MONMOUTH UNIVERSITY

SCHOOL OF SCIENCE

SCHOOL OF SCIENCE

15TH ANNUAL
STUDENT RESEARCH CONFERENCE

Magill Commons

Tuesday, April 19, 2016

ABSTRACTS

MONMOUTH UNIVERSITY

STUDENT SCHOLARSHIP WEEK

MONMOUTH UNIVERSITY
SCHOOL OF SCIENCE

MONMOUTH UNIVERSITY
STUDENT SCHOLARSHIP WEEK

School of Science
15TH Annual
Student Research Conference

Tuesday, April 19, 2016
Magill Commons

1:00 pm – 1:30 pm	**Registration and Poster Set-up** **Magill Commons Club Rooms 107 - 109**
1:30 pm – 2:15 pm	**Keynote Presentation** **Magill Commons Dining Room** **Dr. Adam Resnick, Children's Hospital of Philadelphia** **Introduction by Dr. Martin Hicks, Biology Department**
2:15 pm – 2:30 pm	**Break**
2:30 pm – 4:30 pm	**Poster Session** **Magill Commons Club Rooms 107 - 109** **Welcome by Interim Dean John Tiedemann**
4:30 pm – 5:00 pm	**Wrap-up and Closing Remarks**
5:00 pm – 5:15 pm	**Break**
5:15 pm – 7:00 pm	**Reception & Dean's Awards for Excellence in Research** **Magill Commons Dining Room**

MONMOUTH UNIVERSITY

SCHOOL OF SCIENCE

15TH Annual
Student Research Conference

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MONMOUTH
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DEPARTMENT OF BIOLOGY

WRECK POND AQUATIC VERTEBRAE eDNA PROJECT

Tatiana Castro, Chelsea Soriano and Cayla Sullivan

Department of Biology

Faculty Mentors: Professor Christine Thompson and Dr. Martin Hicks

Jenna Krug, American Littoral Society
Mark Stoeckle, Rockefeller University

ABSTRACT

The Aquatic Vertebrate eDNA Project, conducted by Monmouth University students and faculty and supported by the Urban Coast Institute's Marine Research Initiative, is taking place in Wreck Pond, New Jersey. This study enables the detection of various fish and mammal species found in marine and freshwater habitats. Wreck Pond is currently undergoing a restoration project directed by the American Littoral Society to facilitate fish passage into the pond from the open ocean. With this study, specific species can be identified without causing stress to the organisms. Twice monthly water samples were taken from four locations throughout Wreck Pond and the adjacent ocean from March 2016 through June 2016. Along with obtaining 1,000 mL for each water sample, YSI data and observations of the site are recorded. After collection, water samples undergo vacuum filtration, DNA extraction, amplification of vertebrate DNA using a 12s mitochondrial DNA primer, and Next Generation sequencing. Final readings will be compared to the vertebrate 12s library to determine the species found in Wreck Pond. These identifications will be compared to fish caught in fyke nets by the American Littoral Society during spring tides from March through June. This study is important for further research on anadromous species, like the alewife and blueback herring, because migration patterns for their aggregated spawning can be conducted. A better understanding of fish passage through Wreck Pond will enable further restoration and management for these species in this area. With eDNA identification, these essential species can be protected, conserved, and better understood by the public.

ESSENTIAL OILS AND METHYLGLYOXAL: A POSSIBLE ALTERNATIVE TREATMENT FOR ANTIBIOTIC RESISTANT BACTERIAL INFECTIONS

Erin Cieslak

Department of Biology

Faculty Mentor: Dr. James P. Mack

ABSTRACT

Antibiotic resistant bacteria in healthcare settings have become a serious global problem. These bacteria are evolving much more quickly than are effective treatments to combat them. Due to the indiscriminate and overuse of antibiotics, treatment options to control multidrug resistant bacterial infections are limited at this time. Some natural plant products may be a useful alternative modality for treating these antibiotic resistant bacteria.

In this research, three essential oils (Cassia, Cinnamon, and Thyme White) and Methylglyoxal (the key component in Manuka Honey) were used in conjunction with four carrier oils (Coconut oil, Jojoba oil, Lanolin oil, and Olive oil) as emollients to determine their efficacy in inhibiting Methicillin-resistant *Staphylococcus aureus* (MRSA) and Methicillin-sensitive *Staphylococcus aureus* (MSSA) bacteria. Cassia, Cinnamon, Thyme White, and Methylglyoxal were chosen because, in previous studies done at Monmouth University, these four materials have proven to be effective in treating MRSA and MSSA bacterial infections. Most essential oils are irritating to the skin in their concentrated form, therefore diluted essential oils were used in the study. The dilutions were made using carrier oils that are known to be safe for use on the skin. Using these diluted essential oils and methylglyoxal in the carrier oils, the minimum inhibitory concentration (MIC) of the essential oil or methylglyoxal was determined against the MRSA and MSSA bacteria.

It was determined that a 25% dilution was the MIC of the essential oil or methylglyoxal in various carrier oils, and at this concentration they worked much more effectively than the standard antibiotic, Vancomycin. The emollient even worked at about the same level as the much stronger antibiotic, Rifampin; however, this antibiotic is not used as frequently due to its severe side effects. Having the emollients as alternative treatments for antibiotic resistant bacterial infections, such as MRSA and MSSA, will make more options available to infected patients.

THE EFFECT OF ESSENTIAL OILS AND METHYLGLYOXAL ON *ACINETOBACTER BAUMANNII*

Karla Clavelo and Joseph Kellett

Department of Biology

Faculty Mentor: Dr. James P. Mack

ABSTRACT

Antibiotic resistant bacteria have become a large problem in healthcare settings, primarily due to the overuse and misuse of antibiotics. Consequently, these bacterial infections have become difficult to treat because the bacteria have evolved to make the common commercial antibiotics increasingly ineffective. Alternative treatments using natural products derived from plants are sought to effectively combat these multidrug-resistant bacteria.

In this research, the essential oils cassia, cinnamon bark, oregano, thyme white, and the aldehyde methylglyoxal (the main active antibacterial ingredient in Manuka Honey) were used in conjunction with three carrier oils (olive oil, jojoba oil, and coconut oil) to determine their efficacy in inhibiting the growth of *Acinetobacter baumannii*, a multidrug-resistant bacterium. *Acinetobacter baumannii* is a rapidly emerging pathogen in the healthcare settings, where it causes infections that include bacteremia, pneumonia, meningitis, urinary tract infections, and wound infection. The essential oils we used were diluted to lower concentrations with the carrier oils to determine their minimal inhibitory concentration (MIC) because most essential oils can be irritating to the skin in high concentrations. The results were then compared to colostin, a traditional antibiotic used to treat *Acinetobacter baumannii* infections, to determine their relative effectiveness. The dilutions were made using the carrier oils listed above, which are known to be safe on the skin. The efficacy of the essential oils and methylglyoxal combined with the carrier oils were determined by using the disk diffusion (Kirby-Bauer) method.

