# 1 Tasnim Shikder & Subrina Rafiq  
**Predicting Trends for Data Collected Over Time: A Comparison Study**

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This study is focused on statistical methods for data collected over time. The data used in this project was pulled from two sectors, financial and the public service division, specifically, Apple Stocks and the daily total number of 311 calls. We look at Apple stocks on a daily basis recorded at the closing time from January 2017 to September 2018 (source: NASDAQ). Initial analysis shows evidence of an increasing linear trend and of temporal autocorrelation. The 311 data was sourced from NYC Open Data and aggregated to daily counts for the year 2018. While the distribution of Apple stocks looks bimodal, the 311 daily counts seem to be approximately Gaussian. In the next step, we use mathematical modeling for the estimation and prediction of the mean functions (trends) as functions of time. Model selection including residual diagnostics is then performed, leading to the winning models ARIMA (autoregressive integrated moving average) (5,1,10) for Apple Stocks, and ARIMA (4,1,2) for the 311 daily counts, respectively. Results include five days ahead forecasts based on the selected models and analysis of their accuracy. All descriptive and inferential methods are carried out in R, library TSA.

# 2 Yasmine Oprea  
**Investigating the Role of Potassium Ion Flow in Trypanolysis**

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African trypanosomes are extracellular parasites that cause African trypanosomiasis, or sleeping sickness. They are transmitted by infected tsetse flies to mammalian hosts, but humans and certain primates are able to resist infection by *Trypanosoma brucei brucei* because of innate immune factors known as trypanosome lytic factors (TLFs) which contain the trypanolytic protein Apolipoprotein L-1 (APOL1). APOL1 forms channels in the plasma membrane of the trypanosome, causing ion flux across the plasma membrane. After channel formation in the membrane, there is an initial influx of sodium ions, followed by chloride influx and a loss of osmoregulation resulting from uncontrolled ion flux. We hypothesize that initial sodium influx is counterbalanced by potassium ion efflux through endogenous potassium leak channels. Trypanosomes have a genetically encoded heterodimeric plasma membrane potassium channel that is essential to survival, and we hypothesize that blocking this channel would accelerate lysis. To investigate this, we used potassium channel blocker barium chloride to block the transport of potassium ions across the plasma membrane and performed TLF-mediated trypanolysis assays using TLF-containing high-density lipoprotein isolated from human plasma. We observed that TLF kills parasites more rapidly in the presence of barium, although barium itself does not kill the parasites. However, barium is not entirely specific for potassium channels. Thus, we would like to confirm these biochemical experiments by using reverse genetics via targeted knockdown of the potassium channel in the presence of TLF and repeating these trypanolysis assays. This would help us better understand the mechanism by which APOL1-mediated trypanolysis occurs.
Breast cancer is the leading cause of cancer deaths in women. The current standard of care diagnostic techniques includes mammography, ultrasounds, and MRI scans. Each one has their own obstacles in discriminating between benign and malignant tumor growths. Ultimately invasive biopsies are performed to confirm findings. There’s a need to develop imaging agents to aid in the early detection of malignant tumors and identify possible metastatic spreads. Low pH insertion peptide (pHLIP) targeted optoacoustic imaging targets the acidic microenvironments of cancer. Our strategy offers non-invasive visualization of the heterogeneous distribution of exogenous agents in depth in tissues. We hypothesize that a dark quencher IRDye QC1 pHLIP yields signal. In theory, dark quenchers could convert most of their energy into non-radiative relaxations that generate a larger photoacoustic effect; meanwhile fluorescent dyes convert some of their energy as emitted photons. In this study we used orthotopic mouse breast cancer model for our experiments. Fluorescence imaging and multispectral optoacoustic tomography was used to test both QC1 pHLIP and its fluorescent counterpart. We found that pHLIP-targeted optoacoustic imaging can discriminate between benign and malignant breast cancer tissues in vivo with high signal/noise ratios. In particular, dark quencher QC1 pHLIP demonstrated higher signal intensity in detection of malignant tumors than fluorescent ICG pHLIP. This is encouraging because it has the potential to aid in non-invasive early detection of breast cancer in addition to other types of cancers in a clinical setting.

Myeloproliferative Neoplasms (MPNs) are a group of blood disorders characterized by abnormal proliferation of myeloid cells and a variable affinity for progression towards more aggressive disease. In 2013, whole-exome sequencing of patients with MPNs led to the discovery of calreticulin (CALR) mutations in the majority of previously uncharacterized MPNs (60-70% of JAK2 and thrombopoietin receptor (MPL) wild type (WT) patients). A proteomic approach was used to determine differences in the interactome of wild-type versus mutant CALR in a Ba/F3 cell line. Once differential binding partners were determined, we sought to elucidate how their novel interaction was contributing to leukemogenesis. Mass spectrometry experiments revealed mutant CALR as compared to WT CALR displays enriched binding to Fli1, a megakaryocytic transcription factor, and decreased binding to ERp57, an endoplasmic reticulum (ER) chaperone protein. The formation of this novel interactome is associated with changes in cellular localization of Fli1, ERp57, and CALR especially in the nuclear compartment. We found increased recruitment of Fli1, ERp57, and CALR to the MPL promoter, and increased MPL transcription. Mutations of the CALR gene confer a gain-of-function, which allows mutant CALR to not only constitutively activate the MPL-JAK-STAT signaling axis, but also upregulate MPL transcription by increasing recruitment of
Fli1, CALR and ERp57 to the MPL promoter. Future research will further explore the role of Fli1 and ERp57 in MPN development in order to fully elucidate the mechanism by which mutant CALR contributes to leukemogenesis.

#5 Sophie Hudes

**Analysis of the Binding of RBM22 to U2-U6 and U12-U6atac snRNA Complex of the Human Spliceosome**

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The splicing of precursor messenger (pre-m) RNA is catalyzed by the spliceosome, a dynamic ribonucleoprotein assembly comprising five small nuclear ribonucleic acids (snRNA) and over 100 proteins. Catalysis consists of removing non-coding introns and ligating flanking coding exons together, and is achieved by the RNA components. The catalytic core of the major form of the spliceosome comprises a paired complex of U2 and U6 snRNA, and the minor (low abundance) variant consists of paired U12 and U6atac snRNA. The flexible multi-stem central junction that characterizes the U2-U6 snRNA pairing does not occur in the U12-U6atac complex of the minor spliceosome, making the latter an approachable model for structural analysis. In addition, it is unknown if RBM22, a human protein implicated in folding of the U2-U6 snRNA complex into its catalytic conformation prior to pre-mRNA splicing, maintains a similar role in the minor spliceosome. The goal is to evaluate and compare the interaction of RBM22 with U2-U6 and U12-U6atac snRNA complexes of the spliceosome. Previous research in the laboratory using Electrophoretic Mobility Shift Assay (EMSA) has shown that RBM22 binds the U12-U6atac complex with a dissociation constant (Kd) ~8µM, similar to the Kd for binding of U2-U6 snRNA. Data are now being collected to assay for changes in affinity between RBM22 and mutated sequence elements of U2-U6 and U12-U6atac snRNA to analyze the role of individual nucleotides in binding. Analysis of the interaction of RBM22 with mutated and wild type will create a greater understanding of the molecular determinants of interaction.

#6 Marnie Kotlyar

**Glycosyl Crotylating Agents for the Synthesis of Biologically Relevant Glycolipids**

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KRN7000, also called alpha-galactosylceramine (α-GalCer), is an immunostimulatory glycolipid that comprises an α-O-galactose moiety linked to the C1 position of 2-hexacosanamido-1,3,4-trihydroxy, C-18 lipid chain. KRN7000 stimulates the release of Th1 and Th2 cytokines, which induce inflammatory and immunomodulatory responses, respectively. Regulating Th1/Th2 balance is a promising strategy to combat foreign pathogens, cancer, and certain autoimmune disorders. To this end, KRN7000 analogues with a clear Th1 or Th2 bias and measured potency are needed for clinical development. Thus the immunological evaluation of new analogues of KRN7000 is of considerable interest. Accordingly, the goal of this project is the synthesis of C-glycosides of KRN7000 (analogues in which the glycoside oxygen is replaced with a carbon substituent), for use as mechanistic probes, and as leads for drug development. Our synthetic strategy centers on the reaction of C-glycoside crotylating agents and lipid derived amines. This reaction gives a stereochemically complex glycolipid product that can be transformed to C-glycosides of KRN7000. Critical to the success of this methodology are the key crotylating agents, which should be easily prepared and easy-to-handle. Boron-derived reagents meet these requirements. Accordingly, a suitable C-glycosylborinolate was prepared in six straightforward steps from commercially available D-galactose. The key step in this synthesis was the palladium chloride promoted reaction of a
galactose-derived allylic chloride and bis(pinacolato)diboron, which provided the desired crotylborinate in 65% yield. This material was analyzed using nuclear magnetic resonance spectroscopy (NMR). Our current work is focused on the pivotal reaction of the crotylborinate with imines. These studies have wider relevance to the synthesis of other classes of complex glycomimetics.

#7 Ellesa Naito

**Biotransformation of Tyrosine in Mixed Microbial Culture Derived from Spinach**

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Microorganisms are an important source of potential therapeutic agents, such as antibiotics, anticancer agents, and immunosuppressants. Microbes in soil, in particular, are known as prolific producers of secondary metabolites and studied extensively for the discovery of new drugs. However, little is currently known about the metabolic potential of plant-associated bacteria. To fill this knowledge gap, our group has been examining mixed microbial cultures (MMCs) derived from various plants. Our previous study indicated that an MMC from spinach was capable of transforming tyrosine, a naturally occurring amino acid, into novel metabolites. However, we could not study their chemical structures and biological effects, because the spinach MMC produces only minuscule amounts of tyrosine derivatives. To prepare larger quantities of tyrosine derivatives, we are currently studying the biotransformation of tyrosine in the spinach MMC to see if exogenously added tyrosine increases the yield of tyrosine derivatives. To test this, the spinach MMC was fed with tyrosine and incubated at room temperature for one week. Extractions were performed to isolate the tyrosine derivatives from the culture medium. Thin Layer Chromatography (TLC) of the extracts indicated the production of new metabolites. We are currently conducting a large-scale preparation of the new metabolites for structural characterization. This presentation will include TLC profiles of the extracts, purification of the products of biotransformation, and spectroscopic data of the purified products.

#8 Rawlica Sumner

**Investigation of the Prevalence of Enterovirus 68 in an Oncology Patient Population**

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Introduction: Enterovirus 68 (EV-D68) is a single stranded RNA virus associated with severe respiratory disease in children. In rare cases, EV-D68 was associated with acute flaccid paralysis. The prevalence of EV-D68 infections in oncology settings is unclear. In this study, we investigate the prevalence of EV-D68 in adult and pediatric oncology patients. Methods: Routine detection of Rhinovirus/Enterovirus (R/E) from nasopharyngeal swabs (NPS) was performed using the FilmArray Respiratory Panel (FARP). All patients positive for Rhinovirus/Enterovirus between November 2018 and February 2019 were included if enough remnant sample was available. NPS were stored at 2-8°C for up to 7 days and longer at -20°C prior to RNA extraction on the EasyMag instrument. An internal control was used for each sample. Real-time PCR (qPCR) for EV-D68 was performed as previously described (1). Results: 6,384 NPSs were tested by the FARP. 2,189/6,384 (34.3%) were positive for a respiratory virus with 646/2,189 (29.5%) positive for R/E. 300/646 (46.4%) NPS were available for further testing. To date, 100 NPS have been tested by qPCR for EV-D68. The average age of patients tested was 49-year-old (range: 1-89 years-old), 16 were <18 years of age and 42 were female. 7 samples were excluded due to internal control failure. All 93 samples were negative for EV-D68. Conclusion: Preliminary results suggests that the prevalence of EV-D68 was low or non-existent in this patient population. Testing of the remaining samples by qPCR is pending. Further characterization of the specific Enterovirus genotype by sequencing is on-going.
#9 Christin Rosado

**Progressive Deterioration of Spatial Coding During Epileptogenesis**

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Hunter College Faculty Mentor: Kelle Cruz, Department of Physics and Astronomy

Temporal lobe epilepsy in both human patients and animal models produces cognitive deficits, which can be assessed by examining spatial coding in epileptic mice. Place cells are neurons within the hippocampus that fire at a high rate when humans and animals are positioned in a specific spot within their environment, acting as a cognitive map. Our experiment aimed to understand spatial information processing is altered in an animal model of temporal lobe epilepsy. To test these deficits, we used miniature microscopes enabling in vivo calcium imaging of neuronal activity. Mice ran on a linear track to stimulate place cell activity while we recorded in CA1 (a subregion of the hippocampus). This experiment allowed us to quantify information content and stability of place cells, as well as conduct a time series analysis of place cell stability during the progression of temporal lobe epilepsy. Through imaging CA1 place cells across sessions, we discovered that the spatial processing in CA1 was severely impaired in epileptic mice. Place cells were less stable and carried less information overall. Furthermore, a time series analysis showed that spatial processing deficits became progressively worse across weeks. These results demonstrate the importance of intra-hippocampal communication in the formation of spatial coding and how abnormal firing of neural cells can result in poor spatial processing.

#10 Lon Yin L. Chan

**A Chemical Biology Approach to Exploring the Epichaperome in Cancer**

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Cancer cells continue to thrive in spite of their harsh microenvironments, and have learned to cope with challenges like hypoxia, oxidative stress, nutrient deprivation and immunological surveillance. To adapt, and enhance their survival, cancer cells re-wire important cellular proteins, called collectively the chaperome. By enhancing the interaction strength between participant chaperomes, cancer cells create new entities, called epichaperomes, better suited to deal with the proteome demand present in the malignant state. These epichaperome entities, thermodynamically and functionally distinct from constituent chaperomes, are therefore significantly different from the chaperome units characteristic of healthy cells, and may provide a new target for cancer treatment (Rodina et al, Nature 2016). We hypothesize that an in depth understanding of these tumor-specific epichaperomes and of how the inhibitors influence these complexes in the context of native tumors may enable the design of inhibitors with effective and safe use in the clinic. While currently several inhibitors that target chaperome units have advanced to clinics for cancer, or are in late preclinical development, a study to evaluate their ability to bind tumor epichaperomes, or their selectivity for epichaperomes has yet to be performed. We found that there is a complex time-dependent regulation by the inhibitor. In an initial stage, there is a trapping and stabilization of the epichaperome, followed by subsequent collapse. The functional consequences of this biochemical mechanism include inhibition of onco-protein networks and decreased proliferation and survival of cancer cells.
#11 Safiya Samad & Sharmin Sultan

**Establishing a Method for Recombinant Expression of Disulfide-Rich Venom Peptides**

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Bioactive venom peptides are increasingly being explored as drug leads in pharmaceutical research because of their immense therapeutic potential. However, due to the large number of venomous organisms and the challenges that come with characterizing crude venom arsenals, there is a need to screen and characterize venomous peptides more efficiently in order to expedite the discovery of potential therapeutics. The Holford laboratory primarily studies marine snail venom from Terebridae, an understudied lineage of the predatory marine snails. One of the many challenges of screening and characterizing Terebridae venom is that these snails produce very small amounts of venom. In order to overcome this challenge, we have developed a method to recombinantly express terebrid venom peptides found from next generation sequencing of various species of Terebridae. We successfully synthesized various Terebridae peptides via recombinant expression, which alleviates some of the difficulties of synthesising peptides by solid phase peptide synthesis (SPPS). Our vector design for recombinant expression in *E. coli* cells encodes for a variable peptide region, where any peptide sequence can be inserted, a periplasmic export sequence that targets the peptide to the periplasm to be oxidatively folded, a fusion tag for purification purposes, and a TEV protease recognition site to cleave the variable peptide from its fusion tag. This project will establish a recombinant protocol for successfully generating large quantities of Terebridae venom peptides for further functional analyses in hopes to identify novel potential therapeutic candidates from the Terebridae venom.

#12 Melissa DiMaio

**An All-Optical Implementation of the Deutsch Quantum Algorithm**

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The ability to determine certain properties of functions quickly and efficiently is a primary goal of computing technology today. Quantum computers can perform this task faster and more efficiently than their classical counterparts (Bergou and Hillery 2013). The first efficient quantum algorithm to demonstrate the superiority of quantum computers in this domain was proposed by Deutsch (1985). Its aim is to find symmetry properties of Boolean functions. In the work presented here, we design an all-optical implementation of this celebrated algorithm. The design is based on single-photon multiport quantum interferometry where the unitary transformations corresponding to a particular Boolean function can be realized using beam splitters and phase-shifters in the appropriate beams (Sun, Hillery, and Bergou 2001). Classically, in the simplest case, the function has to be tested for the two possible input values of 0 and 1, so two tests are required. On a quantum computer, a single run can decide whether the function is constant or balanced. Thus, our implementation, which can be built in any optical laboratory from existing components, demonstrates a special case of exponential speed-up in evaluating functions, provided by quantum computers.
The term “superfood” was devised by the food industry to describe foods that benefit health. Although largely done so for marketing purposes, it has brought attention to plants like wheatgrass. Wheatgrass is a concentrated source of nutrients often used to increase hemoglobin production, although the exact mechanism is uncertain. Wheatgrass microbial co-cultures have produced many indole derivatives, which are potential microbial signaling factors. We hypothesized that wheatgrass microbes may process tryptophan to make these indole derivatives, and aimed to utilize small-scale extraction to produce these metabolite molecules more efficiently, in order to shed light on microbe communication. We perform biotransformation of tryptophan into its derivatives using wheatgrass microbes. After initial inoculation, organic extraction of the secondary metabolites produced by the bacteria, and repropagation, we use column chromatography to purify the extract. Preliminary results based on thin-layer chromatography and nuclear magnetic resonance spectroscopy indicate the presence of a tryptophan derivative and a fatty acid, hence a potential novel tryptophan fatty acid metabolite. Our next step to determine the identity of this molecule is to use more precise purification methods to isolate ultrapure compound for mass spectrometry. Our current knowledge of microbial signaling factors is very limited. Recently, tryptophan fatty acid conjugates have been implicated in plant-insect communication. Thus, investigating microbial signaling and communication is of utmost importance not only due to potential medical implications but also to elucidate the many pathways microbes are involved in.
#15 Rebecca Zhang

**Differential Connectivity of the Infralimbic and Prelimbic Cortices with the Basal Forebrain – Amygdala Circuit**

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The study of fear extinction, or the process of learning that a stimulus should no longer signal a fear response, is particularly relevant to the symptoms of post-traumatic stress disorder (PTSD). This project investigates the structural connectivity of brain regions that are implicated in fear extinction. The subregions of the medial prefrontal cortex (mPFC), the infralimbic (IL) and prelimbic (PL) cortices, are frontal lobe structures hypothesized to have opposing functions; fear suppression and expression, respectively. Recall of extinguished fear memories requires the coordinated activation of IL neurons projecting to the basolateral amygdala (BLA), a region responsible for initiating fear-related behaviors. Investigating the indirect projection from the IL to the BLA via the basal forebrain (BF), a region implicated in wakefulness, attention, and learning, adds a new pathway that could attenuate BLA activity following fear extinction. To study the structure of the mPFC–BF–BLA circuit, fluorescent retrograde tracer, cholera toxin subunit B (CTB), was microinjected into the BLA of both hemispheres in mice. An anterograde-tracing virus expressing fluorescent synaptophysin protein was bilaterally microinjected into either the IL or PL. Cholinergic and inhibitory neurons in the BF were immunolabeled, and BF cells were quantified according to subregion, cell type, and mPFC input (IL vs. PL). These experiments have shown that the IL almost exclusively contacts inhibitory BLA-projecting BF neurons. Further behavioral experiments also support our model that during extinction recall, the IL modulates BLA activity both directly and indirectly, by contacting inhibitory projections that go from the BF to the BLA.

