *Blood Journal*, *109*, 1620-1626. Retrieved from bloodjournal.nematologylibrary.org.

3.Yuan, Z., Cao, K., Li, L., Liu, H., Zhao, X., Liu, L.,Deng, H. (2011). The p53 Upregulated Modulator of Apoptosis (PUMA) Chemosensitizes Intrinsically Resistant Ovarian Cancer Cells to Cisplatin by Lowering the Threshold Set by Bcl-xL and Mcl-1. *Molecular Medicine*, *17*(11-12), 1262-1274.

4. Yu, J., Zhang, L., Hwang, P., Kinzler, K., & Vogelstein, B. (2001). PUMA Induces the Rapid Apoptosis of Colorectal Cancer Cells. *Molecular Cell*, *7*, 673-682.

Name(s): Cerovsky, C., Syed, Z., Dendis, A.
Department: Biological Sciences
Faculty Mentor: James Stewart

Project: *AGE/RAGE and PKC-zeta interplay in 3D matrix mediated fibroblast differentiation*

This purpose of this study was to determine whether increases in advanced glycation endproducts (AGEs) in a 3D diabetic collagen matrix will differentiate wild type (WT) cardiac fibroblasts to a profibrotic phenotype. 3D collagen matrices were prepared from collagen extracts from non-diabetic (Db/db) and leptin receptor deficient, diabetic (db/db) mouse tails. Primary cardiac fibroblasts isolated from WT and AGE receptor deficient (R-/-) mice which were seeded onto both Db/db and db/db 3D collagen matrices for 7 days (chronic exposure). In addition, on day 6, these cells were then treated with inhibitors UO126 (ERK 1/2 inhibitor; 10μM) and PKC-zeta Pseudosubstrate (PKC-zeta inhibitor; 1μg/ml) and with a RAGE ligand- glycated albumin (AGE-BSA; 0.5mg/ml) to induce RAGE activation. Chronically exposed R-/- cells were unchanged, however WT cells exhibited functional and phenotypical markers for fibroblast differentiation, such as increased alpha- smooth muscle actin and RAGE expression. Additionally, blockade of ERK1/2 and PKC-zeta restored WT expression to non-diabetic levels. Therefore, chronic exposure to AGE-crosslinked diabetic ECM resulted in phenotypic alterations in WT fibroblasts. These changes were mediated through AGE/RAGE interactions leading to a profibrotic cell phenotype.

Name: Clark, Ronald N.
Major: Computer Science & Engineering
Faculty Mentor: Cindy Bethel

Project Title: *Integrating Autonomous Ground Robotic Systems for Law Enforcement Support*

The aim of this study was to investigate the use of robots in a slow and methodical search with local Law Enforcement Officers and SWAT teams. The initial phase of this research studied the integration of a robot as a team member with the SWAT teams, through the use of tele-operation techniques with the robot. The robot was operated by a non-team member in a manner to simulate the robot exhibiting autonomous behaviors that the SWAT team could respond to and provide directions when the robot did not perform as they expected. The research evaluated how the officers would use the robot for different response scenarios. The officers were observed during their regular training exercises and then the robot was introduced into their training. This allowed for minimizing the officers' potential discomfort by providing a very familiar setting. At the end of the training, the law enforcement officers completed a paper and pencil survey providing their impressions of the incorporation of a robot into their operations. The survey included ratings of different aspects of human-robot interaction, such as: if the team felt uncomfortable with the robot, if the team trusted the robot, if the team thought the robot was useful, and whether the team would want to work with a robot as part of the team in future incident responses. The overall response to the robot was positive. All of the officers (100%) reported that they would want to work with the robot in the future, they felt the robot could be trusted, and that the robot was helpful. The full results were presented in the Summer Symposia poster session.

Name: Comer, Anna
Major: Kinesiology
Mentor: Adam Knight

Project Title: *Effects of Previous Lateral Ankle Sprain on Balance (3 reports)*

First Report PURPOSE: The lateral ankle sprain is the most common athletic injury. Some people who suffer a lateral ankle sprain develop chronic ankle instability (CAI), while others have no residual problems and are known as ankle sprain copers. Balance deficits have been previously reported among participants with CAI. The purpose of the project was to measure the participants' postural sway while standing on one leg and determine the influence of a previous ankle sprain on postural sway. METHODS: Tweny one participants completed the study, including ten participants had no history of a lateral ankle sprain, five participants with a history of a lateral ankle sprain but with no residual symptoms that were ankle sprain copers, and six participants with CAI. Postural sway, as indicated by radial displacement, 95% ellipse area, and average velocity of the center of pressure (COP) was measured using an AMTI force platform. The participants single leg balance was assessed with the eyes open, eyes closed, and on a foam surface. The order of trials was randomized. RESULTS: There were no significant differences (P>.05) between groups for any condition; however across all groups there was a significanlty greater (P>.05) sway velocity (EC=3.66±1.43 in/s; EO=2.15±.75 in/s; FO=2.44±.61 in/s) and radial displacement (EC=.89±1.15 in; EO=.50±.31 in; FO=.57±.53 in) during the trials with the eyes closed. CONCLUSIONS: A previous ankle sprain did not effect static balance. The differences in sway during the eyes closed trials is likely due to the absence of the visual component.

Second Report PURPOSE: Many people who suffer a lateral ankle sprain develop chronic ankle instability (CAI), while others have no residual problems and are known as ankle sprain copers. Lateral ankle sprains commonly occur when landing from a jump. The purpose of the project was to measure the landing kinetics and dynamic postural control after landing from a drop jump. METHODS: The participants perfomed a drop landing off a 45.72 cm high box and were instructed to balance on the landing leg for 3 seconds. Five sucessful trials were completed. Peak vertical ground reaction force, standardized by mutliples of body weight (BW), time to peak vertical force (ms), and dynamic postural sway, as indicated by radial displacement, 95% ellipse area, and average velocity of the center of pressure (COP) was measured using an AMTI force platform. Tweny two participants completed the study, including ten participants had no history of a lateral ankle sprain (NI), five participants that had a previous lateral ankle sprain but were ankle sprain copers, and seven participants that had CAI. RESULTS: There were no significant differences (P>.05) between groups for any variable. The means and SD for the peak vertical force were: NI 3.54 ± .50 BW; ankle sprain coper = 3.44 ± .20 BW; and CAI = 3.24 ± .80 BW.

CONCLUSIONS: The current finding of no difference between groups may be due to small sample size. Further research is needed in order to infer a relationship between previous ankle sprains and landing kinetics.

Third Report PURPOSE: The lateral ankle sprain is the most common athletic injury, and many people who suffer an ankle sprain develop chronic ankle instability (CAI), while some people do not develop residual symptoms and are considered ankle sprain copers. Often times a result of CAI is an increased amount of ankle joint laxity. The purpose of this study was to examine ankle joint laxity using an instrumented arthrometer among participants with no history of ankle injury, those with CAI, and an ankle sprain coper group. METHODS: Twenty-four participants, which included 11 with no previous ankle injury (NI), 5 ankle sprain copers, and 8 with CAI, had their lateral ankle joint laxity assessed using the LigMaster instrumented arthrometer. Three trails of the Talar Inversion test were performed on the previously injured leg of the CAI and coper group and on a matched leg of the NI group. Testing consisted of applying 150 N of force to the medial malleolus while lateral displacement was measured in millimeters (mm). RESULTS: No significant differences in laxity were found between the groups (P>.05). The mean displacement of the NI group was 25.68 ± 4.23 mm. The mean displacement of the ankle sprain coper group was 24.07 ± 1.83 mm. The mean displacement of the CAI group was 26.60 ± 5.88 mm.

CONCLUSIONS: In the present study, CAI did not cause a significant increase in joint laxity. Future research is needed to determine the specific clinical implications of this finding.