The essential oils and methylglyoxal tested were diluted and tested at 100%, 75% and 50% concentrations in carrier oils and compared to the colostin antibiotic. It was determined that at a 50% concentration, the essential oils and methylglyoxal were more effective than colostin in inhibiting the growth of *Acinetobacter baumannii* in the Petri dish experiments. Our results suggests a potential alternative treatment for patients with topical infections by *Acinetobacter baumannii.*

miRNA21a-MEDIATED ANTI-EGFR SiRNA GENE TRANSFER

Medha Dommaraju

Department of Biology

Faculty Mentor: Dr. Martin J. Hicks

ABSTRACT

The most lethal and common malignant primary brain tumor in adults is Glioblastoma Multiforme (GBM). GBM primarily results from specific glial cells, astrocytes, which function in supporting neurons. Due to the high rate of malignancy the median life expectancy for GBM patients ranges from 14-17 months. Current therapies, including radiation and chemotherapy provide some inhibition in the progression of GBM; however many therapies do not pass the blood brain barrier (BBB). Tyrosine kinase receptors (TKR) are often over expressed in GBM making them a potential therapeutic target. One type of TKR, epidermal growth factor receptor (EGFR), is upregulated in about 50% of GBM cases. Our current approach would work from the inside-out, using a gene transfer strategy to deliver the DNA sequence of RNA molecules directed toward the EGFR transcript. Because miRNAs are often up-regulated in GBM, we are taking advantage of the miRNA gene architecture and miRNA processing pathway, including the promoter sequence as well as the pri-miRNA secondary structure to effectively express and deliver the sequences of anti-EGFR siRNAs. The up-regulated miRNA pathways in glioblastoma include miR21a. The miRNA gene provides a promoter region that, as well as the miR21a transcript secondary structure and scaffolding that would direct the siRNA therapy molecule into pri-miRNA processing pathway for more efficient RISC incorporation. It is hypothesized that this novel strategy would lead to a more stable and effective processing of anti-EGFR siRNAs. First, the secondary structure of miR21a was modeled using the 'RNA fold' software program. While maintaining the secondary structure, the secondary structure of miR21a was maintained while replacing with siRNA nucleotides that were complementary to the EGFR gene transcript. The preliminary steps of molecular cloning and synthesis of the siRNA therapy within the miR21a secondary structure have been undertaken. DNA oligos were designed to PCR synthesize and amplify the miRNA21a anti-EGFR insert. Subsequently, the miR21a anti-EGFR insert was ligated into the delivery plasmid adeno-associated virus (pAAV). Currently the efficacy of ligation is being tested using PCR analysis to verify that the clones carry the pAAV miR21a anti-EGFR siRNA therapy vector. I plan to move my project forward by testing this vector therapy in tissue culture using the GBM cell lines. In the future, the same strategy will be used to target additional targets in GBM, such as the CXCR4/CXCL12 axis.

TRANS-SPLICING OF IMMUNOGENS INTO THE EGFR TRANSCRIPT TO BLOCK GROWTH AND REACTIVATE THE IMMUNOGENIC POTENTIAL OF HUMAN GLIOBLASTOMA CELLS

Sarah Falotico[1], Peter Nekrasov[2] and Nicole Sivetz[1]
[1]Monmouth University and [2]Biotechnology High School

Department of Biology

Faculty Mentor: Dr. Martin J. Hicks

ABSTRACT

Glioblastoma multiforme (GBM) is the most common central nervous system malignancy. The current standard of care increases survival to only 14 months. GBM tumors evade the immune system and grow rapidly. Tyrosine kinase receptors, such as epidermal growth factor receptor (EGFR) are often overexpressed in GBM and drive cell proliferation. Current strategies that target EGFR often block activation of the protein receptor after the gene has been transcribed, spliced, translated and sorted to the membrane, possibly too late. A novel approach is to target the EGFR oncogene at the pre-mRNA processing level. Our strategy is to modify the EGFR pre-mRNA transcript by delivering the genetic sequences of a pre-*trans* splicing molecule (PTM) with an immunogenic potential. In the current project, we have designed an immunogenic PTM engineered to splice into a region of the EGFR pre-mRNA transcript, deactivating the growth signal. Two immunogens, one derived from the Human Adenovirus serotype 5 pentose fiber (Ad5-fiber) and one derived from the human cytokine, interleukin-13Rα1-2 were evaluated in the literature for their immunogenic potential. Upon delivery, the hybrid immunogen-PTM would be expressed into the tumor microenvironment. In a future animal model, it is expected that this would re-activate the immune system to the GBM cells expressing the interleukin peptide or the exogeneous Ad5-fiber. This combination may function synergistically with the PTM as a more effective anti-GBM tumor strategy.

USING ESSENTIAL OILS TO COMBAT THE THREAT OF MULTIDRUG RESISTANT BACTERIA, *PSEUDOMONAS AERUGINOSA*

Jenies Grullon

Department of Biology

Faculty Mentor: Dr. James P. Mack

ABSTRACT

The increased occurrence of multidrug resistant bacterial infections has developed to be a major threat in global healthcare settings due to the overuse of antibiotic treatments. The pace at which bacteria are acquiring this resistance is much faster than the development of new drugs to combat this threat. The purpose of our research was to determine if particular essential oils could be used as an alternative method to treat the multidrug resistant bacterium, *Pseudomonas aeruginosa.* Treatment of such infections with essential oils could make a major global impact on the survival of those who now live in underdeveloped countries with limited access to antibiotics. Through our research many essential oils were tested for their ability to inhibit the growth of *Pseudomonas aeruginosa.* Cinnamon Bark and Cassia essential oils were found to be the most effective. Methylglyoxal, the major component of Manuka honey, also had excellent results. Applying essential oils directly to the skin can cause irritation so for our research the essential oils and methylglyoxal were diluted with Lanolin and Jojoba oils to be used as an emollient for safer application. At the minimum inhibitory concentration (MIC) of these emollients their effectiveness in inhibiting *Pseudomonas aeruginosa* was found to be equal to or more than standard antibiotics that are currently used such as Amikacin and Tobramycin. Their MIC however, was not as effective as Ciproflaxin, which according to the U.S. Food and Drug Administration has many adverse side effects such as tendinitis and the possibility for permanent nerve damage. Combinations of essential oils and the antibiotic discs together were also tested but were not found to be more effective than the emollient combinations. The emollients we tested show great promise for their use in topically treating patients with *Pseudomonas aeruginosa* infection in healthcare settings worldwide.

EFFECTS OF mTOR UPREGULATION ON NEURAL DEVELOPMENT

Jamie Himmelreich

Department of Biology

Faculty Mentor: Dr. Cathryn Kubera

ABSTRACT

The mammalian target of rapamycin (mTOR) is an atypical serine/threonine protein kinase that is the central controller of many cellular activities including growth, proliferation, transcription, translation, differentiation, motility, and homeostasis, among others. More specifically, mTOR functions in processes that contribute to normal brain development such as neuronal differentiation, neurite arborization, and synaptic formation and carries out these processes based on signals from a variety of internal and external stimuli. Dysregulation of normal mTOR activity causes abnormal brain development and neural degeneration and is thus implicated in a variety of brain-related diseases including autism, epilepsy, and Alzheimer's, to name a few. Experience-induced and spontaneous elevations in intracellular calcium levels have also been shown to regulate various cell functions and control neural development and hence may be involved in brain-related diseases, as well.

No known previous experiments have assessed the relationship between mTOR and calcium specific to their combined effects on neural development. Hence, this study examines whether there is a connection between upregulated mTOR activity and calcium signaling by comparing the frequency and intensity of calcium spikes in neuro2a cells with artificially driven mTOR activity and non-manipulated cells. mTOR activity was upregulated in the experimental cells by transfecting them with a modified version of the upstream activator Rheb known as constitutively active (CA)-Rheb, which is a small GTPase signaling molecule that is fixed in an "on" state. This mechanism of activation phosphorylates the ribosomal protein S6, producing phospho S6 (pS6), which was used as an indicator of high mTOR activity. Both the experimental and control cells were transfected with the genetically encoded calcium sensor, GCaMP3, to visualize the calcium signals. Live calcium movies were then taken of random fields of a coverslip of both the experimental and control cells using a fluorescence microscope.

GHOST FISHING: IDENTIFICATION AND RETRIEVAL OF DERELICT CRAB POTS IN BARNEGAT BAY

Adam Iatesta

Department of Biology / Urban Coast Institute

Faculty Mentor: Professor James Nickels

ABSTRACT

In the past decade, the Barnegat Bay Estuary has become an area of intensified recreational and commercial fishing pressure on the local blue crab population. As a result, an increased amount of crab pots and traps have been dispersed throughout the region. In combination with the dynamic nature of the bay characterized by heavy boat traffic, strong bottom currents, seasonal icing, and susceptibility to storm impacts, this may increase the quantity of fishing gear that is lost or damaged each year. “Ghost fishing” occurs when this gear remains in the environment and continues to trap organisms. The objective of this project was to mitigate the impacts that the marine debris has on the region. These negative effects include the death of many marine organisms, an economic loss to the fishing industry, negative impacts to human health, and a navigational hazard for boaters. In order to identify and remove these traps, Monmouth University surveyed the northern sector of the bay using side sonar equipment to detect probable derelict gear locations, and then returned on separate occasions to retrieve the gear. A map was created using ArcGIS software in order to summarize and display these results. The removal of the derelict gear will decrease the risks associated with ghost fishing. In combination with similar datasets from partner organizations, the results will generate estimates to better inform managers of the severity and scope of this issue in Barnegat Bay.

