



**Poster Session Abstracts
Undergraduate Category**



SCIENTISTA SYMPOSIUM 2017

UG-1

Increased scleroderma disease activity correlated with low education levels

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The link between education and disease is well documented in several cases in the medical community. Socioeconomic inequalities oftentimes lead to inadequate healthcare or follow-ups, lack of rehabilitation or multidisciplinary support because educational and social systems are crucial to the healing process. Scleroderma and systemic lupus erythematosus (SLE) are two autoimmune diseases in which the body's immune system mistakenly attacks healthy tissues in the body. The purpose of the current study was to demonstrate the potential relationship between education levels in patients with SLE or scleroderma and disease activity scores using validated measures. This research was conducted through the STOP Scleroderma and GW Lupus Study), biospecimen and data repositories approved by The George Washington University IRB (051427, 031614). 54 patients from STOP Scleroderma and 16 from the GW Lupus Study were included in this analysis. In the population of patients with lower education and scleroderma, there is a significantly higher patient and physician disease activity score. In the Medseger Severity Scale, the average report scores for high school, undergraduate, and post-graduate patients are 7.33 ± 5.56 , 4.11 ± 2.88 , and 2.61 ± 2.48 , respectively ($p = 0.0271$). Similarly, the mRSS physician scores for high school, undergraduate, and post-graduate patients are 19.33 ± 6.60 , 5.21 ± 3.64 and 5.00 ± 6.056 , respectively ($p = 0.0002$). Patient reported scores on the S-HAQ are 1.31 ± 0.753 , 0.305 ± 0.372 , and 0.331 ± 0.600 , respectively ($p = 0.0035$). We were able to show significance between lowered education levels and increased patient disease activity in individuals with scleroderma. The same phenomenon is not seen in patients with SLE. This suggests that individuals with a lower education level are less likely to have increased control over their disease outcomes and activity in scleroderma.



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UG-2

Improvements in clinical trials information will improve the reproductive health and fertility of cancer patients

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There are a number of barriers that result in cancer patients not being referred for oncofertility care which includes knowledge about reproductive risks of anti-neoplastic agents. Without this information, clinicians do not always make recommendations for oncofertility care. The objective of this study was to describe the level of reproductive information and recommendations that clinicians have available in clinical trial protocols regarding oncofertility management and follow up and the information that patients may receive in clinical trials patient information sheets or consent forms. A literature review of the 71 anti-neoplastic drugs included in the 68 clinical trials protocols showed that 68% of the anti-neoplastic drugs had gonadotoxic animal data, 32% had gonadotoxic human data, 83% had teratogenic animal data and 32% had teratogenic human data. When the clinical trials protocols were reviewed only 22% of the protocols reported the teratogenic risks and 32% of the protocols reported the gonadotoxic risk. Only 56% of Phase 3 protocols had gonadotoxic information and 13% of Phase 3 protocols had teratogenic information. 9% of the protocols provided fertility preservation recommendations and 4% provided reproductive information in the follow-up and survivorship period. 26% had a section in the clinical trials protocol which identified oncofertility information easily. When gonadotoxic and teratogenic effects of treatment were known they were not consistently included in the clinical trials protocols and the lack of data for new drugs was not reported. Very few protocols gave recommendations for oncofertility management and follow-up following the completion of cancer treatment. The research team proposes a number of recommendations that should be required for clinicians and pharmaceutical companies developing new trials.



SCIENTISTA SYMPOSIUM 2017

UG-3

Applying CRISPR/Cas9 to Identify Immunity-Associated Genes in Tomato

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This project focuses on immunity-associated genes in tomato to determine if they play a role in resistance to a bacterial pathogen. The expression of the two genes, which encode putative transporter proteins, was found to be induced when tomato leaves are exposed to specific virulence proteins expressed by the pathogen *Pseudomonas syringae* pv. *tomato*. The pathogen causes speck disease, which manifests as blemishes on tomato fruits and decreases yield thereby negatively impacting grower's profits. CRISPR/Cas9 technology was used to generate plants carrying mutations in each of the transporter genes to determine the effect of the mutations on resistance to *P. s.* pv. *tomato*. Specifically, DNA was extracted from each of 47 plants generated by CRISPR/Cas9 mutagenesis. The DNA was used for PCR amplification of each transporter gene and the PCR products were sequenced. The sequences were then compared to the wild type gene sequence to determine discrepancies indicative of a mutation and whether the mutations are homozygous or heterozygous. Plants with apparent mutations in the heterozygous state were analyzed further to determine if both alleles had distinct mutations or if a wild type allele was present. Additionally, notes were taken of any aberrant morphological phenotypes of the plants. Plants with a heterozygous mutation expressed a normal phenotype when one of the alleles present was wild type. If both alleles were mutated in the plant, this resulted in a stunted, 'boron-deficiency'-like phenotype. These results reveal a possible connection between a boron-deficiency phenotype and biallelic mutations in tomato. Future experiments will include disease assays to characterize the immune response of the transporter mutant plants to *P. pv. syringae*.



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UG-4

Evaluating and Upgrading a Fast Compact Laser Shutter Prototype

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In Atomic, Molecular and Optical (AMO) physics experiments, it is sometimes necessary to control the radiation that reaches molecules or atoms at specific times. Previous work has reported on different types of shutters, but there remains a demand for shutters that are inexpensive, fast, easy to replicate, produce little vibration on an optical table, and are capable of blocking high laser power. In 2015, Zhang *et al.* reported an inexpensive shutter design that meets all these requirements. Their shutter consisted of a body and a blade that were 3D printed as well as of a RC circuit and a DC motor that rotates the shutter's blade. We report additional performance data on the shutter described by Zhang *et al.* (2015). After making some small changes to the shutter, including the use of a different blade material and minor changes to the driving circuit, we measured the shutter blade's speed and quantified the laser power handling capability. We found that the 3D printed plastic blade can safely support up to 700 mW. With a plastic blade, we measured the shutter blocking speed to be as high as 2.14 ± 0.13 m/s. We also tested stainless steel blades capable of blocking higher laser powers.



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UG-5

Identification of Putative Methyltransferase 2 Homologues in *Giardia lamblia*: Characterization using tRNA Substrate Analysis

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Prior research in our laboratory has detected very low levels of DNA methylation in *Giardia lamblia* and shown that this methylation is required for parasite viability. Like many other single-celled eukaryotes, *Giardia* is apparently missing DNMT1 and DNMT3 homologues, but we have identified four DNA Methyltransferase 2 (DNMT2) enzyme candidates in *G. lamblia* through bioinformatics analysis. We expect DNMT2 to methylate both DNA and tRNA within *G. lamblia*, as this dual methylation capability has been characterized in the DNMT2 enzymes of *Drosophila melanogaster*, *Dictyostelium discoideum*, and the protozoan parasites, *Entamoeba histolytica* and *Trypanosoma brucei*. In order to identify the hypothesized *G. lamblia* DNMT2 homolog and characterize the functionality of the enzyme, I am investigating: the capability of recombinant putative DNMT2 homologues from *G. lamblia* to methylate *in vitro* transcribed tRNA molecules; the presence and frequency of tRNA methylation in wild type *G. lamblia*; and the relative activity and substrate specificity of putative DNMT2 enzymes in *G. lamblia*. Here I show successful design and synthesis of *in vitro* transcribed tRNA molecules, as well as the utilization of liquid chromatography-tandem mass spectrometry (LC-MS/MS) to identify methylated cytidine within tRNA nucleic acids. Furthermore, I have established minimum levels of detection of methylated cytidine using LC-MS/MS, demonstrating that LC-MS/MS is a useful tool for further substrate characterization. With these methods developed, I am using LC-MS/MS to analyze nucleic acid composition and then detect the presence of methyl group modification in both tRNA molecules extracted from parasites and *in vitro* transcribed tRNA molecules that have been incubated with recombinant methyltransferase enzymes. These studies aim to provide preliminary evidence of predicted tRNA methylation by a DNMT2 homolog in *G. lamblia*, and will garner necessary evidence to proceed with genetic manipulations of parasite lines, including the design of knock-downs and dominant-negatives targeting the putative DNMT2.



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UG-6

Curating and Digitizing the Cleveland Museum of Natural History's Apoidea Collection

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Over the course of history, specimens have been curated for the purpose of research and documentation of an area's biological heritage. Research utilizing curated specimens has been hindered due to the inaccessibility of data that has not been transcribed. When many keystone organisms, such as several genera of bees, are under climactic stress, this data is critical for tracking shifts in dispersion and population dynamics. Because of the recent demand for baseline data provided through properly curated specimens, this research aimed to first, identify the Cleveland Museum of Natural History's collection of bees to genus specie, then to digitize this data for posterity. Research began with the identification of bee genera, starting with *Bombus*, through the application of taxonomic keys. Identity was ascertained using several morphological traits highlighted in these keys as indicators, including: sex, angle of midleg basitarsus, oculo-malar area, presence of corbicula, and abdominal patterning. Any specimens that were previously misidentified were corrected and recorded to ensure accuracy of the database; rationale of re-correction was also recorded for future identification purposes. Once proper documentation of each genus was completed, digital transcription commenced. Locality, determiner, date, and indicative morphological traits were also included in the database. According to preliminary data, 30 formerly identified bees were misidentified, necessitating re-identification. Additionally, 103 bees were newly identified amongst a pool of undetermined Apiformes, including 5 *Bombus* species previously unaccounted for. Results display a higher diversity amongst the museum collection at a specie level than previously recorded. Preliminary results also indicate the necessity of the identity corroboration process to species.