#16 Dina Vukel

**Deletion of a wild type SCN5A gene in human induced Pluripotent Stem Cells (hiPSCs)**

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SCN5A is part of a group of genes that encode the proteins that form voltage-gated sodium ion channels (NaV1.5 channels) required for action potentials in heart cells. These channels are essential for maintaining normal electrical pulses and heart rhythm. Structural mutations in SCN5A can cause diseases such as Long QT syndrome and Brugada syndrome, which increase risk of fatal cardiac arrhythmias. Full gene knockouts of SCN5A have shown an increase in fatal cardiac arrhythmias in mice. Our goal was to perform a knockout of SCN5A in human induced Pluripotent Stem Cells (hiPSCs) to better understand the role of SCN5A in human heart function. We targeted a TGG codon in exon 5 using CRISPR to change the sequence to a stop codon, TGA, TAG, or TAA. Our first step was constructing a plasmid expression vector that expressed both guide RNA and Cas9. We then used lipofectamine to transfect the plasmid into the human stem cell line. DNA from transfected cell clones was used to amplify the exon5 region of the endogenous SCN5A gene by polymerase chain reaction (PCR). PCR products were analyzed by gel electrophoresis to determine DNA lengths, and were then sequenced to see if a stop codon had been created. Several clones carried the desired mutation on both SCN5A alleles. Next steps in this project will include differentiating the human induced Pluripotent Stem Cells (hiPSCs) into...
human induced Pluripotent Stem Cell-derived Cardiomyocytes (hiPSC-CMs) and performing RNA profiling and electrophysiological analysis of the mutated hiPSC-CMs.

#17 Kandra N. Cruz

Macronutrient Composition of Foods Eaten by Owl Monkeys (Aotus azarae)

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Understanding food nutrients eaten by primates can offer insight into other areas of ecological studies. While we know much about the different food items that neotropical primates eat, we know little about the nutrients contained within them. We estimated the nutritional composition of foods eaten by the owl monkey (Aotus azarae), in Formosa, Argentina, by observing the monkeys via scan sampling between September 2013 – August 2015. We collected plant parts from the same trees where the animals fed, recorded the date, and processed them in the same manner in which the monkeys ate them. Using wet chemistry methods, the plant parts (N=99) were analyzed for their fiber concentrations (neutral detergent fiber (NDF), acid detergent fiber (ADL), and lignin), crude protein, and lipids. Total non-structural carbohydrates (TNC) were calculated by difference. Since A. azarae live in a highly seasonal environment, our findings demonstrate that during the wet seasons, the owl monkeys appear to be energy maximizers. By contrast, during the dry season, we found that the owl monkeys may have to fallback to lower quality foods higher in protein and fiber. Similar to other studies, our findings suggest non-fig fruits were highest in non-structural carbohydrates and lipids, whereas leaves and flowers were highest in protein. Patterns in diet may help shed some light on the owl monkeys life history and habitat choice.

#18 Frederick Yen

Acetyl-CoA becomes essential under Lysosomal pH Inhibition

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Lysosomes are essential multifunctional membrane-bound organelles involved in macromolecular digestion, metabolism and nutrient signaling. Although lysosomes require the vacuolar type H+ ATPase (v-ATPase) to maintain a significantly lower pH than the rest of the cell, neither the essential function of lysosomal pH nor the metabolic liabilities associated with inhibiting lysosomal acidification are known. To address these questions, we performed a metabolism focused CRISPR/Cas9 genetic screen and identified Pyruvate Dehydrogenase B (PDHB) as an essential gene when Ammonia or Bafilomycin A1 inhibited lysosomal pH. The mitochondrially localized Pyruvate Dehydrogenase Complex converts pyruvate to acetyl-CoA, linking glycolysis in the cytosol to the Citric Acid Cycle in mitochondria. Liquid Chromatography-Mass Spectroscopy (LC-MS) metabolite profiling has shown altered cholesterol and fatty acid synthesis in PDHB-CRISPR knockout cells, thereby suggesting a potential mechanism underlying loss of cell viability. Furthermore, the sensitivity of PDHB knockout cells to lysosomal pH inhibition could be rescued by supplementing acetate, thus, bypassing the need for PDHB-dependent acetyl-CoA synthesis. Finally, although acetate rescues viability, it does not change the lysosomal metabolome, suggesting a requirement for acetyl-CoA distinct from the metabolic changes observed in lysosomes. Taken together, our results suggest that acetyl-CoA is an essential metabolite during lysosomal pH inhibition, functioning in the TCA Cycle as well as cholesterol and fatty acid biosynthesis.
#19 Milana Khaitova

The Effects of Caloric Restriction on Adipocyte Lipid Droplet Size

Milana Khaitova1,2; Ada Weinstock2; Edward A. Fisher2

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Approximately 40% of Americans are obese and this number increases yearly. Obesity may lead to heart disease, stroke, diabetes, cancer and inflammation of adipose tissue, the main site of fat storage. Adipose tissue is stratified into 3 main types with distinct functions: 1) brown adipose tissue, which uses lipids rapidly to produce heat, 2) subcutaneous white and 3) visceral white adipose tissue, which store lipids as an accessible energy source. During obesity, fat cell (adipocyte) size increases as lipids accumulate and are stored, which contributes to the tissue inflammation. Thus, mitigating adipose tissue inflammation is highly desirable. Caloric restriction was shown in multiple species to be anti-inflammatory.

In this study, we wanted to test the hypothesis that mild, short-term calorie restriction will introduce beneficial changes to the obese adipose tissue. Mice were fed a high-fat diet for 24 weeks, after which one group was harvested. The other group was put on a calorie-restricted diet consisting of 70% of their normal food intake of the same high-fat diet for 2 additional weeks before harvest. Adipose tissues were then dissected and analyzed for adipocyte size. Our data show that caloric restriction promotes a decrease in lipid droplet size in the visceral adipose tissue, but not in the subcutaneous adipose tissue.

To conclude, our data suggest that short-term calorie restriction promotes beneficial change to the visceral adipose tissue. Coupled with ongoing studies of the inflammation in adipose tissue, we will determine how calorie restriction influences multiple parameters of adipose tissue biology.

#20 Amanda Onoichenco

The Role of Sex Steroids on Coping Strategy Flexibility, a Novel Female Stress Model

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According to the World Health Organization, major depression is currently the chief cause of disease burden in women, lowering life quality and shortening the lifespan. Upon reaching puberty, young women having the highest risk, globally, of developing depression or other affective disorders. We have found that coping strategies for stress are sex-specific, with females demonstrating increased flexibility in stress response. They show increased variability in choosing between a flight or fight response, which can have implications for future therapeutic treatments. The dopamine reward system is crucial in regulating these responses. Dysregulation of dopaminergic neuron firing rates in the ventral tegmental area (VTA) can be predictive of coping response to stress and, thus, susceptibility to depression and anxiety. While stress paradigms exist, many are designed for male mice and intense physical stress. We have designed a female-specific stress model. Using this model we are able to consider the effects of the of the fluctuating levels of estrogen and progesterone on stress susceptibility or resilience. Through a series of acute variable social stressors, we are able to simulate stressors similar in effect to those we experience daily. The stressors include overcrowding, home cage instability, exposure to predator odor, restraint, and witnessing restraint. Through enzyme-linked immunosorbent assays, we found that levels of corticosterone, a hormone involved in the stress response, increases during the four different social stresses. Utilizing a social interaction test, our preliminary results indicate that following these stressors a subset of females demonstrate social withdrawal, while a subset increases social interaction as compared to control stress naïve mice. This diverse response to stress indicates that females demonstrate flexibility in coping strategy when faced with social stress. We anticipate underlying differences within the dopaminergic system to be driving this behavioral response. Further preliminary results indicate that
estradiol level during stress modulates the coping strategy and behavioral response during social interaction, with estrogen withdrawal increasing stress susceptibility. As a counterpoint, in the upcoming stages of our research, we will be simultaneously measuring the corticosterone and estradiol levels determining the interaction.

#21 Rufina Kamaletdinova

**Role of the Mesocortical Pathway in Resilience to Stress**

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Exposure to stress is an important environmental factor that induces changes in the brain circuitry. It has been shown that mice susceptible to stress exhibit a decreased firing of the ventral tegmental area (VTA) projecting to medial prefrontal cortex (mPFC) neurons as compared to resilient mice. However, the role of the mPFC neuronal feedback to the VTA in this context is unclear. We hypothesize that the mPFC neurons projecting to the VTA have a role in mediating the behavioral stress response, and that these interactions change as the result of stress exposure. Previous studies have shown that repetitive transcranial magnetic stimulation (rTMS) had a positive effect on people's mood when administered on the right prefrontal cortex, but not the left prefrontal cortex. By exploring the lateralization of the mPFC-VTA projections, we hope to learn more about how rTMS can be used to target more specific brain areas in the treatment of depression. We aim to determine lateralization of the mPFC-VTA projections, identify stress mediated changes in the mPFC-VTA projection that contribute to stress vulnerability and resilience, and determine functional relevance of the changes in the mPFC-VTA pathway. We have performed intracranial injections of two different color retrograde tracers into the VTA. We found that this tracer is taken up into the neurons of the mPFC that project to the VTA. Utilizing confocal microscopy, we have visualized the two different color retrograde tracers and have confirmed our injection site in the VTA. We are performing a cell count analysis of the number of mPFC-VTA neurons and determining if there is a quantitative difference the two sides of the brain. Given that the long-term goal of the study is to understand the mechanisms in the brain that are responsible for stress resilience we will be further characterizing these neurons electrophysiologically. We predict that the mice with a stronger connection and exhibited increased plasticity from the mPFC to the VTA will show more robust resilient behavior.

#22 Nailya Khalizova

**Depleting Extracellular Ca²⁺ leads to a Decrease in Cytotoxicity due to Enhanced Trypanosome-protective Variants of APOL1**

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Trypanosomes are a major agricultural barrier in Sub-Saharan Africa, affecting livestock. Humans, however, are immune to some species of trypanosomes due to immunity conferred by an innate immunity protein, Apolipoprotein-L1 (APOL1). The recently evolved variants of APOL1 in humans are linked to an increased risk of developing kidney disease. While the trafficking of APOL1 in trypanosomes has been widely characterized, the pathway of APOL1 toxicity in the kidney is not clear. To elucidate APOL1's role in increased kidney toxicity, we looked at the trafficking of APOL1 in a mammalian cell system. Using live wide-field fluorescent microscopy, we previously showed that APOL1 forms Ca²⁺ conductive channels at the surface of mammalian cells. In order to elucidate the role of Ca²⁺ conductance in APOL1 toxicity, we measured cell death induced by APOL1 in cells that were treated with different amounts of ethylene glycol tetraacetic acid (EGTA), a Ca²⁺ chelator. Based on the results so far, reducing extracellular Ca²⁺ levels with 1.5 mM EGTA leads to ~25% reduction in toxicity caused by kidney disease variants *in vitro*. 
Currently, we are working on confirming our results and further elucidating the role of Ca2+ conductance in APOL1 toxicity. Eventually, understanding the role of Ca2+ in APOL1 cell toxicity pathway could be useful for targeted drug development in the future.

#23 Angelica Y. Rozenfeld

**Photochemical Printing of Multiplexed Glycan Microarrays for Glycan Recognition Studies**

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Glycan recognition studies provide us with insight on vital biological processes by helping detect antigens, develop vaccines and discover different bio-markers. Glycan microarrays, consisting of glycans patterned onto a surface with micrometer-scale feature diameters, can test binding interactions. With the use of a new printer, which combines microfluidics, a digital micromirror device, and a photochemical thiol-ene click reaction, we aim to generate glycan microarrays that can minimize the amount of expensive glycan needed in binding studies, and help to explore the effect of cooperative and multivalent interactions on glycan-lectin interactions. Two different types of glycan microarrays were printed to test the validity of this microarray platform for studying glycan recognition: a multiplexed glycan microarray in which different glycans were immobilized to test lectin-glycan binding combinations, and a microarray with varying densities of a single glycan to probe the role of valency in lectin-glycan binding. The former showed that the binding specificities of the immobilized glycans were consistent with known trends, and the latter revealed that altering density allows for studying subtle surface effects—both of which render the use of these spatially-encoded glycan microarrays an efficient way of mimicking the biological activity of immobilized glycans in the glycocalyx. This approach to studying glycan-lectin recognition furthers our understanding of glycan binding in biological processes, like inflammation and tumor metastasis, and allows for the cultivation of newer and more specific remedies.

#24 Desiree Pante

**Lyme Disease Vaccine Development: Optimizing Bacterial Production of Recombinant Antigens**

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Lyme disease is the most prevalent vector-borne disease in the United States that affects 25,000-30,000 people annually. Lyme disease is caused by, *Borrelia burgdorferi*, a bacterial pathogen transferred from ticks to a host species including humans. Local populations of *Borrelia burgdorferi* consist of a diverse set of strains, making it hard to develop a broadly effective vaccine. We want to find an effective recombinant antigen that would recognize and cross-react to different outer surface protein C (OspC) antigens. The *B. burgdorferi* OspC is a vaccine candidate due to its high expression during host invasion. Twenty *ospC* alleles have been cloned into plasmids and expressed in *E.coli*. By measuring growth conditions for strains with individual alleles, we aim to maximize the yield of recombinant proteins. We use R to obtain statistical estimates of parameters of the growth curves. A statistical method has been developed to estimate growth rates in R/Rstudio. This experiment is ongoing and we have used this method on four out of twenty alleles, which allowed us to maximize the production of these antigens.
Diagnostic Differences in Patterns of Threat-Related Attention Bias
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Threat-related attention bias (AB), or selective and exaggerated attention towards threat-relevant stimuli, is a core feature of anxiety disorders (Bar-haim, Lamy, Pergamin, Bakermans-Kranenburg, & van Ijzendoorn, 2007). However, it remains unclear whether generalized anxiety disorder (GAD) and major depressive disorder (MDD) are associated with similar or distinct patterns of AB. The aim of this study was to compare patterns of AB in people with a primary diagnosis of GAD versus MDD. Three distinct metrics of AB were calculated from the dot probe (DP) task: threat bias, vigilance, and difficulty disengaging. Additionally, an exploratory measure of AB trial-level variability was assessed to further explore AB differences amongst a community sample of adults (N = 64) with moderate to severe anxiety, as reported by the shortened Depression Anxiety and Stress Scale (DASS-21). In place of self-report questionnaires, this study utilized the Mini International Neuropsychiatric Interview (Version 6.0), a structured clinical interview for Diagnostic and Statistical Manual of Mental Disorders (DSM-IV-TR), psychiatric disorders to categorize participants into diagnostic groups of primary GAD, MDD and healthy controls, in order to compare the distinct patterns of AB amongst the groups (Sheehan et al., 1998). Only those with a primary diagnosis of MDD showed significantly greater AB compared to healthy controls. However, those with a primary GAD diagnosis showed greater AB variability compared to healthy controls. This suggests that dynamic, temporal elements of AB are important to examine amongst those with GAD. Future studies should assess whether co-morbidity of GAD and MDD impact expression of AB.

Expression and Interaction of the RNA Methyltransferase Enzymes METTL14 and METTL3
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Chemical modification of mRNA is known to be involved in RNA metabolism, splicing, and localization. The N6–methyladenosine (m6A) modification is the most common form of mRNA modification where a methyl group is transferred onto RNA transcripts at amino acid residues within specific motifs. This process is done by the methyltransferase enzymes METTL3 and METTL14, which form the core subunits of the m6A modification complex. RNA methylation has been implicated in several biological processes and diseases. METTL3 interacts with METTL14 via its methyltransferase domain (MTD). This interaction is essential for the methyltransferase activity of the METTL3/METTL14 complex. These proteins contain multiple phosphorylation sites that are thought to be involved in their dynamic regulation. We focused on a Serine residue in position 399 of METTL14, which is in the MTD. We hypothesized that phosphorylation at this site is important for METTL3/METTL14 complex formation. Therefore we mutated the S399 residue to show its effect on METTL14 binding to METTL3. We tested this hypothesis by expression of our proteins in bacteria. We cloned wild type METTL3 and METTL14 genes into a bacterial expression vector and showed expression of the proteins in bacteria by Western blotting. In the absence of post-translational modification at the S399 residue, we expected no interaction between the proteins. We next cloned METTL14 with a phospho-mimick glutamic acid mutation in the S399 residue. Immunoprecipitation of METTL14 will be used to demonstrate the effect of S399 mutation on binding with METTL3 in WT versus mutated METTL14.
#27 Philip Golubowski

**Impact of Structured Reengagement on HCV Testing**

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Background: Since the hepatitis C virus (HCV) infection cannot be vaccinated against, HCV screening in Emergency Departments (EDs) can have positive public health impacts. In a universal, non-targeted, HCV screening program, 70% of ED patients refused an initial nurse offer of HCV testing. We sought to determine the effect of structured reengagement on HCV testing outcomes after initial test refusal.

Methods: A program evaluation of HCV screening was conducted on patients presenting to an urban ED between June 6, 2018 and November 27, 2018. All adults 18 years or older were offered HCV testing during the initial nurse assessment. Patients who declined the nurse testing offer were reengaged by research associates (RAs).

Results: During the evaluation period, there were 40,679 adult ED visits and 4,649 reengagement encounters. Most (93.5%, n=4,345) reengagement encounters were in patients who refused the nurse offer of HCV testing. In nearly all cases (99%, n=4,614/4,649), patients were approachable for reengagement. In total, 54% (n=2,305/4,247) of all reengagements resulted in a discussion about HCV testing, after which 820 patients (36%, 803/2,305) agreed to HCV testing and 76% (n=636/803) had HCV test performed. This accounted for 12% of the total number of HCV tests performed (636/5,270). Out of 636 tests performed after reengagement, 53 were HCV Ab+ (Antibody positive); almost half (47%, n=25/53) were VL+(viral load positive).

Conclusion: Reengaging patients resulted in a moderate (12%) increase in the number of HCV tests performed in screening program. Patients with active HCV infection, who might have otherwise refused testing, were convinced to test after reengagement, enabling identification of their infection and linkage to care.

#28 Kimberlee McPherson

**WASP acts downstream of Paxillin during plaque formation**

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Cancer is prevalent in today’s society. While a localised tumor can be removed surgically once cells leave the tumor and metastasize treatment becomes much more difficult. Understanding the migratory behavior of cells will aid in the process of controlling and reducing metastasis the number of cancer cells that exist.

The actin cytoskeleton is important for cell migration. It forms a complex network of filaments whose regulation is important for processes such as chemotaxis, endocytosis, exocytosis, and multicellular development. While much is known about actin cytoskeleton, we still have some unanswered questions about the pathway of the phenotypes involved in cell motility. Both Paxillin and WASP play a crucial role in actin-based processes. The laboratory studies the role of extracellular factors in regulating cell behavior in Dictyostelium discoideum, a simple eukaryote. In their studies, they have identified PaxB (Paxillin) and WasA (WASP), two genes that appear to regulate similar actin-based processes. From our experiment, we determined the generic relationship between PaxB and WasA by using plaque assays. We found that PaxB- cells formed large plaques while WasA- cells formed small plaques. The PaxB-/WasA- cells formed small plaques which suggested that both genes were acting in linear pathways, in which WasA was downstream to PaxB. Understanding the genotypes involved in cell motility will allow us to understand cell behavior and will help with reducing cancer cells in cancer biology.
Background/Hypothesis: Glioblastomas are the most aggressive brain tumors, and enhancing lesions on brain imaging studies are usually interpreted as worsening of tumor. After immunotherapy, lesions may enhance from an inflammatory response. This “pseudoprogression” may confound assessment of treatment response. We hypothesize that texture analysis, which measures spatial arrangements of image intensity, may improve prediction of survival in patients with glioblastomas. Methods: We retrospectively analyzed data on 16 immunotherapy patients with glioblastomas. Enhancing lesions were manually segmented (3D Slicer) on magnetic resonance (MR) images and their maps (Ktrans and VP) before immunotherapy. An in-house software extracted 49 texture features, and 3 relevant texture features were selected using regression analysis (LASSO). Selected features were segregated by median values and correlated with progression-free survival (PFS) and overall survival (OS) by Kaplan-Meier analysis (p<0.05). Results: Among 16 patients, median age was 51.5 with 9:7 female to male ratio. Median recurrences per patient was 3; median treatment doses were 4. Median PFS from start of immunotherapy was 2.5 months; median OS was 5.7 months. All tumors were successfully segmented. Using LASSO, two of three textures significantly correlated with survival. Correlation with PFS and OS, respectively, for selected texture features were: “mean Gabor8,” p=0.028 and p=0.037; “correlation VP,” p=0.011 and 0.01; and “standard deviation Gabor1”, p=0.27 and 0.81. Conclusions: Our small series suggests that texture analysis has the potential to predict survival in patients with glioblastomas. Larger prospective studies are needed to further evaluate this promising technique.