EXPRESSION OF VARIOUS GENES FOLLOWING UPREGULATION OF mTOR ACTIVITY BY CONSTITUTIVELY ACTIVE Rheb

Emily Lucas

Department of Biology

Faculty Mentor: Dr. Cathryn Kubera

ABSTRACT

The mammalian target of rapamycin (mTOR) is a highly conserved serine and threonine kinase in the cell which has an important role on many cellular activities including translation, homeostasis, cellular growth and proliferation. It has been recently shown that the regulation of mTOR can play a critical role in the expression of various different genes with in the cell. When mTOR is stimulated by a small ribosomal G protein Rheb, the signaling pathway is activated and cellular growth and proliferation occurs. Making Rheb constitutively active (CA-Rheb) by introduction of a mutation (S16H) causes mTOR to be constantly activated, and the activity of the cell is drastically altered. In our research, we use human derived A172 glioblastoma cells to examine the effect that the upregulation of mTOR has on different signaling genes surrounding the mTOR pathway. Primers specific for eight different genes were used to probe mRNA expression levels in A172 cells transfected with CA-Reb using RT-PCR and qPCR. A172 cells showed varying levels of expression in these genes when mTOR was upregulated.

STATISTICAL ANALYSIS AND MODELING OF TKR LEVELS IN GLIOBLASTOMA CELLS

Danielle Melillo and Natalie Toro

Department of Biology

Faculty Mentor: Dr. Martin J. Hicks

ABSTRACT

Since RNA has multiple involvements in many cell properties, it is important to study RNA and its contributions towards different diseases, such as cancer. One cancer, specifically, is Glioblastoma, which is a stage 4 brain cancer. The existing treatment for this type of cancer is limited to chemotherapy, resection, and radiation. This experiment is an introduction to gene therapy where a gene encoding an RNA that alters the Tyrosine Kinase Receptor (TKR) expression is transferred and blocks the activation of the TKR growth.

In conjunction with data collected from Dr. Hicks' lab, the levels of TKR in cells that underwent no treatment, control treatment, or Dr. Hicks' gene therapy treatment will be analyzed. Tests ran included ANOVA, Planned Comparisons, and the non-parametric Kruskall-Wallis test. Each test performed yielded significant results stating that the levels of TKR in Dr. Hicks' gene therapy were, in fact, different than those of no treatment and control treatment. This allowed Dr. Hicks to continue with real time PCR tests. Going forward, piecewise linear regression will be used on the results of the real time PCR to determine where the threshold is for each of the three different treatments, and then compare the thresholds between treatments.

EFFECTS OF ALCOHOL AND CAFFEINE ON LIPID RAFT-ASSOCIATED RECEPTORS WITHIN THE ADOLESCENT BRAIN

Calliope O'Shea, Marisa Paolella and Marta Telatin

Department of Biology

Faculty Mentor: Dr. Dennis Rhoads

ABSTRACT

Co-consumption of alcohol with stimulants such as caffeine and amphetamine has become increasingly prevalent, particularly among students prone to binge drinking. Based on behavioral studies of adolescent Long-Evans rats, caffeine and amphetamine each appeared to have a "masking" effect against alcohol withdrawal symptoms, which in people might lessen the awareness of growing dependence on alcohol. Our lab is interested in the effects of alcohol and stimulants on the pattern of receptor protein expression in the adolescent brain. Recent work has shown that alcohol alters the levels of several different brain receptors including dopamine D1, adenosine A1, and the AMPA and NMDA glutamate receptors. Lipid rafts are less fluid regions in the cell membrane, allowing for certain receptors and proteins to be fixed in a mutual location. In turn, the common localization of receptors in lipid rafts provides a potential mechanism for associated proteins to interact more efficiently. Rafts may also serve as a common target for alcohol and stimulants. Detergent resistant membrane fragments (presumed lipid rafts) were isolated following solubilization of selected brain regions in Triton X-100 and 18 hours of ultracentrifugation in a discontinuous sucrose gradient. Western blotting was used to identify the raft "marker" protein flotilin and thus to confirm successful isolation of lipid rafts from the membrane fractions. Additionally, Western blotting confirmed the presence of two important targets of alcohol, dopamine D1 and NMDA receptors within the lipid rafts. This sets the stage for studying the role of lipid rafts in the brain's responses to alcohol and caffeine. Our goal is to better understand the adolescent brain, its response to alcohol and stimulants, and the important 'masking' effects that stimulants may have on the consequences of alcohol abuse.

DESIGN OF A GENE TRANSFER VECTOR TO DELIVER A STABILIZED anti-EGFR RNA APTAMER TO THE GLIOBLASTOMA MICROENVIRONMENT

Sachin Parikh

Department of Biology

Faculty Mentor: Dr. Martin J. Hicks

ABSTRACT

Glioblastoma multiforme (GBM) is an incurable and aggressive type of brain tumor. It is the most common central nervous system (CNS) malignancy with a median survival of only 14 months. The epidermal growth factor receptor (EGFR) is a type of tyrosine kinase receptor (TKR) dysregulated in about 40% of GBM tumors. EGFR amplification and over-expression leads to angiogenesis and uncontrolled growth and proliferation of GBM. Although a great deal is known about the biology exhibited by EGFR-activated GBM, the application of therapies against the biologic processes is limited by the blood-brain barrier, which restricts systemically administered therapies from reaching the brain. We are creating an *in vivo* tissue culture model to develop a novel strategy to bypass these barriers by developing a gene transfer vector to deliver the genetic sequences of a known anti-EGFR RNA therapy aptamer that binds with high affinity against EGFR. In this approach, we will use a gene transfer system to modify GBM and CNS cells to express the therapeutic anti-cancer RNA aptamer molecule, and using an extracellular RNA "exRNA" localization element, the RNA aptamer will be transported and spread throughout the tumor microenvironment where EGFR is abundant. In addition, we have added an RNA structural element (an inactivated hammerhead ribozyme) important for the stabilization of the RNA therapeutic molecule.

MicroRNA EXPRESSION FOLLOWING LIPOPOLYSACCHARIDE-INDUCED INFLAMMATION OF RAT TESTIS

Mitchell I. Parker

Department of Biology

Faculty Mentor: Dr. Michael A. Palladino

ABSTRACT

MicroRNAs (miRNAs) are a group of small RNA molecules that do not encode for proteins. Instead, they regulate gene expression. Reproductive biologists are interested in miRNAs because proper expression of these molecules has been linked to normal testis development and spermatogenesis, while atypical expression of certain miRNAs has been implicated in testicular cancer formation and male infertility. Our lab is interested in how miRNAs may be involved in defending the male reproductive tract from infection and the response to inflammation. We hypothesized that control of gene expression by miRNAs plays a significant role in the antimicrobial protection of rat testis and the response to inflammation. The objective of this study was to identify inflammatory-related miRNAs (miRNAs that regulate inflammatory genes) that are up-regulated and/or down-regulated following lipopolysaccharide (LPS)-induced inflammation of rat testis. A Qiagen Rat Inflammatory Response & Autoimmunity miRNA PCR Array (MIRN-105Z) was used to evaluate expression of 84 inflammatory-related miRNAs. Testis total RNA was purified from retired Sprague-Dawley breeder rats that were sacrificed 3 or 6 hours after receiving a 5 mg/kg injection of LPS (n=4) or saline (n=2), and examined by quantitative real-time polymerase chain reaction (qPCR). Results showed 5 inflammatory-related miRNAs with a greater than 2 fold down-regulation (p<0.05) in rats from the 3h group, and 5 inflammatory-related miRNAs with a greater than 2 fold down-regulation (p<0.05) in rats from the 6h group. Review of the literature has revealed that these miRNAs also play major roles in the maintenance of fertility, formation and elimination of cancer, and development of the male reproductive tract. Further study of these miRNAs, and their roles in male reproductive tissues, might lead to advanced therapeutics for treatment, novel biomarkers for detection, and a greater understanding of male reproduction and related health issues.