Name: Cooper, Jennifer
Major: Kinesiology
Faculty Mentor: Stamatis Agiovlasitis

Project Title: *Energetic Optimization During Graded Walking*

Over the course of this project, twenty participants have been tested. In order to complete data collection for one participant, three sessions were conducted. The first session consisted of providing a general overview of the procedures to the participant, calculating participant's body composition using the Bod Pod, determining preferred walking speed of the participant, and familiarizing the participant with the various combinations of speeds and grades on the treadmill. During the second and third sessions, the participant wore a heart rate monitor, a belt with two pedometers and an accelerometer, and a breathing apparatus that allowed his or her expired air to be processed using a metabolic cart. Over the course of these two appointments, the participant walked at the fifteen speed and grade combinations for six minutes each. Following each walking trial, the participant rested for six minutes before proceeding with the next trial.

In addition to completing data collection, initial processing for all participants has been completed including body composition analysis, energy expenditure analysis, and data analysis from pedometers and accelerometers. Statistical analysis will be completed in the near future. Also, a review of additional literature regarding the subject matter will be done in order to aid in the educational process. Results and findings will be presented at the Honors Undergraduate Research Symposium in the spring.

Name: Davis, Katherine Taylor
Major: Psychology
Mentor: Carolyn Adams-Price

Project Title: *Generativity, Activities, and Creative Identity in Midlife Research Project*

The purpose of our study was to examine the link between creative identity and agentic generativity, making one's mark on the world by creating products or ideas, with well-being. We wanted to see if having many creative hobbies corresponds with a higher degree of benefits than does having a single or a few, heavily pursued hobbies.

During our preparation, we spent time selecting the measures to use, and included some new ones such as a creative identity scale and a serious leisure scale. Once we compiled the survey together, we posted it to *Survey Monkey*. We recruited participants by posting an advertisement with a link to the survey on various online discussion forums for different hobbies. By the time we finished gathering data, there had been over 500 participants, and 376 of them answered nearly every question.

During our analysis, we found that pursuing multiple hobbies is more closely linked to creative identity and generativity than is time spent on a single hobby. We found that a creative lifestyle, a creative identity, number of creative hobbies, and ethos (which involves participating in group activities) are predictors of generativity, and generativity predicts well-being. Time spent on primary and additional hobbies, perseverance, effort, and benefits from creative activity are not predictors of generativity.

It would be interesting for future research to compare how much creative identity influences an individual to pursue more creative activities and the degree to which participating in these types of activities leads a person to assume a creative identity. Such research would fill a gap in our current knowledge of creative identity—we know that creative identity is positively correlated to the number of hobbies a person has, but the correlation does not tell us why. It would also be interesting to explore the development of creative identity in adolescents and young adults. In sum, persons with numerous creative hobbies are more likely to have a creative identity and are more generative than are people who only pursue a few.

Name: Fast, Kayla
Major: Biological Sciences
Mentor: Diana Outlaw

Project Title: *Prevalence of Malaria Parasites in Northern Cardinals (Cardinalis cardinalis)*

Through the generosity of the Shackouls Honors College, I was able to take part in a summer undergraduate research program. I was given the opportunity to participate in a project being conducted in Dr. Diana Outlaw's lab in the biological sciences department. My project looked at the prevalence and distribution of malaria parasites in a single host species, the Northern Cardinal (*Cardinalis cardinalis*). This project applied several molecular laboratory techniques to determine whether or not the birds were infected with avian malaria parasites.

The cause of malaria is a bloodborne parasite transmitted to a host, such as the cardinal, via several possible insect vectors. An infected insect injects the parasite into a host through its bite. Subsequently, the host's fitness may be hindered by the presence of malaria parasites. The parasite's ability to infect different species of birds and even different subspecies is an important research focus, because different bird species or subspecies may have different susceptibilities to malaria parasites. The cardinal has been separated into six genetically different subspecies, each with a specific geographic range in North America (Smith et al. 2011). It is important to study the infection of individuals within each subspecies and the details of the parasite causing the infection. Another area of interest includes whether or not malaria parasites act as generalists infecting many lineages of cardinals or as specialists that are more limited, i.e., at the subspecies level.

Cardinals were tested for malaria parasite infection across their entire range in the United States and Mexico. Samples were obtained in the form of either blood or tissue museum- vouchered specimens. Whole genomic DNA was extracted and the product used as a template in the polymerase chain reaction (PCR). PCR was used to amplify the cytochrome *b* gene of the parasite as an indicator for positive infection with avian malaria. A positive or negative infection was determined based on the presence or absence of the appropriate band after conducting electrophoresis on an agarose gel. The DNA samples were then sequenced in order to properly identify the genus of parasite causing the infection and for comparative measures between other malaria parasite individuals.

In this study, parasites were identified as members of either the *Plasmodium* or *Parahaemoproteus* genera. A total of 186 cardinals were tested from 20 different locations in North America. The overall prevalence of malaria in the Northern Cardinal was 63 percent. Of these infections, 67.7 percent were caused by *Parahaemoproteus* and 32.3 percent by *Plasmodium*. Ecological niche models were also created to predict the most likely geographic areas for Northern Cardinals to become infected with malaria. A mitochondrial phylogenetic tree was formed to show genetic similarities between individual parasites. Different parasite lineages were evaluated with respect to the cardinal subspecies each lineage infected and geographic location.

Although an estimated prevalence of infection was determined, accuracy may increase with further testing. Current data indicates that the malaria parasite acts as a generalist and does not selectively infect cardinals, and that specific malaria parasite lineages are not specific to cardinal subspecies. For future directions of this work, data collected in this study may be used in making predictions with regard to future climate change scenarios. Moreover, information gained here may provide essential data needed to make further advances in understanding the co- evolution of host-parasite relationships.

References

Smith B, Escalante P, Hernandez Banos B, et al. (2011) The role of historical and contemporary processes on phylogeographic structure and genetic diversity in the Northern Cardinal, Cardinalis cardinalis. BMC Evolutionary Biology 11, 136.

Name: Favaloro, Anthony
Major: Aerospace Engineering
Faculty Mentor: Thomas E. Lacy, Jr.

Project Title: *Use of Energy-Harvesting Piezoelectric Actuators in an All-Composite Unmanned Aerial Vehicle*

Mississippi State University (MSU) has an established history in the design, analysis, and testing of lightweight unmanned aerial vehicles (UAVs) including short-range, remotely-piloted, small surveillance aerial vehicles [1] and the 155-lb (empty weight) 36 ft wingspan "Owl" UAV [2-4] seen in Figure 1. One key challenge is to optimize the UAV airframe and sensor package to maximize the duration of typical missions.

Figure 1: CAD Model of Owl UL-UAV [2]

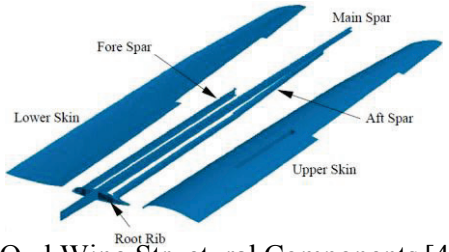


Figure 2: Owl Wing Structural Components [4]

Problem Statement:
In this research, the utility of energy-harvesting piezoelectric sensors for UAV power generation is investigated. The existing full-scale ABAQUS [5] FE model for the Owl wing seen in figure 2 is used to predict main spar strains throughout the wing that are consistent with measured strains associated with individual maneuvers, where a scaled aerodynamic lift distribution is assumed. The temporally varying spar strains along the entire wing is inferred from measured flight strain time histories. The global ABAQUS finite element air vehicle model will be modified to include specialized piezoelectric elements that can be used to predict the power generated from fights comprised of a variety of maneuvers. The total estimated power generated during typical flights will be used to assess the viability of energy-harvesting piezoelectric devices for extending UAV mission durations.