Alzheimer’s Disease (AD) is a progressive neurodegenerative disorder and the sixth leading cause of death in the US. A hallmark of AD is chronic neuroinflammation caused by overactive microglia, the resident immune cells of the CNS. The inability to reduce this inflammatory response leads to chronic neuroinflammation. AD drugs have a 99.6% failure rate and because of the difficulty and costliness of creating novel drugs, our study aims to repurpose existing drugs for treating AD. A bioinformatics approach identified four drugs with potential targets in the AD neurodegenerative pathways: Diazoxide (DZ) a potassium channel activator, Rolipram and Ibudilast, both phosphodiesterase inhibitors, and Dibenzoylemethane (DIB), which alleviates ER stress. Upon drug treatment, human microglia (HMC3) were analyzed for viability (MTT assay) and cytokine secretion (ELISA). We established that DIB was toxic. DZ and Rolipram showed no significant cytotoxicity, while Ibudilast was toxic only at the highest concentrations tested. Moreover, Ibudilast was the only drug that significantly changed the microglia cytokine profile. At 10 µM, Ibudilast increased the levels of IL-13, an anti-inflammatory and neuroprotective cytokine, while at 100 µM Ibudilast lowered the levels of IL-13 while raising IL-6, a pro-inflammatory, neurotoxic cytokine. These data complement the MTT results. Based on our results and those of others, we are assessing the therapeutic effects of Ibudilast in a transgenic rat model of AD.
Examining whether these drugs modulate the release of neurotoxic and neuroprotective cytokines by microglia has potential for treating neuroinflammation in AD. Support: NIH 1R01AG057555-01A1 [to LX (PI), PS, PR, MEF-P]

#31 Eleonora Achrak
Unlocking the Glow: Characterize of Bioluminescent Genes in Fireworm (Odontosyllis enopla)

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Odontosyllis enopla is a fireworm that is typically found in Bermuda that has a fascinating and impressive bioluminescent mating technique. A few minutes after a full moon rises female worms will come to the surface of the ocean and make a green glowing bioluminescent display that attracts male worms for mating. The female’s bioluminescent glow is controlled by the enzyme luciferase, which regulates oxidation of the protein luciferin allowing it to glow. The initial discovery of the luciferase gene was reported as a novel gene due to lack of homology to genes in public databases. However, recent findings indicate some orthology and paralogy between transcriptomes from non-bioluminescent genus from the same family (Syllidae) and a bioluminescent species from the sister family (Harmothoe areolata). This revelation can indicate a rapid evolution of the luciferase different species. In order to fully test the hypothesis that luciferase has convergently evolved we will analyze transcriptome and genomic data from Odontosyllis enopla. Preliminary data indicates syllid luciferase gene may have been evolved through duplication and neofunctionalization. To determine the evolutionary rate, we compared nonsynonymous substitutions to synonymous substitutions in the luciferase gene. The genes in question were assembled and annotated using Velvet, Rascaf, and Augustus. After creation of scaffolds, a series of BLAST operations were performed to characterize genes and their location. The final step of this project was to combine all the data to create a robust genomic and transcriptomic database to address the question of luciferase evolution in Odontosyllis enopla.

#32 Jessica Gjonaj
Impact on Mortality by Number of Vasoactive Agents Used Prior Mechanical Circulatory Support for Cardiogenic Shock

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Modern treatment for Cardiogenic Shock (CS) which is the result of inadequate blood flow to the body’s organs due to a dysfunction of the heart’s ventricles, also includes use of mechanical support including venoarterial extracorporeal membrane oxygenation (VA-ECMO), left ventricular assist devices, such as the Impella heart pump and combination VA-ECMO with Impella (ECPELLA). As mechanical support is initiated, many patients are still treated with vasoactive agents first. This prospective observational study of patients with refractory CS requiring Impella, VA-ECMO or ECPELLA identified 85 patients. The primary endpoint was number of vasoactive agents used prior to start of mechanical support and 30-day mortality. Secondary outcomes were survival to explant, removal of mechanical support, and survival to discharge. There was a numerical increase in explant survival for 0-2 agents used vs. 3 or more (73% vs 62%; p 0.3). This increase in survival for 0-2 agents used was seen for ECPELLA alone (88% vs 98%; p
0.16) but not for Impella or VA-ECMO. Similar trends in 30-day survival and survival to discharge were seen in the total cohort and ECPELLA group. Lower use of vasoactive agents was numerically associated with improved mortality but did not reach statistical significance. We hypothesize that this lack of difference is due to small sample size and that a larger trial is necessary to better assess if fewer vasoactive agents would increase survival for patients in CS.

#33 Jordy Sepulveda
Therapeutics to Target Amyloid Beta and Tau in Fibroblasts from a Familial Alzheimer’s Disease Patient: Relevance to Drug Repurposing
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Alzheimer’s Disease (AD) is a progressive neurodegenerative disorder that accounts for 60-70% of dementia cases. In AD, the A42 fragment of the amyloid precursor protein (APP) and hyperphosphorylation of the microtubule-associated protein tau, play important roles in disease pathology. Moreover, familial AD is associated with higher levels of A42. Drug discovery for AD has had limited success. Repurposing of FDA-approved drugs could streamline the identification of AD therapeutics. Our in silico studies predicted the following: (1) Diazoxide (DZ), which is FDA-approved for hypertension, is a potassium channel activator that could activate multiple AD-relevant kinases. (2) The anti-inflammatory Ibudilast (IBU) and the antidepressant Rolipram (ROL) could inhibit AD-relevant phosphodiesterases. (3) The cancer-preventing Dibenzoylmethane (DIB) could induce the expression of antioxidant enzymes. We investigated the therapeutic potential of these four drugs against A42 and A40 production in skin fibroblasts from a familial AD patient carrying the A246E mutation in the presenilin 1 gene. Cell viability (MTT) assays established that DZ, DIB, and ROL are not toxic, but DIB is. Assessing A42 and A40 secretion with ELISAs demonstrated that DZ and IBU decrease A42 production, suggesting that these drugs may reduce AD pathology. The effect of these drugs on tau hyperphosphorylation is also being determined. Moreover, we are testing whether the in vitro anti-AD effects of IBU will be reproduced in a transgenic rat model of AD, thus offering a new treatment strategy for this disease.
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#34 Emily Makowicz
Post-Transcriptional Regulation of Maternal mRNAs by Nonsense-mediated Decay
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Upf1 is an ATP-dependent RNA helicase known for its canonical role during nonsense-mediated mRNA decay (NMD). Upon splicing, it dynamically associates with the exon junction complex (EJC) and recruits downstream factors, including exonucleases, that degrade transcripts (1) harboring a premature termination codon (PTC) or (2) to downregulate endogenous levels of certain genes. During D. melanogaster oogenesis, core EJC factors have been shown to regulate a key maternal transcript, oskar, but Upf1’s role in this process is poorly understood. Here we characterize Upf1’s localization pattern during oogenesis and propose a role for it in clearing oskar mRNA following bulk translation. Additionally, we find that the MAP kinase cascade that regulates gurken mRNA translation may also be affected when one of Upf1’s targets, gadd45, is not properly degraded.
#35 Pavan Khosla

Shannon Information as a Measure of Codon Bias: an Application in the Genomes of Lyme Disease Bacteria

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The spirochetal bacterium \textit{Borrelia burgdorferi} is infamous for causing Lyme disease, which is the most prevalent arthropod-borne infection in the United States. To test the hypotheses that plasmids and genes vary in codon bias – nonrandom use of synonymous codons – due to evolutionary history and gene function, we developed a new measure of codon bias based on the Shannon Information index. Codon biases were compared among three Lyme disease strains: i) B31, ii) PBr, and iii) PKo, as well as among two major \textit{B. burgdorferi} plasmids, cp26 and lp54. Outcomes revealed significant differences in the codon bias in all of the strain-plasmid pairs examined in this study: i) B31-\textit{cp26} with 13/24 (54\%) noted loci, ii) PBr-\textit{cp26} with 17/25 (68\%) noted loci, iii) PKo-\textit{cp26} with 18/26 (69\%) noted loci, iv) B31-lp54 with 16/61 (26\%) noted loci, v) PBr-lp54 with 21/49 (43\%) noted loci, and vi) PKo-lp54 with 13/52 (25\%) noted loci. This data may one day contribute to the identification of highly expressed surface proteins as vaccine candidates as well as to reconstruct history of genome evolution in \textit{B. burgdorferi}. This project was made possible with NIH funding.

#36 Paul Dyduch

Using Hyperspectral Imaging and Artificial Neural Networks to Detect \textit{E. coli} on Romaine Lettuce and Spinach

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A recent outbreak of pathogenic \textit{Escherichia coli} in romaine lettuce has renewed calls to find a rapid and effective means of detecting potentially harmful bacteria on fresh produce before it is released into the supply chain and consumed. The goal of this study was to use hyperspectral imaging as a means of detecting \textit{E. coli} on romaine and spinach leaves; collected data was then used to train an artificial neural network to distinguish between contaminated and non-contaminated leaves. Leaf samples were inoculated with a mixture of non-pathogenic \textit{E. coli} and then analyzed using a hyperspectral instrument with a 400-1000nm excitation range to produce a reflectance of 82 bands per pixel. We anticipated the inoculated leaves would emit a different reflectance, due to the presence of the bacteria themselves and their metabolic wastes. The collected hyperspectral images were displayed and processed in Environment for Visualizing Images (ENVI) software to extract data by pixel, which was then averaged across each sample class collected. Comparison of mean data shows a discernable difference between \textit{E. coli} treated and control samples, suggesting that hyperspectral imaging is potentially an effective means of detecting produce contamination. Chemometric analysis in the form of a multilayer artificial neural network was up to 100\% effective in distinguishing contaminated from non-contaminated spinach samples. The 72\% efficiency in the case of romaine lettuce can be attributed to error in data processing. Nevertheless, the high efficiency of the artificial neural network suggests coupling it with hyperspectral imaging may be a beneficial means of rapid detection. This project was made possible by NSF funding.
#37 Muhammad Nazim

Improved Epitope Prediction on the Outer Surface Protein C

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The outer surface protein C (OspC) is a highly expressed surface antigen of Lyme disease pathogen, *Borrelia burgdorferi*, and therefore is a prime vaccine target. In the United States, there are at least 23 distinctive OspC alleles carried in *B. burgdorferi* populations, such that a Lyme disease infection with one strain does not induce immunity to later infections from other strains. Identifying key and, in some cases, shared epitopes (i.e. antibody binding sites) on the allelic OspC proteins is essential for the design of polyvalent vaccines that will be effective against multiple antigen alleles. In a previously published study, the sera of 55 adult patients and 23 mice were used to generate the pairwise cross-reactivity correlation data between alleles. We have subsequently improved epitope identification in three ways. First, we applied statistical normalization among individual human and mouse samples. Second, we used the latest genomic sequences to obtain N-Terminus sequences of the alleles, information that was lacking in the original study. As a result, we identified a previously unknown, stronger epitope at the N-Terminus of OspC. Third, we generated confidence intervals for predicted epitopes as well as web-interactive visualization of pairwise allele cross-reactivity. This improved epitope prediction model will help the design of polyvalent OspC-based vaccines against Lyme disease.

#38 Juan A. Cambeiro

Cup Is Necessary for Translational Repression of *oskar* mRNA and Maintenance of P-bodies

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Regulation of gene expression at the mRNA level is fundamental for normal cellular function. In *D. melanogaster*, mRNAs essential for embryonic development encode proteins critical to several specific regulatory processes such as cell division and development. During oogenesis, these essential developmental mRNAs are transported from nurse cells into the oocyte in a translationally repressed state. *oskar* mRNA is localized and translated at the posterior, where it initiates the anterior-posterior axis specification and germ plasm assembly. Cup protein is involved in the translational repression of *oskar* until it is localized, but this mechanism is not entirely clear. Here we show that Cup forms a stable association with *oskar* throughout oogenesis and that it is indispensable for its translational repression during early oogenesis. Moreover, absence of Cup results in altered P-body morphology, suggesting that Cup also supports the formation and/or maintenance of P-bodies. Together, these results help elucidate an intertwined mechanism of post-transcriptional gene expression regulation, where Cup serves as a master regulator for coordinating several cellular processes.
The U.S. is in the midst of a terrible opioid epidemic, and identifying novel opioid-responsive circuits may be key in development of novel therapeutics to treat addiction. The Dorsal Peduncular Cortex (DP) contains glutamatergic neurons that primarily project to the rostromedial tegmental area (RMTg) and the trigeminal nucleus (TGN), which regulate aversion and pain responses, respectively. The DP has not previously been studied for its role in reward or aversion, but data indicate much higher expression of the µ opioid receptor (MOR) in the DP than in surrounding medial prefrontal regions, hinting at a role in actions of opioids. Following i.p. injection of 5mg/kg oxycodone into mice, whole brain mapping of c-fos expression revealed that the DP is indeed a highly oxycodone-responsive region. Interestingly, optogenetic stimulation of the DP resulted in real-time avoidance behaviors in mice. Thus, we hypothesize that oxycodone acts through the G(i)-coupled MOR to inhibit this aversive circuitry, producing reward through negative reinforcement. While it is apparent that there is a significant induction of c-fos in the DP following acute injection of a rewarding dose of oxycodone, it is unknown how this region is involved in more complex models of addiction. Ongoing studies are investigating the behavioral role of this region in conditioned place aversion, conditioned oxycodone withdrawal following chronic administration, and the ability of oxycodone to attenuate DP-stimulation-induced aversion.

In vivo and in vitro targeting with fluorescent proteins (FPs) is widely used tool in research. Commonly employed FPs in far-red spectra (mCardinal, mKelly1 and mKelly2) have proven and stable characteristics such as excitation and emission spectra and maturation time. However, their excitation spectra overlap with the mCherry spectrum, which does not allow us to use both FPs in one organism. We are interested in developing one or more FPs in far-red spectrum to allow simultaneous targeting several proteins of interest in a single organism and to minimize background noise due to natural light emission in animal tissues. We have several mutations of red and far-red FPs, which showed their potential to exhibit non-overlapping emission spectra. We expressed those proteins in Escherichia coli and extracted them to analyze their stability, excitation and emission spectra, quantum number, maturation time and other parameters. We have characterized a novel FP with excitation spectra at 640 nm and up and a variation in mCherry protein with green shifted excitation spectra, which resulted in reduced overlap between them. The development of novel FP in red and far-red spectra may increase the yield of information we can obtain from a single organism by visualizing different structures of interest simultaneously. This project was supported in part by the Office of the President of Hunter College.
Erica M. Rosario

Identifying HIV-1 Rev Cellular Cofactors

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HIV requires its own unspliced RNA to be exported from the nucleus and transported to the cytoplasm in order to translate proteins and assemble virions needed for viral replication. The HIV-1 Rev protein is essential for the nucleocytoplasmic export of partially spliced and unspliced viral transcripts, which makes it an attractive target for drug development. Our aim is to identify cellular factors that are essential for Rev protein function by using RNA interference (RNAi). In humans, the DDX6 protein binds HIV-1 RNA before it leaves the nucleus to enter into the cytoplasm. Depletion of the DDX6 protein reduces the propagation of HIV in human cells. We find that under nutritional stress, Me31B and Rev-EGFP are accumulated in stress granules, which serve as cytoplasmic RNA storage sites. We hypothesize that Me31B, the fruit fly homolog of DDX6, may be a Rev cofactor, and that down-regulation of me31B gene expression will affect transport of intron-containing viral RNAs. To test our hypothesis, we generated two fly stocks that express subgenomic viral RNA (pgTat) and Rev-EGFP under UAS/Gal4 control; one of these stocks expresses endogenous Me31B protein, while in the other stock, me31B gene expression is knocked down through RNAi. Using spinning disk confocal microscopy, we analyzed pgTat RNA distribution pattern in fixed egg chambers via single-molecule RNA FISH and found that when expression of me31B gene is down regulated, the HIV-1 RNA aggregates at the anterior cortex of the oocyte. We co-visualized HIV-1 Tat RNA and Rev-EGFP distribution in the nurse cells, and observed that they colocalize in large aggregates, indicating that Me31B is important for efficient trafficking of both viral RNA and Rev protein.

Daniel R. Antohi

The Impact of Early Life Stress on Anxiety and Depression Predisposition in Later Life

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Major Depressive Disorder affects 8-10% of adults in the United States, and is the leading cause of disability worldwide. Previous research indicates that early life stress is a risk factor for developing impaired cognitive function and mental illnesses in adulthood. Our experiments therefore aim to investigate how early life stress can affect brain function and anxiety- or depressive-like behavior using a mouse model. To achieve this, we used the limited bedding model of early adversity. In this model the dam and her pups are housed on a wire mesh platform in the cage, and provided with one-third of the usual amount of bedding. The limited bedding results in the dam becoming uncomfortable and stressed when nesting. This translates into impaired maternal care, which is known to be a stressor for the pups. Shortly after the mice are weaned they begin testing for anxiety- and depressive-like behavior using the open field test (OFT), elevated plus maze (EPM), and social interaction tests. Our ongoing behavioral analyses in pups aged 35 days to 45 days will determine whether differences exist between mice that received early life stress and the mice that served as controls in the time these mice spend in anxiogenic compartments of the OFT and EPM, as well as in the time interacting with an adult conspecific. Ultimately, this study aims to provide insight into the extent to which early life stress impacts vulnerability to anxiety, stress, and depression later in life.
#43 Darlene Urena

**Purifying Serum Resistance Associated Protein in African Trypanosomes to Study its Structure**

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African Trypanosomes cause trypanosomiasis, also known as African sleeping sickness. There are several subspecies of trypanosomes that include *T. b. brucei* and *T. b. rhodesiense*. Humans are unable to kill *T. b. brucei* because of a high-density lipoprotein called trypanosome lytic factor (TLF). Apolipoprotein L-I (APOL1) is the lytic component of TLF that is taken up by the parasite. APOL1 inserts into the endosomal membrane at an acidic pH. It is then recycled back up to the plasma membrane where it encounters a neutral pH. APOL1 then opens as a cation channel, leading to parasite death. However, humans are not resistant to *T. b. rhodesiense* due to serum resistance associated protein (SRA) synthesized by the parasite. Unlike *T. b. brucei*, SRA is present in *T. b. rhodesiense* and binds to APOL1, preventing lysis. SRA has a glycosylphosphatidylinositol (GPI) anchor that anchors it to the membrane. While other GPI-anchored proteins are extracellular, SRA is both intracellular and extracellular, where it interacts with APOL1. It is important to further analyze the structure of SRA to better understand why and how SRA binds to APOL1. We hypothesize that SRA’s GPI anchor has unique modifications that affects its localization. Our objective is to purify SRA from trypanosomes to analyze its GPI anchor. We plan to do so by affinity chromatography using an antibody to SRA. However, to do so we need to better characterize how these antibodies bind and release SRA. We are currently testing different antibodies to refine our SRA purification protocol.

#44 Michelle Savran

**Natural IgM antibodies bind to Trypanosome Lytic Factor 1 to form Trypanosome lytic factor 2**

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Trypanosome lytic factors 1 and 2 (TLF) are lipoprotein complexes that mediate human immunity by delivering the channel-forming apolipoprotein 1 (APOL1) to African trypanosomes. TLF2 is distinguished from TLF1 by non-covalently associated immunoglobulin M (IgM) antibodies. TLF2 is present in all human serum regardless of infection history, but at a lower quantity than TLF1. We hypothesized that infection leads to an increase in IgM available to bind to TLF1, resulting in TLF2 increasing. We assessed this by measuring TLF1 and TLF2 in human serum and observed a shift in equilibrium from TLF1 to TLF2 after infection in sleeping sickness patients. We recapitulated this shift using mice expressing APOL1 and haptoglobin-related protein (Hpr) after hydrodynamic gene delivery (HGD) and observed that while mice make only TLF1 initially, TLF2 is produced after infection. TLF2 production correlates with the rise of IgM antibody in serum in humans and animal models, suggesting that the TLF2 associated IgM is trypanosome elicited. However, since all human serum samples contain TLF2 regardless of infection history, we hypothesized that these IgMs could be natural IgMs. We investigated the origin of the antibody by challenging mice without activation-induced cytidine deaminase (AID), an enzyme that facilitates class-switch recombination and somatic hypermutation of antibodies, resulting in mice that only produce natural IgM antibody. We found AID-/ mice clear parasite infection at similar rates to wild-type mice, indicating that natural IgM antibodies play a primary role in the immune response to trypanosomes and suggesting that TLF2-associated antibodies are natural IgMs.
Tardigrades, multicellular microscopic organisms, survive extreme environments through cryptobiosis. During cryptobiosis, these creatures synthesize protective proteins called Late Embryonic Abundant (LEA) proteins. This research expressed these tardigrade proteins in E. coli to investigate their utility as stabilizing agents for storage and transportation of live cells and purified proteins. Out of many LEA proteins produced by tardigrades, two (HDLEA1 and MAHS) showed promise for cloning. Gene sequences for these candidates were codon-optimized for E. coli, the codon region were synthesized, they were cloned into a vector, and the proper insertion was confirmed through DNA sequencing. Plasmid lacking tardigrade protein coding sequences (REF), were used as a control. E. coli were transfected with each plasmid, plasmid-containing colonies recovered, and then the E. coli were dessicated. Samples of dessicated E. coli were reconstituted in time intervals (t=0,4,7,22.5 hours) and numbers of viable E. coli counted and compared. While viable E. coli recovered after desiccation declined with time for those carrying either REF or HDLEA1 plasmids, the number of HDLEA1-E. coli recovered was significantly higher. For example, at t=7, this number was 3.2-fold higher than the number recovered carrying the REF plasmid. At t=22.5, the difference was 2.5-fold. However, E. coli carrying the MAHS-encoding plasmid showed no improvement in desiccation survivability. The approximately three-fold improvement in survivability of E. coli expressing HDLEA1 validates the hypothesis that the protective properties of the tardigrade LEA proteins are transferable. This finding could lead to the development of new methods for long-term storage and transportation of medical and industrial proteins.