GENETIC DELIVERY OF A miRNA CLUSTER WITH POLYCISTRONIC siRNAs REDUCES mRNA EXPRESSION OF EPIDERMAL GROWTH FACTOR RECEPTOR IN HUMAN GLIOBLASTOMA CELLS.

Imari Patel[1] and Zainab Faiz[2]
[1]Drexel University, [2]Monmouth University

Department of Biology

Faculty Mentor: Dr. Martin J. Hicks

ABSTRACT

Glioblastoma multiforme (GBM), the most common central nervous system malignancy, is clinically documented as a grade IV astrocytoma. Therefore GBM is one of the most rapidly growing and invasive types of glial tumors of the central nervous system. The standard therapy includes surgical removal, radiation, and chemotherapy with a survival rate of about one year. In addition, systemic therapies are limited by the blood-brain barrier. To bypass the barrier, we are constructing a delivery strategy that inhibits the gene expression of tyrosine kinase receptors (TKR), which are commonly upregulated in GBM. One TKR, epidermal growth factor receptor (EGFR), is overexpressed in GBM leading to uncontrolled growth and proliferation. Our approach is to enlist the RNA interference pathway. Although small interfering RNAs (siRNAs) are often utilized to silence gene expression, exogenously expressed siRNAs are not an effective strategy to treat human disease due to both extracellular and intracellular nucleases as well as activation of cellular immunity against foreign nucleic acids. To bypass these degradatory mechanisms, we are using a natural miRNA cluster genetic background to effectively deliver the DNA encoding multiple anti-EGFR siRNAs by cloning them into the structure of the miRNA cluster, miR-17-92. The anti-EGFR polycistronic miRNA cluster (pAAV-miR-IP1) expresses six siRNAs directed against EGFR specifically targeting the extracellular ligand binding domain, transmembrane domain, intracellular tyrosine kinase domain and 3' untranslated region of the EGFR gene. The therapy vector, pAAV-miR-IP1, was transfected into the human GBM cell line, A172. Results show that pAAV-miR-IP1 was expressed at high levels in the A172 cell line with a subsequent reduction in EGFR mRNA expression. Future strategies include using the polycistronic delivery mechanism to target multiple TKRs in addition to EGFR.

RNA MULTIFUNCTIONAL ANTISENSE GENE TRANSFER STRATEGY TO ALTER HGFR EXPRESSION IN GBM

Priyal Patel

Department of Biology

Faculty Mentor: Dr. Martin J. Hicks

ABSTRACT

The most common central nervous system malignancy is glioblastoma multiforme (GBM). The aggressive tumor spreads rapidly migrating through the white matter of the brain. Current therapy includes surgical removal, radiation and chemotherapy extending survival to about 14 months. Furthermore, the blood-brain barrier is a challenge to direct therapy into the central nervous system (CNS). To bypass this barrier, our research is to develop a novel gene transfer vector to deliver the DNA encoding an antisense RNA (ASR) to alter the splicing pattern of the hepatocyte growth factor receptor (HGFR) within the tumor microenvironment. In this approach, the ASR blocks recognition of splice sites and splicing enhancers. The current strategy targets the splicing of exons 11 to12 of the HGFR pre-mRNA transcript. Blockage of this splicing event leads to retention of intron 11. Because this intron includes 14 intronic alternative polyadenylation (IPA) signals, there is great potential to generate a shortened transcript and its subsequent soluble therapeutic HGFR decoy peptide. A 1st generation construct containing an antisense with a human U7 snRNA was transfected into human glioblastoma cell lines, A172 and U87MG. The 1st generation therapy was successfully expressed in transfected cell lines. To optimize therapeutic efficiency, we have designed a 2nd generation gene transfer construct with multiple elements with distinct functions. These include the ASR with an hnRNPA1 splicing inhibitory element and an sm-Opt U7snRNA (sm-Opt/U7) localization signal with the novel tertiary ‘kiss domain’. The ASR targets the 5’ splice site of Exon 11, the sm-Opt/U7 signal stabilizes and directs the ASR into the spliceosome of the nucleus, the hnRNPA1 tail blocks the splicing machinery and the ‘kiss domain’ stabilizes tertiary structure of the therapy vector. The new design makes use of the U7 promoter and 3’ transcription termination element to allow more efficient transcription. Using the 1st generation therapy vector we have developed assays to measure efficiency of therapy vector delivery, as well as levels of pre-mRNA and spliced HGFR transcript. In the next steps, we are delivering the 2nd generation therapy vector to measure the efficacy to increase the abundance of shortened transcript and reduction of full length HGFR in the GBM cells. Real-time polymerase chain reaction (RT-PCR) and ELISA will be used to determine the ratios of the pre-mRNA, mRNA and decoy in the cell and in the media.

THE ROLE OF $GABA_A$ RECEPTORS WITHIN *PARAMECIUM CAUDATUM*

Jessica Stanton

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Faculty Mentor: Dr. Cathryn Kubera

ABSTRACT

Paramecium caudatum is a type of unicellular eukaryote primarily found in marine and freshwater environments, with bodies that are covered in minute hair structures called cilia. These cilia are the primary means by which *P. caudatum* are able to move and feed. The ciliary beat of *P. caudatum*, consisting of an effective stroke and a recovery stroke, controls locomotion. These strokes propel the Paramecium through the water as it spirals. If Paramecia encounter an obstacle, the ciliary action is reversed and the organism begins swimming backward. It has previously been shown that ciliary reversal is influenced by GABA and calcium signaling in *Paramecium primaurelia* (Ramoino, 2003).

GABA is the primary inhibitory neurotransmitter within the mammalian central nervous system as well as a signaling molecule responsible for neuronal precursor proliferation, neuronal migration and differentiation, and the formation of neuronal networks. $GABA_A$ receptors are a type of GABA receptor created from a possible 21 subunits, but typically consisting of an α, β, and γ_2 subunit. $GABA_A$ receptors have also been illustrated to impact the calcium content within cerebellar granule cell pre-cursors as a result of depolarization (Dave, 2009)

The primary purpose of this study is to not only identify that $GABA_A$ receptor subunits are present within *P. caudatum*, but also to explore the effect that manipulation of these receptors has on the organism's locomotion through the use of calcium imaging. The desired result of this study is to be able to support the hypothesis that there is an evolutionary conservation of the $GABA_A$ receptor role within eukaryotic species – to illustrate that the $GABA_A$ receptors influence calcium levels within the organism similarly to higher level eukaryotes and, as a result, have an effect on the organism's ciliary beat and ciliary reversal.

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DETERMINATION OF THE EBOLA VIRUS 5′-UTR SECONDARY STRUCTURE

Stephan Andersen

Department of Chemistry and Physics

Faculty Mentor: Dr. Jonathan Ouellet

ABSTRACT

Ebola is a single stranded RNA virus that has affected about 28,000 people since last year, mostly in North West African countries. The outbreaks in Africa are getting under control but without a current vaccine or an established method of treatment for Ebola, it is only a matter of time until the next outbreak.

Like any other RNA strands of genetic material, Ebola's RNA genome consists of coding regions and non-coding regions. The coding regions encode for the proteins of the virus, which are structural and non-structural (such as enzymes). The non-coding regions on the virus, which are located at the 5′- and 3′-ends of the RNA, are responsible for the maintenance and replication regulation of the virus. These untranslated regions (UTR) fold into a secondary structure independently from the coding regions.

Determining the secondary structures at the 5′-end is the goal of this project. Ebola UTRs have specific secondary structure features such as base-paired stems and single-stranded regions. To determine RNA secondary structure, Selective 2′-Hydroxyl Acylation analyzed by Primer Extension (SHAPE) experiment that partially acylates the single stranded areas of the RNA has been shown to be effective.