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UG-7

NuRD Paralogs CHD-3/LET-418 Promote Meiotic Double-Stranded Break Repair in *C. elegans*

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Normal meiotic progression requires that double stranded breaks (DSBs) are induced within the DNA of all chromosomes. Unrepaired DSBs lead to defective gametes, which cause severe problems such as miscarriages, chromosomal disorders such as Down syndrome, and predisposition to cancer. Accordingly, DSBs must be faithfully repaired by a series of conserved mechanisms involving chromatin modifiers, proteins that epigenetically modify the structure of DNA. We have demonstrated a role for the nucleosome remodeling (NuRD) complex in DSB repair, wherein the Chromodomain helicase DNA binding protein CHD-3 and its paralog LET-418 promote normal meiotic progression and DSB repair in *C. elegans*. We discovered that the absence of these components leads to chromosome fragmentation, indicative of faulty repair mechanisms. Using an antibody against the DSB marker RAD-51, we found that DSBs abnormally persist in meiotic nuclei of *chd-3* and *let-418* mutant germ lines. We are currently generating several strains which will help us to further understand the molecular nature of these defects. Taken together, these experiments will enable us to determine the role of the NuRD complex in meiotic DSB repair, which can be applied to other organisms such as humans.



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UG-8

Molecular Features of an Epigenetic Regulatory Element at *Rasgrf1* in Mouse

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“Epigenetics” refers to chemical changes in traits that regulate gene expression without changing the DNA sequence. Non-coding RNAs (ncRNA) have been shown to influence the regulation of the epigenome by regulating transcriptional activity, transposon silencing, and chromatin state. However, little is known about how factors locally (in *cis*) contribute to the establishment of epigenetic marks such as DNA methylation. It is critical to investigate epigenetic state as the epigenome influences several biological mechanisms such as cell identity, gene expression, cell growth and fertility. We study the *Rasgrf1* imprinting control region (ICR), a *cis*-acting regulatory region that is methylated on the paternal allele. Previous research in the lab has shown that a ncRNA, pit-RNA, is necessary for the establishment of DNA methylation at *Rasgrf1*. This occurs in *cis* via the piRNA pathway at the differentially methylated domain of *Rasgrf1* in mouse germ cells. However, the mechanism in which the pitRNA controls epigenetic state at the *Rasgrf1* ICR is not well understood. The focus of my project is to investigate the influence of pit-RNA binding proteins on epigenetic and transcriptional state at the *Rasgrf1* ICR in germ cells. Ptpb1 has been identified by mass spectrometry to interact with the pitRNA, and we hypothesize it to regulate the pit-RNA and DNA methylation at the locus. CRISPR/Cas9 was used to knock out Ptpb1 in germ cell derived cells (RST7Ar19) to examine its effects on the expression of pit-RNA and maintenance of DNA methylation at the *Rasgrf1* ICR. Investigation of the influence of Ptpb1 on the expression of pit-RNA and retrotransposons and epigenetic state (DNA methylation) at *Rasgrf1* is ongoing.



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UG-9

Bacterial Growth Studies of Gut Microbes Including *Lactobacillus Rhamnosus GG* and *Escherichia Coli HS* Using UV-VIS Spectrophotometry and Quantitative PCR (QPCR)

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The long term goal of this project is to understand the symbiosis among gut microbes and the current goal of the project is to develop a quantitative analysis method to measure the growth of specific gut microbes including *Escherichia coli HS* and *Lactobacillus Rhamnosus GG* in cell mass or at an RNA level. In this paper, we discussed the early stage of our development including the growth study of the target bacteria using UV-VIS spectrophotometry and quantitative PCR analysis. The specific strains of the two target bacteria in use have been identified using common 16S rRNA sequencing. The growth studies of both bacteria were completed under aerobic and anaerobic conditions. For the UV-VIS spectrophotometry analysis, an OD₆₀₀ measurement was used and the result clearly showed the differences in the growth phases of the two different bacterial strains under the same growth conditions (Tryptic soy broth media, 37°C and aerobic or anaerobic). For the QPCR analysis, a 16S rRNA template was employed and the results showed similar outcomes with the growth studies using the UV-VIS spectrophotometry for *E.coli HS*. Currently, we are trying to connect the two different quantitative bacterial growth analysis techniques including cell mass analysis using UV-VIS spectrophotometry and quantification of 16S rRNA using quantitative PCR. In the future, this combination of the two different methods may provide us one of the possible tools to quantitate a specific bacteria strain from a mixture of different microbes using strain specific PCR primers.



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UG-10

Incorporating Antibiotic Resistance in the Modeling of Tuberculosis in the United States

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According to WHO, one third of the world's population is infected with tuberculosis (TB), with drug resistance posing another challenge to the management of TB. Strains resistant to the most common drugs for treatment (e.g. isoniazid, rifampin) are already widespread. To address the issue, we constructed a mathematical compartmental model described by differential equations showing the transmission of TB in the US. The model encompasses four strains of different resistance to antibiotics, while taking into consideration immigration, which greatly contributes to the excessive transmission of latent TB. We fitted parameters to recent CDC data on TB morbidity and mortality, producing reliable fits, by generating random parameter values within the ranges obtained from real-world data. We then algorithmically adjusted parameter values to better fit CDC and census data in three categories (total US population, active cases of TB, total TB deaths). Our focus now is improving the algorithm by understanding its behavior through various tests and modifying it to obtain more reliable fits. The final goal is to use the model to identify effective strategies against TB.



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UG-11

Human papillomavirus (HPV) infection

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HPV is the most common sexually transmitted infection, and while most mucosal HPV strains are benign, several strains can lead to genital warts and cancers such as cervical, vaginal, and oropharyngeal. HPV 16 and 18 alone account for 50 and 18 percent of all cervical cancer cases respectively. The HPV virus consists of DNA held within a protein shell, or capsid. The protein capsid of HPV is composed of two major proteins: L1 and L2. The L2 protein has been shown to be necessary for infection. In this project, we mutated an L2-syntaxin 18 binding motif to see if the region is necessary for HPV16 infection. We found that by changing just one of four amino acids, of the five amino acid motif, the pseudovirus was not infectious. Not only does this result highlight the importance of this L2-syntaxin 18 interaction in viral trafficking, but the motif could serve as a potential vaccine target.



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UG-12

Nurd Chromatin Remodelers Attenuate Meiotic Checkpoints in *Caenorhabditis Elegans*

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Errors in meiosis result in infertility, miscarriages, and chromosomal disorders in humans. Using the nematode model *C. elegans*, we investigated the role of the Nucleosome Remodeling and Deacetylase (NuRD) chromatin remodeling complex during meiosis. Previously, we discovered that mutations in the genes encoding Chromodomain helicase DNA binding protein CHD-3 and its paralog LET-418 result in persisting DNA damage and chromosome fragmentation that are coincident with increased germline apoptosis. Here, we investigate the genetic, cellular and molecular role of the NuRD complex and its relationship with meiotic checkpoint signaling and the execution of error-free DNA repair during gamete formation. We found that NuRD mutants have higher levels of the phosphorylated checkpoint protein CHK-1 (pCHK-1) versus controls as well as elevated mRNA expression of its downstream targets. These data are corroborated by cellular evidence in which pCHK-1 foci are detected in NuRD mutants, as well as genetic evidence demonstrating that *chk-1(RNAi)* and its downstream effector *cep-1(p53)* suppress apoptosis in when NuRD function is compromised. Strikingly, we also found that NuRD mutants readily engage in error-prone DNA repair pathways, which are normally blocked during meiotic recombination. Taken together, these results support a model wherein the NuRD complex ensures error-free gamete formation by attenuating meiotic checkpoints and preventing usage of error-prone repair pathways during meiosis.



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UG-13

Taking inventory: Presence of a fungal pathogen (Genus: *Ascospaera*) in *Osmia cornifrons* nests among varying landscape composition

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Wild bees impact crop productivity and can be functionally complementary to managed honey bees in agricultural settings, serving as backup and redundancy for honey bee declines. These are important findings since European honey bee colonies, *Apis mellifera*, have been in decline since 2006. Population decrease of *A. mellifera* and many wild bee species are suggested to be onset by multiple combined factors, including emerging infectious diseases. Thus, it is becoming more essential to investigate the impact pathogens have on pollination services and bee biodiversity. My research explores the presence of a common fungal pathogen, *Ascospaera*, and its infection rate within nests and among landscapes of the solitary mason bee, *Osmia cornifrons*.

In this project I screened overwintered trap nests of *O. cornifrons* with two techniques, the first being visual identification and the second through PCR analysis. The bees were collected from 17 sites in the Finger Lakes region of New York, which varied in surrounding landscape composition. Pictures were also taken of all nests and the contents were saved for later visual identification. Additionally, a phylogenetic tree was constructed from DNA extracts of infected individuals for species level identification of the *Ascospaera*. I chose to use both molecular and classical techniques for this study because it is one of the few exploring the presence of *Ascospaera* in a solitary bee, and knowledge on what tool is more effective for pathology is still under question.

In this study I have found difference in body size, inter-tegular distance, and sex ratio among the *O. cornifrons* bees infected with *Ascospaera* in different landscapes. I also found a variety of both pathogenic and saprotrophic species of *Ascospaera* among nests.



SCIENTISTA SYMPOSIUM 2017

UG-14

Patient Specific 3D Printed Therapy to Treat Heart Failure

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Despite improvements in preventative medicine, this year an estimated 1.3 million Americans will suffer a myocardial infarct (MI). Advancements in treatments of MI have resulted in a large number of survivors, however most MI patients develop heart failure as the infarct region expands and the left ventricle (LV) remodels. Remodeling is characterized by an increase in LV volumes and decrease in ejection fraction. As patients with heart failure outnumber available hearts for transplantation, new therapeutic approaches are needed to not only halt the progression of remodeling, but also reverse ventricular chamber dilation and systolic dysfunction.