The mammalian target of rapamycin complex 1 (mTORC1) contributes to the regulation of the cell cycle, as well as cellular metabolism. It does so by phosphorylating targets involved in cellular growth pathways (such as S6 Kinase, 4EBP1, and GRB10). Given that mTORC1 is a nutrient-sensor, the phosphorylation of its downstream targets rely on the sufficient presence of amino acids. It has been shown that glutamine is the only amino acid that activates mTORC1 without the presence of the essential amino acid sensing RAG proteins. RAS-mutant cell lines are especially dependent on the presence of glutamine for their growth and proliferation. We report that for these cells to have phosphorylated S6K, not only must glutamine be present, but ERGIC (ER-Golgi Intermediate Compartment) to Golgi trafficking must be functional. Rab1, Arf1, and Arf3 are a few examples of compounds that mediate vesicle formation between these two compartments. We demonstrate that with the disruption or knockdown of these compounds, mTORC1 phosphorylates 4EBP1, but cannot reach S6K. Through the techniques of western blotting and immunofluorescence, our lab has been able to relate how the localization of mTORC1 differentially effects its targets. In addition to deconstructing a portion of the trafficking system, we have also been able to note how reconstitution of that trafficking system hyper-activates mTORC1 in a manner
that allows for the phosphorylation of S6K and GRB10. Such a temporal mapping of mTORc1 and its activities should be relevant to all labs interested in mechanisms of nutrient sensing and cell proliferation.

#47 Lizandra Donnelly

**The molecular mechanism underlying type I interferon-promoted DNA damage responses in innate immune cells.**

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Maintenance of genome integrity is critical for cell survival; however, cells are perpetually exposed to environmental and physiologic DNA damaging agents. Among the most insidious lesions are DNA double-strand breaks (DSBs), as they can lead to chromosomal translocations if they persist unrepaired. Previous work has shown that, when activated upon exposure to the bacterial pathogen *Listeria monocytogenes*, innate immune cells such as macrophages produce reactive nitrogen intermediates that damage macrophage genomic DNA. This damage initiates a DNA damage response (DDR) that, in contrast to other cell types, depends on the production of type I interferon. In this study, we will elucidate the mechanisms by which type I interferon augments the DDR in a murine macrophage cell line, RAW264.7. Notably, we find that after treatment with the DNA DSB-inducing agent bleomycin, RAW264.7 macrophages do not initiate a DNA damage response unless co-treated with type I interferon. Preliminary results suggest that type I interferon alters the chromatin structure in activated macrophages, allowing DNA damage response factors to access DNA DSB sites. Additionally, it is possible that type I interferon promotes the expression of key DNA damage response factors. And finally, it is possible that type I interferon enhances interaction among limited DDR factors. In the future, we plan to distinguish, experimentally, among these non-mutually exclusive possibilities. This will give us a clearer understanding of how DNA damage responses are regulated in leukocytes and thus, insight into the prevention of myeloid-derived tumorigenesis.

#48 Courtney L. Chambers

**Advanced Molecular Lithography Tools for Controlling Surface Architecture**

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Controlling the architecture of surfaces (chemical composition along x-, y-, and z-axes) with nanometer resolution is a central challenge to applications including smart surfaces, soft electronics, microarrays, sensors, and lab-on-a-chip devices. Polymer brushes, defined as polymer chains covalently tethered to a surface, can modify the chemistry and morphology of surfaces. Using a Digital Micro-mirror Device (DMD), where more than 750,000 micro-mirrors can be individually controlled to project light onto the surface, and incorporating an oxygen-free chamber, we are now able to obtain combinatorial, multi-compositional Polymer Brush patterns with unprecedented chemical and architectural control. The light, directed onto a surface, initiates living photo-polymerizations such as atom-transfer radical polymerization (ATRP) or reversible addition-fragmentation chain transfer polymerization (RAFT) from initiators immobilized on Si/SiO2 wafers. Using this new platform we have already produced multiplexed polymer brush arrays and block-co-polymer arrays, where the position and composition of each of the >750,000 pixels can be independently controlled, with micrometer-scale feature resolution. We are currently expanding the chemical variety of patterns and substrates while making the conditions to produce such patterns (light, environmental restrictions, time, etc.) less vigorous. We envision future patterning tools that will fabricate surfaces with the complexity similar to bio-interfaces.
This work was carried out under government support from the National Science Foundation, a MURI award from the Department of Defense, an Air Force Office of Science and Research, and an AFOSR National Defense Science and Engineering Graduate Fellowship.

#49 Syed Daniyal

Control of Cocaine Reward by the a5 Subunit of the Nicotinic Acetylcholine Receptor

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Genome-wide association studies have identified a single nucleotide polymorphism (SNP) in the gene coding for α5 nAChR (α5 nicotinic acetylcholine receptor subunit) that is linked to the development of nicotine dependence. Paradoxically, this same SNP also appears to be protective against the development of cocaine dependence. However, the circuit-level mechanisms underlying the disparate role of this subunit in modulating the rewarding aspects of different drugs of abuse is unknown. Here, we used a combination of genetically modified mice, behavioral assays of cocaine reward, DREADDs (designer receptor exclusively activated by designer drug) to manipulate α5-expressing cells in specific brain regions, optogenetics, and whole cell current clamp recordings in order to deduce the neural mechanisms underlying the ability of α5 nAChR to differently modulate cocaine reward when compared to nicotine reward. We found evidence to suggest that the α5 nAChR plays a role in mediating the rewarding properties of cocaine, by modulating the parafascicular nucleus (Pfn). A major target of projections from the Pfn are the cholinergic interneurons (CINs) in the nucleus accumbens (NAcc), which are also key in signaling cocaine reward. We found that in animals lacking the α5 nAChR, both basal and optogenetically evoked, CIN activity was altered, as was the response of these specialized cells to cocaine. Our results suggest that diminished α5 function in the Pfn leads to altered recruitment of CINs which leads to reduced cocaine reward. Together, these data provide a mechanism through which cocaine efficacy was reduced in α5 KO mice, and highlights the importance of Pfn modulation of CINs in regulating cocaine reward.

#50 Mariya Kasiyanyk & Molly Bekbolatova

MicroRNA-1205 Directly Targets FRYL in Prostate Cancer

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Prostate cancer (PCa) is one of the deadliest cancers in the United States, in which 1 in 9 men are estimated to be diagnosed with PCa in 2019. The 8q24 chromosomal locus is highly associated with increased PCa risk. Within this locus lies the c-MYC and PVT1 genes, which are two oncogenes often amplified in many cancers, including PCa. PVT1 is alternatively spliced and encodes a long non-coding RNA along with six microRNAs (miRNAs), including miR-1205. However, the function of miR-1205 has yet to be fully elucidated. Currently, it has been established that microRNAs regulate gene expression by binding to the 3’UTR of target genes leading to their degradation. Our lab has discovered that miR-1205 is underexpressed in PCa tissue and has a tumor suppressive role in PCa. To elucidate the molecular mechanism of miR-1205 in PCa, FRYL has been identified as a putative miRNA target through target prediction databases. The aim of this study was to validate if miR-1205 directly targets FRYL using the RNA pulldown technique. A biotinylated scramble (control) and miR-1205 duplex were transfected into PCa cells and RNA was isolated using TRIzol method after 24 hours. The lysate was incubated with streptavidin beads overnight at 4C and targets were isolated and quantified using NanoDrop. QPCR analysis demonstrated that FRYL was enriched in PCa cells that were transfected with the miR-1205
biotinylated duplex indicating that miR-1205 directly binds to FRYL. In future studies, we hope to further elucidate the significance of miR-1205 regulation of FRYL in PCa.

#51 Mehriniso Khaydarova
Molecular Diagnostic Yield of Chromosomal Microarray Analysis in Patients with Developmental Disorders
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Chromosomal microarray analysis (CMA) is a powerful molecular diagnostic exam to detect genomic imbalances and study disease mechanism and pathogenesis. Along with Whole-Exome Sequencing (WES), CMA has become the standard in clinical diagnostic testing for individuals with congenital anomalies and developmental disabilities. Our aim was to determine the frequency of genomic imbalances in CMA and WES testing. We hypothesized that the percent diagnostic yield for genomic imbalances would align with the current standard 7-9% yield. To test our hypothesis, we conducted a retrospective medical review of 243 patients with a variety of developmental delay/disorders without any identifiable causes who were assessed and referred by a developmental specialist. CMA was performed on all n=243 patients and WES was performed on n=39 patients. Laboratory results were scanned for genetic mutations such as deletion, duplication, inversion, and translocation of chromosomes. Probands were stratified into 2 essential groups: positive and negative based on the presence of genomic imbalances. Among 243 probands, 5.5% (n=13) abnormal pathogenic chromosomal alterations were observed (deletion n=11, duplication n=2). Furthermore, CMA detected Variants of Unknown Significance (VUS) in the genome of 17.6% probands (n=43) and Areas of Homozygosity (AOH) in 11.5% (n=28) probands. Overall, CMA was able to identify genomic imbalances among 35% (n=84) of the total patient sample. This set of clinical results demonstrates the need for improvement in sensitivity of CMA for the detection of clinically relevant genomic imbalances and highlights the need for comprehensive genetic counseling to facilitate accurate clinical correlation and interpretation.

#52 Jordan Gugliotta & Nicole Rakhmanova
Biotransformation of Tryptophan by Wheatgrass Microbes
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Chemical signaling is a fundamental mechanism by which bacterial microbes are able to communicate amongst each other. The compounds produced serve as “chemical words” allowing for microorganisms to adapt and thrive in their environments. The purpose of our research is to maximize and classify these chemical signals produced by wheatgrass microbes in the presence of tryptophan. Tryptophan is the substrate of choice due to previous findings that the microbes in question are capable of producing tryptophan derivatives from other substrates. In theory, by administering tryptophan to the bacteria it is quite possible that larger volumes of the tryptophan derivatives will be produced. By manipulating the environment of the wheatgrass microbes and altering the concentration of tryptophan, we hope to discover tryptophan derived compounds that function as significant chemical signal and hope to determine how they may serve a purpose in the survival of the microbes. Through methods such as extraction, thin-layer chromatography, column chromatography, and nuclear magnetic resonance (NMR), we are able to analyze the derivatives produced and classify them based on their specific properties. Thus far, we have isolated two compounds of interest which we will continue to amplify, purify via column chromatography and analyze through NMR. Using these methods we expect to produce enough material...
to be able to definitively determine the tryptophan derivative and hopefully find meaning in its ability to serve as chemical words.

#53 Sreejan Saha
**Using Hydroxyapatite's Adsorption Capabilities to Detect Anthrax**
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*Bacillus anthracis*, the primary bacterium responsible for the spreading of anthrax, has been known to release 2,6-pyridinedicarboxylic acid (DPA) in its bacterial spores. Hydroxyapatite (HAP), a structural calcium phosphate complex found in our bones and teeth, possesses affinities for compounds other than itself, possibly classifying it as an adsorbent. HAP is currently being contacted with various substances, such as industrial dyes, metal ions, and toxic biomolecules in order to test for its proposed adsorbent qualities for future uses in environmental remediation and as a potential biological marker. Working with the disodium salt derivative of DPA, I contact HAP and its synthesized modified derivatives (mHAP), which are proposed to have higher affinities than HAP itself, with DPA. After a series of contacts, HAP has been shown to adsorb DPA in a monolayer, conforming to the Langmuir adsorption isotherm model and mHAP has been shown to adsorb DPA in a multilayer, conforming to the S-shaped adsorption isotherm model.

#54 Alexandria Velasquez
**Characterizing Microbial Communication Compounds Produced in Wheatgrass-Derived Bacterial Co-Cultures**
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Microbes communicate with one another using chemicals to coordinate and regulate mass behaviors such as producing biofilm. However, in microbiology, scientists are only beginning to uncover the molecules used in microbial communications. By understanding the chemical language of microbes, we can begin to understand and control microbial behaviors to our benefit. Our lab focuses on deciphering the structures and biological activities of the ‘chemical words’ used between microbes. A limitation of traditional methods of microbial molecular discovery is the use of monocultures. Monocultures disallow interspecies communication, limiting both the variety of chemical factors and bacterial species generated in vitro. In contrast, our approach treats a community of microbes as a single biological entity in a co-culture, while altering the culture conditions. I hypothesized, if the living environment of the mixed microbial culture changes then the bacteria would be forced to suppress or produce different molecules to adapt to their new surroundings. My project studies the communication between bacteria that grow on the surface of wheatgrass. A sterilized porous synthetic matrix was introduced to alter the environment of the culture. Our studies revealed that indole, phenol, and fatty-acid derivatives were present in the culture and indole was induced in the presence of the matrix. Prior literature suggests that these may be significant communication molecules. Overall, these results indicate that growing bacteria as a co-culture and changing their environment is a promising approach to uncover molecules for microbial communication.

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#55 Rebecca Deng

**Polonium-210 Present in Tobacco**

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Ionizing radiation is a form of particles or electromagnetic waves emitted from unstable nuclei that have enough energy to remove electrons from other atoms. One radioactive isotope present terrestrially is uranium-238 (\(^{238}\)U) which decays to polonium-210 (\(^{210}\)Po, \(t_{1/2}=138.376 \pm 0.002\) days). Although \(^{210}\)Po is present in the environment at low dosages, the properties of this isotope make it susceptible to possible ingestion due to its presence in the soil. When polonium-210 enters the body, such as through tobacco, high concentrations may lead smokers to a higher risk of radiation exposure and higher dosage. Two new approaches were investigated to measure polonium in tobacco. Both are based on radiochemical separation followed by employing alpha spectrometry or liquid scintillation for assaying the radiation levels of polonium-210 in different tobacco samples. For use in alpha spectrometry, the polonium was separated by acidic digestion followed by Po spontaneous deposition over a copper foil. Alternatively, polonium was separated from digested samples by mean of tributylphosphate (TBP) extractant in para-xylene solvent followed by measurement over liquid scintillation. Results using alpha spectrometry revealed that the polonium is equal to 25.98 ± 1.96 mBq per cigarette. The collective committed effective dose resulting from the use of one of the commercially available cigarettes per year is estimated to be 219 ± 16.5 μSv.

#56 Wasie Karim

**Identifying Key Proteins Associated with Inflammation in Active Crohn’s Disease**

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Crohn’s Disease is an autoimmune condition of the gastrointestinal (GI) tract that affects millions across the developed world. The immune system malfunctions, attacking the GI tract anywhere from the mouth to the anus. Due to its multifactorial nature, its exact cause is unknown. Extensive genomic studies have been performed on Crohn’s Disease, though limited proteomic studies exist. The goal of this project is to identify inflammatory protein biomarkers (analytes) that may predict recurrence of inflammation in post-operative resection cases of Crohn’s Disease – specifically whole or partial ileum resection. The hypothesis is that at surgery, patients’ inflammatory analytes will be at their highest, and removal of inflamed bowel during surgery will act as a “reset” switch, returning analyte levels to normal, uninflamed levels. Then, differences in analyte levels may be measured between baseline surgery levels and levels at remission. Blood serum samples were collected from patients at surgery, and at first and second follow-up colonoscopies following surgery. Blood serum samples were submitted to Olink Proteomics for analysis. Then, R and Microsoft Excel were used to analyze the data and generate charts. Patients’ clinical information and disease conditions were also collected. Findings showed that 29 analytes had statistically significant differences in serum levels between surgery and health first follow-up colonoscopy. Furthermore, regression analysis suggests that 49.9% of variance in disease condition can be attributed to analyte’s readouts. Ultimately, findings in the data may be used in the future to predict inflammation in post-operative resection cases of Crohn’s Disease based on the patient’s proteome.
#57 Dajana Reci

Synthesis and Biological Evaluation of Selective D3 Antagonists with an Aryl Linker Moiety
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Dopamine D3 receptor (D3R) antagonists appear to be promising for the treatment of substance abuse disorders. However, several known D3R antagonists are plagued with poor pharmacokinetic properties and unfavorable selectivity, particularly in comparison to structurally related dopamine D2 receptors (D2R). These pharmacodynamic and pharmacokinetic issues have contributed to the clinical unavailability of selective D3R antagonists as treatment for substance abuse. Utilizing in silico docking, synthesis and dopamine receptor binding assays, we have designed, synthesized and evaluated novel molecules using a known D3R pharmacophore. This pharmacophore contains three key regions: i) an amine-containing “head” group, ii) a hydrocarbon “ linker” moiety and iii) an arylamide “tail” region. Here we will present our structure-activity findings on a sub-set of analogs that contain a tetrahydroisoquinoline (THIQ) motif as the “head” portion and with a variety of aryl “ linker” moieties and arylamide “tail” regions. Our data indicates that introduction of an aryl “ linker” portion is generally unfavorable for D3R affinity. However, D3R affinity appears to be sensitive to the type and the position of the substitutions in the arylamide “tail” regions. Specifically, the addition of methoxy substituents increased both selectivity and potency of D3R, potentially due to additional interactions with Ser 192 in the orthosteric binding site. Further consideration of substitutions in the arylamide “tail” region must be considered for further advancement of selectivity and potency. This structure-activity study has identified a number of new, selective D3 antagonists and has provided important revelations for further optimization of the arylamide “tail” region in subsequent analog generations.