Current Progress:
At this time, a complete FEM simulation in ABAQUS for power generation has not been completed. However, many initial estimates using simplified methods have been performed. All of these initial estimates have shown unfortunately, negligible power generation.The primary reason that the complete FEM simulation has not been run is due to the complexities of the existing Owl wing models (seen in Figures 3 and 4) and the additional piezoelectric elements that must be added for power generation. There are two existing and experimentally validated models for the wing. One model was for prediction and comparison with the static testing wing; the other model was for prediction and comparison with the vibration testing of the wing. Therefore, a great amount of time has been dedicated to understanding the proper use of the existing models for useful strain measurement and to understanding the function of the piezoelectric element.

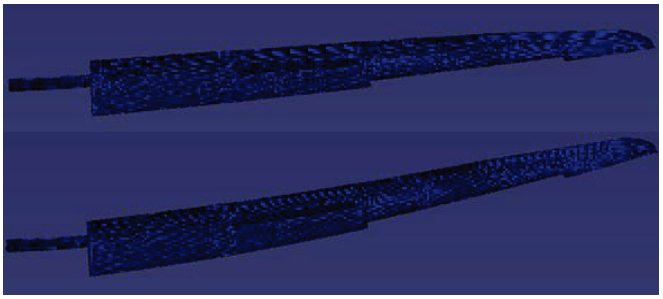


Figure 3: Static Owl Wing Model

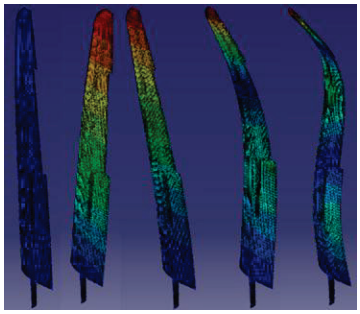


Figure 4: Dynamic Owl Wing Model

The current progress is as follows: the two existing FEM models of the Owl wing have been obtained, these models have been tested and verified to be the experimentally validated models, the raw data from the flight testing of the Owl has been obtained, this data has been reduced into meaningful strain data during a known flight maneuver, using the FEM model an equivalent stiffness and natural frequency have been obtained in order to model the wing as a simple cantilever beam with a piezoelectric patch, and the piezoelectric FEM element has been investigated for its ability to generate power and deform under an applied load on a simple beam. A sample of the reduced flight test data can be seen below in Figures 5 and 6. This data is for a 4g pull up maneuver.

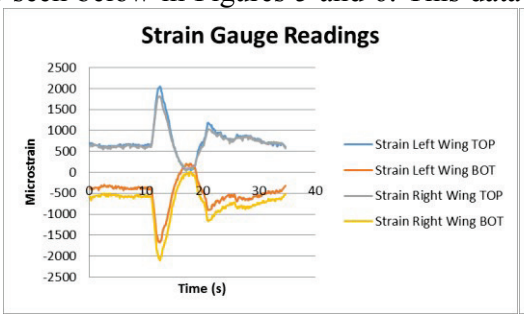


Figure 5: Strain Gauge Data

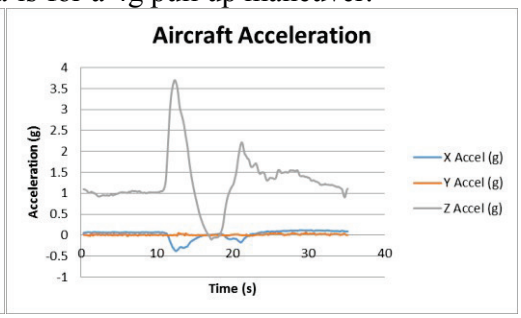


Figure 6: Aircraft Acceleration Data

Future Work: The next step in this project is to begin to integrate the piezoelectric FEM elements into the spar models. Once this is completed, voltage histories (as seen in figure 7 for a simple case) can be obtained and, thereby, power generation can be estimated.

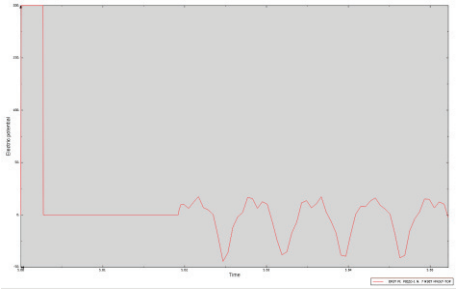


Figure 7: Voltage Time History of a Simple Piezoelectric System

References

[1] "Xawk 5 UAS," *Xipiter UAS Integrated Products Team*, Mississippi State University, 2011. [http://xipiter.org/web/xawk-5/. Accessed 4/9/2012.]

[2] Sullivan, R., Hwang, Y., Rais-Rohani, M., and Lacy, T., 2009, "Structural Analysis and Testing of an Ultralight UAV Carbon Composite Wing," *AIAA Journal of Aircraft*, 46(3), 814-820.

[3] Sullivan, R.W., Hwang, Y., Rais-Rohani, M., Lacy, T.E., and Wiwattananon, P., "Static Response of a Composite Wing Under a Whiffletree Loading," in the Proceedings of the ASC 22nd Annual Technical Conference, Seattle, Washington, September 17-19, 2007.

[4] Sullivan, R. Rais-Rohani, M., Lacy, T., and Alday, N, "Structural Testing of an Ultralight Composite UAV," in the Proceedings of the 47th AIAA/ ASME/ ASCE/ AHS/ ASC Structures, Structural Dynamics, and Materials Conference, Newport, Rhode Island, May 1-4, 2006.

[5] ABAQUS Ver. 6.4, Hibbitt, Karlsson & Sorensen, Inc., 2003.

Name: Hall, Christian
Major: Computer Science and Engineering
Faculty Mentor: Dr. T.J. Jankun-Kelly
Project Title: *Semi-automatic Color Map Generator Web App for Visualization*

This research project involved building upon a web application that had been started the previous year. The web application, titled Kill the Rainbow, is a tool that aims to help eliminate the "rainbow color map." Research in visualization has clearly shown that this color map, which is the default in many applications, is detrimental in helping people accurately perceive features in visualized data.

Several papers were read over the summer that outlined the exact problems this color scheme causes. Complications included unnecessary color banding, insufficient luminance variation, and other perceptual issues in visualized data. These problems confuse or mislead people interpreting the information, resulting in a lack of comprehension or incorrect conclusions about the data. Unfortunately, these erroneous color schemes are widespread and are difficult to edit so that perceptually appropriate choices are selected, making it difficult to solve this problem. This is the problem Kill the Rainbow attempts to solve.

Before this summer, the application foundation had been completed, but it lacked the ability to generate color maps. The focus this year was placed on adding visualizations with color changing functionality based on data given by EPSCoR researchers. The foundation was built using HTML5, CSS3, and jQuery, and the additions made this summer were implemented primarily with a JavaScript library focused on data driven documents called d3.js.

One of the three planned visualizations was completed with all color map generation this summer. Once the other two are complete, the final goal before initial release is to implement a way for users to download the color map they choose from the application. If enough people begin using the correct color maps, the "rainbow color map" may fade from use.

Name: King, Taylor
Major: Animal & Dairy Sciences
Faculty Mentor: Mariola Edelmann

Project Title: *Quantifying Polyubiquitination in Salmonellae Infection*

Pathogenic *Salmonellae* are one of the leading causes of bacterial food-borne illness. The great increase of drug-resistant strains makes the discovery of new treatments imperative. One aspect of *Salmonellae* infection that sparks unique interest is ubiquitination of proteins. Ubiquitin is a small regulatory protein that modifies its protein targets post-translationally resulting in changes of protein function and stability. Ubiquitin pathways, including enzymes that control ubiquitination and deubiquitination, are essential to some bacterial infections including those by *Salmonellae.* However, the function of protein ubiquitination has never been studied systematically in *Salmonellae* infection.