The experimental goal was to develop an approach that mechanically alters LV geometry secondary to remodeling. To do this, an implantable device was developed for clinical use that is placed on the pericardial surface and can alter LV dimension in chronically remodeled post MI heart. The device is designed using 3D modeling to graphically visualize and incorporate ventricular curvature. From that 3D model the device is fabricated using 3D printing. To determine the function of the device in-vivo animal models of heart failure secondary to MI were used. Data was obtained using high resolution cardiac MRI. These images were used to measure the LV volume and myocardial strain.

Experiments found that acutely changing the device volume significantly altered the LV shape returning to pre infarct dimensions. Control animals continued to remodel, while remodeling was halted or reversed in treated animals. This was confirmed with MR images, which indicated the device led to permanent reverse remodeling and restored LV geometry and wall thickness. Follow up studies using this device are pending NIH funding. The goal is to perform “first in man” study of the device on heart transplant patients; these studies will serve as data for a full clinical trial.



SCIENTISTA SYMPOSIUM 2017

UG-15

Dancing with Electrons: Non-Trivial Behavior in Topological Superconductors

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When many people think physics, they might imagine complicated particle accelerators or our expanding galaxy, but physics is beautiful down to seemingly the most banal system in the 21st century: the transistor. Indeed, electrons in transistor-like devices interact and dance with each other in unexpected ways. The 'environmental conditions' of a material allow us to probe and visualize exotic quantum states of matter that behave just as beautifully as, say, stars in distant galaxies. This research focuses on the dancing of electrons in a unique class of materials called "topological insulators," which have remarkable energy- and computing-based potential. Topological insulators are characterized by the presence of conducting surface or edge electrons despite having an insulating bulk. These surface electrons are protected from backscattering (collisions, essentially) and hence give us a new paradigm of perfect electronic transport. However, the experimental challenge begins with revealing and manipulating the unique electronic states in topological insulators. In this work, I take a topological insulator material system and experimentally probe it at near absolute-zero temperatures. Informed by past experiments and theory, and enabled by modern nanotechnological methods, I hope to reveal interesting electronic behavior guided by topological transport.



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UG-16

Co-limitation of nitrogen and phosphorus as a bottom-up control on algal biomass in a mesotrophic lake

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Lake Minnewaska, located in a state park in New York, has been recovering over the last 30 years from acidification; concurrently, water clarity has decreased raising concern amongst park managers and visitors. As lake acidity decreased *Notemigonus crysoleucas* (golden shiner), a zooplanktivore, and *Micropterus salmoides* (largemouth bass), a piscivorous species, were unintentionally introduced, resulting in a trophic cascade with increasing algal growth and decreasing water clarity. In this study we investigated bottom up controls on algal biomass by performing a nutrient limitation experiment. Focusing on Lake Minnewaska, a mesotrophic lake, we predicted the co-limitation of both nitrogen and phosphorus on phytoplankton biomass. The experiment included introduced treatments of unamended lake water control (C), and three treatments amended with nitrogen (N), phosphorus (P), and a combination (N+P). The samples incubated in-situ for one week during both June and September 2016 on Minnewaska's surface. Retrieval of the samples, was followed by chlorophyll *a* (chl *a*) concentration measurement as a proxy for algal biomass.



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UG-17

Grafting Organic Molecules to Metal Surfaces through the Reduction of Aryl Diazonium Salts.

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Energy demands are increasing worldwide and the effects on the environment cannot be overlooked. Recent developments in energy storage have involved the use of conducting polymers as a means of electron transfer. Some applications of these conducting polymers include lightweight and rechargeable batteries, light emitting diodes, sensors and molecular electronics, among others. The reduction of diazonium salts is one of the known methods for chemically modifying electrode surfaces. This is achieved by grafting molecular chains onto the surface of materials through covalent bonding. Various monomers can be employed to provide distinctive electronic properties. We explored the reaction of various aromatic amines with nickel foam surfaces via diazonium chemistry. The reduction of aryl diazonium salts allows for the grafting of different aryl groups on the metal surface. In the first step, several aromatic amines were added to an acidic medium, generating the diazonium salt. Grafting was then achieved by simply dipping the metal into the salt solution. Samples were analyzed using Scanning Electron Microscopy, with 4-bromoaniline yielding the most significant visual surface change. Sonication served as an indirect method of assessing surface modification, as the interaction between diazonium derived films and metallic substrates are stable enough to withstand ultrasonic treatment, boiling in solvents, and prolonged exposure to various temperature conditions.



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UG-18

The Molecular Mechanisms of Sensory Synapse Formation

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Estimated to cost the country over 635 billion dollars per year, in both treatment costs and lost productivity, pain is an extremely exigent issue in society today. Therefore, it is critical to develop a more comprehensive understanding of the mechanism with which these pain signals are processed, potentially opening up new ideas for possible treatments. Studies have shown that two classes of proteins, neurexins and neuroligins, play a large role in the specificity of synaptic connectivity, leading to the hypothesis that the expression patterns of these neuroligins and neurexins create a code for connectivity. With this in mind, we propose the hypothesis: β neurexins in sensory neurons influence interactions with neuroligins, in turn altering aspects of synapse formation. Utilizing a co-culture of sensory neurons, cultured from mouse dorsal root ganglia, and fibroblast COS7 cells transfected with purified neuroligin DNA adhesion molecules and presynaptic terminals were be immunostained and then imaged – allowing for quantitative analysis of synapse formation utilizing the images from the confocal. To isolate the effects of the neurexin gene, a conditional gene knockout technique using viral vectors was implemented in order to knockout the genes coding for β neurexins. Under the premise of our hypothesis – that β Neurexins in sensory neurons influence interactions with neuroligins, there would be distinctly increased synapse formation in sensory neuron cultures containing the Neurexin gene than those with the genes knocked out. This would be visually indicated by the number of stained adhesion molecules and presynaptic terminals in the contrasting confocal images, showing that trans-synaptic interactions of neurexins and neuroligins play a large role in the specification of synaptic connections.



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UG-19

Single Molecule Conductance of PTM and PTM Radical

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The study of molecular electronics has increased over the past decade due to innovations in techniques used to measure single molecule conductance. One particular technique, which uses scanning tunneling microscopy (STM) in break junction measurements (STM-BJ), has allowed us to study the conductance of various small organic molecules. STM-BJ has also allowed us to deduce the relative levels of highest occupied molecular orbital (HOMO) and lowest unoccupied molecular orbitals (LUMO) to determine the conductance pathway. In this study, we have synthesized particularly interesting organic molecules, PTM and the uniquely-stable PTM radical. Through the synthesis of PTM and its radical counterpart, we hope to determine the effect of radicalization in molecular conductance as well as determine how the presence of the singly occupied molecular orbital (SOMO) affects the conductance pathway.



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UG-20

Calculating fits for data contributing to a lattice QCD approach to determining the anomalous magnetic dipole moment of the muon.

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For this project, we attempted to extrapolate the photon vacuum polarization as a function of momentum to 0 from a calculation previously conducted using lattice QCD to determine the anomalous magnetic dipole moment of the muon, a_μ . To do this, we used Python to first extract and analyze raw data from the initial lattice program and then to perform calculations using fit functions such as Padè approximants and conformal polynomials in order to determine a_μ and the error associated with its calculation. The overall goal of research into the anomalous magnetic moment of the muon is to calculate the value within a small degree of error using lattice QCD. Lattice QCD is being used to calculate this value because currently there is a discrepancy between calculations done using the Standard Model of particle physics and measurements taken during experiments. Currently, our results show that the discrepancy is persisting, though not to a significant enough degree. We recently obtained a new set of data from FermiLab and are working on processing it to see if we can get a result with even more certainty. If the discrepancy between the Standard Model calculation and the experimental measurements persists in our calculations, then we can possibly look for effects in physics beyond the Standard Model.



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UG-21

National Access to Children's Hospitals provided by Affordable Care Act (ACA) Silver Insurance Plans

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The objective of this longitudinal study is to examine access to children's hospitals provided by ACA Silver insurance plans throughout the United States starting from 2015 to present day. Aims of this project include assessing health equity as provided by current federal insurance plan policy as well as determining the need for possible quality improvement of national pediatric healthcare access. The Health.gov website has been used to create a cohort of Silver ACA insurance plans in all 50 states (including the District of Columbia) which includes 124 Children's Hospital Association (CHA) member children's hospitals and 2,229 Silver insurance plans. Accessibility is determined by measuring geographic proximity to general acute care hospitals –data from hospitals within a 25-mile radius of identified major cities in each state are being collected. Preliminary data analysis shows that, on average, only 56% of hospitals are accepted by < 70% of Silver ACA insurance plans throughout the United States. Furthermore, in regions with only one accessible children's hospital, an average of 27% of plans are not contracted with a children's hospital. As such, a general trend from the 2015-2016 data can be determined that emphasizes a narrowing of healthcare plans, ultimately limiting access to children's hospitals within the span of one year due to national trends in healthcare coverage and availability. It is therefore evident that the recent political and economic atmospheres play a crucial role in providing substantial access to children's hospitals, and thus, pediatric medical services.



SCIENTISTA SYMPOSIUM 2017

UG-22

Gazed At, Groped, and Assaulted: The Too Much Information of Being an Adolescent Girl

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** These authors contributed equally to this work*

In October 2015, New Paltz High School tenth-grader Maya Gold took her own life. In an article published on January 7, 2016, in the *New Paltz Times*, Gold's parents said they'd found sexually objectifying text messages on their late daughter's cell phone, which they believed contributed to her suicide. Being sexually objectified is a common occurrence for adolescent girls, with 30% of students reporting sexual harassment through text, email or social media (Hill & Kearn, 2011). In partnership with the TMI Project twelve college students participated in a 10-week memoir writing and storytelling workshop on experiences of sexual objectification and harassment which culminate in a live performance at the New Paltz High School. In our conference presentation, we will discuss the process of taking memoirs to the stage (performative research) as well as share the results of data collected on the psychological benefits of telling and listening to the too-much-information stories that we too often hide out of shame.