#58 Daniela Yakobashvili

Novel Magnetic Nanoparticle-Based Gene Delivery Carriers in Cancer Therapeutics
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In recent years, RNA interference (RNAi), a novel technique that involves the inhibition of gene expression, has caught the attention of many cancer researchers because of its viability in preventing tumor growth. With the development of this method, however, comes the demand for carrier systems that could efficiently transfect RNA and release it at desired times and specific locations. Among the potential candidates are superparamagnetic iron-oxide nanoparticles, particularly those possessing a cage shape (IO-NCage). A significant advantage is that the IO-NCage can incorporate RNA inside its cavity, thereby protecting the RNA from denaturing prior to release. In this study, we examined the efficacy in RNA delivery to luciferase-expressing melanoma cells using IO-NCages as carriers. In vitro, IO-NCages were found to be successful in the uptake and release of RNA with no signs of degradation. IO-NCages further proved superior to liposomal agents in RNA transfection when oscillating magnetic fields were applied to cell media. This outcome indicates that the magnetic field can be applied to trigger the release of RNA, demonstrating that IO-NCages can serve as effective RNA transfection agents in cancer therapeutics.
In vivo pretargeting is a promising approach to targeting tumors using radioactive elements. Using the radioactive Tc-99m isotope, we are able to target tumors for visualizing them in the mice’s bodies. Tc-99m is a widely used and available radioisotope used in medical imaging and could provide benefits due to its improved targeting capabilities. We use Re (Rhenium) as a non-radioactive analog of technetium-99m in order to facilitate chemical characterization of complexes; rhenium and technetium are in the same group of the periodic table, therefore they have very similar properties. This project involves pre-targeting approaches wherein the targeting vector, an antibody containing a transcycloclooctene (TCO), is administered into the mice, and the small molecule Tc-99m –tetrazine (Tz) construct is administered a day later. The antibody takes about a day or more to localize at the tumor, while the radioactive Tc-99m-tetrazine reacts with the TCO-antibody at the tumor site to form a covalent complex. This occurs by an Inverse Electron Demand Diels Alder click reaction. Theoretically, the small molecule Tc-99m-tetrazine that does not react with the TCO will clear from non-target tissues as quickly as possible. Pretargeting is a strategy to decrease the radioactive dose in healthy tissues. We built the small molecule tetrazine Tc and Re complexes using small peptides to complex the metals to ultimately form Tc-99m and Re peptide tetrazine complexes. The major part of my project specifically focused on synthesis of the macroscopic non-radioactive Re complexes for characterization and to identify the composition and structures of the Tc-99m constructs. This synthesis was accomplished by reacting a Re(V) oxo complex with tri- and tetra-peptides such as phe-lys-cys (FKC), ser-lys-cys (SKC), glu-lys-cys (DKC), and phe-lys-cys-arg (FKCR) to form the Re(V)oxo complex of the peptides. We found that the Re(V) binds to the first three amino acids of the peptide and the cysteine forms a strong Re(V)-S bond that contributes to the complex stability. Next, we reacted the Re(V) peptide with a N-succinimidyl –tetrazine or N-succinimidy1-PEG5-tetrazine that reacts with the lysine part of the peptide to form, for example, ReFK(PEG5-Tz) CR. These complexes were purified by preparative HPLC and characterized. Mass spectrometry verifies the formulation of the Re peptide tetrazine constructs. As a secondary component of the project, we worked with the graduate student to prepare the Tc-99m peptide-Tz constructs and verified their composition by HPLC co-elution studies. The Tc-99m peptide-tetrazine constructs were tested in vivo in pretargeting reactions using the antibody-TCO constructs. Our results show that there was tumor uptake using the 99mTc-FK(PEG5-Tz)CR that confirmed the in vivo click reaction. This construct exhibited improved tumor:intestinal uptake over the Tc-99mDKC –Tz and Tc99m DKC-Tz constructs.
arsenals. This has led to an increasing number of novel uncharacterized peptides found in venom. In order to characterize the molecular mechanisms of venomous peptides, our strategy is to create HaloTag-peptide fusions of specific venomous peptides and test their bioactivity in functional assays. HaloTag technology is based on bacterial haloalkane dehalogenase from *Rhodococcus rhodochrous*, and designed to study multiple areas of protein-protein interactions using a single genetic construct. The HaloTag construct is versatile in the fact it can bind covalently to various multi-functionalized ligands. To create various peptide-HaloTag fusions, we developed a vector that encodes: a histidine tag for affinity purification, a thrombin protease cleavage site to remove the histidine tag, a variable peptide region, a TEV protease cleavage site to cut the variable peptide region if needed, and lastly the HaloTag construct. We successfully recombinantly expressed and purified three vectors encoding for three different venom peptides: Tv1, MVIIA, and DendroToxin-K. Methods used to isolate and purify the peptide fusions were enzymatic cell lysis and nickel-sepharose affinity chromatography. The purified products were confirmed and characterized by SDS PAGE gels and mass spectrometry. Future studies will test the peptide HaloTag fusions binding activity on ion channels in an electrophysiological assay.

**#61 John Portelli**

**Synthesis of a Mannose-Rich Tetracyclan**

**John Portelli**

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Mannose-rich glycans are expressed on the surface of many pathogens and their binding to receptors on host cells plays an important role in pathogen infectivity. Thus, small molecule mimics of these pathogenic glycans are of interest for studying disease pathways. Moreover, by acting as antagonists to the attachment of pathogens to host cells, these molecules have potential as agents against pathogen infection. In this context, the goal of this research was the synthesis of the mannose-rich tetracyclan. This molecule was prepared in a modular fashion from the tetra-yne and the glycosyl-azide, which were readily obtained from pentaerythritol and from D-mannose, respectively. The glycosyl-azide was made by performing an SN2 reaction on the chain, swapping a Cl group for an azide group. The chain was attached to penta-acetylated mannose using the Lewis acid BF3-EtO in methylene chloride. The core of the compound was prepared by using pentaerythritol and propargyl bromide with TBAI (tetrabutylammonium iodide) as a catalyst and NaH in DMF (dimethylformamide). After the Cul-catalyzed “Click” reaction on and provided the tetra-triazole-glycan in 10% yield from 31 mg. Removal of the acetate protecting groups from provided the target compound. The biological applications of the compound have not been characterized since biological assays are still pending. The presentation will focus on the synthesis of the compound and accompanying reactions. The result is the synthesis of the compound and the Nuclear Magnetic Resonance Spectroscopy (NMR) and Mass Spectrometry (MS) data.

**#62 Yu Qi Huang**

**Riluzole Targets Yes Associated Protein (YAP) to induce Apoptosis in Osteosarcoma**

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Osteosarcoma is a primary cancer of bone, prevalent in children and young adults. Metastasis is either present at the time of diagnosis or develops later during the course of treatment in most patients. The survival rate with metastatic osteosarcoma is very low, therefore new treatment options need to be developed. Our lab is interested in studying Riluzole as an anti osteosarcoma agent. Our lab has demonstrated that Riluzole effectively inhibits proliferation and induces apoptosis both in human and mouse osteosarcoma cells. We have also demonstrated that Riluzole blocks the activity of mGluR5
receptor signaling to inhibit growth in osteosarcoma cells. Currently, our lab is investigating the role of Yes Associated Protein, (YAP), a transcription co-activator, in Riluzole-induced apoptosis. Riluzole changes subcellular localization of Yap from cytoplasm to nucleus. We hypothesized that the increase in nuclear localization of Yap facilitates transcription of pro-apoptotic genes upon Riluzole treatment. Our recent data provided by immunocytotoxicity, immunoblotting and toxicity assays using WT and Yap KO cells suggests that Riluzole activates C-Abl kinase to phosphorylate YAP at Y357. The data shows that Riluzole switches YAP activity from pro-proliferative to pro-apoptotic by promoting phosphorylation of YAP at Y357.

#63 Sarah Hollmann
Role of the Distal RNA Loops in Stabilizing the Catalytic Conformation of the Hairpin Ribozyme
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Ribozymes, or enzymes composed entirely of RNA, maintain critical roles in catalyzing important reactions in prokaryotes and organelles of eukaryotes. The hairpin ribozyme performs a fundamental catalytic function in reproduction of certain plant viruses. Nucleotides from the internal loops of two of the four stem loops comprising the ribozyme interact to create the catalytic core, which then performs a self-cleavage reaction. There are, in addition, additional loop structures beyond the interacting catalytic regions of each of the stem loops that have complementary sequences. We hypothesize that these distal loop sequences pair to stabilize the catalytic interaction and to enhance the rate of catalysis. We measured binding affinity between independent RNA fragments corresponding to the sequences of the two stem loops comprising the catalytic site by electrophoretic mobility shift assay (EMSA). EMSA results showed greater affinity for stem loops containing the the wild type sequences for the distal loops (~80% binding at 1:1 stoichiometry) than for mutant distal loops that would discourage interaction (~20% binding at 1:1 stoichiometry). Preliminary data for catalytic activity of wild type vs. mutants suggest ~50% greater activity by hairpin ribozymes with wild type distal sequences than mutant distal sequences. These findings suggest that the distal interaction contributes to the affinity between, and thus the catalytic rate of the hairpin ribozyme. Knowledge from these studies may assist in the design of artificial enzymes and will contribute to the overall understanding of the structural components of hairpin ribozymes that are also found in other viruses.

#64 Yu Qing Xu
Role of Estrogen Signaling in Regulating mRNA 3' End Processing and Gene Expression in MCF7 Breast Cancer Cells.
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Messenger RNA (mRNA) 3’ end processing plays important roles in balancing biosynthesis and turnover of transcripts, thus regulating their steady-state levels and contributing to gene expression control. We have shown that removal of the poly(A) tail at the mRNAs 3’ end, a process known as deadenylation, is regulated by functional interactions between nuclear poly(A)-specific ribonuclease (PARN) and tumor suppressor factors, such as p53 and BRCA1/BARD1 under normal and DNA damage conditions in HCT116 colorectal cells. Here, we extend these studies to determine whether estrogen treatment regulates mRNA 3’ end processing and gene expression in MCF7 human breast adenocarcinoma cells. Estrogen signaling is primarily mediated by estrogen receptors, ERα and ERβ. Excessive estrogen signaling leads to increased cell proliferation and cancer development in breast cells, with over 75% of breast cancers being ER-positive. Studies have suggested that there is a feedback loop between p53 and
ERα. Thus, we hypothesize that the interplay between estrogen signaling, specifically through ERα, p53, and deadenylation factors will play a role in regulating mRNA 3' processing, affecting the cellular transcriptome and hence, gene expression. Using radiolabeled capped poly(A)+ RNA substrates, we showed that 2 hour estrogen treatment (10nM) activates nuclear deadenylation in MCF7 cells. Furthermore, small-interfering RNA (siRNA) mediated knockdown of ERα and fulvestrant treatment (a selective ER degrader) results in a decrease in nuclear deadenylation, suggesting ERα may act as an activator of nuclear deadenylation. Understanding the role of estrogen in this regulation will contribute to the development of new therapies for breast cancer.

#65 Steven Medvedovky & Timothy Lau
A Novel Synthesis of Iron Oxide Nanotube and Their Applications in Efficient Drug Delivery Systems.
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This research investigates the facile synthesis of iron-oxide nanotubes (IO-NTubes) (through consecutive galvanic replacement from a silver nanowire template) and their in vitro cell uptake. Iron-oxide nanostructures have seen medical application as MRI-active imaging agents and FDA-approved drug vectors. Since considerable research have shown high-aspect ratio nanoparticles may be more effective in these medical applications due to longer body circulation times, we designed tubular iron-oxide nanoparticles for clinical translation. Here, we first developed a synthesis protocol utilizing consecutive galvanic replacement reactions to generate tubular IO-NTubes from silver nanowire templates. The IO-NTube’s diameter is 40 nm, extremely small and expected to escape the liver and kidney for longer body circulation. We then compared in vitro cell uptake of high-aspect ratio IO-NTubes by osteosarcoma (LM7) cancer cells with low-aspect ratio iron-oxide nanoparticles. IO-NTubes were coated in polyethylene glycol (PEG) surfactant to avoid aggregation, fluorescently labeled using (Cy5) dye for visibility in cells, and incubated with LM7 cells. Our results showed IO-NTubes had greater uptake than the other nanoparticles, confirming our hypothesis. IO-Ntubes also showed no cell toxicity, opening the possibility for use in animal models. Investigation into drug-delivery efficiency and in vivo performance of IO-NTubes is still desired as this nanoparticle can be applied to various therapeutic treatments for cancer, neurodegenerative diseases, and/or gene therapy. Additionally, IO-NTube’s superparamagnetic property could be used in magnetic hyperthermia and external magnetic field-guided organ targeting. Iron-oxide nanotubes may make a variety of therapeutic and imaging combinations possible, potentially opening a new route for the clinical translation of nanotechnology.

#66 Mark Yusufov
Biotransformation of Oleic Acid by Wheatgrass Microbial Culture
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Microbes living in soil and on the surface of plants include a wide range of organisms, such as bacteria, fungi, archaea, protists, and microscopic animals that interact with each other and with their environment through chemical signals. Studying the chemical signals produced by microbes for communication between themselves and between microbes and plants, and microbes and animals, may lead to novel discoveries about the effect of such signals and the role that they play in cell metabolism and cell communication. One microbial community we are studying comes from a sample of wheatgrass. Wheatgrass are the first leaves of the common wheat plant and have recently become popular for their
nutritional value and supposedly curative properties. Currently, we know that wheatgrass culture is equipped with metabolic genes that are capable of hydrating monounsaturated fatty acids to form hydroxy fatty acids (HFA), however, the roles of HFAs in microbial communication is yet unknown so further studies must be done to understand what role these metabolites play. In order to obtain enough product to analyze, the wheatgrass microbial community is cultured with oleic acid, a monounsaturated fatty acid, and the products of interest are extracted, purified, and analyzed with spectroscopy. Our results indicate that wheatgrass microbes transform oleic acid into hydroxystearic acid. 12-hydroxystearic acid is used as a low molecular weight gelator. Our hypothesis is that the hydroxystearic acid from our culture may function in a similar fashion, which may have potential application as a regulator of cell plasma membrane permeability.

#67 Rodolfo Olivares

Excretory Pathways of Technetium-99m SPECT Imaging Agents Based on Biorthogonal Diels-Alder Click Chemistry

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Tc-99m impact in medical imaging begins with success of targeting tumor of interest, producing contemporary images of the tumor in question. Through properties of similar reactivity, we used the non-radioactive analog of Tc-99, Rhenium (Re), in order to catalyze chemical characterization of complexes shared by both elements, making the study of Tc-99m easier to accomplish, with respect to keeping the compounds clickable moiety (tetrazine moiety). To use these radioactive compounds in imaging we had to decrease their presence in healthy tissues; to accomplish this we’d administer the targeting vector and then the radioisotope separately into the body, for then they react and integrate in vivo. Doing so with an antibody that is tagged through a reactive bioorthogonal group that is implemented into the animal of study. After this reaction is accomplished, the final expectation is for the radioactive isotope to be clear from the tissue with no interest as quickly as possible through the furtherance of secretions. Hence, for these expected outcomes to occur we are to expect a Tc-99m complex that is able to be isolatable, react with antibodies that has been altered and produce a high tumor to background ratio, while keeping its integrity with the Diels-Alder reaction that accomplishes the resulting products. Two expected products are produced with the amino groups we used (FKC (FKCR), DKC, SKC), which are diastereomers to each other in the form of an anti and syn conformation of the complex, nonetheless images were produced with each having varying results.

#68 Aqsa Ghaffar

The Effects of Adding Zinc to the Yeast Spliceosomal Protein Cwc2

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Spliceosomes catalyze the removal of non-coding introns from precursor messenger RNA (pre-mRNA) and ligate the coding exon regions. Spliceosomes assemble from five small nuclear snRNAs (U1, U2, U4, U5, and U6) and numerous proteins. Catalysis is performed by the snRNA components, in particular by a complex formed by pairing between the U2 and U6 snRNA. However, correct folding into the catalytically active conformation requires interaction with specific spliceosomal proteins. One of these proteins in yeast is Cwc2 (analogous to the human RBM22) which is associated with the Prp-19 complex. A crystal structure of the Cwc2 functional core reveals three RNA binding modules: an RNA recognition motif.
(RRM), zinc finger (ZnF), and an intervening connector element, which are tightly integrated into a compact globular structure. It remains unclear how Cwc2 interacts with RNA to fulfill its role. To investigate this further we express and purify the Cwc2 protein. It is possible for the zinc cofactor of the ZnF to be lost from the protein during purification, which would inhibit proper folding and binding to its RNA target. We are therefore analyzing the effects of supplementing the purified protein with zinc on these functions by use of gel electrophoresis techniques. These experiments will help us to gain a greater understanding of how Cwc2 interacts with RNA to fulfill its biological role.

### #69 Reecan Juarez

**Synthesis of Apomorphine Analogs Towards Novel Dopamine Receptor Agonists**

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Hypofunction at dopamine D1 and D2 receptors plays a significant role in Parkinson’s Disease (PD). Apomorphine (brand name Apokyn) is an eminent D1 and D2 receptor agonist and PD medication. However, the catechol moiety of apomorphine metabolically hinders the medicine’s efficacy in clinical treatment. Chemically modifying the catechol moiety can metabolically stabilize apomorphine and ultimately increase apomorphine’s efficacy. Thus, this project aims to design, synthesize, and pharmacologically characterize a collection of unique apomorphine analogs that feature a modified catechol moiety. Functionalized aniline moieties replace the phenolic groups of the catechol moiety. The analogs were synthesized in 7 steps and had 40 to 50% overall yield from readily available starting materials. A key reaction in each analog’s synthesis involved direct arylation on a bromobenzyl tetrahydroisoquinoline intermediate, which accomplished formation of the tetracyclic apomorphine scaffold. Chemically manipulating the aniline moieties produced the collection of target compounds. Structures of the analogs were confirmed via mass spectrometry and nuclear magnetic resonance (NMR) spectroscopy. Favorable overall yield and NMR data highlight the efficiency of the synthesis and permit biological testing of the analogs. Structure-activity relationship (SAR) analyses have measured the binding affinity and functional activity of five analogs at human D1 and D2 receptors. At the D1 receptor, two analogs show comparable affinity to apomorphine. If the remaining analogs exhibit favorable pharmacokinetic properties, affinity, and agonist activity at D1 and D2 receptors, these analogs can potentially be used as novel drug leads in PD treatment and chemical probes for D1 and D2 receptors.(NIH Grant No. SC1GM092282 & Hunter College Grant # R25GM060665-18)

### #70 David Nemirovsky

**The Appeal of Using Inorganic Titanium-Based Materials for Removing Technetium-99 from Contaminated Ground Water**

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The legacy of nuclear events, represented by nuclear accidents, nuclear weapon experiments, and the wastes generated from nuclear energy production contribute to the contamination of water with highly toxic, long-lived radionuclides. Technetium-99 (Tc-99) is a radioactive element (half-life: 2.1x10⁵ years) found in relatively large quantities in nuclear wastes and is contributing significantly to the long-term radiation risk to humans. Its prevalent oxidation state, +7, as pertechnetate (TcO₄⁻), has high solubility in water and is not adsorbed by most soils and subsurface minerals, which lead to its high mobility in the surrounding environment. In this context, evaluating and designing novel materials, which are capable to reduce and extract Tc-99 from environment and nuclear waste sources, are crucially required. In the present work, titanium-based inorganic ion-exchangers were synthesized and evaluated for the reduction and uptake of (TcO₄⁻) pertechnetate. These synthesized ion-exchangers have two structural forms, poorly crystalline silicotitanate (PCST) and sodium nonatitanate (SNT). The approach is based on photocatalytic
oxidation using UV radiation. Since all technetium isotopes are radioactive, rhenium (Re) was used as a non-radioactive surrogate of Tc-99 in these studies to minimize the radiation exposure dose while optimizing the best conditions for Tc-99 uptake over SNT or PCST. Different parameters were optimized, including the influence of solution acidity, time of equilibration, concentration of metal, and stability of the materials. Our results revealed that 100% of Re was taken-up from a solution mixture using SNT ion-exchangers at an optimized condition of pH 5 with equilibration time of 7 days.

#71 Kyrillos Akhnoukh

Does The Histidine Tag Affect The Folding of RBM22?

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The splicing of pre-messenger RNA (pre-mRNA) entails removal of noncoding introns and ligation of the coding exons in a pre-mRNA message prior to protein synthesis. The process is catalyzed by the spliceosome, a large and dynamic ribonucleoprotein particle comprising small nuclear RNAs (snRNAs) U1, U2, U4, U5, and U6 and many proteins. The catalytic component of the spliceosome is formed by the U2 and U6 snRNAs, but a protein called RBM22 has been shown to be essential for aiding in the folding of the correct conformation of the catalytic center in the human spliceosome. The expression system of RBM22 that we use includes a tag of 6 Histidine amino acids (“his-tag”) on the N-terminus of the protein to aid in purification by affinity chromatography on a Ni2+ column. After purification of the protein, the his-tag can be removed with the use of a protease that is specific for the sequence between the His-tag and RBM22. This is a tedious process, so we ask whether the presence of the his-tag on the N-terminus affects the folding or RNA binding properties of the protein. The question of whether or not the his-tag is removed by our treatment and whether its presence affects relative folding of the protein will be assayed by SDS gel electrophoresis and a nondenaturing gel, respectively; binding to RNA will be assayed by horizontal electrophoretic mobility shift assay (EMSA). These studies will assist in our understanding of the structural role of the N-terminal end of the protein.