The primary goal of this project was to develop a method for the enrichment of polyubiquitinated proteins in combination with an integrated proteomics approach to quantify polyubiquitination of specific proteins during *Salmonellae* infection. Several methods of purification of polyubiquitinated proteins were tested, but the enrichment by TUBEs (tandem ubiquitin binding entities) was determined to be the most efficient approach. Having optimized experimental conditions for enrichment and elution, the polyubiquitinated proteins were isolated by TUBEs from uninfected and wildtype *Salmonellae* infected HeLa cells. The protein extracts were subjected to western blotting for visualization. The results indicate a significant regulation of polyubiquitination in *Salmonellae* infection which may contribute to the control of bacterial pathogenesis processes including innate immunity. The TUBEs-extracted polyubquitinated proteins will be subjected to analysis by HPLC-OrbiTrap LTQ Velos mass spectrometry and quantitative post-analysis by Proteome Discoverer 1.3 and Proteo IQ. Ubiquitin pathways will be mapped using Ingenuity Pathway Analysis software.

This data will be used to understand the role of polyubiquitination in *Salmonellae* infection and to identify polyubiquitinated protein substrates of deubiquitinating enzymes that regulate *Salmonellae* infection. Subsequently, a more accurate understanding of the molecular basis to host-pathogen relationships in *Salmonellae* infection will be contributed in order to develop more effective antimicrobials.

Name: LaFrance, Robert Andrew
Major: Computer Science & Engineering
Faculty Mentor: Dr. Cindy Bethel

Project Title: *Therabot Study*

The purpose of this study is twofold. First, we are questioning therapists and counselors to determine how useful a robotic companion would be in comforting their patients that have undergone various traumas, such as assault or abuse. Secondly, we are performing a web-based survey to determine the preferences of common people towards several different forms of animals for the purposes of creating the therapeutic robot companion, named Therabot. Ideally, once marketed, the Therabot would fulfill several helpful tasks for therapists. Some of the features we hope to have in the Therabot include the ability to sense the stress levels of the patients (and make reassuring noises appropriately), verbally leading the patients through calming exercises, and replay therapy sessions for help while the patient is at home. We hope to have a variety of different animal types and covering available, so that each patient's Therabot would be an expression of their personality. When the time comes to end therapy, the patients would be able to receive a stuffed animal version of their robot to keep with them, if the therapists believe that would be helpful to further recovery.

Name: Martin, Jessica
Department: Biological Sciences
Faculty Mentors: Charles Knapp, Giuliano Colosimo, Mark Welch

***Project Title*:** *Importance of Communal Nesting to the Survival Of Iguana delicatissima*

Iguana delicatissima, the Lesser Antillean Iguana, is an endangered Caribbean endemic. Due to its relatively undeveloped state, the island of Dominica hosts the largest populations of *I. delicatissima*, but even there the species faces many threats to survival including predation, hunting, and loss of habitat. Based on previous genetic analyses of adult iguanas, some populations on Dominica show increased levels of heterozygosity and reproductive success, and may serve as important source populations for the island. Nesting sites also play an essential role in species preservation, and identifying these areas is critical for conservation management. *Iguana delicatissima* is known to nest communally, and large numbers of iguanas travel from their home ranges to nest together in these specific areas. This research aims to aid conservation management by prioritizing areas with genetically diverse source populations and nesting sites for protection. It was hypothesized that known communal nesting sites serve multiple local populations. It was predicted that the expected heterozygosity,H_E, in hatchlings from these nesting sites would be greater than the H_E among adults living in these areas. It was further predicted that observed heterozygosity,H_O, in the hatchlings would be lower than H_E, meaning they would show excess homozygosity. Allele frequencies at three loci revealed that H_E in the hatchlings at Batali Beach, a known communal nesting site, did not exceed that of the surrounding adult populations. However, genotypic frequencies revealed that there was excess homozygosity at these loci in the hatchling population. With regard to the hypothesis, these two results are in conflict. More data would need to be collected to determine whether sample sizes are affecting estimates of H_E or whether the findings reflect some other aspect in the species' life history.

Name: McKnight, Morgan
Department: Biological Sciences
Faculty Mentor: Brian Counterman

Project Title: *Population genetic structure in passion vine butterflies and lab rearing the Southern Dogface Butterfly*

This summer I worked on two projects dealing with two butterfly systems. One project aims to gain a better understanding of the evolutionary processes that drive adaptive divergence. By observing patterns of genetic variation among populations of *Heliconius* butterflies, we were testing the hypothesis that color pattern diversity in *Heliconius* is due to genetic drift rather than natural selection. Using Amplified Fragment Length Polymorphisms (AFLPs), we will conduct genome-wide scans for genetic variation from ~200 individuals collected across a 30km^2 region in French Guiana. The region is centered on a hybrid zone with divergent color pattern races of *Heliconius erato*.

We completed AFLPs for a set of twenty-four samples from the hybrid zone. We began preliminary data analyses and were currently expanding our number of individuals and AFLP primer pairs.

The second project I worked on was establishing the first recorded laboratory stock colony of the Southern Dogface, *Zerene cesonia.* We collected 10 female individuals from the local Osborne prairie. We successfully had several females oviposit eggs on native prairie clover (>200 eggs) and false indigo (<10 eggs). We reared 30 larva to pupation and ~10 adult butterflies eclosed in the lab. We were in our second generation of adults and started the process of mating. We were well on our way to having our third generation of adults. We plan to use these individuals for future studies of oviposition, wing pattern development and mate preference.

Collectively, this summer I learned about the biology of butterflies, from field collecting, caretaking, behavioral and genetic perspectives.

Name: McLaurin, Tyler
Department: Biological Sciences
Faculty Mentor: Janet Donaldson

Project Title: *Effect Of Citrus Pulp On The Viability Of The Probiotic Saccharomyces Cerevisiae Boulardii And Subsequent Effects In Presence Of Pathogens*

A high rate of weight gain in piglets is one of the goals for those working in the food production division of agribusiness. Farmers often supplement the diets of nursing sows and weaned piglets with the yeast probiotic *Saccharomyces cerevisiae* subtype *boulardii*, marketed as Levucell SB, to properly maintain gut flora, intestinal health, and to promote weight gain. Previous research has shown that the addition of citrus pulp to the piglets' diets has decreased the average daily weight gain of the piglets when they were subjected to the enteric bacterium *Salmonella*. This study was conducted to determine if the results from the previous study may have occurred due to interactions between the yeast, *Salmonella*, and the citrus pulp, and to test if similar results would be obtained from utilizing an alternative enteric pathogen, *Escherichia coli* O157:H7. Interactions were tested *in vitro* by growing cultures of Levucell SB yeast, *Salmonella*, and *E. coli* O157:H7 in pig fecal fluid supplemented with 0% citrus pulp and 5% citrus pulp with samples plated for viable plate counts over 48 hours at 39°C. Results showed that yeast viability was reduced after 48 hours of exposure to citrus pulp by $1.5\log_{10}$, indicating probable fungicidal properties in citrus pulp. When *Salmonella* and yeast were co-cultured, yeast counts decreased again by ~ $1.5\log_{10}$. However, when *Salmonella* and yeast co-cultures were supplemented with 5% citrus pulp, viability of both organisms decreased more than when cultured separately and supplemented with citrus pulp. Viability results, coupled with reduced weight gain observed in previous studies, could indicate that when challenged with yeast and citrus pulp, *Salmonella* might increase cytotoxin production, enhancing the immune response. Results differed when *E. coli* cultures were tested. While growth of *E. coli* was inhibited in cultures supplemented with 5% citrus pulp, the bacteria seemed relatively unaffected when co-cultured with yeast and no citrus pulp. In fact, by testing the viability of *E. coli* grown in media supplemented with yeast supernatant and yeast grown in media containing *E. coli* supernatant, it was found that *E. coli* could utilize carbon sources obtained from lysed yeast cells. This finding suggests that the presence of yeast could provide protection to *E. coli* in nutrient starved environments. The overall results of the experiment show that *E. coli* responds differently to yeast and citrus pulp than *Salmonella*, and that Levucell SB, which is intended to promote intestinal health, may actually provide protection to enteric pathogens in the guts of pigs.

Name: Melton, Wesley
Department: Aerospace Engineering
Faculty Mentor: Thomas E. Lacy, Jr.

