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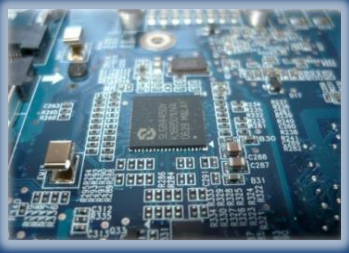

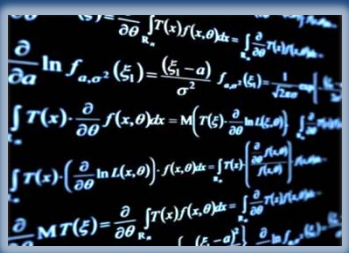

COLUMBIA UNIVERSITY UNDERGRADUATE SCIENCE & ENGINEERING RESEARCH SHOWCASE ABSTRACTS

Friday, October 21st, 2016
11:00 am-12:30 pm
Roone Arledge Auditorium
Lerner Hall

Abstracts

Maylis Basturk, Evolutionary Biology of the Human Species

Contact: mkb2170@columbia.edu
Faculty Mentor: Professor Mimi Shirasu-Hiza, Department of Genetics and Development, Columbia University Medical Center
Title: A multifaceted approach to traumatic brain injury in Drosophila

Abstract: Traumatic brain injury (TBI) is the leading cause of death for individuals under the age of 40, with an estimated 5.3 million Americans living with a traumatic brain injury-related disability. Most commonly, TBI results from blunt force trauma, inertial acceleration, or deceleration force causing the brain to ricochet inside the skull. While hospitals and insurance companies often characterize traumatic brain injury as a singular event, those who suffer from a TBI sustain more than just primary injuries. TBI patients incur secondary injuries resulting from cellular and molecular responses to the primary injury, that often persist over time. Much of the research characterizing the effects and outcomes of TBI consists of retrospective human clinical studies. However, there exists immense heterogeneity in the TBI patient population, in terms of genetic, socioeconomic and environmental factors, which create significant barriers in TBI research. In this study, we investigated the effect of environmental and epigenetic factors, such as parental age, acute and developmental stress, on survival following TBI. Moreover, we developed new protocol to inflict mild repetitive TBI. While our study did not find a significant effect of parental age and stress on survival of TBI, our data provide the foundation for future studies of other factors that influence survival. Ultimately, this study provides insight into using the fly as a model for TBI, to potentially identify future therapeutic interventions.

Jenna Bergmann, Cell and Molecular Biology; Latin

Contact: jmb2381@barnard.edu
Faculty Mentor: Professor Jennifer Mansfield, Department of Biology, Barnard College
Title: Determining mechanisms of Hoxa5 function: testing contribution of Hoxa5 expressing cells to muscle-related cell types and its ta

Abstract: Hoxa5 is one of 39 mammalian Hox genes, a family of transcription factors that are essential for the proper morphological development of tissues along the body axis, including the vertebral column. The Hoxa5 loss of function phenotype is perinatal lethal and includes homeotic transformations in the cervical and thoracic regions. The mechanisms through which Hoxa5 contributes to these structures, including its transcriptional targets and the tissue types in which Hoxa5 acts, have not been elucidated. Here, we asked whether Hoxa5 expressing cells contribute to muscle connective tissue and other muscle-related cell types. Preliminary data showed that descendants of Hoxa5 expressing cells include fibroblast-like cells within muscle but not differentiated muscle cells themselves. We collected embryos mapped for Hoxa5 using Cre recombinase lineage tracing, a method of permanently marking cells that have expressed Hoxa5 with red fluorescence. We then used immunohistochemistry to detect Tcf-4, a protein expressed in muscle connective tissue, actin, a protein in muscle cells, and the Hoxa5 descendants and compared the cells expressing each protein with a compound microscope. The same technique was also used to detect Pax7, a marker of muscle satellite cells. These experiments suggest that Hoxa5 expressing cells contribute neither to muscle connective tissue nor muscle satellite cell precursors. In a second approach, we are using relative quantification of gene expression in Hoxa5 loss of function embryos to identify potential target genes regulated by Hoxa5,including Wnt-related and regulated genes Paxillin, Nkd1, and Axin2.