#72 Artem Duda

What is Old is New: Removal of Deposited Uranium from Teeth Employing Carbonate

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Following a nuclear event, particles containing actinides such as uranium may be released into the environment. The impacts of uranium, a radioactive element with long half-life, on living organisms is both chemical and radiological. Uranium is transported as uranyl cation (UO22+) in the bloodstream where it forms complexes with small ligands, mainly carbonates, and some serum protein targets. It accumulates mainly in bone and up to now, no treatment is efficient enough to remove all the uranyl. As hydroxypatites (HAP) are involved in the formation of bone and teeth, we investigate their potential uptake to uranyl. Initial studies included optimizing varies conditions for the uptake (pH, kinetics, buffer, and metal concentration) and removal of uranyl (common household soda and sodium bicarbonate, Na2CO3) were performed. Our preliminary data revealed a fast and high uptake of uranyl on hydroxypatite. Further studies showed the possible release of uranyl from HAP after treatment with sodium bicarbonate. Following studies, using human teeth as targets, revealed the uptake of uranium nearing 10% from a solution of 10ppm of UO22+. These studies were done to better understand the accumulation and removal of the deposited uranium in the case of human contamination. The final goal of these studies is to develop a solution, safe for human intake, which will completely remove ingested uranium from the body.
#73 Suchwinder Singh
Biotransformation of Tryptophan by a Mixed Microbial Culture (MMC) Derived from Aloe Vera

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Microorganisms are present everywhere and produce a variety of natural products. Some microbial natural products have resulted in pharmaceutical/clinical uses as drugs ranging from antibiotics to immunosuppressants. While numerous studies have examined the production of natural products by soil microorganisms, little is currently known about the metabolites produced by plant-associated microbes. In order to gain new insights into the metabolic potential of plant-associated microbes, we have obtained a mixed microbial culture (MMC) from Aloe vera. Aloe vera is known to have a variety of uses such as laxatives and anti-inflammatory responses, and can have microbes useful in the production of other compounds. Our preliminary data indicated that the Aloe vera MMC produces derivatives of tryptophan. Yet, the amounts of those derivatives are too small to conduct chemical and biological characterizations. In order to increase the production yields of tryptophan derivatives, tryptophan was introduced as a substrate into the Aloe vera MMC. Thin-layer chromatography of the products indicated that Aloe vera MMC indeed transformed tryptophan into several products. We are currently accumulating biotransformed tryptophan derivatives for structural characterization. Biomedical implications of our findings will be discussed.

#74 Jafar Ali
Synthesis of Novel HOPO (Hydroxypyridinone) Multidentate Ligands for Radiometal Decorporation

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Impromptu exposure to radionuclides in the environment due to anthropogenic events pose potentially long-term catastrophic effects to the human body, such as organ damage and cancer. For the purpose of nuclear medicine, there is a constant need to both synthesize and design chelators that can function as decorporating agents for removing toxic radioactive elements. Within this context, the 3,4,3-LI(1,2 HOPO) ligand was previously investigated as a chelating agent for heavy metal decorporation, such as for uranium, by Younes et al. 3,4,3-LI(1,2 HOPO) is composed of four 1-hydroxy-pyridin-2-one (1,2-HOPO) units linked to a spermine scaffold through amide linkages, and has the ability to form stable complexes with a high selectivity for metal ions with large charge/radius ratios via its eight coordination sites. The synthesis of different multidentate HOPO ligands (five/six units of 1,2-HOPO, with ten/twelve coordination sites) was investigated to increase the stability of metal-ligand complexation, and to facilitate the stable coordination of radionuclides with high coordination numbers, particularly the lanthanides and the actinides. The protected 1,2-HOPOBn acid chloride was synthesized from commercially available 6-hydroxypicolinic acid and inserted into a spermine scaffold. The penta and hexasubstituted ligands were produced, and characterized by HRMS (high resolution mass spectrometry) and HNMR, CNMR, COSYNMR and DEPTNMR (hydrogen, carbon, correlation spectroscopy, and distortionless enhancement by polarization transfer nuclear magnetic resonance spectroscopy, respectively). 3,4,3-LI(1,2 HOPO) was also readily produced and characterized in the same vein, and an optimized synthesis of 3,4,3-LI(1,2 HOPO) is presented. Such compounds, due to their previously reported solubility in water and low chemical toxicity, can potentially provide very viable avenues to remove toxic radioactive elements in vivo.
#75 Minhua Cao

**Improved Synthesis of the Bifunctional p-SCN-Bn-HOPO for PET imaging**

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Nuclear medicine utilizes radionuclides attached to plasma membrane antibodies for targeting and imaging and tumor cells. A specific imaging modality, Positron Emission Tomography (PET) uses positron emitting radionuclides as tracers for imaging tumors. For this purpose, bifunctional chelators are employed to firmly bind a radionuclide and attach the radiometal to antibodies. In this context, the octadentate 3,4,3-LI(1,2-HOPO) ligand, named here as HOPO (hydroxypyridone), is a promising chelator with selectivity for tetravalent f-elements. It has water solubility, lower toxicity, and oral availability. Deri et. al (2015) has explored the potential of the bifunctional p-SCN-Bn-HOPO, a derivative of the HOPO ligand, to chelate zirconium-89 for PET imaging applications. *In vivo* studies demonstrated that the bifunctional HOPO ligand has a higher stability with zirconium-89 than the clinical utilized desferrioxamine chelator (DFO) and delivered a good tumor-to-organ contrast. The potential application of the HOPO-ligand derivative instigated our interest in optimizing and improving the synthesis of p-SCN-Bn-HOPO to achieve a higher yield. The bifunctional p-SCN-Bn-HOPO ligand can be synthesized in a nine step reaction from the commercially available spermine with a 1.4% yield. Here, we were able to improve the yield of the first 4 steps by 20%. This was achieved by modifying the reaction parameters and solvent conditions. The compound obtained was characterized by liquid chromatography mass spectrometry (LCMS), proton nuclear magnetic resonance (1H NMR), and carbon-13 nuclear magnetic resonance (13C NMR).

#76 Matthew Ho

**Biotransformation of Oleic Acid in Mixed Microbial Culture**

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Microbial signaling is examined in this research. The human body contains trillions of microorganisms, and roughly 70% of the cells inside the body being microbial cells. Microbes play an important role in the regulating our metabolism, regulating our immune system, and extracting energy from food. The diverse microbial environment in our body requires microbe-microbe communication. While current knowledge on microbial signaling is limited, there are certain known signaling factors, such as diffusible signaling factors (DSF), which are cis-2-unsaturated fatty acids. Our recent study, however, detected a series of hydroxylated fatty acids in the culture broths of various mixed microbial cultures (MMCs). The finding opened a possibility that microbial communities use hydroxylated fatty acids as well as DSFs for communications. The exact chemical structures and biological effects of hydroxylated fatty acids, however, could not be determined because the amounts recovered from MMCs were limited. In order to obtain larger amounts of hydroxylated fatty acids, we examined the utility of MMCs to convert exogenously added fatty acids into hydroxylated fatty acids. The addition of oleic acid to an MMC derived from ginseng indeed produced a new fatty acid with a hydroxyl group as determined by nuclear magnetic resonance. The finding indicates that MMC biotransformation can serve as a simple yet powerful approach to generate various hydroxylated fatty acids from simple and inexpensive fatty acids. This presentation will outline our biotransformation experiments and structural characterization of the biotransformation products. In addition, the biomedical implications of our finding will be discussed.
#77 Arif I. Mahmud

**NLRP3 Signaling Drives Macrophage-Induced Adaptive Immune Suppression in Pancreatic Carcinoma**

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The tumor microenvironment (TME) in pancreatic ductal adenocarcinoma (PDA) is characterized by immune tolerance, which enables disease to progress unabated by adaptive immunity. However, the drivers of this tolerogenic program are incompletely defined. In this study, we found that NLRP3 promotes expansion of immune-suppressive macrophages in PDA. NLRP3 signaling in macrophages drives the differentiation of CD4+ T cells into tumor-promoting T helper type 2 cell (Th2 cell), Th17 cell, and regulatory T cell populations while suppressing Th1 cell polarization and cytotoxic CD8+ T cell activation. The suppressive effects of NLRP3 signaling were IL-10 dependent. Pharmacological inhibition or deletion of NLRP3, ASC (apoptosis-associated speck-like protein containing a CARD complex), or caspase-1 protected against PDA and was associated with immunogenic reprogramming of innate and adaptive immunity within the TME. Similarly, transfer of PDA-entrained macrophages or T cells from NLRP3−/− hosts was protective. These data suggest that targeting NLRP3 holds the promise for the immunotherapy of PDA.

This work was supported by NIH grants (CA168611, CA155649, and CA206105 to GM), the Department of Defense Peer Reviewed Medical Research Program (GM), the Lustgarten Foundation (GM), the American Association for Cancer Research Pancreatic Cancer Action Network (GM), the Hirshberg Foundation for Pancreatic Cancer Research (GM), and the Irene and Bernard Schwartz Fellowship in Gastrointestinal Oncology (DD).

#78 William Deng

**Synthesis and Disulfide Mapping of a Bioactive Terebrid Snail Venom Peptide Tsu 1.1**

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Disulfide-rich peptides found in the venom of marine snails are highly efficient and effective tools for the development of novel therapeutics. One example of a peptide-based pharmaceutical derived from marine snail venom is Prialt, a non-addictive analgesic that relieves chronic pain in cancer and HIV patients. The work in our lab focuses on the structural and biological characterization of terebrid marine snail venom peptides in the hope of discovering potential therapeutics. Previous studies from our lab have shown that a peptide named Tsu 1.1 — from a terebrid marine snail venom — has the potential to be an orexigenic agent in fruit flies. The sequencing of Tsu1.1 was initially obtained from transcriptomic analysis, and it was chemically synthesized in the lab via solid phase peptide synthesis. In this project, I employed a new method for the synthesis of Tsu1.1 using the Biotage Alstra peptide synthesized with a yield of 58%, a value which dramatically exceeds the 9% yield obtained using an older method on the CEM Liberty Blue synthesizer. This methodology for the synthesis of terebrid peptides will reduce the time spent on their purification. The overall time for this method is approximately one week of active bench work from start to finish. The higher yield of marine snail venom peptide provided by this approach can facilitate additional screening for bioactive molecules as well as the disulfide mapping of the peptides.
#79 Charlene Redhead

Heavy Metal Determination in Hair Samples from Feral Dogs living in the Chernobyl Exclusion Zone

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Following the Chernobyl nuclear disaster, more than 2,400 tons of lead powder were dropped by helicopters onto the damaged nuclear reactor to shield workers from radiation. To estimate the level of environmental heavy metal contamination, hair samples were taken from feral dogs living in the area and compared to control, unexposed dog populations. Metal concentrations in unwashed hair were compared to those of washed samples to estimate actual body burden vs surface contamination. Extrapolation of this data will inform us of effects of human exposure. Hair samples were obtained from dogs living near the nuclear power plant, Chernobyl, Slavutych, and from a veterinary clinic in New York City. Unwashed hair was digested in concentrated nitric acid, while washed hair was treated with successive washes of deionized water, acetone, and triton X-100 solution before digestion and reweighing. Metals analysis was performed using inductively coupled plasma mass spectrometry. A pilot experiment was first conducted using hair from three Chernobyl dogs and four unexposed, controls. Comparisons of hair from Chernobyl vs Control Dogs identified significant (p<0.05) differences in 14 out of 25 heavy metals analyzed in this experiment. Preliminary data show higher concentrations of several potentially toxic and/or carcinogenic heavy metals in hair samples from dogs living near the nuclear reactor. Further analysis of hair from a larger population of animals may strengthen these initial conclusions. This research is funded by the NIEHS Grant Number: 1-R25-ES025505-04. It is an initiative of the summer program, PrI MER, at Columbia University.

#80 Paula Laziuk

Optimization of the Production of Collagen Mimetic Peptide Col877 using Bacterial Expression.

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The interest in collagen formation and sequence composition has resulted in the production of designed collagen proteins. The expression and purification of these peptides allows for the determination of factors that are crucial for the proper folding and assembly of collagen fibrils. Col877, a 398 residue mimetic protein, contains three repeating sequences and a foldon domain, which prevents the end-on-end stacking of collagen triple helices. The amino acid sequence has been optimized for optimal tRNA function within the E. coli expression system. The plasmid containing the Col877 protein sequence was introduced to variations of the E. coli cell strain BL21. Previous purifications focused on the elution of the His-tagged protein using either large-scale metal affinity chromatography and imidazole or small-scale spin column purification. Since Col877 can exist as a disulfide-linked trimer, a dimer or a monomer, the identification of the protein band on SDS-PAGE gels became difficult. Optimization of protein expression must be accomplished in order to increase protein yield. The concentration of IPTG, and the period and temperature of induction have been varied. The BL21-CodonPlus-(DE3)-RP cell strain was incorporated as an alternative expression system since it features additional tRNA for proline and arginine residues. The effectiveness of this cell strain has been compared to BL21, but protein yield was poor and the band remained unidentifiable. Other studies have concluded that the addition of a small amount of ethanol within the growth medium has beneficial effects on the expression of proteins using bacterial expression techniques. The effectiveness of this method on the expression of Col877 will be investigated.
Cancer cells face demanding nutrient conditions when undergoing proliferation, but often face nutrient limited resources. Acquisition of nutrients is achieved through various transporters or through the regulated form of endocytosis that mediates non-selective uptake of nutrients. Furthermore, nutrient uptake is achieved when amino acids such as glutamate and asparagine are able to act as an exchange factor and exchange with extracellular amino acid pool. Pancreatic Ductal Adenocarcinoma (PDAC) cell models often experience a glutamine and asparagine low micro-environment which further limits their growth. To meet appropriate nutrient conditions, dependency on the de novo synthesis of these amino acids becomes a priority but also a vulnerability in targeted therapy. As glutamine synthesis is limited, the synthesis of asparagine from aspartate and glutamine is also limited because of the low expression of Asparagine Synthetase (ASNS) in PDAC cell models. Shown in literature, supplemented cell culture medium with asparagine is able to rescue PDAC cell models and further allow proliferation. The mechanism of action is still not well understood, as the same effect has been seen in other cancer models, but it is suspected that asparagine is able to rescue cell proliferation by restoring global protein synthesis. Further study of the mechanism of action of asparagine rescue will allow for therapies in which ASNS is targeted.

Bodies of water have been polluted for decades with dyes, metal ions, and other toxic byproducts from a multitude of industries that devastate homeostatic ecological conditions. Methylene blue, a heterocyclic dye, is widely used in paper, plastic and textiles. It is important to be able to purify industrial wastewater since methylene blue causes many ecological and health complications when it is improperly disposed of. This dye is suspected to be a possible carcinogen and endocrine gland disruptor in humans. Since current purification techniques are costly, these industries don’t bother to properly dispose of their chemical waste. Hydroxyapatite (HAP), the main inorganic compound found in bones, is an ideal waste management candidate for these plants to decrease their ecological footprint. HAP’s inexpensive production can be exploited for use in the purification of water due to its possible adsorbent qualities. Despite its biocompatibility, HAP is not widely utilized because of its low capacity and lack of selectivity. For this reason, bisphosphonate compounds, specifically 1-hydroxyethane-1,1-diphosphonic acid (HEDPA), are used to convert HAP to a calcium bisphosphonate matrix which amplifies its affinity for methylene blue. This new molecule, modified hydroxyapatite (mHAP), proves to be a better sorbent than HAP due to the addition of phosphonate groups. HAP’s and mHAP’s biocompatibility thus make them ideal molecules to use for environmental remediation.
#83 Marcus Bonoan

**Analysis of Ototoxicity in Pediatric Osteosarcoma Patients**

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Cisplatin is an important chemotherapeutic agent that is used to treat localized and metastatic osteosarcoma. Acute and progressive high frequency ototoxicity, or hearing loss, is a well-known toxicity of the platinum compounds found in cisplatin, however questions remain regarding the influence of dose schedule and genomic factors on the development of ototoxicity. To address this issue, we reviewed the medical charts of osteosarcoma patients treated at Memorial Sloan Kettering Cancer Center who received at least one dose of cisplatin. Our retrospective review documented relevant clinical and demographic information about each patient. We reviewed audiograms for each patient, documenting their hearing deficit with the International Society of Pediatric Oncology (SIOP) Boston Ototoxicity Scale. We identified 49 patients that received at least one dose of cisplatin as part of their treatment for osteosarcoma. Of those 49, 40 patients, or about 82%, developed ototoxicity of any grade, which is similar to previous reports. Seven patients (14%) developed grade 3 or higher hearing loss and 25 (51%) patients developed grade 2 or higher hearing loss. Hearing loss was correlated with number of doses of cisplatin, however no correlations with age were seen as have been previously reported. From our results, we concluded that cisplatin administered on a 120mg/m² x 1 day dosing schedule leads to significantly higher ototoxicity then a dosing schedule of 60 mg/m² x 2 days. In the future, we plan to do further genetic studies to identify the prevalence of otoprotective germline single nucleotide polymorphisms in our patient cohort.

#84 David Guber

**BRCA1/BARD1 polyubiquitinates the RNA Recognition Motif 3 of HuR-bound to the 3’ Untranslated Region of TP53 mRNA.**

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Human Antigen R (HuR, ELAV1) is an RNA binding protein that regulates the stability of mRNA targets involved in DNA damage response by binding to 3’ untranslated regions (3’UTR), usually increasing their stability. Control of mRNA stability is essential for regulation of gene expression during different cellular conditions. HuR is released from its target mRNAs by ubiquitination under non-stress conditions. It is known that poly(Ub) chains attached to Lys313 and Lys326 of RNA recognition motif 3 (RRM3) signal dissociation of HuR from CDKN1A mRNA. However, the identity of the E3 ubiquitin (Ub) ligase responsible for HuR modification is not known yet. Our results indicate that the E3 Ub ligase BRCA1/BARD1 can modify HuR in in vitro ubiquitination reactions. Furthermore, siRNA-mediated knockdown of BRCA1/BARD1 decreased HuR ubiquitination in HCT116 cells. Interestingly, in vitro ubiquitination reactions with HuR bound to biotinylated TP53 3’UTR resulted in HuR polyubiquitination. My data indicate that polyubiquitination of HuR by BRCA1/BARD1 happens mainly through Lys6 of Ub. Using different HuR derivatives, we determined that BRCA1/BARD1-mediated ubiquitination of HuR mostly occurs in HuR’s RRM3. To further analyze which Lys residues in the HuR RRM3 domain are ubiquitinated by BRCA1/BARD1, we used a panel of Lys mutants (Lys274Arg, Lys283/285Arg, Lys313Arg, Lys326Arg, Lys313/326Arg). While BRCA1/BARD1 can mono- or poly-ubiquitinate most of the RRM3 mutants, the replacement of Lys313 for Arg significantly decreased RRM3 ubiquitination. These results indicate that BRCA1/BARD1 regulates the signaling of HuR-mRNAs interaction resulting in the regulation of gene expression during the DNA damage response.
#85 Ahmet Doymaz

**Cell Cycle Arrest Protein p21 Function Is Regulated by Non-Coding RNA from CDKN1A Gene Generated by Alternative Polyadenylation during DNA Damage Response.**

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After being subject to DNA damage, mammalian cells undergo coordinated and dynamic responses to regulate cellular functions after stress. A mechanism to control cellular conditions during the DNA damage response is regulation of mRNA processing, such as the regulation of cleavage and polyadenylation (CpA) during transcription. CpA can occur at more than one mutually exclusive location within a gene termed “alternative polyadenylation” (APA). The long-term goal of this research project is to understand the role of APA in the regulation of gene expression during the cellular response to DNA damage. We have characterized a long non-coding RNA (lncRNA) produced through intronic APA in the CDKN1A gene, which canonically encodes for the cell cycle arrest protein p21. To further explore the mechanisms of this lncRNA’s function we performed siRNA-mediated knockdown of its expression. Depletion of this CDKN1A lncRNA resulted in a significant decrease in p21 protein, without affecting CDKN1A full-length mRNA levels. Consistent with this, overexpression of the intronic-APA lncRNA increased p21 protein levels but did not affect CDKN1A full-length mRNA levels. These studies suggest that this lncRNA regulates p21 protein levels post-transcriptionally. To test whether CDKN1A-APA transcript regulates p21 levels at the translational level, I propose to treat lncRNA-depleted cells with the translation inhibitor cycloheximide. I will also analyze CDKN1A-APA transcript functions under different stresses which induce p21, such as etoposide. Understanding the role of lncRNAs in cancer is a novel approach to design new diagnostic tools and therapies.