SCIENTISTA SYMPOSIUM 2017

UG-23

Computational Investigation on the Pyrolysis of Polyethylene

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Knowledge of pyrolysis is crucial for the understanding of the chemistry behind polymer combustion and flammability of plastics, which is vital to the scientific contributions toward fire safety. Polyethylene, being the most common plastic, has been most frequently involved in various kinetic studies consisting of different elementary reactions. Such chemical processes have achieved considerable success in recent studies. Computational research has been conducted on the pyrolysis of polyethylene with both methyl end groups as well as CH₂ radical end groups. Pyrolysis is the dissociation of bonds at high temperatures in the absence of oxygen. However, the temperatures are high enough to supply the energy needed to separate the bonds. We plan to computationally investigate the dissociation of various polyethylene chains at multiple temperatures to study the dissociation of the chains themselves. The dissociation of C-C bonds in various polyethylene chains were studied using reactive molecular dynamics simulations in vacuum. Three types of polyethylene chains were simulated under both constant density and constant pressure. These chains consisted of 500 molecules of PE-1 (ethane), 250 molecules of PE-2 (butane), and 200 molecules of PE-2.5 (pentane). These polyethylene chains ended in methyl groups rather than leaving the terminal carbon as a radical. We will report rate constants and mechanistic details for the pyrolysis of molecules under investigation.



SCIENTISTA SYMPOSIUM 2017

UG-24

New Enzyme Configuration to Optimize Power Output of a Biofuel Cell

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The Diabetes epidemic in the United States alone has inflicted close to thirty million people. Diabetes patients struggle with maintaining healthy insulin levels. The main application of our research is to develop an artificial pancreas, which will monitor glucose levels and power an insulin pump. A nanobiofuel cell will power this device.

Our nanobiofuel cell currently uses glucose oxidase and laccase enzymes to oxidize glucose and reduce oxygen in order to produce a current, which travels through single-wall carbon nanotubes (SWCNT). In effort to optimize our fuel cell, we tried replacing glucose oxidase with a new enzyme, glucose dehydrogenase. For our experiment we looked at four combinations of enzymes and SWCNTs: glucose oxidase and a bare SWCNT, glucose oxidase and laccase, glucose dehydrogenase and a bare SWCNT, and glucose dehydrogenase and laccase.

With these configurations we used a Keithley 6517A meter, which has an input impedance of $200\ \Omega$, to measure the voltage produced by the fuel cell as a function of load resistance. We also used a custom-built computer controlled circuit designed to vary the load across the biofuel cell from $100\text{M}\Omega$ to $1\text{K}\Omega$ in increments. This data was then transformed into a graph of the power produced by the fuel cell as a function of the load resistance. The highest output was generated by the glucose dehydrogenase and laccase combination. This combination increased our power output by 3500%. Future work will be dedicated to understanding the relevant properties of glucose dehydrogenase and continuing to optimize the nanobiofuel cell.



SCIENTISTA SYMPOSIUM 2017

UG-25

Newest Kid on the Block: Characterization of the novel multidrug-resistant pathogen, *Candida auris*

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Candida auris is a novel and emerging fungal pathogen capable of causing invasive, and often fatal, bloodstream and wound infections in immunocompromised patients. Several outbreaks have been reported in hospitals across the world, including the United States, and predominantly in New York. *C. auris* exhibits extensive multidrug resistance that has never been seen in any *Candida* species, and is often misdiagnosed for other *Candida* species, thus limiting treatment options for patients. Our laboratory obtained 10 *C. auris* isolates in order to perform *in vitro* antifungal susceptibility testing and determine the Minimum Inhibitory Concentration (MIC) under Clinical and Laboratory Standards Institute guidelines. An alarming percentage (70%) of *C. auris* isolates exhibited a strong resistance to the commonly prescribed drug, fluconazole (MICs of 128 ug/mL or above). Many of these strains are projected to have an elevated resistance to other classes of drugs, such as polyenes and echinocandins. An *in vivo* model using the waxworm, *Galleria mellonella*, was used to further study the highly-resistant *C. auris* strains, which demonstrated significantly different virulence in this host. Outbreaks of *C. auris* continue to increase on a worldwide scale, posing an immediate global health risk. *In vitro* and *in vivo* studies to characterize *C. auris* pathogenesis are imperative and fundamental to the proper diagnosis and treatment of this emerging threat.



SCIENTISTA SYMPOSIUM 2017

UG-26

Origins of highly-inclined TNOs: the Early Solar System and Planet Nine

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Current models of solar system evolution fail to explain a small (but expanding) population of highly inclined objects orbiting outside Neptune. In my work, I endeavor to show that the existence of a distant, Neptune-like, and as-yet undetected planet - known colloquially as “Planet Nine” - is responsible for the seemingly aberrant dynamics of this population of trans-neptunian objects (TNOs). In order to demonstrate this dynamical interaction, I simulate the evolution of Kuiper belt objects in the presence of Planet Nine, and compare their final orbits to those of the highly inclined TNOs we see in the solar system today.



SCIENTISTA SYMPOSIUM 2017

UG-27

The Effects of a Semester of Aerobic Exercise on Fitness, Cognition and Mood in College Students

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Long-term aerobic exercise enhances mood state and improves a range of cognitive functions including attention, information processing speed and both short- and long-term memory. Though a recent study found that first-year medical school students who regularly exercised attained higher grades than those who remained sedentary, little has been done to assess whether long-term exercise in undergraduate students positively influences academic performance and learning and study strategies. Therefore, the present longitudinal study examined the effects of an exercise intervention on mood, cognitive function and academic performance in first-year college students. Thirteen healthy, sedentary students from New York University completed a cardiopulmonary fitness test (VO₂ max test), a battery of neuropsychological tasks and a series of self-reported mood and study strategies questionnaires at the beginning and end of one semester in which they maintained their sedentary lifestyles. At the beginning and end of the following semester, they repeated these tasks, but increased their exercise regimens to include three or more aerobic exercise sessions per week lasting 45 minutes or longer. Overall grade point average (GPA) was obtained for each semester as well. Compared to the sedentary semester, the exercise intervention significantly increased cardiopulmonary fitness (Time x Semester: VO₂ peak $F(1,13)=15.246$, $p=0.002$), quality of life (Time x Semester: $F(1,10)=4.771$, $p=0.05$) and information processing speed as measured by the Eriksen Flanker Task (Time x Semester: congruent trials $F(1,10)=9.093$, $p=0.013$; incongruent trials $F(1,10)=8.060$, $p=0.018$). Changes in academic performance and learning and study strategies are currently being analyzed. These results suggest that even a single semester of exercise can improve cardiopulmonary fitness, cognition, and mood in previously sedentary, first-year college students.



SCIENTISTA SYMPOSIUM 2017

UG-28

Positive Influence of the Special Supplemental Nutrition Program for Women, Infants, and Children (WIC) on Diet

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Poor diet quality is a significant barrier to maintaining a healthy life. The use of federal food and nutrition assistance programs is one strategy to overcoming this barrier by expanding access to healthy foods in low-income communities. The Special Supplemental Nutrition Program for Women, Infants, and Children (WIC) has the capacity to influence the eating habits of low-income youth. Previous research has focused on the effect that WIC programming has on purchasing patterns, which is not necessarily reflective of changes in consumption. Data from a nationally representative sample of children age 2 – 5 who participated in the 2011-2014 National Health and Nutrition Examination Surveys (NHANES) was used for this study. Data regarding WIC utilization was collected at the household level for NHANES participants. Dietary intake was for children younger than six using a proxy. All data were analyzed using SAS 9.4 survey procedures to account for the unequal sampling probability and complex survey design of the NHANES. Children currently receiving WIC benefits have higher quality diets than children who do not receive WIC benefits. Compared to non-WIC participants, children who are currently receiving WIC benefits eat more protein, more legumes and less refined grains but consume more fat. The results demonstrate the mostly positive influence WIC participation has on diet quality among low-income youth. The effectiveness of WIC participation varied by racial group, with WIC participation having a more significant impact on the diets of Non-Hispanic White and Mexican-American children than Non-Hispanic Black children and children of other racial groups.



SCIENTISTA SYMPOSIUM 2017

UG-29

Spatio-temporal patterns of the 1918–1919 influenza pandemic in India: does transportation predict the historical spread of a deadly infectious disease?

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From the spread of bubonic plague via trade routes in the medieval period, to the spread of Ebola and Zika via air travel in recent years, infectious diseases and human transportation share a strong link. The influenza pandemic of 1918, which was responsible for 50 to 100 million deaths worldwide, was likely also facilitated by human travel. Our study focuses on the role that travel may have played within British India in the spread of the 1918 influenza pandemic. Based on excellent public health and transportation records from the era, we first examined weekly death rates from fever diseases across 30 districts of India during the period of January 1916 to December 1921 and estimated influenza related deaths relative to baseline mortality. We then explored the relationship between pandemic mortality and a number of environmental and demographic factors, including population density, age structure, urbanization, temperature and rainfall. Our analysis revealed geographic heterogeneity in pandemic mortality. Mortality rates were found to be unusually high among young adults, which is consistent with pandemic patterns from other countries. Mortality was also highest for western districts, and those with the largest population size. Motivated by this analysis, we developed a mathematical model to ask whether travel via the robust railroad system of British India predicted the spread of pandemic influenza during 1918-1919. Our study revealed that railroad travel between districts significantly explained the spread of the 1918 influenza pandemic and highlights the importance of transportation in propagating infection. With no end in sight to the continued growth in global travel, we must account for the high speed and volume of modern transportation in developing prompt disease surveillance and efficient disease control strategies.