Ramona Bledea, Neuroscience and Behavior

Contact: rb3032@columbia.edu
Faculty Mentor: Professor Edmund Griffin, Department of Psychiatry, Columbia University Medical Center / New York State Psychiatric Institute
Title: Chronic Alcohol Use Creates a Permissive Epigenetic Environment for Compulsive Cocaine Self-Administration

Abstract: The Gateway Hypothesis proposes that certain "gateway" drugs can enhance the likelihood of addiction to stronger, more illicit substances such as cocaine occurring later on in life. Insight into the molecular changes behind this effect is a critical step towards the development of treatments for addiction. In this study, we propose that chronic abuse of the gateway drug alcohol will potentiate the effects of cocaine on behavior, and that it does so by directly mediating the activation of calcium-calmodulin kinase II-alpha through the alteration of Ca2+ levels through changes to AMPA and NMDA channel expression in post synaptic densities in the nucleus accumbens. Phosphorylated calcium-calmodulin kinase II-alpha in turn can mediate the degradation of histone deacetylase 4 in the nucleus by activation of the proteasome. Since histone deacetylase 4 has the capacity to regulate gene expression, its presence provides an opportunity for epigenetic priming for addiction to occur in response to alcohol abuse. Thus far, our data supports that as the bloodstream is deprived of alcohol after a period of chronic use, the nucleus is the site of histone deacetylase 4 degradation, and that alcohol priming enhances motivation and compulsivity for cocaine use.

Adam Block, Mathematics

Contact: abb2190@columbia.edu
Faculty Mentor: Dr. Daniel Litt, Department of Mathematics, Columbia University
Title: Schur Functors and Exact Sequences

Abstract: Much study has been done on the representation theory of the general linear groups of vector spaces both in zero and prime characteristics. As such, the study of Schur Functors, indexed by integer partitions, is important. In 1974, Carter and Lusztig demonstrated the existence of an exact sequence of Schur Functors indexed by hook partitions over prime fields. We develop the representation theory of the algebraic de Rham complex in an attempt to extend their result to arbitrary finite fields, a result that has consequences for the proving of certain vanishing theorems in algebraic geometry.

Paul Bloom, Neuroscience and Behavior

Contact: pab2163@columbia.edu
Faculty Mentor: Professor Janet Metcalfe, Department of Psychology, Columbia University
Title: The Tip of the Tongue (TOT) State as an Impetus for Curiosity

Abstract: The "tip of the tongue" (TOT) state occurs when one cannot recall something, yet feels sure that the desired information is familiar (Brown & McNeill, 1966). While the TOT state has been studied as a form of partial (Maril et al., 2001) or failed memory retrieval (Schwartz & Metcalfe, 2011), little work has been done thus far to understand its potential motivational or cognitive functions. We hypothesize that the often frustrating nature of the TOT state increases curiosity for the wanted information and serves as an impetus for knowledge seeking. In a behavioral study (N = 46) using general information questions, we found that being in the TOT state elicited a higher frequency of answer-seeking as compared to not knowing the answer. Additionally, in another study in progress, we

are examining event-related potentials (ERPs) in response to feedback (correct answers) to general information questions. Preliminary analyses (N = 17) suggest that feedback while in the TOT state, as compared to feedback after not knowing the answer, may evoke a heightened positivity at the midline between 300-600ms post-stimulus. This possible heightened positivity, if consistent between individuals, may indicate greater attention and recruitment of cognitive resources to feedback following the TOT state (Polich, 2007).

Chiara Butler, Chemistry

Contact: cjb2208@columbia.edu
Faculty Mentor: Dr. Xavier Roy, Department of Chemistry, Columbia University
Title: Synthesis and Characterization of a Nickel Phosphide Molecular Cluster

Abstract: Molecular clusters are inorganic molecules sometimes called “superatoms” because of their atomically-precise structures and characteristic electronic properties. A novel nickel phosphide cluster, Ni12[PMe]10(PEt3)8, was synthesized from an organocyclophosphane precursor. It features a unique, oblong core geometry as well as uncapped nickel atoms not covered by coordinating ligands. The cluster was characterized by single crystal and powder X-ray diffraction and analyzed with ultraviolet-visible spectroscopy, thermogravimetric analysis, and differential scanning calorimetry.