A consensus sequence of the first 80 nucleotides was determined out of 160 Ebola sequenced genomes. DNA oligonucleotides were purchased and amplified through PCR and transcribed. The RNA includes an extra sequence where a fluorescent primer can bind for reverse transcription initiation.

The next step is to perform the SHAPE experiment to determine the RNA secondary structure of the 5′-UTR. The following step of the project will be to perform SHAPE on a non-consensus Ebola UTR sequence to compare the structures. Moreover, incubation of the RNA with cell extracts before the SHAPE experiment may be envisaged to monitor potential protein binding to the Ebola 5′-UTR.

COLLECTION AND ANALYSIS OF PHYSICO-CHEMICAL PARAMETERS OF WATER FOR ASSESSMENT OF INTERTIDAL COASTAL ECOSYSTEMS

Crystal Diaz

Department of Chemistry and Physics / Department of Biology

Faculty Mentors: Dr. Dmytro Kosenkov / Dr. Pedram Daneshgar

ABSTRACT

Atmospheric warming has the potential to cause evident change in the salinity of seawater, due to evaporative loss of surface waters. Much marine life live within a certain salinity range and any significant changes can cause them to migrate elsewhere, causing invasive species in marine ecosystems, or even succumb to the changes in their environment. Mangrove and coastal ecosystems can also be impacted. These ecosystems are important to humans and Earth for various reasons including: nutrient cycling, gas and climate regulation, and bioremediation of waste. The first step in preserving these ecosystems is to understand how any changes can negatively affect them. Hence, the goal of this project is to assess how global warming is affecting the salinity of intertidal coastal ecosystems.

The experiment is being carried out using a data station assembled with both temperature and salinity probes to obtain data for about 20-40 hours. This information will be stored in a database for further analysis. The experiment is first being executed in a laboratory setting using dilutions of salt water made from a stock solution. Different environments will be stimulated in the lab such as increasing temperatures and recording salinity as it cools and also recording salinity evaporating solution over time. Once the experiment is tested and finalized in the laboratory it will then be performed in a green house and left over night to collect data. My hypothesis is that the results will show an increase in overall salinity and a correlation will be made between increase salinity and atmospheric warming.

SYNTHESIS and DNA BINDING of NOVEL Pd-(II) CURCUMINOIDS

Kristen Flynn, Mary Easop and Stephanie Bellinger-Buckley

Department of Chemistry and Physics

Faculty Mentors: Dr. Jonathan J. Rochford and Dr. Massimiliano Lamberto

ABSTRACT

Over the past 20 years the reverse transcriptase enzyme telomerase has become a very important target in the development of novel anticancer therapeutics due to its over-expression in 80-85% of cancer cell types. One of the strategies used for telomerase inhibition involves the folding of telomeric DNA into stable G-Quadruplex structures by small molecules. We here report the synthesis of novel Pd (II) curcuminoid complexes and their preliminary binding studies to telomeric DNA. These molecules represent a very promising class of potential anticancer drugs.

MODELING SELECTIVITY OF BINDING OF POLYCYCLIC AROMATIC LIGANDS TO DNA

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Faculty Mentors: Dr. Dmytro Kosenkov and Dr. Massimiliano Lamberto

ABSTRACT

The binding of organic ligands to telomeric G-quadruplex DNA (gqDNA) may acts as an anti-cancer therapy. While some molecules are known to bind and stabilize this gqDNA structure, when placed into an environment that contains double stranded DNA (dsDNA), the binding tends to favor dsDNA as opposed to gqDNA structure leading to toxic effects. A higher binding affinity to the dsDNA may affect gene replication depending on the place of binding.
The modeling presented here has been to test the relative affinities (binding energies) of DNA-ligand binding in order to establish the ligand structure that will provide the best selectivity for gqDNA. In order to correctly assess this, several computational trials have been conducted using various methodologies (e.g., molecular docking, molecular dynamics simulations) with the purpose of simulating a natural molecular environment. This work is focused on the testing of the interactions of recently synthesized polycyclic aromatic ligands including: two naphthalene diimide ligands, 9-[4-(N,N-dimethylamino)phenylamino]-3,6-bis(3-pyrrolodinopropionamido) acridine[1] and a quinone methide ligand[2].

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ISOLATION AND SEQUENCING OF AN APTAMER

Krima Patel

Department of Chemistry and Physics

Faculty Mentor: Dr. Jonathan Ouellet

ABSTRACT

There are many current treatments for cancer such as chemotherapy but they entail numerous side effects. With my project, the ultimate long term goal is to develop a cancer-specific therapy for cancer cells using RNA. This particular type of RNA that binds to a small molecule is known as an aptamer. An aptamer targets a specific molecule which, in this case, is 2-hydroxyglutarate found strictly in myelogenous leukemia and gliomas.

Two years ago I started my project and I have been able to develop a pool of aptamers that bind the oncometabolite, 2-HG. In the past three months, I have learned the molecular biology techniques to isolate and sequence the most effective aptamers which involved cloning the pool of aptamers. Cloning is a technique that will be used to effectively isolate the individual aptamers. Then, the individual aptamers will be transcribed and assayed for 2-HG binding. As a short term goal for my project, I will be able to sequence the most effective aptamers and perform bioinformatics analysis.

Next, the designed aptamer will be used to make a riboswitch to control gene expression. With numerous clinical trials, the goal is to develop the sequenced aptamers into a riboswitch which would act as a biosensor for 2-HG, allowing early cancer detection. With early cancer detection, this project may be a new platform for developing new treatments for cancer patients.

DESIGN OF A NOVEL ANALOG OF TAXOL (PACLITAXEL)

Anjali Prajapati and Krima Patel

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ABSTRACT

Taxol (Paclitaxel) is a very effective drug that is used throughout the world as an anticancer agent. This particular drug is isolated from the yew tree. It accelerates tubulin polymerization and stabilizes microtubules. Tubulin is a protein found within microtubules that is essential for cell division and is made up of two separate proteins. Paclitaxel binds specifically to the beta-subunit of tubulin. Also, Taxol binds to tubulin using the side chain, acetyl, benzoyl, and oxetane groups, making them the most important binding sites. Furthermore, by stabilizing microtubules, cell division cycle is stopped. The design and synthesis of a novel paclitaxel drug analog will be presented and discussed.

EXCITON ENERGY TRANSFER IN LIGHT HARVESTING PROTEINS WITH COVALENTLY BOUND PIGMENTS: THE ROLE OF ELECTRONIC COUPLING

Brittany Reed, Michael DeFilippo and Danielle Valdez

Department of Chemistry and Physics

Faculty Mentor: Dr. Dmytro Kosenkov

ABSTRACT

In today's field of scientific research, the desire for the advancement in solar cell technology has grown exponentially. Through the use of solar cell technology natural energy, such as sunlight, can be converted into other functional forms of energy. The main goal of this research is to find a way to develop more efficient solar cells through the use of different computational methods.

Our research has focused on specific photosynthetic light-harvesting complexes, such as the Fenna-Matthews-Olson (FMO) protein complex, the Peridinin Chlorophyll Protein (PCP) complex, and cryptophyte algae molecular species Phycoerythrin 545 (PE545) and Phycocyanin 645 (PC645). These protein complexes are being studied because of their ability in absorbing natural light, making use of this energy, and ultimately transferring this energy to the chlorophyll molecules making up the complex.

In this scientific study, the protein fragments making up these light-harvesting complexes were first modeled in ArgusLab software. The computational program Gaussian09 was then used to obtain the UV-Vis spectra at the wB97xD/6-31+G* level of theory, ultimately allowing the molecule's excited states to be determined. Finally, using a custom PyFREC program implementing the Förster theory, the isolated proteins and excited energy states were analyzed to determine the coupling energy between the different molecular fragments of each respective light harvesting complex.

It is concluded that the strength of coupling between molecular fragments in these light-harvesting complexes increases as distance decreases and depends on their mutual orientation. The delocalization of the electronic excited states of separate fragments was also observed. Further investigations of the molecular dynamics for the different light-harvesting complexes are needed to develop more efficient types of solar cells.