SCIENTISTA SYMPOSIUM 2017

UG-30

Assessing In-group vs. Out-group Aggression via Fabricated Tangram Competition

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Intergroup biases in empathy and harm can be driven by actual competitions for resources or by symbolic competitions for status. Interventions that aim to reduce bias might work for one kind of competition, but not the other. We tested whether priming secure attachment figures would reduce biases when there was symbolic competition, but not when there was an actual competition for resources. In our study, subjects from the University of Michigan were told they would complete tangram puzzles for a prize, and they were either in direct competition with a rival school or they were not in direct competition with the rival school. Half of these subjects additionally wrote about a secure attachment figure. Later subjects reported how much they empathized with students from their own school and from the rival school who experienced positive and negative events. Afterwards, they had the opportunity to assign difficult puzzles to students from both schools to harm them, or easy puzzles to students from both schools to help them. We predicted that we would find a bias that Michigan students had towards other Michigan students in assigning the puzzles – they would get easier puzzles and students from the rival school would get harder puzzles. However, we also predicted that this would not directly correlate to their ability to empathize with students from both schools who experience positive or negative events. The results from the study will demonstrate that different kinds of competition may require different kinds of interventions to reduce intergroup bias.



SCIENTISTA SYMPOSIUM 2017

UG-31

An Application of the Phillips Curve to the Indian Economy

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Using macroeconomic data from the Indian economy spanning January 1980 to August 2016, I find that the tradeoff between inflation and unemployment implied by the Phillips Curve is nonexistent. Using supply shock variables for liberalization, droughts and oil prices, I fit a New-Keynesian Phillips Curve (NKPC) to the Indian economy. The NKPC proves to be of little applicability to the Indian case, despite the inclusion of supply shocks, and despite the usage of both OLS and GMM estimators. Indeed, my estimations' rejections of the unemployment-inflation tradeoff, the low R-squared of my GMM estimations and the rejection of the Hansen J-Statistic provide insight to some serious misspecification issues, despite the application of several frameworks within the NKPC.

My results are a departure from the findings of recent literature on the NKPC in the Indian economy, demonstrating a need for reevaluation of traditional macroeconomic models, and more specifically, their applicability to developing economies. I can now ask whether lagged effects of recent events such as the financial crisis of 2007-09 have put the existence of the NKPC tradeoff in jeopardy for the Indian economy. Perhaps, in line with historical trends, Indian WPI inflation has returned to its previous unpredictability. The inapplicability of the NKPC to the Indian economy in my research may imply the unemployment inflation tradeoff only applies to advanced economies, although further research on the NKPC in developing economies is necessary before reaching this conclusion.



**Uncovering the transcriptional regulation of ClpC during sporulation in
*Bacillus subtilis***

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ClpC is an AAA+ ATPase chaperone/unfoldase that interacts with the ClpP protease during proteolysis in the gram-positive bacterium *Bacillus subtilis*. ClpC has additional roles in sporulation, cell competence, cell division and degradative enzyme production. ClpC, while present during normal growth, is known to be produced in high quantities under stressful conditions to degrade protein aggregates. It has been shown previously that ClpCP preferentially localizes to the forespore during sporulation and functions to degrade proteins. However, very little is known about the spatial and temporal regulation of ClpC. A number of putative promoters have been suggested by *in silico* predictive analyses, but no specific transcriptional regulators have been defined to date. We propose that there are sporulation-specific promoters that activate additional *clpC* expression. We used PCR to amplify increasing amount of DNA upstream of *clpC* (each sequence encompassing different numbers of putative promoters) and cloned the DNA into a HindIII/EcoRI digested plasmid containing the *lacZ* reporter gene. The newly formed plasmids were then transformed into *B. subtilis* and tested for β -galactosidase activity spectrophotometrically. All data analysis was carried out using Microsoft Excel Spreadsheets. We here present evidence that ClpC is part of a complex regulatory network involving multiple alternative sigma factors. An increase in β -galactosidase activity around the second hour of sporulation coinciding with the time the σ^H is active was observed. A knockout mutant of this sigma factor eliminated this activity. Our results suggest that ClpC is at least partially under control of σ^H , prior to entry into sporulation. This work not only tells us how ClpC is specifically regulated in *B subtilis* during sporulation, it also contributes to our general understanding of the spatial, temporal, and developmental control of proteolysis in prokaryotes.



SCIENTISTA SYMPOSIUM 2017

UG-33

Investigating Notch2 as a potential binding partner of Progranulin: Implications for Neurodegenerative Disease

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Pharmaceuticals designed to treat neurodegeneration are often inefficient in halting or slowing disease progression, thus necessitating investigation of more efficacious forms of treatment. Progranulin (PGRN), a secreted glycoprotein of 7.5 granulin repeats, has been implicated in Frontotemporal Lobar Degeneration (FTLD); however, the mechanisms behind PGRN's effects, specifically those behind neuronal growth and survival, are not fully understood. In an attempt to elucidate how PGRN promotes neuronal growth and survival, the current study investigated Notch2, a Type 1 transmembrane receptor protein characterized as a neurotrophin, as a binding partner of PGRN. To determine if PGRN and Notch2 bind, PGRN and Notch2 were immunoprecipitated and a cell surface and uptake assay was performed. Data revealed that PGRN and Notch2 bind at the cell surface. These results identify Notch2 as a binding partner of PGRN, which with further study, may elucidate the mechanisms behind PGRN's effects and identify Notch2 as a pharmaceutical target for neurodegenerative disease.



SCIENTISTA SYMPOSIUM 2017

UG-34

The Heart might not Always Want What it Wants: The Effect of Dietary Patterns on Heart Disease

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Cardiovascular disease is one of the more pressing issues in America today. In order to understand the risks of heart disease among the American people, it is important to study their dietary patterns. In order to get a comprehensive data set of the American people, the CDC's program the National Health and Nutrition Examination Survey (NHANES) was used. The study sample consisted of the individuals with a complete anthropometric data set and was cleaned to isolate adults. Individuals with heart disease were defined by displaying likely contributors to or had ever been diagnosed with a heart related disease.

Eating habits of individuals was assessed in the interview stage of the NHANES, and this study focused on how many times dinners that were consumed was cooked at home, and the energy density of foods consumed. All statistical analyses were performed using SAS University Edition. All models were adjusted for age, sex, race/ethnicity, and level of education, with significance determined at $P < 0.05$.

Those who cooked dinner zero times per week has a greater heart disease disparity than those who cooked dinner six times per (1.27 vs. 0.73, $P = 0.018$ vs $P = 0.046$), suggesting a significant inverse relationship between these variables. Individuals who are eating dinner that was cooked at home zero times are eating foods that are significantly higher in energy density than those who are eating a dinner cooked at home seven times a week. (1.88 vs 1.73, $P < 0.0001$).

This suggests that eating meals that are prepared at home can have an overall positive effect on one's health. This data is important for advances in preventative medicine.



SCIENTISTA SYMPOSIUM 2017

UG-35

Are Exon 11-Associated Variants of the OPRM Gene Involved in Alcohol Reward?

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Alcohol use remains a global problem with approximately 10-20% of chronic alcohol users becoming alcoholics. Despite severe consequences, alcohol continues to be a rewarding substance for many and may be just as addictive as other drugs of abuse. Recent work in our laboratories has led to a successful manipulation of a gene targeting one of the exons that makes up the opiate receptor gene (OPRM). By knocking-out exon 11 (E11) of the OPRM gene in mice, heroin failed to elicit any significant analgesia or rewarding effect in the knockout mice. Many narcotics such as morphine and heroin activate the mu opiate receptor and cause a pleasurable feeling that may be psychologically similar to what alcoholics feel when consuming alcohol. The present study evaluated chronic alcohol consumption in wild-type and E11 knockout (KO) mice. To see if E11 is also involved in the rewarding effects of alcohol intake, the present study was designed to evaluate the effects of alcohol in E11 KO mice. E11 and C57 wild-type control mice were evaluated using a 2 bottle choice paradigm. Total consumption was measured over a 30-day period with escalating concentrations of alcohol (2-10%). Results showed E11 knockout mice drank significantly higher amounts of alcohol as compared to C57 control mice, raising the possibility that E11 is also involved in the rewarding effects of alcohol. Although alcohol is presumed to have a very different mechanism of action than heroin, the physiological properties of reward might use a common E11 genetic map.



SCIENTISTA SYMPOSIUM 2017

UG-36

Peer Mentoring as a Retention Intervention for Underrepresented Computer Science Majors

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Nation-wide statistics have historically acknowledged women, as well as non-White and non-Asian minorities, as the two underrepresented groups in STEM, particularly in computing fields. Research indicates that recruitment and retention are the two key areas needed to resolve the gap. Focusing on retention, this study investigates intervention approaches for college students currently in Computer Science and related majors, with the case study being St. John's University. Institutional reports show St. John's University, a highly diverse populated college, has higher enrollment percentages of women and non-White non-Asians compared to the national averages; however, the underrepresentation of them still exists. Informed by literature insights on the characteristics and experience of these minority students, this study utilizes extant mentoring models and faculty resources at St. John's University to propose components for a peer mentoring pilot program that will run in the 2017-2018 academic year.



SCIENTISTA SYMPOSIUM 2017

UG-37

Exploring Physics using Monte Carlo Applications

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This research project focused on exploring Monte Carlo applications, specifically the Metropolis Algorithm and its applications to selected problems encountered in physics and mathematics. The main motivation behind this project was to learn about and become comfortable using random numbers and the metropolis algorithm while also exploring how they can be applied to common physics problems. Specifically, this project focused on using the algorithm alongside other computational methods to find the equilibrium configuration of electrons when they are placed on a conducting sphere. To do this, we used random numbers to choose arbitrary locations on a sphere and used the metropolis algorithm to minimize the electrostatic potential of the set of electrons. Upon observations of the data using various plotting methods, we observed a highly symmetrical configuration, as expected. This observation of symmetry has carried through to investigations into other surfaces including a torus, a cone, a cylinder and an ellipsoid. The codes developed during this research can later be used as an outline for any code attempting to find global extrema of a function.