Richard Cao, Computer Science; Mathamatics

Contact: rrc2130@columbia.edu
Faculty Mentor: Professor William H. Robinson, Department of Immunology and Rheumatology, Stanford University
Title: Identification and Validation of Autoantibody Targets in Pulmonary Arterial Hypertension

Abstract: Pulmonary arterial hypertension (PAH) is a disease of the pulmonary vasculature, characterized by hyper-proliferation of endothelial cells, and increased pulmonary blood pressure that lead to heart failure and death. Roughly 1,000 PAH patients are identified in the U.S. each year, and only 34% of patients with PAH survive past five years without treatment.1 No treatments curb the progression of PAH, therefore a better understanding of PAH’s pathogenesis is desired. This project aims to explore the role of autoantibodies in the pathogenesis of PAH.

Elevated levels of plasmablasts, as well as IgG and IgA in PAH peripheral blood were detected previously. PAH patient peripheral blood plasmablasts were sequenced to identify PAH-specific autoantibody genes, which were used to generate recombinant, monoclonal IgG antibodies. These recombinant IgGs were tested for reactivity against a panel of autoantigens using protein microarrays. Twenty-five reactive IgGs were identified for further verification. In order to verify chosen IgGs’ reactivity to self-antigens, indirect Enzyme Linked Immuno-Sorbent Assays (ELISAs) were performed. One IgG bound to PCNA, one bound to sp100, and another to ssDNA. Small ubiquitin-like modifier proteins (SUMO) were hypothesized to be the antigens to these antibodies. Therefore, further testing to determine whether PCNA, sp100, and PCNA are SUMOylated, was conducted using western blotting; however, the presence of SUMO was not found. Furthermore, the aforementioned antibodies were also tested for reactivity towards SUMO using western blotting. Again, no binding was detected.

PAH plasmablast-derived recombinant monoclonal IgGs can specifically bind to self-antigens such as PCNA, sp100 and SSDNA, which suggests that PAH may be an autoimmune disease. These PAH plasmablast-derived recombinant monoclonal IgGs can serve as targets for novel diagnostics. Further in-

vitro and in-vivo studies need to be conducted to investigate the pathways in which autoantibodies and their respective antigens cooperate to initiate and exacerbate PAH.

Ting Cao, Biochemistry

Contact: tc2743@columbia.edu
Faculty Mentor: Dr. Brent Stockwell, Department of Biological Sciences, Columbia University
Title: Synthesis and Evaluation of Ester and Amide Substituted Ferrostatin Analogues

Abstract: Ferroptosis is a regulated form of non-apoptotic, iron-dependent, oxidative cell death that has been shown to be involved in many degenerative diseases.1 Ferrostatin-1 (Fer-1) is a small molecule that is a potent inhibitor of ferroptosis. Fer-1 effectively inhibits oxidative lipid damage but is metabolically unstable, thus limiting its in vivo application. Our group's earlier studies had shown that replacement of the ester moiety in Fer-1 with an amide moiety resulted in significantly decreased potency. More recently, it has been reported that amide substituted analogues of Fer-1 have increased stability while retaining high potency. In this study, we sought to verify if this was true. We synthesized ester and amide substituted ferrostatin analogues. We tested for the ability of these analogues to inhibit ferroptotic cell death, and attempted to establish a clearer structure-activity relationship by comparing their potency.