ACARBOSE ANALOGS AS NOVEL TREATMENT METHODS FOR TYPE 2 DIABETES

Angela Russell and Shreeja Kadakia

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Faculty Mentor: Dr. Massimiliano Lamberto

ABSTRACT

For our project, we focused on medications for Type 2 diabetes. There are eight different classes of medications that are currently available in the American market. The class of medications we chose to focus on was Alpha-glucosidase inhibitors, because these medications do not increase cellular insulin secretion and prevent weight gain effects that other medications have, which may lead to increased risks of cardiovascular disease and various other side effects. For our project, we will modify the structure so that we can change the functional group that interacts with two major digestive enzymes: alpha amylase and alpha-glucoside hydrolase. This will be done so as to increase the affinity and consequently, the binding of the drug to the enzymes. We will also examine how modifications give rise to or diminish other side effects by analyzing how the analog would interact with the other enzymes that it does not directly impact.

ROLE OF MICROPLASTICS ON THE BIOGEOCHEMISTRY OF HEAVY METAL(LOID)S IN THE AQUATIC SYSTEM

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Faculty Mentor: Dr. Tsananguraayi Tongesayi

ABSTRACT

One of the principal sources of water contamination is wastewater; a combined flow of raw sewage, industrial and commercial effluents, and storm water. Among its slew of contaminants are microplastics, a class of pollutants which is emerging as one of the major water quality challenges of this century. Microplastics are comprised of (i) synthetic polymer products manufactured as additives in various consumer products such as hand, facial, and body cleansers; (ii) small pieces from degrading industrial and domestic polymer products; (iii) polymeric fibers released by washing of synthetic clothing and plastic abrasion during dishwashing; and (iv) preproduction pellets that are used in plastic production. They occur in various shapes that include spheres, fibers, and fragments, and enter the aquatic environment primarily via improper waste disposal, insufficient waste management, and urban runoffs. In addition to being pollutants, microplastics adsorb other chemical pollutants and harbor pathogenic organisms which they then distribute widely within the aquatic system thanks to their water-buoyancy, chemical inertness, and durability. As a result, microplastics can introduce pathogenic organisms and chemical toxicants from wastewater to freshwater and marine habitats. By adsorbing chemical pollutants and microorganisms on their surfaces, mircoplastics can influence the biogeochemistry of metal(loid)s and hence can alter the speciation, mobility, bioavailability, and toxicity of the chemical pollutants in water. One of the major goals of this study is to study the role of microplastics on the biogeochemistry and speciation of toxic chemical species in the aquatic environment.

MONITORING GENE EXPRESSION VIA FLUORESCENCE MODULATED BY A RIBOSWITCH

James Tilton

Department of Chemistry and Physics

Faculty Mentor: Dr. Jonathan Ouellet

ABSTRACT

My main focus of research is to develop a plasmid system that would act as a biosensor for theophylline. Theophylline is a small molecule used as a bronchodilator in inhalers for treatment of asthma. More importantly with the laboratory main end-goals, an aptamer has been developed and often used as a proof of concept for theophylline. The RNA that binds tightly and specifically (aptamer) binds 10,000 times more to theophylline than to caffeine, even though they differ in structure by only one methyl group. In order to know if the RNA has bound to theophylline, an expression platform needs to be paired with the aptamer (riboswitch) to see on/off modulation of gene expression with florescence.

Through molecular cloning, PCR, and bioengineering, a riboswitch known to bind to theophylline was inserted into a plasmid between mCherry and GFP genes. The final cloned plasmid consists of a single promoter, mCherry gene, riboswitch and the GFP gene. In such system, mCherry is constitutively expressed in the bacteria while GFP should be expressed only in the presence of theophylline. This allows for measuring fluorescence ratio gene expression of mCherry vs. GFP and we can see the effectiveness of the riboswitch as a biosensor.

In the future, new biosensors can be made by replacing this riboswitch by other aptamers such as glucose or 2-hydroyglutarate (2-HG) also being researched by the Ouellet lab.

As a side project, I have been working to find an acrylamide gel stain to measure by densitometry the cleavage of DNA fragments without the use of radiation. This is useful for many institutions that wish to follow nucleic acid cleavage kinetics without radiolabeling. The model DNA is intended to self-cleave in the presence of zinc into fragments of 14 and 51 nt; visualized with different sensitivities under different stains.

ANALYSIS OF ELECTRONIC EXCITED STATES OF SOLVATOCHROMIC DYES IN SOLVENTS OF VARYING POLARITY

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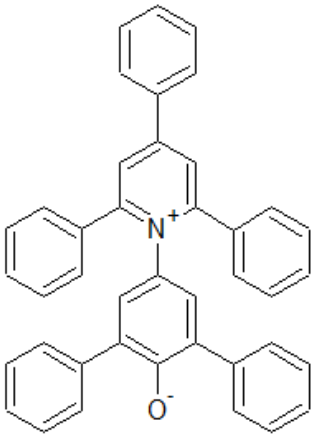
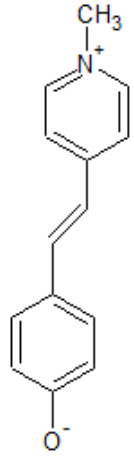
Faculty Mentor: Dr. Dmytro Kosenkov

ABSTRACT

The investigation of electronic excitations in condensed phase is important for understanding of fundamental mechanisms of the excitation energy transfer in artificial and natural photochemical systems. Pyridinium N-phenolate betadine dyes, such as Reichardt's betaine[1] and Brooker's merocyanine[1] are highly sensitive molecular probes frequently used as empirical indicators for solvent polarity. This solvatochromic behavior of the dyes was examined with UV-Vis spectroscopy and the density functional theory. The solvatochromic behavior of these molecules was investigated in solvents of varying polarity, ranging from nonpolar (e.g. dioxane) to polar (e.g. water) solvents using polarizable continuum and explicit solvent models.



Dye 1. 2,6-Diphenyl-4-(2,4,6-triphenyl-1-pyridinio) phenolate



Dye 2. 4-[(1-methyl-4(1H)-pyridinylidene) ethylidene]-2,5-cyclohexadien-1-one

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DEPARTMENT OF
COMPUTER SCIENCE AND SOFTWARE ENGINEERING

BUILD A STORY

Peter Camamis

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ABSTRACT

As more and more parents struggle to provide for their children, they frequently take on jobs and cannot always be around for their children. *Build a Story* was created to help connect remote parents with their young ones. In addition to providing an application to author interactive bedtime stories, the results may be shared remotely with the community of parents, including interactive feedback to give the author a sense of satisfaction. Authors may build their stories including associated media capable of attaching to words during composition. Formal documentations and methods have been processed including task estimations and wireframes. The application is written in Swift 2.2 for iOS 8+ and in particular for iPad tablet computers. It uses Amazon Web Services for network capabilities. Amazon services used are Cognito for authentication, DynamoDB for remote data storage, S3 for remote associated media, Route 53 for internet infrastructure and SNS for mobile notifications. Service analytics are powered by Crashlytics providing crash reporting, mobile analytics, mobile identity as well as growth, monetization, infrastructure and UX analysis.

SWARM SIMULATION

Philip DiMarco

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ABSTRACT

From birds, and fish to ants and bees, swarming plays a critical role in how animals interact and live. The emergent behavior that results from swarming allows complex problems to be solved without any centralized control structure. Swarming, as it applies to control of groups of robots is particularly exciting. This research focused on the simulation of multi agent systems, where the movement of each agent is determined by the surrounding local environment. Stated in a more concrete way, we can think about this problem space as consisting of a group of lawn mowers trying to cut the entire area of a lawn, where each lawn mower is locally attracted to high grass, and its movement is determined by the relative positions of all surrounding lawn mowers. The behaviors of these lawn mowers is designed to mimic the behavior of herds of sheep.

Each swarm member operates on the following principles:

1. Every agent can sense the relative distance and angle of all other agents around it.
2. Agents are able to coordinate their movement through the use of an attraction/repulsion force (attraction over far distances, repulsion over short distances, 0 at some equilibrium point).
3. Agents are attracted to high grass.