SCIENTISTA SYMPOSIUM 2017

UG-38

Small molecule pharmacological chaperone has potential to improve protein trafficking in the lysosomal storage disease sialidosis

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Sialidosis is a rare lysosomal storage disorder (LSD) caused by a deficiency of Neuraminidase 1 (NEU1) in the lysosomes, which leads to substrate accumulation and disease symptoms. There are currently no cause-based treatments available. Pharmacological chaperone therapy (PCT) is a treatment approach which has been approved for Fabry disease, another LSD. A small molecule pharmacological chaperone helps to stabilize the deficient enzyme and increase its trafficking from the endoplasmic reticulum to the lysosome. Since mutated enzyme retains partial activity, it can metabolize substrate upon reaching the lysosome and thus prevent substrate buildup and disease symptoms. The Garman lab at the University of Massachusetts Amherst identified a potential pharmacological chaperone and performed *in vitro* and *ex vivo* proof-of-concept studies validating the use of this small molecule in PCT. Pulse proteolysis shows that purified NEU1 can resist degradation by a protease when incubated with the pharmacological chaperone beforehand. The pharmacological chaperone also increases the activity of wild-type NEU1 and some common disease mutations of NEU1. Finally, using fluorescence microscopy, we have shown that the pharmacological chaperone can increase trafficking of wild-type and mutant NEU1 to the lysosomes. These findings suggest PCT may be an effective treatment for sialidosis and provide a molecular scaffold for a new treatment avenue.



**Poster Session Abstracts
Graduate Category**



SCIENTISTA SYMPOSIUM 2017

G-1

Robot Motion Planning in Heterogeneous Space

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Motion planning algorithms has shown tremendous results for the navigation of robots in the past. However, there is no formal way to determine if any motion planning algorithms is applicable in all varying environments. The continuous improvement on the capabilities of robots and the complexity of environments in which they successfully traverse, there is a need to formally define these complex environments. These environments are naturally heterogeneous and hence a single motion planning algorithm will not work universally. In our work we give a formal definition of heterogeneous spaces based on the concept of expansiveness and homotopy representations of the planning space. We have defined different phases i.e. free space, obstacle/blocked space, narrow passage space and cluttered region, that make up a heterogeneous environment. These descriptions give more insight into the complexity and planning properties of configuration space and develop a better understanding of environment. The properties of heterogeneous space has been applied to generate two-dimensional and three-dimensional space environments. We apply machine learning algorithms on created configuration space to map various regions of the environment during our experiments. We analysed the efficiency of these techniques and combined them to improve upon the algorithm for the motion of robots in the changing environment. Our results include an improvement on the time taken to solve a query when the topology of the space is taken into consideration, the number of edges by sample needed to solve the query and the number of total to valid samples generated. In our future work, we plan to look into more complex and dynamic environments and investigate how this affects the heterogeneous nature of the planning space.



SCIENTISTA SYMPOSIUM 2017

G-2

Usefulness of the eDNA (environmental DNA) method for detection of rare native and invasive *Myriophyllum* species at low densities

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In northeastern United States the aquatic plant genus *Myriophyllum* is represented by seven native and two invasive species. Most of the native species are rare and endangered and their small population sizes make their detection difficult at many locations. At the same time, it is hard to notice the presence of invasive *Myriophyllum* species at early stages of introduction. Accurate information on plant species presence or absence is crucial for their management.

Here, we report that an eDNA (environmental DNA) method can detect rare and endangered *Myriophyllum* species as well as invasive *Myriophyllum* species in their early stages of introduction in northeastern United States. The eDNA method was recently developed to detect aquatic species hard to find due to their low densities. Small debris that potentially contains tissues of target organisms are collected by filtering environmental water and serve to detect species DNA signals using molecular methods, e.g., DNA sequencing and DNA fingerprinting. This method has been demonstrated as potentially useful for early detection of invasive *M. spicatum* infestations.

In this study, we optimized the method to detect different native and invasive *Myriophyllum* species in Ponkapoag pond, MA. Two invasive species, *M. spicatum* and *M. heterophyllum*, were detected in the waters of that pond, both of which are present there in abundance. At the same location we were also able to detect native *M. sibiricum*, a species that went virtually extinct in Massachusetts, and contrary to any expectations, *M. quitense*, which has never been reported in northeastern United States, but is known as non-native in east-coast Canada. The eDNA method proved useful for our purpose and further work will be performed on other locations and species.



SCIENTISTA SYMPOSIUM 2017

G-3

Effect of Metal Ions on Polyelectrolyte Mechanics

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Polyelectrolytes based hydrogel fibers can mimic extracellular matrix, and have various biomedical applications such as drug delivery and tissue scaffolding. Metal ions have been shown to stabilize hydrogel fiber networks through the interactions between the carboxylic group of the polyacrylic acid and metal ions. However, how ions modulate the mechanical properties of individual polyelectrolyte polymers is still unknown. In this study, electrospun polyacrylic acid (PAA) with chitosan (CS) is used as a model system to evaluate how ferric ions (Fe^{3+}) affect both fiber length and bending stiffness using dark field microscopy images and persistence length analysis. We demonstrate that increasing ferric ions leads to a reduction in fiber length and an increase of bending stiffness. Our work suggests that metal ions can regulate single polyelectrolyte fiber mechanics, thereby providing designs to fabricate hydrogel with controllable stiffness.



SCIENTISTA SYMPOSIUM 2017

G-4

Nanoscale investigation of biophysicochemical responses to induced stress in *Rhodococcus opacus*

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Creating a more in-depth knowledge base of bacterial existence and evolution in a chemical, physical, and biological sense has become increasingly relevant, especially with the growing number of treatment-resistant bacteria. Some of the most important factors regarding how bacteria become infectious relate to the biomechanical properties: stiffness, adhesion, and binding interactions. Our study aims to investigate the nano-molecular measurements of these factors, establish chemical compositions of cell walls, and understand the biophysicochemical responses associated to stress on bacterial systems.

Here we focus on the plant-based bacteria *Rhodococcus opacus* and their response to varying growth adaptations. First, we study the physical attributes of the bacterial system with atomic force microscopy (AFM). Additionally, we use mechanical measurements to understand the biomechanical properties associated with the bacterial cell membranes. This allows for the measurement of stiffness and adhesion, Young's modulus, and relative hydrophobicity/hydrophilicity. We use Raman spectroscopy to understand the biophysicochemical properties and identify/quantify molecular details, which can be further explored with nanoscale-IR spectroscopy. By exploring all associated properties and bacterial responses to stress at the nanoscale level, we propose a new approach with exciting implications, such as potential clues for the development of more potent treatments for resistant bacteria.



SCIENTISTA SYMPOSIUM 2017

G-5

Affective State and Exercise Motivation:

Does baseline mood regulate exercise motivation?

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Exercise is beneficial for many areas of the body and brain including cardiovascular, cognitive, and affective domains. However, only 20.9% of the U.S. population meet the requirements for the Physical Activity Guidelines, indicating a clear issue for the motivation to exercise. Recent animal research has shown that the motivation to exercise is regulated by brain regions within the motivational circuitry, including the nucleus accumbens (NA) and prefrontal cortex (PFC). Additionally, research in both animals and humans has shown a link between the neural mechanisms that regulate motivation and those that regulate mood. For example, depressed individuals show decreased levels of motivation, which brain imaging studies reveal is reflected as a decreased activation in the NA. Both acute and long-term exercise improve mood state and are beneficial for symptoms in individuals with mood disorders. Additionally, the affective response to exercise has been shown to predict the motivation for and pursuit of future exercise. Little is known, however, regarding the link between exercise motivation and general baseline affect in healthy populations. Therefore, the present research aims to address this gap and identify the relationship between motivation to exercise and mood state. 177 healthy, non-smoking adults, ages 25-59, were recruited for this cross-sectional study. To assess exercise motivation, participants completed the Exercise Motivations Inventory, the Exercise Regulations Questionnaire, and the Exercise Causality Questionnaire. To assess mood state, participants completed the Profile of Mood States, the Positive and Negative Affect Scale, the Beck Depression Inventory, and the Beck Anxiety Inventory. In order to control for fitness level, participants' cardiopulmonary fitness was measured via a VO₂ max test. We hypothesize that, controlling for fitness level, affective state will predict the level of motivation to exercise.



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G-6

Solution-Cathode Glow Discharge: A Versatile Ion Source for Atomic, Molecular, and Biological Mass Spectrometry

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Mass spectrometry is a technique utilized in many disciplines due to its sensitivity and selectivity. In order to analyze samples that contain many different types of analytes (*e.g.*, polar, non-polar, inorganic) with mass spectrometry, usually several different ionization methods are required. Therefore, a versatile ionization source capable of producing ionic forms of analytes with different physical characteristics would simplify analyses and reduce cost. Here, we present the use of the solution-cathode glow discharge (SCGD) as an ionization source for mass spectrometry.