Project: *Multiscale Modeling of Woven Fiber Composites Using Randomized Fiber Strengths*

Introduction: The Micromechanical Analysis Code with the Generalized Method of Cells (MAC/GMC) [1] was developed by NASA Glenn Research Center to model composite materials based upon Aboudi's method of cells [3-5] through use of Repeating Unit Cells (RUCs). MAC/GMC has also been coupled with the finite element solver ABAQUS using the hybrid code FEAMAC. This software allows progressive failure analyses to be performed on complex structures while performing a global-to-local-to-global finite element analysis. When modeling composites in traditional finite element analyses, the fiber tensile strength is considered a material constant and is homogenized with the matrix properties. However, as-fabricated fibers display a distribution of tensile strengths due to material defects. Therefore, models predicting failure with constant material properties do not reflect actual test data.

Purpose: This work aims to model progressive failure of a woven fiber composite system using fiber failure strengths consistent with manufacturer data. A global-to-local-to-global progressive failure analysis will be performed using FEAMAC and ABAQUS Standard on a composite flexure specimen and compared to experimental data.

Progress: A model representing an ASTM standard test specimen has been constructed in ABAQUS with loading conditions consistent with a three-point flexural test (see Figure 1 in the Appendix). A unidirectional flexure specimen with a constant fiber strength was simulated in FEAMAC/ABAQUS as an initial step. Failure from this simulation is shown in Figure 2 in the Appendix.

Future Work: Now that the model has been simulated, the woven RUC model will be developed in MAC/GMC. Then, a Matlab code will be used to randomize fiber strengths throughout the RUC model and RUCs throughout the finite element mesh. Multiple multiscale progressive simulations will be performed to quantify the effect of statistically varying fiber strengths at the mesoscale on the progressive failure behavior at the macroscale. The results of these analyses will be then compared to experimental flexural test data obtained from the literature.

Appendix:

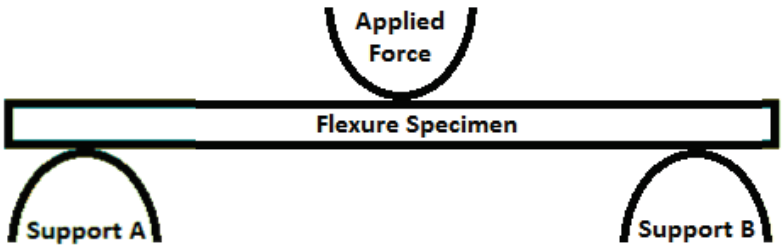


Figure 1: Loading conditions of a three-point bend test model.

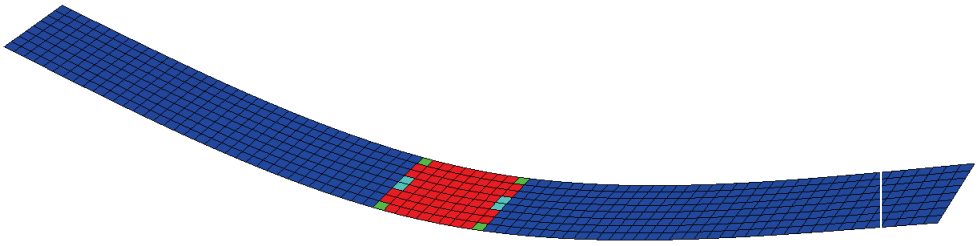


Figure2: Failure Output from a FEAMAC/ABAQUS model for a unidirectional RUC.

References:

[1] Bednarcyk B.A., and Arnold, S.M., "MAC/GMC 4.0 User's Manual – Keywords Manual" NASA/TM-2002-212077/VOL2. 2002.
[2] Ricks, T.M., Lacy, T.E., Bednarcyk, B.A., and Arnold, S.M., "A Multiscale Modeling Methodology for Metal Matrix Composites Including Fiber Strength Stochastics," in the Proceedings of the 53rd AIAA/ASME/ASCE/AHS/ASC Structures, Structural Dynamics, and Materials Conference, Honolulu, Hawaii, April 23-26, 2012.
[3] Aboudi, J., Mechanics of Composite Materials: A Unified Micromechanical Approach, Elsevier, Amsterdam. 1991.
[4] Aboudi, J., "Micromechanical Analysis of Thermoinelastic Multiphase Short-Fiber Composites" Compos Eng, Vol. 5, 1995, pp. 839–850.
[5] Aboudi, J., "Micromechanical Analysis of Composites by the Method of Cells – Update" Appl Mech Rev, Vol.49, 1996, pp. S83–S91.

Name: Mody, Perceus
Department: Biological Sciences
Mentor: Dr. Justin Thornton, Assistant Professor, Dept. of Biological Sciences

Project Title: *Streptococcus pneumoniae induces H_2O_2- mediated DNA damage in mouse bone marrow neutrophils and human lung epithelial cells*

Description: *Streptococcus pneumoniae* (pneumococcus) is a gram-positive bacterium that is the leading cause of community acquired pneumonia and a common cause of otitis, meningitis, and sepsis. During pneumococcal pneumonia, the lung epithelium is adversely affected and neutrophils are recruited in large numbers to help limit bacterial growth. The pneumococcus itself produces hydrogen peroxide as a byproduct of aerobic metabolism via the enzyme, pyruvate oxidase (SpxB). Therefore, we tested our hypothesis that H_2O_2 produced by *S. pneumoniae* induces DNA damage in neutrophils and lung epithelial cells. Comet assays, utilizing single cell electrophoresis, demonstrated the extent of DNA damage induced by *S. pneumoniae.* DNA-damaging agents, H_2O_2 and etoposide, served as controls. We found that exposure to *S. pneumoniae* induces DNA damage in neutrophil progenitors (42.3µm average tail length vs. 20.41µm in controls; $P<0.0001$) and murine derived bone marrow neutrophils. Significant DNA damage was also seen in human A549 lung epithelial cells. ROS inhibitor N-acetyl cysteine and catalase were able to protect neutrophils and A549 cells from DNA damage induced by *S. pneumoniae*. Additionally, an isogenic Δ*spxB* mutant (HPK) did not induce significant DNA damage in either cell type. Moreover, Annexin V/propidium iodide staining and flow cytometry were used to characterize neutrophil apoptosis in response to *S.pneumoniae* and ΔspxB mutants. Since DNA damage was induced by the bacteria, RT^2 Profiler PCR arrays were utilized for transcriptional profiling of DNA damage response genes in human lung epithelial cells exposed to T4R or HPK.

Name: Morgan, Perry
Major: Biological Sciences
Faculty Mentor: Dr. David Chevalier

Project Title: *"Response of the Arabidopsis gene At3G02400 to genotoxins"*

My research focused on the molecular biology and genetics of plant species. Specifically, I examined the biological role of the *Arabidopsis thaliana* gene At3G02400 with regard to its induction via genotoxic agents. At3G02400 is not expressed under normal growth conditions, but when exposed to certain genotoxic agents it is found that the gene is expressed. To date, it has been shown that At3G02400 is induced by gamma radiation, mitomycin C, and camptothecin (CTP).

The goal of my research was to determine the role of At3G02400 in regulating cell division. Additionally, I was concerned with determining the concentrations of CTP and nicotine necessary for the induction of At3G02400. A cyclin:GUS (beta-glucronidase) reporter system was used to determine the role of At3G02400 in regulating cell division (i.e. whether it was more prevalent, less prevalent, or unaltered when At3G02400 is expressed). Additionally, using a GUS reporter system and gradient concentration treatments of CTP and nicotine respectively, I was able to determine the concentration of each compound necessary for the expression of At3G02400.

The results of my research show that At3G02400's role in the regulation of cell division is largely negligible. That is, there was little difference in the rate of cell division between the untreated cyclin:GUS mutants and those that were treated with CTP. Additionally, it was shown that nicotine does not induce the expression of At3G02400 at the concentrations tested (1.5 – 0 mM)while CTP causes expression to occur at concentrations as a low as 15 μM. At3G02400's role in the response of *Arabidopsis thaliana* to genotoxins remains unclear, but given the possibilities of its function, is worth continued study.