Joshua Choe, Biology

Contact: jc4685@columbia.edu
Faculty Mentor: Dr. Jung-whan Kim, Department of Biological Sciences, University of Texas at Dallas
Title: Distinct Metabolic Phenotypes within Non-small Cell Lung Cancer Define Selective Vulnerability to Glycolytic Inhibition of Lung

Abstract: Adenocarcinoma (ADC) and squamous cell carcinoma (SqCC) are the two predominant subtypes of non-small cell lung cancer (NSCLC), a set of diseases distinct in their histological, molecular, and clinical presentation. However, targetable metabolic signatures specific to individual NSCLC subtypes remain unknown. Our integrative analysis of human NSCLC tumor samples, patient-derived xenografts, the KrasG12D; Lkb1-/- murine model of NSCLC, NSCLC cell lines, and The Cancer Genome Atlas (TCGA) has uncovered markedly elevated expression of the GLUT1 glucose transporter in lung SqCC, which augments glucose uptake and fuels glycolytic flux as core metabolic features. We demonstrate that a critical reliance on glycolysis renders lung SqCC vulnerable to inhibition of GLUT1-mediated glycolytic metabolism, while lung ADC exhibits significant glucose independence. Clinically, elevated GLUT1-mediated glycolysis in lung SqCC strongly correlates with distinctly high 18F-FDG uptake in PET scan and poor prognosis. Our findings reveal previously undescribed metabolic heterogeneity of NSCLC subtypes and implicate significant potential for the development of diagnostic, prognostic, and targeted therapeutic strategies for NSCLC, including the potential to exploit the unique glycolytic reliance of lung SqCC, a cancer for which existing treatments have proven to be clinically insufficient.

Kristy Choi, Data Science

Contact: eyc2120@columbia.edu
Faculty Mentor: Dana Pe'er, Department of Biological Sciences, Columbia University
Title: Algorithmic approaches for analyzing single-cell RNA-sequencing data

Abstract: Recent advances in the development of single-cell RNA-sequencing (scRNA-seq) technologies have enabled the discovery of significant biological findings, ranging from the characterization of rare cellular subpopulations to the uncovering of novel gene expression patterns. However, the overabundance of dropout that prevails in the data's structure poses computational challenges for widely-used tools designed to analyze traditional bulk RNA-seq or DNA microarray experiments. If scRNA-seq data is not processed correctly prior to downstream analysis, the presence of errors and technological artifacts can mask and distort true biological signal. Therefore, we developed a new data analysis framework called SEquence Quality Control (SEQC) in order to streamline the pre-processing, alignment, and post-processing steps in scRNA-seq analysis. Then we sequenced mouse embryonic stem cell (mESC) samples with different methods for scRNA-seq (In-drop, Drop-seq, Mars-seq, 10X) in order to (1) test the effectiveness of the pipeline and (2) compare differences across technological platforms. We discovered that after filtering the sequenced data for artifactual reads and resolving errors by leveraging the information from known barcodes, we were able to recover a much more noticeable structure in the data with stronger biological signal. Several patterns specific to technologies, such as cell yield and coverage, also emerged from the analysis. Taken together, this result suggests that SEQC can be used for analyzing a wide variety of scRNA-seq experiments and provides a new standard for working with and interpreting scRNA-seq data.

Alexander Cody, Biology

Contact: asc2197@columbia.edu
Faculty Mentor: Dr. Gary C. Sieck, Department of Physiology & Biomedical Engineering, Mayo Clinic
Title: Rewarming Shock Decreases Oxygen Consumption Rate in Cardiomyocytes

Abstract: Hypothermia/Rewarming (H/R) induces cardiac contractile dysfunction; however the underlying intracellular mechanisms remain elusive. We hypothesized that in cardiomyocytes, H/R decreases oxygen consumption rate (OCR), which may be related to reduced myocardial dysfunction due to insufficient matching of the metabolic demand. To test this hypothesis, isolated cardiomyocytes from 6 rats underwent the H/R protocol as follows: cardiomyocytes were electrically stimulated (every 2 s) throughout the protocol; experimental temperature was cooled from 35oC to 15oC in 30 min, maintained at 15oC for 2 h, and then rewarmed back to 35oC in 30 min. Time-matched control cardiomyocytes were stimulated every 2 s for 3 h at 35oC. After 3 h, control and H/R cardiomyocytes were placed into separate chambers of an Oroboros Oxygraph (high-resolution respirometry) to measure OCR under varying conditions. Initially basal OCR was measured for 5 min followed serial exposure to oligomycin (1 µM for 5 min) to block ATP synthase activity, FCCP (0.5 µM repeated 3 times for 5 min each) an H+ ionophore to dissipate mitochondrial membrane potential; and antimycin-A (0.5 µM for 5 min) to block the electron transport chain. This procedure allows us to assess the key parameters of mitochondrial respiratory function: basal and maximal respiration (after FCCP exposure), ATP production and proton leak (after oligomycin), and reserve respiratory capacity (calculated after antimycin-A). H/R decreased all of these key parameters of mitochondrial function, which suggests that decreased OCR following rewarming may contribute to contractile dysfunction due insufficient matching of ATP supply and demand, as well as by contributing to a decline in cell viability (e.g., triggering apoptosis).