The combination of attraction/repulsion forces and attraction to high grass allow the agents to move as a swarm and cut the entire area of a lawn.

The research performed here examines various functional mechanisms for computing attractive and repulsive forces, the resultant behaviors dictated by how forces are computed, and the efficiency of the swarm in mowing a lawn.

XERCISE FITNESS

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ABSTRACT

Xercise Fitness is a personalized fitness iOS application offering users a fully immersive personal health experience. There are two main focuses for the Xercise Fitness application, and they involve exercises/workouts and macronutrients. The main feature of the application consists of the ability to randomly generate a single exercise or entire workout for the user based on two simple criteria, a main muscle group and a sub muscle group. Personalization is another key feature for Xercise Fitness, so users have the ability to create, save, and share their own personal exercises/workouts or those created by other users. Finally, users can track their own macronutrients including carbohydrates, fats, and proteins. They are also provided with the ability to set a goal, track a running total, and see their progress for the day compared to the goal they set for themselves. The objective was to target a wide range of users, those who may need a jumpstart in the gym, those who may be looking for something new in their workouts, or those who want to track a healthy lifestyle. The team followed agile software development practices in order to achieve the goals set for this project. Through agile development, the team incremented work through iterative sprints of planned work, which differs from the traditional functions of waterfall development. The group developed requirements specifications, detailed mock designs, a project management plan, and test documentation in order to facilitate the success of the application while in development. Thus far, our results from Xercise Fitness have directly correlated to the goals we set out to achieve. Making minor adjustments during the course of development, we never once steered away from the achievable goals that we set out to do in the start of the project.

AUTOMATED REPEATABLE RELEASABLE HOLDBACK BAR (AARHB) TEST FIXTURE IMMERSIVE UNITY OPERATIONAL/MAINTENANCE TRAINER

Jason Gaglione, Ryan Curto, Rich Allindogan and Christopher Mott

Department of Computer Science and Software Engineering

Faculty Mentor: Dr. Daniela Rosca

ABSTRACT

The project sponsor, supporter, and acquirer is the United States Navy. Prospective users will be United States Navy trainees. The purpose of the Automated Repeatable Releasable Holdback Bar (AARHB) Unity 3D project is to simulate the process of operating the AARHB in a virtual environment to serve as a virtual reality training simulator. We have created a simulation of the computer graphical user interface (GUI) to further simulate the actions that are done in the AARHB laboratory. The 3D simulation begins with the trainee being dropped into the AARHB testing fixture laboratory with the ability to walk around freely. The user will be able to walk up to the testing fixture, computer or any walls within the laboratory. During the Fall 2015 semester our team worked on documentation such as the Software Requirements Specification (SRS), Software Architecture Document (SAD) and Software Project Plan (SPP). We are in constant communication with the team (our client) at the naval base, making sure to keep them in the loop and understanding where we stand in the development of the simulation. During the Spring 2016 semester our team is participating in an agile process for our development phase.

Our agile process is broken down into two week sprints in which we dedicated each sprint to a specific aspect of the project. We planned out five two-week sprints which allows the whole team to look forward to a finished simulation on April 9th, 2016. We also use a System/Subsystem Design Description (SSDD) document to help organize our sprints and really understand what we wanted our end goal of each sprint to be.

ENHANCING NAMED-ENTITY RECOGNITION WITH DBpedia

Ramya Kalathingal and Maurani Saha

Department of Computer Science and Software Engineering

Faculty Mentor: Dr. Richard Scherl

ABSTRACT

We are using a state-of-the-art parser to process natural language texts such as news articles. The parser uses a named-entity recognizer to identify phrases as names of people, organizations, and locations. DBpedia is a semantically organized database that is automatically created from the structured content of Wikipedia. In accordance with the principles of the Semantic Web, DBpedia has an ontology that further categorizes people, organizations, and locations. By accessing the latest archives of DBpedia, we are experimenting with matching the named entities found in the text with those categorized by DBpedia to obtain a finer-grained categorization. For example, this technique allows us to identify people as scientists or politicians, and organizations as companies or universities. Our goal is to use this information to improve the performance of text clustering and classification methods.

A ROBOT TO IMPROVE SOCIAL SKILLS OF CHILDREN WITH AUTISM

Ramya Kalathingal, Maurani Saha, and Himabindu Yalamanchili, Teena Gopi and Swethana Gopisetti

Department of Computer Science and Software Engineering

Faculty Mentors: Dr. Patrizia Bonaventura and Dr. Richard Scherl

ABSTRACT

The presentation describes the first stage of a proposed research project on testing a zoomorphic robot as a therapy tool for children with autism. The diagnosis of Autism Spectrum Disorders (ASD) is currently on the rise, with 1 in 68 children currently affected by this disorder. ASD affects social communication and causes lack of appropriate social interaction of the children with their peers and caregivers, inability to decode and express emotions, lack of ability to communicate verbally, and aggressive behavior.

Interaction with robots has been shown to improve communication skills by children with autism, but issues related to ethical and social acceptability of these technological tools are still debated. Previous research on the most acceptable appearance of the robot shows that zoomorphic robots elicit better social interaction of the children with autism than human-like robots.

However, there are very few studies that have tested the robots with real ASD patients. The present exploratory research, which has not entered data collection, aims to bridge this gap and test the effect of a zoomorphic robot on verbal and non-verbal interaction with children with autism.

The poster reports the first stage of the research: the construction of a relatively simple robot using the inexpensive EV3 platform. The robot is programmed to move up to the child and say several sentences. An infrared sensor is used to calculate the exact position of the child, as the robot moves towards the child. The robot starts talking when the sensor indicates that the child is within a distance threshold.

The data to be gathered concerning the children's interaction with the robot will be important for increasing our understanding of ASD and developing better therapies. Future work will involve recording and analyzing the children's speech in response to the robot, and using a more sophisticated robot.

T-TRAIN: A TYPING PLATFORM COOPERATED WITH MULTI-DISCIPLINES

Lotachukwu E. Onwumelu and Yuxi Yang

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Faculty Mentor: Dr. Cui Yu

ABSTRACT

T-Train is a special typing platform that can be cooperated with multiple disciplines in the university. It provides functions to train typing, practice spelling, simulate flash-card learning, save and share writing, and even support cognitive exercises that involve reading (listening), understanding, remembering and repeating. It is a flexible platform that users can choose how to use for various needs. This project is an example demonstrating how a computer system can exploit simple tools and empower them with approaches and findings from multiple disciplines to become more useful. Take typing tools as the example; there are many typing programs available, but they mostly focus on typing training for positioning, accuracy and speed. In this project, we experiment to add elements from literature language (English) education, engaging-learning, social connection, cognitive neurology theory, and special needs therapy practices. This is the first version of implementation aiming to prove the concept. Future improvement will be forthcoming.

FEED

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ABSTRACT

The FEED system is a web application for gathering, organizing, and displaying of interests and ideas. Although a multitude of social media outlets exist that allow users to sort and share content, the goal of this application is to give them a private place to organize their many interests and ideas. The currently available systems can be used to store and organize content, but they often limit the type of content that users can store, lack multiple options for organization, and are based on social media concepts. The FEED system will match what we feel is an area where current software falls short.

Modern computer power users are assaulted with a variety of content (web pages, tweets, things to take note of, photos, videos, lyrics, documents, etc.). Users need to be able to return to information which they have saved in a quick and reliable manner. To solve this issue, we are proposing a system that:

- Saves all these types of items as well as associated metadata
- Provides natural methods of organizing and searching through these items

FEED lets users access their stored items across multiple views including a timeline view and a mind map view. While the timeline view helps users to quickly find items based on the time they were saved, the mind map view allows uses to organize items in a hierarchical format which is particularly useful for brainstorming new ideas.

The FEED system was developed at Monmouth University as a Software Engineering Practicum project during the fall 2015 and spring 2016 semesters. The system runs on an nginx/unicorn/postgres stack, using ansible to manage development, testing, staging, and deployment. The application was written in Ruby on Rails with a Bootstrap and AngularJS user interface. Agile development strategies and test-driven development methods were used throughout the project.