Name: Murnan, Charlotte
Major: Mathematics and Statistics
Faculty Mentor: Dr. Daniel Carruth, CAVs

Project: *"Developing Algorithms for Automated Analysis of Athlete Motion"*

This project started with a need for a more efficient way for trainers to evaluate athletes. There are simple exercises, such as the overhead squat, that can be performed by athletes and evaluated by trainers that reflect muscle imbalances. If caught early enough, these imbalances can be corrected before they result in injury. The problem with this process is that it can be very time consuming for the trainers and athletes, thus only performed about three times a year. To automate this evaluation would increase the efficiency of this procedure, and could also increase how often it can be performed. My research project this summer was a start towards the automation process, and further work can lead to the desired outcome.

To start this project, I needed to know what metrics needed to be identified in order to determine the muscle imbalances. For these metrics, I consulted *Clinical Movement Analysis to Identify Muscle Imbalances and Guide Exercise* by Christopher Hirth in which an overhead squat was evaluated. The five main issues I found to watch for in an overhead squat were if the toes turned out, the knees turned in or out, the heels raised, the arms fell forward, or the trunk leaned too far forward. Once I knew what to look for, I selected training data of 20 student athletes performing at least three repetitions of an overhead squat from a large set of anonymous motion data. Using this data, I identified some measures that could find the five metrics mathematically rather than visually. After the measures were identified, I set threshold parameters for each metric based on what I interpreted in Hirth's article. With measures identified and parameters set, I then created formulas in Microsoft Excel to calculate the key measures. The measures, formulas, and parameters are described in the table below.

Key Metric	Measures	Formula	Threshold Parameter
Toe Out	Distance between toes divided by distance between heels	FRR = Dist(R_Foot, L_Foot) / Dist(R_Heel, L_Heel)	>1.2
Knees turn in/out	Difference in distance between the knees at endpoint and start point	$\Delta KP = Dist_{EP}(R\_Knee\_Med, L\_Knee\_Med) - Dist_{SP}(R\_Knee\_Med, L\_Knee\_Med)$	5 cm
Heels Raise	Maximum value of the two feet for the difference between z-values for start and end points	$\Delta HR = MAX(R\_Heel_{ZEP} - R\_Heel_{ZSP}, L\_Heel_{ZEP} - L\_Heel_{ZSP})$	>2 cm
Arms Fall Forward	Shoulder Flexion	$SF = ANGLE(\ Proj_{SAG}(V_{R\_Acromion,\ T10}), Proj_{SAG}\ (V_{R\ \ Acromion,\ R\ \ Elbow\ \ Lat})\ )$	<30°
Trunk Lean	Angle between trunk and lower leg	$\theta TL = ANGLE(\ Proj_{SAG}(V_{R\_Acromion,\ R\_Hip}), Proj_{SAG}\ (V_{R\_Knee\_Med,\ R\_Ankle\_Med}))$	>20°

Once the formulas were running in Excel and producing the measures properly, I applied the formulas to the data for all 20 student athletes. Looking at the results for all the subjects, I realized some of my set parameters may not be realistic. This is why it is important to have professional trainers evaluate my data, and compare their visual findings to my automated ones. Once they verify that my process can produce correct results given the proper parameters, I can continue towards the end results. Ideally, the end result of the automated process would utilize a more cost-efficient motion tracking system, such as Microsoft's Kinect. Reduced cost and improvements to efficiency would then allow athletes at all levels to benefit from regular evaluations.

Name: Myers, Kaci
Major: Psychology
Faculty Advisor: Deborah Eakin

Project Title: The Effects of Imagery & Misinformation on Eyewitness Memory

In the spring semester of 2012, I ran a pilot study on The Effects of Imagery & Misinformation on Eyewitness Memory. I spent the summer analyzing the data I collected from the pilot study, preparing for the final run of the experiment and data analysis in the fall, and writing my thesis paper. The proposed study investigated how exposure to misleading post-event information affects a person's ability to recall details of a witnessed event when the misleading information is accompanied by a misleading versus a veridical image. Preliminary findings suggest providing a photograph increased false memories, but also increased veridical ones.

Near the end of spring semester, our data analysis computers had significantly slowed down or had issues that prevented them from being used for data analysis at all. We used a portion of the miscellaneous expenses from the grant to help enhance/replace these machines to increase lab productivity. In addition, we needed new E-Prime software, which the grant also helped us obtain. In my experiment, participants work in a set of two paper booklets per person. The grant money went towards lab expenses for paper as well as any other materials needed, such as pencils. Overall, the grant greatly helped with my research over the summer and for the following fall semester.

Name: Offenberger, Sean
Major: Aerospace Engineering
Faculty Advisor: Dr. Thomas Lacy

Project Title: *Characterization of Debris Cloud Distribution and Damage Caused by Hypervelocity Impacts on Vapor Grown Carbon Nanofiber Reinforced Laminate Shielding*

Hypervelocity impacts (HVIs) generally involve impact velocities greater than 3km/s and large impact energies, even for the case of very small projectile masses. The near-Earth space environment contains a flux depending on the altitude above Earth and position of the Earth's orbit of man-made orbital debris, meteoroids, and micrometeoroids that can impact spacecraft with an average impact velocity in the range of 8-19km/s [1]. Consequently, spacecraft with prolonged operation in this environment will certainly experience high velocity/high energy impacts from small objects with diameters approximately 1m and smaller. HVIs can be simulated using light gas guns such as Mississippi State University's (MSU) micro two-stage light gas gun.

A commonly employed small particle impact mitigation technique is to attach a thin nonstructural shielding layer outside the main structural wall. This serves to break up the projectile into an expanding debris cloud behind the shield, thereby dispersing its kinetic energy over a larger area of the main structural wall. Early shields were made of a single thin plate of aluminum, but more recent shield designs include multiple layers and composite materials [2].The addition of nanoreinforcements such as VGCNFs to composite hypervelocity shielding materials hasn't been investigated in depth. In this work, the debris cloud impacts on the aluminum back wall caused by HVIs on two types of plain weave cross ply shielding were compared: woven fabric E-glass/vinyl ester (VE) laminate composite and E-glass/VE/VGCNF hybrid laminate composite with 0.5 parts per hundred resin (phr) VGCNFs. This small amount of VGCNFs is about 0.3 volume % of the VE resin.

METHODS: Specimens Production: In order to validate the capabilities of the two stage light gas gun, plain weave cross ply E-glass composites were fabricated with either a neat VE resin (Derakane 441-400) or a VE resin reinforced with 0.5phr oxidized vapor grown carbon nanofibers (Applied Sciences Inc., PR-24-XT-LHT-OX)with average length of 50-200 μm. The batches of resin were prepared and cured using the methodology specified in [3]. These nanoreinforced VE resins are more suited to land and marine applications rather than to space applications, but they were used in this work for convenience. Future tests will involve materials better suited to space applications such as epoxy resins or bismaleimide resins, both reinforced with carbon fibers.

7.6cm x 7.6cm specimens were cut out of cured laminates using a water saw. Laminated composite and hybrid composite panels with a $[0^{o}{}_{5}]$ layup were prepared using a wet lay-up vacuum bagging procedure. The thickness of the cured laminates was approximately 1.27mm.

A 19.1mm thick wooden spacer was used for convenience to set the standoff distance between the 7.6cm x 7.6cm composite shielding targets and a 6061 aluminum back wall. The composite shield (target), spacer, and back wall were assembled using tape.

Gas Gun Operation: The target specimens were attached to a mounting plate inside the target chamber with small diameter rubber o-rings as shown in Figure 2 to cushion the interaction between the target and mounting plate. Projectile velocities were measured using an oscilloscope, which recorded the time between signals from one photodiode located at the exit of the projectile barrel and one located in the target chamber. The impact velocity was calculated by dividing the distance between the photodiodes by the time between voltage readings on the oscilloscope. The following approximate firing parameters were used: 0.55g gunpowder, 0.45gHDPE piston, 1.135MPa helium, 0.005g 6-6 Nylon projectile, and 413 Pa prevailing pressure inside the vacuum tube.