Willie Dong, Mathematics

Contact: wgd2105@columbia.edu
Faculty Mentors: Dr. Daniel Halpern-Leistner and Dr. Daniel Litt, Department of Mathematics, Columbia University
Title: Rational Points of Elliptic Curves over Finite Fields

Abstract: The Weil conjectures are influential proposals regarding the behavior of local zeta functions of algebraic varieties over finite fields. Specifically, much study has been given to rational points on elliptic curves over finite fields and its relation to the Weil conjectures. Corresponding to elliptic curves over finite fields, per the conjectures, are associated linear recurrences and characteristic polynomials that yield specific formulas for point counts over finite fields. Using the software Sage, we look at the distribution and corresponding statistics of the arguments of the roots of these characteristic polynomials, via both exhaustive and Monte Carlo methods. We compare these statistics to data generated by matrix-based models and analyze the relationship between these two data sets. (Work done in conjunction with Theodore Coyne.)

Ailis Dooner, Undeclared

Contact: acd2174@columbia.edu
Faculty Mentor: Dr. Cherie Motti, Department of Chemistry, Australian Institute of Marine Sciences
Title: Behavioral Analysis of the Crown-of-Thorns Starfish

Abstract: The Crown-of-Thorns Starfish (CoTS), Acanthaster planci, preys on coral, and is a major culprit in the diminishing of coral ecosystems of the Great Barrier Reef (GBR) off the coast of Northern Queensland, Australia (Teruya et al, 2001), causing more reef loss than has coral bleaching (D'eath et al, 2012). Presently, toxic injection of individual CoTS is a common management technique on the GBR; while this approach can minimize aesthetic deterioration and keep tourist operations afloat along specific swathes of the Reef (GBRMPA, 2014), it is not broadly implementable. In order to address and lessen CoTS' ecological impact, a more nuanced understanding of the starfish's behavior and biochemical sensitivity (to both potential cues from other organisms and fellow CoTS) is needed. This study entailed a three-pronged examination of CoTS' behavior involving analysis of: a.) CoTS' response to the presence of live spider conch snails, Lambis lambis b.) CoTS aggregation patterns in the winter season, and c.). single-organism sensitivity to two chemicals found in corals, dimethylsulfoniopropionate (DMSP) and acrylate. CoTS' response to Lambis lambis was analyzed using a Y-shaped maze tank, in which water from a snail-containing header tank flowed into a prong of the Y, and CoTS' movement patterns were analyzed with heat-mapping software. CoTS were not deterred significantly by the water-borne aroma of Lambis lambis, perhaps because it is not a perceived threat. Aggregation behavior was analyzed with an 8 sector round-tank aggregation assay, and (Southern Hemisphere) wintertime aggregation was observed to be lower than summertime aggregation patterns, which the research group previously analyzed in the (Southern Hemisphere) summer of 2015-2016. Sensitivity to DMSP and acrylate was tested with a dropper assay, in which 1mL of 0.001 M solution was ejected over a single arm of the specimens, and response was recorded with a numerical ranking system. Analysis of the assay is still in progress. This study gives insight into certain behaviors of the Crown-of-Thorns Starfish, which could potentially be useful information in future development of management techniques.