#86 Yasir Naeem

**Synthesis of Trimannan Associated with Pathogen Infection**

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Complex, high mannose glycans on the surface of a variety of pathogens (HIV, TB, Ebola, Dengue and Zika) are believed to bind carbohydrate receptors on host cells, thereby facilitating the early stages of infection. Thus, there is considerable interest in small molecule fragments of these more complex pathogenic glycans for use as biomechanistic probes and as potential therapeutic agents. This research involves the synthesis of such a fragment - a branched mannose trisaccharide which is a widely occurring subunit of these high mannose glycans. This molecule was prepared from mannose in eight steps and 20% overall yield in essentially complete stereoselectivity for the two glycoside bonds. The structure was characterized by nuclear magnetic resonance spectroscopy and mass spectrometry. Details of this synthesis and future applications of this trisaccharide will be presented.
Oregano plant produces many different types of secondary metabolites that have been exploited in the food and pharmaceutical industry for decades. Recent studies, however, indicate that some bioactive metabolites in oregano are produced not by the oregano plant but by the microbes associated with the plant. At present, little is known about oregano-associated microbes and how environmental factors interfere with their metabolic profile. This is an important problem, because, without the knowledge of oregano-associated microbes and their metabolites, it would not be possible to fully understand the therapeutic effects of oregano. A previous study in our lab characterized and identified a secondary metabolite produced by the oregano microbiota called Piliferolide A. This compound has shown to present antifungal properties against pink snow mold, a fungus that affects cereal crops. Microbial metabolites serve as a way of communication amongst microbes and their hosts for maintenance and homeostasis. This allows microbes to cope with a range of adverse conditions. The interactions between microbes and their biotic and abiotic environment is not well understood. To address this problem, this study obtained liquid chromatography-mass spectrometry (LC/MS) profiles from the extracts of the oregano microbiota and screened for the presence of metabolites in different environmental conditions using metabolomic database search based on tandem mass spectrometry (MS/MS) fingerprinting. The microbial metabolomics study is an important tool for drug discovery, personalized treatment strategies, agricultural and food industries. Further characterizations of these microbial metabolites are underway to understand their chemical structures and biological effects.

Collagen is involved in wound healing processes such as extracellular matrix (ECM) remodeling and deposition. The compact fibrillar structure of collagen makes the access of the major cell interaction sites complicated. How collagen interacts with these cell receptors is not fully understood. Recently, our lab has succeeded in generating collagen mimetic mini-fibrils which can be used to model collagens carrying receptor binding sites. Studies of these mini-fibrils will help in characterizing the collagen-cell receptor interaction at the fibril level. One of the challenges in developing minifibrils is obtaining a good yield through a bacterial expression system. To overcome this difficulty, we have introduced V-domain, which is known to facilitate the expression and folding of bacterial collagen, and inserted the gene in a new expression vector. My project is to optimize the expression of this new vector, Col877pV, and to improve the yield. During the first few runs, we used 2xYT media, and the expression level was still not optimal. We are currently trying different growth temperature, and induction conditions, as well as a new growth medium M9 casamino acid. The yield was analyzed by SDS PAGE and His-tag affinity chromatography. The yield under different conditions will be presented. These studies will help us to effectively produce the mini-fibrils and help move our research of collagen forward.
#89 Shanna-Kay Griffiths

**Biotransformation of Indole-3-carboxaldehyde and Glycine**

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Biotransformation is the modification of a chemical compound by an organism that results in the production of new compounds. Biotransformation can serve as an environmentally friendly and renewable alternative to chemical synthesis to generate molecules that are beneficial for the environment and for the development of new drugs. Our previous study indicated that a mixed microbial culture (MMC) derived from wheatgrass is capable of coupling indole-3-carboxaldehyde and glycine to generate a new heterocyclic molecule. This finding is important because it opens an opportunity to develop new MMC-based “green” processes to produce heterocyclic molecules, which are important for drug development. Furthermore, the heterocyclic product from the wheatgrass MMC, once characterized, will provide a new clue to understand the chemical language spoken in microbial communities. This presentation will explain the biotransformation by wheatgrass MMC, purification of the heterocyclic product, and structural analysis. Implications of our finding in terms of green chemistry and biomedical research will be discussed.

#90 Madeleine D. Tuten

**The Effects of Psychiatric Distress and Male Role Norms on Men’s Attitudes Towards Help-Seeking**

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Research suggests that endorsement of stereotypically masculine norms is related to less favorable attitudes towards help-seeking. However, the role of specific masculine norms on help-seeking attitudes in men experiencing clinically significant psychological distress is not well understood. The current study examined associations among men’s clinical distress, specific male role norms, and attitudes towards help-seeking in a national sample. Five hundred seventy-nine men completed an online survey that assessed psychiatric symptoms, male role norms (i.e. status, toughness, antifemininity), and attitudes towards professional help-seeking (i.e. openness to help-seeking, value in help-seeking, preference to cope on one’s own). A significant negative indirect effect emerged between global psychiatric symptom severity and attitudes towards help-seeking via antifemininity; men endorsing greater psychiatric distress were more likely to endorse antifemininity norms, which in turn were associated with less favorable help-seeking attitudes (Openness $\beta = -0.17$, SE $= .06$, 95% CI $[-.29,-.07]$; Value $\beta = -0.08$, SE $= .04$, 95% CI $[-.17,-.01]$). Results suggest that psychological distress may activate beliefs that men should avoid stereotypically feminine characteristics. As psychological distress itself may be seen by some men as feminine, activation of the antifemininity norm may reinforce negative help-seeking attitudes and inhibit help-seeking. Future work is needed to identify interventions for challenging norms and attitudes that restrict the mental healthcare utilization of those men who need it most.
#91 Simona Lysakova

Examining Asthma Control among Emerging Adults: Utility of Qualitative Methodology

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Background: Emerging adults (EAs; 18-29-year-olds) have the highest asthma prevalence among adults (10.3%). Moreover, mortality rates are four times higher for EAs compared to children. Poor asthma control (i.e., exacerbated symptoms and functional impairment) has been linked to worse health outcomes. Qualitative methods can account for developmental context, allowing for rich understanding of reasons for poor asthma control at this life stage. The study aims are: 1) to assess EAs’ prevalence and asthma control, and 2) to demonstrate the utility of qualitative methods to better understand asthma control among this population. Method: Aim 1 was tested in secondary analysis of 124 adults (aged 22-71) with asthma who completed the Asthma Control Questionnaire (ACQ-5). Aim 2 draws on an ongoing qualitative (interview) study of 30 EAs to understand beliefs and treatment of asthma. Exploratory qualitative analyses will examine the developmental determinants of asthma control at this life stage. Results: Study 1: 10.5% of this sample with asthma were EAs (n = 13). All had uncontrolled asthma (ACQ-5 score ≥ 1.5). This matches the asthma prevalence for EAs nationally (10.3%). Case studies from the qualitative study will illustrate how thematic analyses can uncover developmental influences in the interview data. Discussion: The prevalence of uncontrolled asthma is a salient issue for emerging adults. We expect that by interviewing EAs, we will be able to provide rich data for understanding the determinants of poor asthma control among this age group, which can inform interventions.

#92 Jovanka Noel

Social Support and Depressive Symptoms in Cancer Patients: Is All Support Beneficial?

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Introduction: When faced with chronic illness, individuals often turn to loved ones for social support. The presence of positive social support when needed helps individuals cope with disease and maintain psychological well-being. However, support can be detrimental if it is perceived as unhelpful or inadequate. In the context of cancer, many patients are at risk of developing depression. Our aim was to examine the independent roles of positive and problematic social support on depressive symptoms in the cancer context. Methods: A systematic review of the Contextual Illness Support Scale (CISS) was conducted using seven databases. Peer-reviewed empirical papers and conference proceedings were included if they used the CISS in any language with an illness condition, and were published between 1990 and 2018. Native language speakers reviewed articles for eligibility and performed data extraction. Articles were coded for sample characteristics, internal consistency reliability, and the relation of the CISS to depressive symptoms. Results: Of the 4,007 references retrieved, 35 studies met inclusion criteria. All of the studies used the German version of the CISS scale instead of the original English version. Cancer type varied by study, with the majority focusing on multiple cancers (57%), breast cancer (14%), or hematological cancer (8%). Depressive symptoms were associated with problematic support and inversely related to positive support, with correlations ranging from - .11 to .35 (p’s < .01). Conclusion: It is not the presence of support but rather the type of support that is associated with higher or fewer depressive symptoms among cancer patients.
#93 Sabina Kubayeva

**PKMζ Protein Expression Increases in Adult Mouse Hippocampus Following Sevoflurane Anesthesia Treatment**

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PKMζ is a brain-specific, autonomously active atypical PKC critical for the formation and maintenance of Long-Term Potentiation (LTP), which is characterized by persistent strengthening of synapses. In addition to being a memory molecule, PKMζ may also serve neuroprotective roles. Sevoflurane (a volatile anesthetic) reinforces neuroprotection by mitigating the aversive effects of hypoxia on neuronal health. Wang et al. (2012) showed that sevoflurane enhances neuronal recovery after hypoxia and increases new PKMζ protein production in the rat hippocampus. Zeta inhibitory peptide (ZIP), a PKMζ inhibitor, blocks improved neuronal survival following sevoflurane, suggesting that neuroprotection conferred by sevoflurane is mediated by the increase in PKMζ. However, postsynaptic whole-cell injection of PKMζ has been shown to cause the potentiation of postsynaptic responses throughout the neuron. Non-specific increases in synaptic strength is expected to introduce noise, aversively affecting memory traces (engrams). Interestingly, no such changes in synaptic strength are observed with sevoflurane, suggesting that newly synthesized PKMζ does not affect pre-existing synaptic pools of PKMζ, but exerts its beneficial effects at another cellular locus. To examine the mechanism that controls the compartmentalization of PKMζ pools and guarantees the integrity of pre-existing engrams in the hippocampus, mice were anesthetized with 2% sevoflurane for 2 hrs. Brain were fixed with paraformaldehyde, sectioned into 40 μm coronal sections and stained with antibodies against PKMζ. The morphological distribution of PKMζ was examined using laser confocal microscopy. Our findings regarding the relationship between PKMζ and sevoflurane can be used to determine more about Alzheimer’s disease pathology.

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#94 Michelle Rangel

**Effects of Chronic Escalating Methamphetamine on 5HT1B Receptor Knockout Mice**

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Although dopamine has been well studied in reward circuitry and drug abuse, less is known about serotonin (5-HT) in response to neurotoxic drugs of abuse such as methamphetamine (MA). Previous research on alcohol and cocaine indicate that 5HT1B knockout (KO) mice have an increase motivation to self-administer these drugs. Additionally, differences in drug use between male and female MA users is noted in the human literature. Our lab investigated the 5HT1B receptor and its role in chronic escalation of MA use. Using a 28-day voluntary oral methamphetamine administration (VOMA) model, mice had access to increasing doses of MA for the first 10 days followed by a free access period of static MA doses from days 11-28. We hypothesized different rates of consumption within genotype along with differences between sexes. Consumption results displayed a main effect of day across all conditions, however, only wild-type mice demonstrated a main effect of both sex and day, as well as an interaction of sex by day that was not evident in KO animals. Chronic methamphetamine users are also known to display weakened cognition therefore after 14 days of abstinence, mice were tested on a radial arm maze task for working memory. Results demonstrated no main effect of sex or genotype but an overall effect of bait. Overall, results suggest a potential role of serotonin in the differential consumption of MA in wild-type male and female mice without a role in working memory in this model. Future research should explore 5HT1A receptors using the VOMA model.
#95 Zianne Cuff

**Self-Recognition in the African Electric Catfish (*Malapterurus electricus*?)**

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Mirror Self-Recognition (MSR) is characterized as the ability for an individual to recognize itself in a mirror while possessing an intrinsic understanding that the image it sees reflects ‘self’. While MSR is typically studied through observing the physical interactions of an individual with a mirror using a host of techniques, these experiments limit our understanding of potential self-recognition in other animals whose primary sense is not vision. The current study investigates *Malapterurus electricus*, the African electric catfish, that relies primarily on electric and olfactory cues. We hypothesize that members of this species can discriminate between self, kin and other. Using a habituation paradigm, we record the fish’s electric activity in response to a gentle mechanical stimulus to its abdomen. This stimulus consists of one of four conditions: untreated cotton swab, a swab containing mucus from a conspecific, from itself, or a prey fish. We will compare the number of habituation stimuli needed across all four conditions, analyze the composition of each electric discharge, and identify possible differences in the chemical make-up of the fish’s mucus using mass spectrochromatography. The current analysis supports the hypothesis. *Malapterurus* responded most frequently to goldfish mucus and untreated swabs, followed by conspecific mucus, and hardly discharged when stimulated with its own mucus. More research is necessary to add *Malapterurus electricus* to the rank of mammalian species exhibiting self-recognition.

#96 Sashana Rowe-Harriott

**Examining the Mediating Role of Emotion Reactivity in the Relation between Non-Suicidal Self-Injury (NSSI) Age of Onset and Severity of NSSI**

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Non-suicidal self-injury (NSSI) refers to the intentional harm of one’s own body tissue without intent to die, and for purposes not socially sanctioned. NSSI prevalence is increasing; moreover, NSSI is a known risk factor for later suicidal behaviors. Consequently, NSSI must be better understood to inform preventative strategies. While studies suggest that adolescents that have early NSSI onset are more likely to engage in severe NSSI, the influence of emotional mechanisms on this relation is understudied. In this project, via two studies we examined the role of emotion reactivity (ER) in the relation between NSSI age of onset and NSSI severity, among a clinical, adolescent sample. We hypothesized that adolescents with higher ER will have younger NSSI age of onset and greater NSSI severity than for adolescents with lower ER. Also, we expected that there will be an indirect path from NSSI age of onset and NSSI severity via ER. Both studies recruited adolescents from local emergency departments and pediatric outpatient clinics after being admitted for suicidal behavior. A combined, analytic sample of 57 adolescents (52.6% female), with a mean age of 15.5 (±2.2) years, responded to a semi-structured interview and completed a battery of self-report questionnaires. Results indicated that there was no significant direct effect between NSSI age of onset and NSSI severity. Additionally, there was no significant indirect effect of the proposed path model. However, ER significantly predicted NSSI severity and urgency. Our results provide insights on what drives NSSI severity.
#97 Gerson Borrero

Examining Substance Use as a Mediator in the Relationship Between Rumination and Suicidal Ideation

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The present study examines the relationship between rumination and suicide ideation via substance use. Rumination involves maladaptive repetitive thinking about the causes and consequences of a negative mood. While research has established that certain ruminative subtypes, such as brooding and reflection, have relationships with suicidal ideation, existing literature has yet to explore possible mediators in these relationships. As such, the current study utilized Selby and Joiner’s Emotional Cascade model as the basis to propose partial mediation models describing how substance use mediates the relationships that ruminative subtypes have with suicide ideation. 353 college students, ages 18-34 (263 female), with or without a history of suicide ideation or attempts and recruited from the Young Adult Study of Emotion and Stress, completed self-report measures of rumination and suicide ideation at baseline, a computerized diagnostic interview one month later, and suicide ideation self-reports at 6-month follow up. We hypothesized that reflection would predict suicide ideation, and that substance use would mediate that relationship. Additionally, brooding was expected to predict suicidal ideation, mediated by substance use or depressive symptoms. We also hypothesized that the relationship between brooding and suicidal ideation would be mediated by both depressive symptoms and substance use in a serial model. We found that brooding predicted suicidal ideation but did not predict substance use. Additionally, reflection predicted suicidal ideation, but this relationship was mediated by depressive symptoms and not substance use. These results suggest that depressive symptoms may be better explain the relationship between reflection and suicide ideation among young adults.

#98 Destinee B. Semidey

Heparan Sulfate Proteoglycan Expression Varies in the Hippocampus and Amygdala of Animal Models for Mood Disorders

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Patients with major depressive disorder show decreased fibroblast growth factor 2 (FGF2) in the hippocampus. Sprague-Dawley rats were bred based on locomotor activity to develop bred High Responder (bHR) and bred Low Responder (bLR), models for externalizing and internalizing mood disorders, respectively. Meta-analysis of bLR/bHR expression data demonstrates differential levels of the FGF2 co-receptors known as heparan sulfate proteoglycans (HSPGs). P14 is a critical period for emotional processing centers while adults show long term changes in brain glycomes. In this study, P14 and adult animals were assessed for HSPGs through in situ hybridization using S35 probe. bLR rats express high levels of the HSPG Glypican-1 and bHR express high levels of the HSPG Syndecan-4. Outbred rats were examined to profile “normal”. Amygdala Glypican-1 expression in the outbred animals was similar to bLRs and similar to bHRS in the hippocampus. The analysis of Syndecan-4 is ongoing. Neurocan, a proteoglycan involved in perineuronal nets (PNNs), also demonstrates differential expression in a meta-analysis, suggesting its role in mood disorders. Further analyses are required, but manipulation of proteoglycan levels may alter behavior and serve as a therapeutic target for mood disorders, like major depressive disorder.
#99 Max Economos

An Investigation of Potential Relationships Between Multiple Measures of Neural Inhibition Within the Visual System of Humans

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Gamma-aminobutyric acid (GABA), the major inhibitory neurotransmitter of the mammalian nervous system, moderates intracortical inhibition within the visual system. Deficiencies of GABAergic inhibitory processes have been associated with the development of various pathologies, and could therefore serve as a valuable diagnostic tool. Cortical activity at the level of the visual cortex is observed by measuring visual evoked potentials (VEP). Quantitatively adjusted visual stimuli were designed to optimize the neural response sizes of the inhibitory mechanisms of interest. Contrast sweeps of bright or dark isolated checks as well as contrast-reversed partial-windmill and windmill-dartboard stimuli were presented to elicit responses of bright and dark shunting inhibition, short-range (Fundamental) and long-range (2nd Harmonic) lateral interactions, respectively. There is a weak positive correlation between our bright and dark measures of shunting inhibition, \( p < .05 \). Weak negative correlations exist between bright shunting and the fundamental response \( (p < .05) \) and between bright shunting and the 2nd harmonic response \( (p < .05) \). There is no significant relationship between dark shunting and either the fundamental or harmonic response \( (p > .05) \); this result was expected, and supports our knowledge of the ON/OFF pathways as separate and distinct underlying mechanisms of the visual system. While most participants fall within a consistent range for both bright and dark shunting, others exhibit very high or very low for one and not the other. Further research should be conducted to determine whether or not population-specific optimal ranges exist for these measures.

#100 Hannah Rosenthal

In Vitro Fertilization: A Study of the Effects of Preimplantation Genetic Diagnosis and Improved Freezing Methods on Embryo Transfer Efficiency

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This project focused on determining how changes in freezing methods and preimplantation genetic diagnosis (PGD) have affected the mean number of embryos transferred during Frozen Embryo Transfers (FET). A typical treatment cycle for PGD begins with hormonal stimulation of the ovaries, surgical collection of eggs that are then fertilized with sperm. Eggs that are successfully fertilized undergo an embryo biopsy, are frozen, and then tested for abnormalities. If found normal, the embryos are thawed and transplanted into the woman’s uterus. Data were collected for 369 patients treated in years 2012-2018. The data were collected from Westchester Fertility and Reproductive Endocrinology. Patients were divided into two groups, based on treatments of embryos: FET with PGD vs. only FET. For years 2012-2013 FET was by the slow freeze method, while from years 2014-2018 it was by vitrification. Comparisons were made between these groups with respect to number of embryo transfers required. Preliminary analyses show that patients in which the slow freeze method was used required an average of 1.9 embryos per transfer (68 patients). When vitrification was used but no PGD, the average was 1.5 (215 patients), and when both vitrification and PGD were used, the average was 1.05 embryos per transfer (85 patients). Preliminary data support the idea that changing the freeze protocol from slow freeze to vitrification, along with the increased use of PGD, allowed for a decrease in number of embryos transferred before a healthy pregnancy.
#101 Aziz Elbasheir

**Environmental Enrichment as a Modulator in the Expression of GFAP and GS in Hippocampal Astrocytes**

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Environmental Enrichment (EE) has been shown to stimulate gliogenesis within the hippocampus. Here we accentuate possible effects of EE on propagation of glial fibrillary acidic protein (GFAP) and GS (glutamine synthetase) expressing astrocytes in response to stress. Preliminary findings suggest EE as a mediator in the expression of both GFAP and GS under a stressor condition. To address this issue, 24 Sprague Dawley rats were equally divided at postnatal day 25 and housed into either EE or standard housing for 30 days. Groups were further split, where half the rodents received an acute single prolonged stressor (SPS), while the other half did not. Two weeks following SPS, brains were then collected. Using immunohistochemistry, GFAP and GS will be tagged and quantified to ascertain any effects of EE on astrocytic gliogenesis. Evidence has shown, under certain enriched conditions, an upregulation of GFAP, which helps preserve the mechanical strength of astrocytes. Additionally, astrocytes have shown to maintain the expression of GS, which functions as a neuroprotector. Therefore, it is expected that in the presence of EE, there will be an upregulation of GFAP and GS expressing astrocytes, which in turn, can increase the resiliency of the hippocampus to the neurodegenerative effects of stress.