RESULTS: Three E-glass/VE and three E-glass/VE/VGCNF shielding specimens were impacted. Measured projectile velocities ranged from 3.4km/s to 4.7km/s, and kinetic energy ranged from 28.9 to 55.2 J. The impact damage and debris cloud were characterized by visually inspecting the shielding and aluminum back wall and viewing the aluminum back wall with a scanning electron microscope (SEM).

Visual Inspection of Shielded Impacts: Damage to Composite Shielding: Both types of composite shields sustained significant impact damage. The E-glass/VE shielding clearly showed complete penetration of the laminate with multiple delaminations through the thickness. The E-glass/VE/VGCNF shielding showed similar penetrations and impact damage. Both types of specimens showed minimal charring of the composite impact hole diameters. For the E-glass/VE laminates, the typical delamination diameters were roughly six times the penetration diameters. The E-glass/VE/VGCNF laminates showed evidence of similar delaminations, but these could not be measured because the VGCNFs discolored the VE dark black leaving them opaque.

DAMAGE TO ALUMINUM BACK WALL: The surface impact damage consists of two primary components: deep gouges and shallow rough areas. The gouges are slender areas with relatively deep penetration depth that tend to concentrate in a ring-like pattern surrounding the center of impact. The rough areas are regions with less severe surface penetration that radiate away from the center of impact. Although not evident in the black and white photographs, there was also significant discoloration of the surface of the aluminum back wall. This is likely due to resin burning resulting from localized heating at impact.

SEM Imaging of Composite Shields: A Carl Zeiss EVO50VP Variable Pressure Scanning Electron Microscope was used for SEM imaging. Based upon SEM images, both types of composite shields led to similar debris cloud formation and surface cratering. As previously noted, the debris cloud impact damage to the aluminum back wall was comprised of relatively deep gouges around the center of impact and regions with widespread shallow surface damage. In the latter case, debris cloud surface damage consisted of distributed shallow indentations due to individual E-glass fibers from the shields impacting the back wall. In general, the troughs formed by E-glass fibers impacting the plate are empty, but occasional E-glass fibers and fiber fragments were embedded in the aluminum surface. It is clear from these images that the E-glass fibers fragmented upon impact with the aluminum plate. The aluminum back wall surfaces with the deep debris cloud gouges were highly irregular

CONCLUSION: HVIs of six plain weave cross ply laminate composite shields were conducted using a two-stage light gas gun. Three E-glass/VE composite shields and three E-glass/VE/VGCNF composite shields served as targets. Both types of shield produced debris cloud impacts with very similar characteristics. The addition of only tiny amounts of VGCNFs (0.5phr, about 0.3 volume % of resin), however, seems to have an effect on the damage seen in the shield itself, resulting in a larger penetration hole and less fraying. To further investigate the damage to the shields, the extent and number of delaminations must be assessed quantitatively.

The expanding debris clouds produced from these impacts consisted of individual broken E-Glass fibers and pieces of resin and projectile material. Some of the SEM images suggest that the gouges were formed before the trough areas, which would be expected from an expanding debris cloud. However, it is not yet known what physical state the material was in that caused the gouging. Future investigations will involve fiber and matrix materials more suited to space applications as well as projectile materials with material properties similar to orbital debris or micrometeoroids.

ACKNOWLEDGEMENTS: The authors would like to thank General Sealants for graciously donating AT-200Y sealant for use in the vacuum bagging process.

REFERENCES

[1] Tribble, A.C., *The Space Environment*, Princeton, Princeton University Press, 2003.

[2] W. P. Schonberg. 2000. "Protecting Spacecraft Against Orbital Debris Impact Damage Using Composite Materials," *Composites: Part A*: 31, 869-878.

[3] S. Nouranian, H. Toghiani, T. Lacy, C. Pittman, and J. DuBien. 2011. "Dynamic Mechanical Analysis and Optimization of Vapor-grown Carbon Nanofiber/Vinyl Ester Nanocomposites Using Design of Experiments," *Journal of Composite Materials*: 45(16), 1647-1657.

Name: Phillips, Kathryn
Department: Anthropology
Faculty Mentor: Janet Rafferty

Project Title: *Project Name: Adding New Knowledge through Seriations and Geophysics*

My research occurred in four stages: (1) artifact collection, (2) cataloguing of artifacts, (3) pottery analysis, and (4) seriation. The artifacts that I used during my research were collected by the 2012 Archaeological Field School that I participated in. The artifacts were collected from sites on South Farm on Mississippi State's campus. When the collections of artifacts got back to the lab, I had to catalogue them by sorting them into categories like sherds, lithics, historics, etc. Once all site collections were catalogued I then analyzed the pottery from each site. To analyze the pottery I first looked at the temper and then subdivided the temper by surface finish. Temper is what is put into the pottery to help equalize shrinkage when the pot is dried and fired and is usually fiber, shell, sand, or fired clay. Surface finish refers to whether the pottery is decorated. This analyzing resulted in multiple pottery types being present in each collection. These groups of artifacts are called assemblages. These assemblages will soon be put into a frequency seriation which will help date the site. There had been a previous archaeological survey at the sites the 2012 Field School surveyed. I took the collections from this older survey and catalogued them. I then took the pottery and analyzed it. The reason for adding this extra collection was to add to the amount of the pottery, thus producing a more reliable date in the frequency seriation.

Name: Randive, Rushil
Department: Biological Sciences
Faculty Mentors: S. Jeyaraj, M. Chotani, & J.A. Stewart, Jr.

Project: *Rap1a mediates ECM remodeling through AGE/RAGE signaling in diabetes mellitus*

Rap1a is a small monomeric G-protein in the Ras-GTPase superfamily that acts as a molecular switch coupling extracellular events to intracellular signaling. There are very few attributed roles of Rap1a in ECM remodeling. Our hypothesis is Rap1a signaling intersects hyperglycemia-mediated AGE/RAGE signaling to alter fibroblast phenotype increasing ECM production and accumulation leading to LV structural remodeling. Rap1a gene ablation and knock-down were used to determine ECM and AGE accumulation, RAGE expression and fibroblast differentiation to determine the molecular interplay between Rap1a- and AGE/RAGE-dependent signaling in isolated diabetic cardiac fibroblasts from Db/db and db/db. We observed left ventricular (LV) collagen levels were significantly decreased by gene abalation. Silencing Rap1a mRNA in diabetic (db/db) fibroblasts returned collagen and RAGE expression to non-diabetic (Db/db) levels. These studies are the first of its kind to provide unique targets for therapeutic strategies aimed at reducing hyperglycemia/AGE-mediated ECM production and accumulation in diabetic patients.

Name: Robinson, Anne
Major: Psychology
Faculty Mentor: Carrick Williams

Project: Project Title: Own-race Bias and Eye Movements: Does Effort Predict Memory?

Introduction: Humans remember faces exceptionally well compared to other objects. It is presumed that there is a special type of processing, typically called holistic processing, that is obligatory and gives faces an advantage because the face is processed as a unified whole. However, people vary in their ability to use holistic processing (Hugenberg & Corneille, 2009). Specifically, a phenomenon known as the own-race bias, whereby people remember faces of their own race better than faces of another race, has been claimed to result from differential holistic processing (Michel, Rossion, Han, Chung, & Caldara, 2006). One way to examine holistic processing of faces is the face inversion effect. When turned upside-down, memory for a face is dramatically worse than when the face is presented in its normal orientation presumably because inverting the face disrupts holistic processing. Critically, inverting other-race faces does not disrupt memory to the same extent that it does own-race faces (Rhodes, Brake, Taylor, & Tan, 1989). The theory behind this is that inverting faces disrupts holistic processing, but, because other-race faces are processed more on the basis of their features, face inversion does not carry the same consequences for subsequent memory. Our experiment examined the relationship between own-race bias and the face inversion effect. Goldinger , He, and Papesh (2009) found that participants made more frequent fixations on the eyes of own-race faces, while focusing more on the nose and mouth of other-race stimuli. They also found, using distance traveled by the eyes as a measure of effort, that participants selectively withdrew effort from other-race faces presumably leading to worse memory for those faces. Extending Goldinger et al.'s study, we wanted to examine if differences in facial feature processing and measures of effort would account for the differences in the face inversion effect for different race faces. In order to accomplish this, we had participants view African American faces, Caucasian faces, and a set of non-face objects (radios) while we tracked their eye movements.