William Falcon, Data Science

Contact: waf2107@columbia.edu
Faculty Mentor: Professor Henning Schulzrinne, Department of Computer Science, Columbia University
Title: Indoor Location: Estimating a User's Floor Level Via Mobile Device Sensor Data

Abstract: During an emergency phone call, precise floor location minimizes emergency response time and maximizes the probability of the victim's survival. GPS does not provide floor location at all. This need is specifically important in urban canyons, such as New York City, where GPS is unreliable and where searching many floors in a building is time consuming.

In this paper we combine Machine Learning techniques with mobile device data to pinpoint a caller to +-1 floor of their floor location using zero infrastructure support. As the system crowdsources more data over time, the prediction accuracy improves as the Maximum Likelihood Estimator (MLE) for each user location improves. We use three insights to predict the user's floor location. First, we use a classifier to determine whether a user is indoors or outdoors. Second we measure device relative altitude change across the indoor/outdoor boundary for the last known significant location change. Third, we crowdsource device readings over time at the same location to determine a ground truth and adjust known floor locations within that building.

Andre Fiks Salem, Neuroscience and Behavior

Contact: af2868@columbia.edu
Faculty Mentor: Dr. Martin Chalfie, Department of Biological Sciences, Columbia University
Title: A method to identify super-sensitive mutants of Caenorhabditis elegans

Abstract: In spite of research that defined the molecules essential to vision, smell, and taste, researchers still do not know or fully understand all the molecules responsible for mechanical senses. Scientists have learned about some of the proteins essential to mechanosensation in mutants of the C. elegans roundworm in which it has been genetically disrupted. The mutations are provoked by random chemical mutagenesis, which should yield insensitive as well as super sensitive mutants. However, the super sensitive mutants have not been studied because their phenotype cannot be discriminated easily from the already responsive wild type in the standard touch assay.

We tested alterations to this assay in order to reduce overall response rate and allow super sensitive mutants to stand out from wild type. We concluded substituting the wild type for the temperature sensitive mec-4(u45) mutant, which has a reduced response rate at 22°C, will be helpful to identify super sensitives. In this new test, response rates to touch would be low and any animal that reverts to a high response should possess, along with the u45 allele, a super sensitive mutation. In the future, we will use this method to test strains with suspected enhanced sensitivity and hopefully allow more research in the genes causing this phenotype so that we can further understand how organisms feel touch.

Rebecca Gellman, Neuroscience and Behavior

Contact: rhg2120@columbia.edu
Faculty Mentor: Dr. Cindy Sears, Department of Medicine, Johns Hopkins University
Title: C. difficile Present in Germ Free APC Mice Inoculated with Colon Biofilms

Abstract: Colorectal cancer (CRC) is one of the top causes of cancer-related death worldwide. Because of the colon's high microbial load, the role of bacteria in the generation and proliferation of colon tumors has been a key area of interest. Previous studies show that biofilms, polymicrobial bacterial aggregates, disrupt the colon's mucosal layer and invade the epithelial cells. The bacteria present in these biofilms cause tumorigenesis by breaking down E-cadherin and triggering a chemical pathway that ultimately results in Stat3 activation and cell proliferation in the epithelium. 16S sequencing of the stool of germ-free (GF) APC mice inoculated with biofilms taken from human colons indicated a small, but significant and enduring, presence of Clostridium difficile. C. diff is an anaerobic, sporogenic bacterium that causes colitis and is a common nosocomial pathogen. In this study, we attempted the isolation of C. diff from the stools of GF APC mice inoculated with biofilms taken from tumor, normal flanking, or healthy biopsy colon tissue samples. C. diff was isolated from the frozen stool samples using heat shock. This method was designed to kill off most vegetative cells present in the stool, but to allow C. diff spores to survive and develop. C. diff was selected on cycloserine, cefoxitin, and fructose agar with horse blood (CCFA-HB). Colonies with the characteristic morphology of C. diff were then subcultured onto brucella blood agar. The morphology of the resulting bacteria were analyzed using gram stain. PCR was then performed to screen for a clostridial glutamate dehydrogenase gene (GDH) and the gene for toxin B (tcdB), one of the toxin proteins produced by C. difficile. The former indicated whether the isolated bacteria was a clostridial species, the latter showed whether or not the C. diff strain was toxigenic. PCR of subcultured single colonies isolated from two tumor, two normal flanking, and one healthy biopsy GF APC stool sample indicated the presence of toxigenic C. diff in one tumor and one healthy biopsy sample. However, no C. diff was isolated from either the normal flanking samples or the additional tumor sample. This study suggests that C. diff is present in human colon biofilms, and can survive when introduced into the guts of GF mice. Future studies will analyze the prevalence and potential tumorigenic role of this bacterial species.