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ASSESSING THE SPATIAL DISTRIBUTION AND RECAPTURE RATE OF *MALACLEMYS TERRAPIN* ON ISLAND BEACH STATE PARK, NEW JERSEY

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Faculty Mentor: Dr. Richard Bastian

ABSTRACT

The focus of this study is to determine the spatial distribution and recapture rate of the diamondback terrapin, *Malaclemys terrapin*, on a barrier island in New Jersey. *M. terrapin* is not currently endangered in New Jersey but their population is threatened by humans and habitat destruction. There are few studies that estimate the abundance of terrapins in New Jersey. As a result, there are few regulations protecting the species.

Stephanie Egger, a wildlife biologist at the Conserve Wildlife Foundation of New Jersey, compiled data on terrapins that were captured on Sedge Island and marked with a tag daily during June, July, and August beginning in 2004 until the summer of 2015. The location, tag number, and whether the turtle was recaptured was recorded for each turtle. The recapture rates will be assessed between monthly and yearly to analyze the abundance of the terrapins. The location of recapture and distance traveled by individuals will also be assessed and taken into account.

ANALYSIS OF mTOR VIA CONSTITUTIVELY ACTIVE Rheb IN GRANULE-CELL PRECURSOR DEVELOPMENT

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ABSTRACT

In conjunction with Dr. Kubera of the Monmouth University Biology Department, data was collected after transfection of a Rheb plasmid. The Rheb plasmid activates the mammalian target of rapamycin (mTOR) cell cascade, which increases axon length and complexity in the development of granule-cell precursors (GCPs). Increased complexity leads to increased grey matter, which makes cerebral processing less efficient and has been linked to multiple sclerosis, Huntington's disease, Alzheimer's disease, and a variety of cancers. Cell complexity was quantified using Scholl analysis, which measures axon length of GCPs based on radii. 85 GCPs were measured at 3 and 5 days. GCP cells were grouped into Rheb plasmid and control (without plasmid). The sums of the dendrite lengths were taken and were compared to their respective controls and to each other. Analysis revealed that GCP complexity was significantly greater at the 5 day growth ($p=0.006$) and against the control and when comparing 3 and 5 day growth ($p<0.001$), using nonparametric analysis. An ANOVA revealed that there is statistical significance among the complexity of the four groupings ($p<0.001$), however an independent Kruskal-Wallis Test only demonstrated significantly greater complexity of GCPs between Rheb 3 and 5 day ($p<0.001$).

STATISTICS OF DENTAL PATHOLOGY IN DIFFERENT EGYPTIAN POPULATIONS

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ABSTRACT

Chelsea Cordle is a graduate student at Monmouth University studying archeology. Her thesis focuses on dental pathology in two ancient Egyptian populations. The two populations were sampled from two tombs in Abydos, Egypt. There was evidence that one tomb (OP 17) was of a lower class than the other (TC 20). She took samples of teeth from each population and took measurements of dental wear, calculus, caries, abscesses, and teeth lost ante-mortem. Based on the categorical data that was collected, Chi-squared tests were used to test for differences in proportions between the levels of each variable and between the two populations. Dental wear was found to have $p=0.477$ which means there is no significant difference between the populations. It was concluded that there was a difference in the percentage of teeth lost ante-mortem ($p=0.000$). The difference in severity of carries between the populations was insignificant with a $p=0.387$. There was no significant difference in the occurrence of calculus between the populations ($p=1.000$), however, there was a significant difference in severity of calculus between the populations ($p=0.026$). Since abscesses were collected as total counts for each population, only a non-statistical comparison between the two populations was done.

CAN WE DESIGN AN EXPERIMENT THAT WILL DETECT THE EXISTENCE OF A SALTWATER GRADIENT?

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ABSTRACT

A question was presented by Dr. Pedram Daneshgar of Monmouth University's Biology Department: How can we detect the existence of a saltwater gradient in at least three of seven mangrove tidal creeks on Cape Eleuthera Island, The Bahamas. Dr. Daneshgar hypothesized that water deeper into the creek (further from the mouth) will exhibit higher salinity values than water closer to the mouth. Since data is to be collected in the upcoming summer (2016), the focus of this project has been on data collection methods, as well as potential analyses to be performed, with the three following propositions: Mixed Model ANOVA, repeated measures ANCOVA, and regression. With various uncontrollable environmental factors to take into consideration, the type of analysis to be performed will vary according to the data that is eventually collected. To better predict what type of results may be found, data is currently being simulated, with the goal of producing data that will accurately represent what Dr. Daneshgar may come across in the Bahamas. The goal of these simulations is to validate the statistical differences in salinity values that the mangrove tidal creeks are expected to show.

THE STATISTICAL ANALYSIS OF THE EFFECTIVENESS OF ANTIBIOTICS ADMINISTERED CONTINUOUSLY VS. INTERMITTENTLY AT MAINTAINING BLOOD ANTIBIOTIC CONCENTRATIONS IN DOGS WITH SEPTIC PERITONITIS

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ABSTRACT

As multidrug resistant infections continue to become more apparent, it is essential for patients to receive a treatment that will cure them in an efficient manner. When treating a patient with beta-lactam antibiotics, it is important to examine the lowest concentration of antibiotic, also known as the minimum inhibitory concentration (MIC), needed to prevent overnight growth of bacteria. If the concentration of antibiotics in the blood drops below the MIC, the bacteria can flourish and become more antibiotic resistant. Dr. Stewart of Massachusetts Veterinary Referral Hospital initiated a study to determine the effectiveness of ampicillin-sulbactam as a continuous infusion versus intermittent injections on dogs with septic peritonitis. The traditional method of intermittent infusion shows spikes in the concentrations of antibiotics in the blood, which can often fall below the MIC. He hypothesized that by using a continuous infusion method; the concentration in the blood will be steadier, therefore, having a greater percentage of time above the MIC. This would result in a quicker recovery rate for the dogs suffering from this infection. The study is small as of now and the sample size will gradually increase as more dogs meet the qualifications. To statistically analyze the small data, the Mann Whitney nonparametric test will be used to compare the concentrations of antibiotics in the blood between the two groups since the data is not normally distributed. By averaging the hours above a given MIC level for each group, continuous versus intermittent, we can determine which group of dogs has a greater time above the MIC level also using the Mann Whitney test.

STATISTICAL ANALYSIS OF THE MONMOUTH UNIVERSITY VINEYARD'S GRAPE YIELD

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ABSTRACT

The purpose for growing a vineyard at Monmouth University was for student experience so that those studying plant biology can have the chance to learn about agriculture and cultivation first hand. The vineyard also provides the opportunity for research; students can engage in experimental design, data collection, and data analysis. The vineyard is comprised of four rows, with four blocks in each row. Each block contains six vines. The three grape varieties in the vineyard are Concord in row 1, Chambourcin in row 2, and Cayuga White in rows 3 and 4. These grape varieties were chosen for several reasons. Concord is a well-known variety, and can withstand environmental factors that other varieties may not be able to. Chambourcin grapes were chosen because this variety is growing in popularity in New Jersey. Cayuga White was chosen because of its popularity in neighboring New York State.

The current study seeks to find a trend in the data that will determine why some vines are more productive than others. The differences in grape yield (measured in pounds) will be compared between grape varieties, vine number, row number, and block. It is hypothesized that there will be a difference in grape yield between the variables; however, a specific difference was not predicted.

Descriptive statistics were analyzed, normality and equal variances were tested. To compare the difference in grape yield between variables, both ANOVA and Nonparametric tests were used. A difference in yield was found in the Chambourcin variety, in comparison to Concord ($p<.001$), and Cayuga White ($p<.001$). Similarly, row 2 was significantly different from row 1 ($p<.001$), row 3 ($p=.036$), and row 4 ($p=.001$). These results suggest that Chambourcin grapes are best suited for the vineyard, in order to maximize grape production, in comparison to Concord and Cayuga White.