Methods: Fifty-seven undergraduate students at Mississippi State University participated in this study for course credit, but because we were interested in own-race bias, we excluded from this analysis any participant who identified themselves as multiracial or a race other than African American or Caucasian. The data are reported for 15 African American and 32 Caucasian participants. Following calibration of the eye tracker, we had each participant study upright African American faces, Caucasian faces, and radios for 10 seconds each for a later memory test. In the subsequent memory test, participants were shown presented and nonpresented exemplars from each category either upright or inverted and indicated whether the stimulus had been previously studied. Eye tracking was performed in both the study and memory test phases.

Results: Results from the memory test showed an own-race bias for both African American and Caucasian participants. In addition, results showed a general face inversion effect for both African American and Caucasian participants as well. Contrary to expectations, though, the face inversion effect was not statistically greater for own-race faces for either participant group, and, in fact, the African American participants showed a numerically larger face inversion effect for Caucasian faces. Thus, the current study, failed to find an indication that holistic processing was especially disrupted for other-race faces.

The next question was whether the own-race bias seen in the memory test could be accounted for by eye movement differences during the study. In contrast to the fixation patterns shown by Goldinger et al. (2009), at study, Caucasian participants showed more fixations on the forehead for own-race stimuli, and more fixations on the eyes and mouth for other-race stimuli. Also at study, African American participants showed more fixations on the mouth for own-race stimuli, and more fixations on the eyes and forehead regions for other-race stimuli. With respect to the "effort" in encoding (the distance the eyes moved within the stimulus), we did find that when memory test accuracy was regressed on the distance moved by the eyes at study, there was a significant relationship that was over and above the number of fixations during study, similar to Goldinger et al

(2009). This finding indicates that effort plays a role in face recognition. However, we also found that distance moved by the eyes was less for Caucasian stimuli than for African American stimuli, regardless of participant race failing to replicate the pattern of Goldinger et al. One possible explanation for this different finding is that our stimuli were real-world photographs and some features of the African American stimuli we used may have attracted more attention (e.g, earrings), causing the eyes to travel more.

Discussion: Overall, we found that there was an own-race bias for both participant groups, but neither differential holistic processing nor effort appeared to explain these findings. Although distance traveled did predict visual memory for faces over and above the total number of fixations on the face, the measure was not different for the own-race and other-race faces. One interesting aspect of the data that might shed light on this finding was that the distance-traveled measure was highly correlated across stimulus types (both own- and other-race faces ($r = .90$) and to a lesser extent to radios, $r \geq .75$) indicating that our participants had highly similar viewing patterns regardless of the type of stimulus. This finding suggests that our subjects may each be using a generalized encoding strategy for all stimuli rather than having a different strategy for each stimulus type.

Name: Sprabery, Read
Major: Electrical and Computer Engineering
Faculty Mentor: Tommy Morris

Project Title: *Power Grid Intrusion Detection*

Over the summer, I worked with Dr. Morris researching methods to better secure the nation's power grid. Currently, there was been a shift to use Phasor Measurement Units (PMU's) which communicate with Phasor Data Concentrators (PDC's) in order to relay information regarding the status of the power grid. These devices communicate using a well-documented protocol developed by the IEEE, C37.118. This protocol defines how Phasor Measurement devices communicate, and failure to adhere to it implies that either a device is malfunctioning or malicious activity is occurring. Attacks can range from simply preventing the machines from communicating, known as a denial of service attack, which, if the data is being used to make a system critical operating decision, can be extremely detrimental. Another more sophisticated attack can intercept data, modify the measurement taken from the grid, and forward incorrect data to another device. This kind of attack is known as a Man in the Middle attack, and can be used to spoof data, possibly causing destructive actions to be taken. When spoofing data, an attacker must ensure that the spoofed data also adheres to the protocol. In addition to adhering to the C37.118, data must adhere to environment specific configurations. One PMU may relay multiple streams of data, thus if a connection from a PMU suddenly shows more or less streams, then there is a violation of that particular environment's configuration.

In order to help identify attacks like these before they cause problems, an Intrusion Detection System (IDS) was developed in the form of a plugin for the popular IDS Snort. Our plugin not only detects what are known as protocol mutations, but ensures that the data streams sent between devices adhere to their corresponding configurations. An initial configuration is sent between devices when they initially connect. The plugin developed with Dr. Morris auto configures itself to scale as more devices come online and transmit their configurations to other devices on the network. In this way, we detect protocol mutations which may be a result of malicious activity and send an alert to a network administrator. The system works by sitting between the PDC's and a network switch. All communication to and from the PDC must go over this single line. With this configuration, our system is easily scalable, and can handle traffic between multiple PMU's and a PDC on one network.

This research has led to a number of questions regarding efficient classification of rules to ensure that the systems are adequately protected in a variety of ways. In addition to this, further research can be done regarding the scalability of the Snort plugin with regards to the number of machines that can be protected with a single node. The summer's work resulted in a usable plugin that adds a layer of security to power grid control systems and can be used as a starting point for further research in the area.

This research has resulted in one accepted conference paper. The paper titled "Protocol Mutation Intrusion Detection for Synchrophasor Communications" will be presented at the 8th Annual Cyber Security and Information Intelligence Research Workshop (CSIIRW8) in Oak Ridge, TN January 8-10, 2013.

Name: Stafford, James
Major: Computer Science and Engineering
Faculty Mentor: Dr. Cindy Bethel

Project: *Conveying Robot Intent For Movement*

In this project, I have developed a system that will convey robot intent to a human using leds and an android device. The robot sends a message about its movements to the android device that it prints to screen and tells the user through an earpiece about its movements. The robot sends the message shortly before it begins to move.

In addition to developing the system, we held human studies to learn which method of the communication is best. The findings will be used for a poster and paper.

Name(s): Cerovsky, C., **Syed, Z**., Dendis, A.
Mentor: Stewart, Jr., JA
Department: Biological Sciences

Project: *AGE/RAGE and PKC-zeta interplay in 3D matrix mediated fibroblast differentiation*

This purpose of this study was to determine whether increases in advanced glycation endproducts (AGEs) in a 3D diabetic collagen matrix will differentiate wild type (WT) cardiac fibroblasts to a profibrotic phenotype. 3D collagen matrices were prepared from collagen extracts from non-diabetic (Db/db) and leptin receptor deficient, diabetic (db/db) mouse tails. Primary cardiac fibroblasts isolated from WT and AGE receptor deficient (R-/-) mice which were seeded onto both Db/db and db/db 3D collagen matrices for 7 days (chronic exposure). In addition, on day 6, these cells were then treated with inhibitors UO126 (ERK 1/2 inhibitor; 10μM) and PKC-zeta Pseudosubstrate (PKC-zeta inhibitor; 1μg/ml) and with a RAGE ligand- glycated albumin (AGE-BSA; 0.5mg/ml) to induce RAGE activation. Chronically exposed R-/- cells were unchanged, however WT cells exhibited functional and phenotypical markers for fibroblast differentiation, such as increased alpha- smooth muscle actin and RAGE expression. Additionally, blockade of ERK1/2 and PKC-zeta restored WT expression to non-diabetic levels. Therefore, chronic exposure to AGE-crosslinked diabetic ECM resulted in phenotypic alterations in WT fibroblasts. These changes were mediated through AGE/RAGE interactions leading to a profibrotic cell phenotype.