The SCGD is an atmospheric-pressure glow discharge that consists of a direct current plasma between a metal anode and a flowing solution cathode. Analytes within the flowing solution are directly sputtered from the solution into the discharge where they can be ionized, energetically excited, and/or atomized. Originally, this discharge was developed as an alternative to the inductively coupled plasma for atomic emission spectroscopy, which produced comparable analytical figures of merit. Here, we explore the versatility of this plasma as an ionization source for mass spectrometry. Specifically, it will be shown that the SCGD is capable of volatilization and ionization of elemental species, small organic molecules, and labile biomolecules. Elemental ion signals were detected in the sub-part-per-billion range. Whereas, molecular species could be ionized directly from the flowing solution or through desorption/ionization of a solid sample held near the glow discharge. Furthermore, the SCGD was found to be capable of producing gas-phase ions of large, labile biomolecules, such as peptides. Finally, the ability to obtain structural information of molecular species with the SCGD will be demonstrated through tunable fragmentation simply with a change in discharge power. In the case of peptides, the tunable fragmentation produced better peptide sequence coverage than ESIMS/MS via collision-induced dissociation.



Reduction and analysis of coupled heterogeneous FitzHugh-Nagumo Oscillators

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Networks of nonlinear neuronal oscillators exhibit complex dynamics that depend on both the network structure and the distribution of external input. Mathematical investigation of the dynamics in oscillator networks can help in understanding the behavior of neurons in the brain. Here, we implement sufficient conditions for synchronization in networks of FitzHugh-Nagumo (FN) neuronal oscillators with electrical gap junction coupling to reduce large networks of neurons to corresponding representative networks that are more tractable to analysis. The FN model, a two-dimensional simplification of the Hodgkin-Huxley equations for neuronal membrane potential dynamics, exhibits input-dependent regimes of dynamical behavior. These regimes can be characterized as firing, quiescent, or saturated. In the reduced network, we explore the contributions of external input heterogeneity and coupling strength to determine whether specific oscillators are firing. We use the relationships between external input distribution and oscillator states in the reduced network to elucidate properties of oscillators in the original network. Complex behavior in the reduced network includes the presence of mixed mode oscillations and asymptotically periodic behavior. Extensions of these results could be used to inform system identification in complex networked oscillatory systems.



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G-8

Bayesian Analysis of Longitudinal Data

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Bayesian models are widely explored and adopted to analyze many different problems for the modern data science era. In real life, expertise has the knowledge and has some ideas and the direction about the problem, and Bayesian approaches consider this expertise belief into the analysis. In fact, Bayesian approaches give the analyst the chance to use previous study results (Prior information) and incorporate them into the new analysis to increase the amount of information (Posterior information). Moreover, if previous information is not available, Bayesian models can still be a valuable choice, since noninformative prior can be adopted for the parameter estimation.

In this study, we are interested in the application of Bayesian models for the analysis of longitudinal data. The growing interest for longitudinal studies derives from the huge application across the scientific disciplines including the medical field. The main focus will be the application of growth models for the study of datasets made of protein measurements collected at different time points and involving different groups of patients. The task will be the discovery of particular patterns and latent subgroups in between the studied groups.



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G-9

A novel role for Plexin A in photoreceptor axon targeting in *Drosophila*

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Normal nervous system functioning is dependent upon very defined and precise network formation during development. Aberrant synaptic connectivity caused by mutations in axon guidance molecules and cell adhesion proteins has been associated with neurodevelopmental and psychiatric disorders such as intelligence disability, epilepsy, Autism Spectrum Disorders, and schizophrenia. The *Drosophila* visual system is an excellent model system for studying the basic mechanisms of axon pathfinding and neural circuit formation. The terminals of R7 and R8 photoreceptors, responsible for color vision, are segregated into distinct target layers of the medulla, a central region of visual processing in the brain. We have found that null mutations in *plexA* cause R7 photoreceptors to prematurely terminate in the R8 layer of the medulla and fail to expand their axon terminals. Labeling of presynaptic sites in R7 axons shows fewer synapses when *plexA* is knocked down in neurons using RNAi. Mosaic analysis and *plexA* RNAi experiments indicate that PlexA is required in the brain and not in the eye. PlexA is strongly expressed in medulla tangential neurons, which occupy the layer just beyond where R7 axons terminate and arise from the tips of the outer proliferation center (OPC). Deleting *plexA* from the progeny of the tips of the OPC using somatic CRISPR/Cas9 causes R7 mistargeting, supporting a function for PlexA in medulla tangential neurons. Misexpression of PlexA in photoreceptor axons results in their hyperfasciculation and premature termination, consistent with PlexA acting to promote attraction or adhesion of R7 axons. R7 mistargeting is not observed in mutants for Semaphorin-1a or Semaphorin-1b, the known PlexA binding partners. One reported splice form of PlexA lacks the Semaphorin-binding Sema domain. We are using misexpression and genome editing to test whether the Sema domain is necessary for PlexA function in the visual system. We are also deleting the cytoplasmic domain in order to determine whether PlexA acts as a receptor or a ligand in this context. Lastly, we are investigating whether a novel receptor may mediate this function of PlexA, which may have implications for how Plexin family members control axon pathfinding in higher organisms.



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G-10

Pairing Your Sox: Cross Species Function of Sox11 in Neural Development

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Neuronal development involves the progression of cells from progenitors to neurons and is guided by precise spatial and temporal expression of transcription factors. Sox transcription factors play critical roles in this process of neuronal development and their expression and function is conserved across species. Sox11, a member of the SoxC gene family, promotes neuronal differentiation in several species including *Xenopus laevis* (frog) and *Mus musculus* (mouse). Our functional studies reveal that frog and mouse Sox11 cannot substitute for one another in neuronal development despite the high level of Sox transcription factor conservation. To address potential causes for functional differences between frog and mouse Sox11, we compared the mouse and frog Sox11 protein domains hypothesized to be involved in protein-protein, and protein-DNA interactions and analyzed the function of cis- regulatory regions. Our results indicate that a single amino acid difference in the highly conserved protein-protein and protein-DNA domain alters the function of Sox11 in these two species and that post-transcriptional regulation via miRNAs is key to the controlling Sox11 spatial and temporal expression across species.



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G-11

Regulation of Microtubule Severing by Katanin

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The cell's cytoskeleton is a dynamic network of microtubules constantly being reorganized to meet the spatiotemporal demands of the cell. Microtubules are organized into subcellular highways to control cell processes such as cell division, cargo transport, and neuronal development and maintenance. Reorganization of this intricate network is tightly regulated by various stabilizing and destabilizing microtubule-associated proteins that decorate the network. Katanin p60 is a microtubule destabilizing enzyme from the ATPases Associated with various Activities (AAA+) family. It recognizes the tubulin carboxy-terminal tails (CTTs) to sever microtubules. Our lab has previously shown free tubulin dimers can inhibit katanin severing *in vitro*. Our results suggests a possible regulatory mechanism of katanin severing in the cell. Using super-resolution microscopy and image analysis, we seek to characterize the regulation of microtubule severing by katanin. We find that the CTT sequence, ionic, hydrophobic, and steric features play a role in determining katanin's activity. A better understanding of how modified CTTs regulate microtubule severing by katanin will help future research aimed to correct katanin severing when this process goes awry as in improper chromosome segregation during mitosis or loss of microtubule integrity in neuronal diseases.



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G-12

A combination of catalysts and adsorbents for in-situ conversion of CO₂ to synthetic natural gas

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We report the advantages of a Dual Function Material (DFM) that combines a CO₂ adsorbent in combination with a catalyst that captures and converts CO₂ in situ to synthetic natural gas (CH₄) with the addition of H₂ produced from excess solar or wind energy via water electrolysis. This technology offers a new approach towards managing CO₂ emissions while producing a useful fuel while closing the carbon cycle. Different loadings of adsorbents (CaO, K₂CO₃ and Na₂CO₃) and catalysts (Ru, and Rh) were compared for CO₂ adsorption and conversion to synthetic natural gas production. All materials rapidly adsorb CO₂ but hydrogenation to CH₄ is highly dependent on the adsorbent and catalyst material. Excellence performance was observed for CO₂ captured on 5% Ru-10% CaO/Al₂O₃. For samples with 20% Na₂CO₃ in combination with 0.5% Rh, the performance was the best of all.



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G-13

Targeting G-quadruplex by Anti-Cancer Drugs

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Molecular targeted therapy is one of the major methods of cancer therapeutic treatments. In this method drugs are designed to specifically moderate the function of proteins or other disease related components. In this therapy small molecules (SMs) that can target cancer cells and penetrate through the cell membrane are used due to their specificity as they cause less damage to normal cells.

G-quadruplex (GQ) structures are DNA structures that form at the end of chromosomes (telomeres) and a number of other regulatory sites that have a G-rich sequence. Stabilizing these structures has emerged as a potential strategy to slow down cancer proliferation. Therefore, GQ stabilizing SMs have attracted attention due to their potential use as anti-cancer drugs and in biotechnological applications where GQ is used as a sensor. In this study, we used single molecule Förster resonance energy transfer to study the interactions between a GQ and a fluorescently labeled SM (L1Cy5-7OTD) that stabilizes it. By placing the fluorophores at different locations on the DNA construct that includes the GQ, we determined that L1Cy5-7OTD stacks on the GQ for extended periods of time, with dwell times in 100-200 s range. The frequency of SM binding and the duration of associated dwell times both correlated with the stability of GQ. Finally, we observed transitions between different binding orientations of L1Cy5-7OTD, without dissociating from GQ. These dynamics were surprising, and potentially significant, as stacking of SMs is typically considered a static binding event.