#102 Ariel Nieves

**Effects of Stress and Environmental Enrichment on GFAP and S100B Immuno-positive Astrocytes.**

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Neuroinflammation in response to severe stressors can lead to behavioral and cognitive deficits as well as pathological changes that may lead to the development of neurodegenerative diseases. Environmental enrichment (EE) has been shown in studies to attenuate several of these deficits. We hypothesize EE is a neuroprotective factor, utilizing time dependent expressions of astrocytes, against the effects of acute stressors. Male Sprague Dawley rats (postnatal day 21) were placed into either EE-housing (N = 12), where they were exposed to social and physical forms of enrichment, or Single-housing (SH, N = 12). After 30 days in respective housing, animals were further separated into an acute stressed or non-stressed cohort. The stress cohort underwent single prolonged stress paradigm (physiological, psychological, and emotional) followed by a rest period of one week. A successful preliminary immunohistochemistry test stain was used to assess the expression of astrocytic immune-positive cells with cytokine markers Glial fibrillary acidic protein (GFAP) and S100 calcium-binding protein B (S100B). Astrocytes retract cytoskeletal processes before migration to site of injury. Due to this mechanism we predict that there will be increased GFAP expression and decreased S100B expression in the hippocampus of EE animals because of a decreased neuroinflammatory response and therefore a reduced mobilization of astrocytes.

This work was supported by PCS CUNY, Undergraduate Research Initiative, and National Institute of Health: Blueprint for Enhancing Neuroscience Diversity through Undergraduate Research Education Experiences (ENDURE)
In addition to its involvement in motor control, the cerebellum might be implicated in affect processing and the pathophysiology of post-traumatic stress disorder (e.g., Baldacara et al., 2011). Lower activity in the cerebellar vermis has been associated with more trauma-related symptoms in young adults with a history of childhood maltreatment (Teicher, 2000). Vermal hypoactivity in trauma-exposed people might be related to atypical functional connectivity between the vermis and the limbic system. Resting-state connectivity, a measure of spontaneous activity synchronization between brain regions, is a common index of baseline functional coupling of neural circuits. We hypothesized that trauma exposure would be associated with greater resting connectivity between the vermis and bilateral amygdalae and hippocampi. 24 trauma-exposed women (age M=22.9, SD=5.5) and 20 no-trauma controls (age M=21.1, SD=3.2) completed a clinical interview and a resting-state functional magnetic resonance imaging scan. Trauma-exposed women did not differ from no-trauma controls in resting vermis-amygdala or vermis-hippocampus connectivity (all \( p\)s>0.05). Age was inversely associated with vermal connectivity with the left amygdala (\( r=\text{-.451, p=\text{.002}}\)), left hippocampus (\( r=\text{-.505, p=\text{.001}}\)), and right hippocampus (\( r=\text{-.335, p=\text{.028}}\)). Controlling for age, trauma-exposed women showed a trend towards greater left amygdala-vermis connectivity compared to controls (\( F(1, 40)=3.61, p=\text{.065, part. \eta}_2=\text{.083})\). These results suggest that trauma exposure is associated with stronger functional coupling between the cerebellum and the limbic system. Further understanding of cerebello-limbic connectivity might provide insight into the pathophysiology of trauma-related disorders.

Phelan McDermid Syndrome (PMS) is a genetic disorder that results from a disruption or deletion on the terminal end of Chromosome 22, specifically in the 22q13 region. SHANK3 is one of the genes that is found in genes that is found in this area. Symptoms of PMS include developmental delays such as absent or delayed speech. We hypothesized that mice with deletion of all SHANK3 isoforms would have communication deficiencies. Ultrasonic vocalizations of two different batches of mice were recorded at 6 and 12 days old. The 6 day old batch consisted of untouched mice that have never been separated from their mother. Being both younger and smaller they are more sensitive to the cold, calling to their mothers as a result. This age is also the peak of vocalization in mice. In the 12 day old cohort, the mice already participated in daily testing and were separated from their mothers before. They were also more resistant to the cold and called less as a result. Upon analysis of 3 minute recordings of each cohort, no phenotypic difference was seen in the 12 day old mice. In the 6 day old group, however, the KO genotype had the least number of calls and shortest calling time, while the WT had the most number of calls and a longer calling time. In conclusion, the 6 day old group supported the hypothesis of communication deficiencies while the 12 day old group did not. For future studies, the two different cohorts may be studied at different temperatures.
#105 Giovanni Green

**The Black Panther Party and Community Health**

Giovanni Green¹

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In a response to discrimination, communities organize, assess their resources, and develop interventions that address the traumas associated with poor living conditions. There has been scholarly work on the Black Panther Party and the social justice interventions they brought to communities as a response to the inadequate social welfare programs administered by the government. United States government documents also reveal the often violent objectives and methods for silencing and repressing the actions of the Black Panther Party and other political groups who were perceived as dissenters through COINTELPRO. This study will focus on the survival programs of the Black Panther Party and the tyrannical approach taken by public officials to repress any form of community-based health activism efforts. There was the criminalization of the People’s Free Breakfast Programs, the People’s Free Health Clinics, and other interventions that eased the hardships associated with the built environments inhabited by people of color. To understand this process of criminalization there will be an examination of the space marginalized groups have been relegated to live within and the traumas associated with their built environments, the interventions developed by the Black Panther Party to ameliorate the increased rates of morbidity and mortality due to systemic racism, and the pressure placed on organizations to discontinue collaboration with the Black Panther Party. While the organization of the party may have deteriorated, the impact of their efforts still reverberates through society and results in models of community organizing around social justice issues in the present.

#106 Hristiana Stoynova

**Biogenic Carbon Storage and Fluxes in a Heterogeneous Suburban Landscape: A Case Study at the National Institute of Standards and Technology in Gaithersburg, Maryland**

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Currently three percent of Earth’s land surface is urbanized, yet relatively little is known about spatial and temporal patterns in biogenic carbon (C) storage and fluxes in urban environments compared to rural areas. Urban environments tend to be considerably warmer than rural environments because of the urban heat island effect and vegetation in urban ecosystems tend to have greater access to sunlight and nutrients. Most urban vegetation is fragmented and exposed to high concentrations of pollution, changing the growth rate and, therefore, the amount of C being sequestered. For these reasons, intact rural forest might not serve as a reliable analog for urban systems. The objective of our research is to use empirical field ecological measurements in a GIS framework to develop a spatially-explicit model of biological carbon storage and fluxes across a fragmented, heterogeneous suburban landscape, which are often overlooked in regional carbon balance estimates. We collected data from the 372.7 ha campus of the National Institute of Standards and Technology (NIST) in Gaithersburg, Maryland, a suburb of Washington, D.C. Vegetation productivity and C storage was assessed using leaf-level measurements of photosynthetic rates and field-based measurements of biomass and net ecosystem productivity across the different vegetation types. Our early results suggest that urban forests can be surprisingly productive and that letting intensively managed urban grasslands (lawns) revert back to unmanaged grasslands can result in increased carbon storage.
#107 Michael Abdool

Does ABCA1 Contribute to the Formation of TLFs?

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Humans have a subset of high-density lipoproteins (HDL) known as trypanosome lytic factors (TLF) found in the bloodstream, which are responsible for immunity against African trypanosomes. TLFs are made up of apolipoprotein L-1 (APOL1), apolipoprotein A-I (APOA-I), haptoglobin-related protein (HPR), and hemoglobin (HB). Knowing the components that make up TLF, our goal is to learn more about how TLF assembles into a complex. ATP-binding cassette transporter (ABCA1) is a protein known for mediating the transport of phospholipids and cholesterol to extracellular APOA-I for the initial generation of HDL. We want to know if ABCA1 plays a role in the generation of TLFs. We began by acquiring a cell line (HEP G2) known to express ABCA1 endogenously, and compared it to Nterra, HeLa and HEK293 cell lines via western blot. Upon western blot analysis, we observed bands in the Nterra and HEP G2 lanes, but they were larger than expected. Transient transfection of HEK 293 cells, with a plasmid containing the APOA-I gene, revealed expression of APOA-I in cell lysates and in the media, which tells us that APOA-I is being secreted outside of the cells. This indicates that HEK293 cells have ABCA1, even though we were unable to detect the protein. For future experiments, we will test whether the proteins previously detected are indeed ABCA1. ABCA1 is a protein that lipidates and transports molecules across the plasma membrane and could potentially play a key role in creating TLFs.

#108 Ariane Marchese

29Si MAS NMR of Heat-Treated Serpentine Materials for CO2 Capture Under Different Leaching Conditions

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The large and increasing content of greenhouse gases in the earth's atmosphere is unprecedented and poses a threat to the stability of current environmental conditions. Included among the strategies geared towards ameliorating rising atmospheric CO2 levels is the development of materials capable of absorbing/converting atmospheric CO2. Mineral carbonation using heat-treated serpentine (HTS) is one of the more promising approaches in this regard. This sequestration material is central in the step-wise conversion of atmospheric CO2 to an inorganic solid carbonate form via the availability of reactive Mg2+. Accompanying conversion to the carbonate, the mineral silicate environment is transformed from a modified state (Mg2SiO4) to SiO2. The conversion efficiency to MgCO3 closely follows the evolution of the silicate environment, i.e. from Q0 to Q4 structural units. In this research, 29Si magic-angle spinning nuclear magnetic resonance (MAS NMR) is used to analyze the silicate environment distribution (Qn, where the number of bridging oxygen atoms, n = 0,1,2,3,4) in various HTS samples throughout a step-wise acid-leaching route. The results provide insight into the synthesis of effective agents for carbon capture.
#109 Vanessa Pinto

**Star Photometry**

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The main focus of my research is to apply photometry to the exoplanet transit method to find new planets. By studying the constant brightness of a star, we can detect when it decreases due to another astronomical body, typically a planet, passing between the star and the earth. Through examining this change in brightness, we can determine the size of the planet, its orbit and the relative distance. Using a new program called AstroImageJ, it is possible to analyze the image data during a transit, including data reduction processes that require combining different types of frames such as flats, darks, and biases. We also employ the functionality of Astrometry.net, to obtain the precise coordinates of the star so AstroImageJ can easily process multiple images by matching coordinates instead of the pixels in the picture.

#110 William Chakalis

**Astronomical Imaging**

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My research focuses on the data analysis of .FITS files (Flexible Image Transfer System). FITS images are n-dimensional arrays of data that astronomers use to store images. One common task is combining multiple FITS images to create the magnificent astronomical vistas that appeal to so many people. Problems arise when these images are not aligned correctly, which is not uncommon when observing astronomical bodies within our solar system that move at rates different from the sidereal rate that bodies such as stars do. The FITS file format is almost 40 years old, and the most common means of processing them known as Image Reduction and Analysis Facility (IRAF) has become obsolete. Astropy is a widely used python-coding package among astronomers around the world, and the community is developing new modules to handle FITS files as older solutions have become antiquated. The ultimate purpose of this project is to develop a new module that can align FITS images with the hope of developing a new module for Astropy.

#111 Christopher Mallia

**High-Pressure Nuclear Magnetic Resonance for Characterizing Volume Dependent Molecular Dynamics**

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Nuclear Magnetic Resonance (NMR) spectroscopic techniques have proven powerful and robust in characterizing material systems across scientific fields. Their application in lithium-ion battery chemistries as a non-invasive technique to target specific nuclei is indispensable to finding materials that are better performing and safe. One such variation of NMR is High Pressure (HP) NMR, whereby varied hydrostatic pressure is applied to the system, allowing for characterization of volume dependent dynamic processes. HP-NMR has proven to be particularly insightful for studying polymeric systems and ionic liquids (molten salts) for use as electrolytes in lithium-ion batteries. These materials retain a high level of ionic motional...
freedom at atmospheric pressures, and by restricting these motions under high pressures, one can isolate the interactions that are independent of relative space. Such materials have highly desirable properties that would enable the creation of batteries with no risk of thermal runaway, and stable structural properties that allow for use in extreme environments. To fully be able to understand these systems, and to inform the scientific community at large in which direction materials research needs to go, effective and enlightening experiments are needed. HP-NMR represents such an experiment, by allowing access to dynamic variable such as Spin-Lattice Relaxation Time (T1) and Diffusion Coefficient (D) measurements as functions of a thermodynamic variable besides temperature. The novel polymer electrolyte research in this work was funded by grants from Advanced Research Projects Agency - Energy (ARPA-E) and Ionic Materials Inc. Studies of glycerol based eutectic solvents were funded by Department of Energy Office of Science, through Case Western University Breakthrough Electrolytes for Energy Storage (BEES) program.

#112 Ysaris Sosa
Ion Transport and Association Study of Glyme-Based Electrolytes with Lithium and Sodium Salts

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The ever-increasing demand for energy storage has prompted continuous research into newer and better performing materials. Electric Double-Layer Capacitors (EDLCs) have gained much attention, due to their ability to store substantially more charge than conventional solid-state capacitors. The choice of electrolyte in an EDLC is important in determining various characteristics, such as energy density, cycle life, and stability. In this project, electrolyte salts were studied in various types of solvents, known as glymes (low molecular mass ethers); these salts and solvents included LiPF6 and NaPF6, as well as monoglyme (G1), diglyme (G2), and tetraglyme (G4), respectively, in various concentrations. Glyme-based electrolytes were chosen as electrolyte materials due to their chemical and thermal stability. Ionic and molecular self-diffusion measurements were performed on these materials, using Nuclear Magnetic Resonance (NMR) spectroscopy, specifically Pulse Field Gradient (PFG) diffusometry, in order to characterize the mobilities of the cations, anions, and solvents. By comparing the NMR diffusion data with direct ionic conductivity measurements, the degree of ionic association of each material was found. Out of all the materials studied, it was found that NaPF6 in G2 showed the best balance of low ionic association and high conductivity.

#114 Iurii Gurkov
Elucidating Virulence in Parasites: Studying Leishmaniasis using Dictyostelium discoideum

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Leishmaniasis, caused by the parasite Leishmania major, affects 12 million and puts at risk 350 million people worldwide. There is a need for new treatments as available drugs are toxic and modestly effective, and drug resistance is widespread. Virulence in L. major is known to be driven by ether phospholipids, whose precursors are synthesized by Fatty Acyl Reductase (FAR) and Dihydroxyacetonephosphate Acyl Transferase (DAT), making these enzymes potential drug targets. Rational drug design requires structural and functional analysis of FAR and DAT enzymes. However, it is expensive and difficult to perform such analysis in L. major. The model organism Dictyostelium discoideum much like L. major utilizes ether phospholipids which it produces from a single, bifunctional enzyme FAR-DAT. In order to establish D.
discoideum as a platform for studying FAR and DAT, cells that lack or overexpress the enzymes were created. Cells that overexpress the enzyme were characterized for growth, maximum cell density, and chemotaxis. Preliminary data suggest that cells that overexpress FAR or DAT have a larger doubling time relative to wild type cells. Cells that overexpress FAR reach stationary phase at lower cell density than wild type cells. Cells that overexpress both FAR and DAT together form smaller plaques on bacterial lawns than wild type cells. Taken together, these experiments suggest that ether-linked phospholipids are important for growth in D. discoideum. Such insight can be used to design assays to test the function of FAR and DAT with the goal of better understanding the mechanism of virulence in leishmaniasis.

#115 Jennifer Ferd & Trami Dang

Developing a Bioinformatics Pipeline for Characterizing Venom Peptides from Terebrid Snails

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More than 1.5 billion people worldwide suffer from moderate to severe chronic pain. Existing drugs for the treatment of pain are often associated with serious side effects and rapid development of tolerance, thus, there is a need for new, more selective, molecules. Venom peptides, such as MVIIA from the venomous snail Conus magus, are very effective in modulating molecular targets that play an important role in pain response. Each venomous snail can produce between 50-200 unique peptides in its venom arsenal. Considering there are 400 species of terebrid snails, this is a significant amount of novel peptides to characterize. This project applies a user-friendly bioinformatics automated workflow via a Galaxy pipeline to identify novel venom peptides from the transcriptomes of terebrid snails. Using RNA-Seq data, we performed quality control reports using FastQC, removed any low-quality reads and sequence adapters using Trimmomatic, and then assembled the reads de novo to develop a transcriptome with Trinity. From the transcripts, we applied GetORF to create open reading frames (ORFs) and predict genes that are then parsed by a python script to filter putative toxins with the help of SignalP. Upon completion of the bioinformatics pipeline a database of viable venom peptides is generated. These peptides will then be experimentally characterized for bioactivity. By expanding the discovery of new putative terebrid venom peptides this work can lead to new therapeutics for pain relief.

#116 Tahir Ramzan

Human Microbiome and Minority Health: Unravelling Variations Associated with Disease and Health Disparities

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Over the past decade, human microbiome research has made strides in relating disease and health to microbiome composition and diversity. More specifically, certain human microbiome profiles have been associated with increased risk of cancer, infectious, metabolic and autoimmune diseases. Type 2 diabetes, most notably, has become an epidemic health problem that has been linked to alterations in gut microbiomes. Previous research has shown a relationship between the dysbiosis of gut microbiomes and
an increased risk of diabetes however, little effort has been made to explore variations in microbiomes of diabetes patients in relation to their ethnicity. Here, we examined the differences in the taxonomic composition, diversity, and structure of gut and nasal cavity microbiomes (n = 128) studied in Caucasian, African American, Asian, and Hispanic prediabetic patients (n = 76) in the US. Specifically, we utilized raw 16S rRNA sequences generated by the Integrative-Human-Microbiome-Project and analyzed the data using the R environment. Our preliminary results suggest that the diversity and structure in gut (Kruskal-Wallis Test, P = 0.30; PERMANOVA, P = 0.12) and nasal (Kruskal-Wallis Test, P = 0.06; PERMANOVA, P = 0.13) microbiomes of prediabetes patients did not significantly differ among most ethnic groups. We conclude that unlike in healthy individuals who vary in their microbiome profiles based on their ethnic origin, human microbiomes in prediabetes become less distinguishable by ethnicity and race. Further studies are needed to increase our understanding how socioeconomic, behavioral, biological, and cultural factors impact microbiomes in health and disease.

#117 Mohammed Rahman
MicrobiomeExplorer: An interactive and web-based R Shiny analysis platform for microbiome research
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Understanding the complex microbial world opens new doors to study biology, improve health, and address some of the most pressing challenges of today’s world. Microbiome research has been a quickly advancing scientific field due to the rapid development of next-generation sequencing technologies generating large-scale, high-throughput data, requiring scientists to have advanced skills in bioinformatics and statistics. Here, we developed MicrobiomeExplorer, an easy-to-use, web-based R Shiny application, providing users an interactive and intuitive bioinformatics platform that complements current analysis tools in addition to combining functions of several R packages currently available for microbiome analysis. Specifically, the application allows users with little coding expertise to generate microbiome data summary statistics, pre-process data (e.g., rarefaction, subsampling), and run in-depth analysis of taxonomic composition, diversity, and structure of microbiomes. MicrobiomeExplorer also provides easy access to different visualizations and a suite of statistical analyses, including univariate and multivariate community inference commonly used in microbiome research. In conclusion, MicrobiomeExplorer offers a user-friendly graphical interface that guides users through a sophisticated analysis workflow which enables the efficient exploration and visualization of complex microbiome data.

#118 Cassandra Lee
Implementation of Targeted Temperature Management with Hypothermia Therapy on Post-Cardiac Arrest Patient’s Morbidity and Mortality: A Limited Literature Review
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In 2016, there were over 550,000 reported cases of cardiac arrest in the United States that caused morbidity and mortality. Patients who survive cardiac arrest suffer from permanent neurological damage caused by increased cerebral metabolic demands, edema, tissue hypoxia and apoptosis. The objective of this review is to learn whether targeted temperature therapy (TTM) with hypothermia therapy (HT) can minimize and/or prevent these damages. A limited literature review of 12 articles from CINAHL, EBSCO,
ProQuest, BioMed Central, Cochrane Library, Google Scholar, International Liaison Committee on Resuscitation (ILCOR), and American Heart Association (AHA) was utilized to verify usefulness of TTM with HT on post-cardiac arrest. Inclusion criteria were full peer-reviewed articles within the past 5 years, and exclusions included non-English articles and pediatric population. Results of this review showed that many patient variables are still being considered when determining the usefulness of TTM with HT post-cardiac arrest. These include but are not limited to age, gender, comorbidities, presenting rhythm, time of return of spontaneous circulation, Glasgow Coma Scale, and initiation of therapy. Based on this limited review, evidence remains thin and inconclusive on improving patient’s neurological outcomes and mortality. However current guidelines from AHA and ILCOR continue to recommend TTM with HT on post-cardiac arrest as best practice. Therefore, further research is necessary to conclusively determine its usefulness.