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G-14

Cool lives of of the Dirt-y Tundra Soil Bacteria Active at Subzero Temperatures

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Polar environments cover large biomes on the planet, harbor vast carbon reserves, and are home to microbes. These microbes are responsible for cycling greenhouse gases as well as Earth's important nutrients such as carbon, nitrogen, etc. Climate change is expected to impact these vulnerable Arctic environments with temperature fluctuations, and thereby affect microbial populations and activities, even within subzero temperature ranges. While there are bacterial studies that examine the effect of temperature thaw above 0°C, very little is known about the effect of temperature on bacteria within subzero temperatures in polar soils. This study investigates the effect of temperature on the active subzero bacteriome in Arctic tundra soils by using Stable Isotope Probing (SIP) and DNA sequencing. Arctic tundra soil from Kilpisjärvi, Finland was amended with a common tundra carbon-substrate (13cellobiose) and incubated at 0, -5, and -16°C for 5-40 weeks. This study demonstrates that there are distinct bacterial families active such as the *Caulobacteraceae*, *Candidatus Brocadiaceae*, *Pelobacteraceae*, *Acetobacteraceae*, *Armatimonadaceae*, *Desulfobacteraceae* at -16°C that were undetected at 0, -5°C, or as the initial resident community. Similarly, some bacterial families were detected at 0°C of the *Prochloroccoceae*, *Thermaceae*, and *Nocardiae*, but not at -5°C or -16°C. Therefore, this study suggests that the impact of temperature shifts even with subzero ranges may influence bacterial populations, whose activities may thus affect global biogeochemical cycles.



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G-15

Spectroscopic Optical Coherence Elastography of White and Grey Matter in a Mouse Brain

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Spectroscopic Optical Coherence Elastography (S-OCE) is a new biomedical imaging technique that can provide high resolution imaging capability by measuring frequency-dependent responses. Similar to ultrasound, OCE delivers mechanical excitation to the sample of interest and detects the response of the sample. Our source of excitation is radiation pressure of focused ultrasound, and the displacement response is quantified by the optical coherence tomography (OCT) system. As a result, the response detected in OCE is dependent on the mechanical properties of the sample. In this experiment, OCE was used to evaluate the mechanical response of a mouse-brain model by distinctively analyzing white and grey matter. The results of the study show that the response displacements were significantly different between white and grey matter, indicating distinguishable mechanical properties. Using OCE, mechanical properties of the white and grey matter can be observed at the nanometer scale.



Serial Isolates of *Cryptococcus neoformans* Demonstrate Altered Resilience to Nutritional Stress

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Cryptococcus neoformans is an opportunistic fungal pathogen that causes fatal meningitis in immunocompromised individuals, especially HIV+/AIDS patients. It has a high propensity to persist and relapse despite antifungal therapy. Cerebrospinal fluid from recurrent infections is routinely drawn, and raises the question of whether later isolates survive host stresses better than earlier isolates. Previous studies have shown that the two aging models of chronological and replicative lifespan are altered by nutrition deficiency, and advanced age cells show phenotypic variations during chronic infections. Therefore, both mitotic and post-mitotic aging of cells may play an important role in maintaining their fitness in the host. We hypothesized that later isolates respond differently to nutritional stresses, such as glucose availability, which is significantly reduced in cerebrospinal fluid. We investigated the fitness of serial isolates from several patients in New York City, USA, by measuring their growth rates and viability in media with severely restricted glucose comparable to spinal fluid, or complete lack of nutrition. Further *in vitro* and *in vivo* characterization of the isolates was performed. The fitness of later isolates was comparably improved compared to earlier isolates depending on the patient, and the length of time between the isolates. This study stresses the importance of studying multiple isolates, rather than only the first isolate, in the case of recurrent infections. We propose that in patients where later isolates show improved fitness, the strains be investigated for differences to help understand why the infection persisted as this may lead to improved therapy against recurrent infections.



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G-17

Comparison between different methods to purify nematic liquid crystals(NLCs) by measuring the concentration of ions using numerical analysis of ion transient

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It is essential to understand the electrical transport behavior of ions in order to understand the performance of devices based on NLCs. In order to utilize NLCs as semiconductors, one must control ion concentrations. There are many different methods to purify NLCs, such as vacuum sublimation, treatment with ionic exchange resins, dispersion in ultra-pure water, and so on. However, it is important to know which method is more efficient when compared to others. We use a technique to measure the concentration of ions by using numerical analysis of ion current transients. We will discuss the above purification methods and compare results of each method by analyzing the ionic transport behavior.



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G-18

Twelve years later: Re-assessing Visual and Olfactory Cues Raccoons Use to Find Diamondback Terrapin Nests

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As is true for many North American turtles, nest predation by Raccoons (*Procyon lotor*) is the primary cause of mortality of Diamondback Terrapins (*Malaclemys terrapin*) eggs laid at Jamaica Bay, New York. Previous research using artificial nests at this site indicated that Raccoons located nests based on soil disturbance and ocean water scent. In addition, they were found to be repelled by human scent, and vinyl marking flags used by researchers did not increase predation rates. To test whether more than a decade of subsequent field work at the same site resulted in a change in Raccoon behavior, we replicated the previous experiments by constructing the same types of artificial nests and adding a design to further test the effects of seven potential cues used for locating and predation of nests: moisture, human scent, terrapin scent, ocean water scent, fresh water scent, soil disturbance and flag markers. Our results corroborate previous research that flag markers are not important cues for Raccoons locating terrapin nests. Contrary to previous research, we found that ocean water scent no longer increases Raccoon predation, and human scent does not repel Raccoons. We conclude that Raccoons have not learned to use signs left by humans. Raccoons in Jamaica Bay continue to locate nests primarily by relying on the tactile cue of soil disturbance rather than visual markers, moisture, or olfactory cues.



The Role of Ruthenium in CO₂ Capture and Catalytic Conversion to Fuel by Dual Function Material (DFM)

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Development of sustainable energy technologies and reduction of carbon dioxide in the atmosphere are the two effective strategies in dealing with current environmental issues. Herein we report a Dual Function Material (DFM) consisting of supported sodium carbonate in intimate contact with dispersed Ru as a promising catalytic solution for combining both approaches. The Ru-Na₂CO₃ DFM deposited on Al₂O₃ captures CO₂ from a flue gas and catalytically converts it to synthetic natural gas (i.e. methane) using H₂ generated from renewable sources. The methane produced is recycled to the inlet of the power plant for reuse maintaining a closed carbon cycle. The Ru in the DFM, in combination with H₂, catalytically hydrogenates both adsorbed CO₂ and the bulk Na₂CO₃ forming methane. The depleted sites adsorb CO₂ through a carbonate reformation process and in addition adsorb CO₂ on its surface. This material functions well in O₂- and H₂O-containing flue gas where the favorable Ru redox property allows RuO_x, formed during flue gas exposure, to be reduced during the hydrogenation cycle. As a combined CO₂ capture and utilization scheme, this technology overcomes many of the limitations of the conventional liquid amine-based CO₂ sorbent technology.

The original DFM contained nano- dispersed calcium oxide and ruthenium, functioning as CO₂ adsorbent and metal catalyst respectively, on a high surface gamma alumina support. We have now found that supported carbonate materials, intimately in contact with a catalyst, show further improvements in performance.

We report the basic chemistry and catalysis associated with the DFM process. Cyclic aging tests for simulated flue gas operations, with and without steam and O₂ present, will be reported. The influence of critical process parameters will be discussed as well.



Spherical Nanostructured Kaolin-Bound SAPO-34 Catalyst for Conversion of Methanol to Light Olefins in a Fluidized Bed Reactor

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Methanol-to-olefins process was taken in to account as a promising alternative non-oil route to produce light olefins. Methanol is one of the largest chemical commodities that can be produced from natural gas, biomass or from coal via synthesis gas. SAPO-34 molecular sieve exhibits higher selectivity toward light olefins among all the implemented catalysts. However, rapid deactivation and short lifetime are challenges for SAPO-34 catalysts. To overcome these drawbacks, fluidized bed reactor was suggested by consideration of reactor design principles. It provides the possibility of catalyst regeneration. In this study, the successful synthesis of kaolin-bound SAPO-34 catalyst by using alumina sol was achieved. SAPO-34 catalysts with different morphologies were synthesized. Then, slurries with constant ratios of SAPO-34 catalysts, kaolin (as matrix) and alumina sol (as binder) were subjected to the spray dryer at constant operational conditions. Different physiochemical characterization methods including XRD, FESEM, BET and FTIR techniques were applied. At first, the catalysts activities were examined in a fixed bed reactor and then the catalyst with the best performance in MTO reaction was used in fluidized bed reactor. The post characterization was also investigated by using TGA and FTIR analysis. Application of TEOS as Si source and DEA/TEA/TEAOH as template combination leads to the smallest particles of SAPO-34 which is a crucial criterion in spraying process to micro spherical particles production.



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G-21

Catalysts promoted with niobium oxides for air pollution abatement

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Pt containing catalysts are currently used commercially to convert carbon monoxide (CO) and hydrocarbon (HCs) pollutants from stationary chemical and petroleum plants that emit volatile organic compounds (VOC). However, Pt containing catalysts are limited by high price and availability. The goal of the research is to find alternative and less expensive catalysts to replace Pt for these applications. We have found that niobium oxides (Nb₂O₅) as supports for certain transition metal oxides promote their activity while maintaining stability and make them possible alternatives to Pt.

The present work reports that the orthorhombic structure of niobium oxide (pre-calcined at 800 °C in air) promotes Co₃O₄ towards the oxidation of both CO and propane, common pollutants in VOC applications. This was surprising result since orthorhombic niobium oxide has a very low surface area (about 2 m²/g relative to the more traditional Al₂O₃ supports 120 m²/g). The results indicate that 1% Co₃O₄/Nb₂O₅ has comparable catalytic activity to 1% Pt/Al₂O₃ and to 1% Pt/Nb₂O₅. Furthermore, 6% Co₃O₄/Nb₂O₅ outperforms 1% Pt/Al₂O₃ both in catalytic activity and thermal stability. These results suggest a strong interaction between niobium oxide and active component, cobalt oxide, likely by inducing an oxygen defect structure with oxygen vacancies leading to enhanced activity towards the oxidation of CO and Propane.