Silas Grossberndt, Physics; Mathematics

Contact: skg2131@columbia.edu
Faculty Mentor: Dr. Andy Haas, Department of Physics, New York University
Title: A New Detector for the Observation of Milli-charge (Dark sector) Fermions at the LHC

Abstract: Our group is in the process of creating a new experiment at the Large Hadron Collider (LHC) that offers a model-independent probing detector for milli-charged particles. This experiment should be sensitive to charges in the range of 10-3 to 10-1 time the electron chare in mass ranges of 0.1 to 100 GeV. This window is chosen as it is the least constrained window in which we may find non-Standard Model particles at the LHC. The detector shall be placed in the old counting room at CMS, will feature plastic scintillators divided into four segments and approximately 100 photomultiplier tubes using a coincidence design to reduce background. Currently, we are focused on creating a good estimation of background rate using the scintillator in conjunction with the photomultiplier tube and an off the shelf ADC, and optimal operating voltage.

Saiti Srabonti Halder, Biomedical Engineering

Contact: ssh2164@columbia.edu
Faculty Mentor: Dr. Clark T. Hung, Cellular Engineering Laboratory, Department of Biomedical Engineering, Columbia University
Title: Assaying Permeability of Pre-treated Bovine Synovium using Flourescent Dextran

Abstract: Osteoarthritis is a common disease of the join characterized by deterioration of integrity of the joint cartilage and synovium eventually leading to inflammation. Although mechanical knee replacement surgeries are becoming common, the process is still extremely expensive, invasive, and unavailable in many parts of the world. The need to devise a less invasive and less expensive strategy requires a better understanding of the behavior of the synovium, a thin lining of cells responsible for nourishing the cartilage and synthesizing various important lubricant molecules.

The aim of this study was to observe and assess the permeability of the synovium under control and treatment conditions. Trans-wells fitted with synovium samples pre-treated with different combinations of chemicals were utilized to mimic the different possible chemical conditions in an osteoarthritic joint. First, fluorescently labelled dextran solution was added to the upper chamber of the trans-well and samples were collected from the bottom chamber at regular intervals. Then, these samples were assayed and the resulting data was analyzed to compare the differences in permeability. Our results show that there exists a negative correlation between any kind of treatment and permeability, with the unadulterated synovium showing the highest flow through of dextran molecules. These preliminary findings indicate that an osteoarthritic joint might prove vulnerable to various chemical stimulants and further optimization of the experiment can give us a better idea of transport properties of the synovium, allowing us to devise drugs and strategies with minimum side-effects.

Caroline Haoud, Biochemistry

Contact: ceh2189@columbia.edu
Faculty Mentor: Dr. Makoto Ishii, Department of Neurology, Feil Family Brain and Mind Research Institute, Weill Cornell Medical College
Title: Distribution of Amyloid-Beta Peptide Plaques and Its Impact on Basal Cellular Activity in Knock-In Mice with Mutations in Amyloi

Abstract: One major neuropathological hallmark of Alzheimer's disease (AD) is extracellular amyloid plaques which are comprised of abnormally aggregated amyloid-beta (Aβ) peptides. Aβ is naturally produced by proteolytic processing of the amyloid precursor protein (APP). While the exact etiology of AD is unknown, specific mutations in the APP gene that lead to an increase in Aβ levels and increased aggregation of Aβ have been identified in autosomal dominant familial forms of AD, strongly suggesting that Aβ may play an important pathogenic role in AD. The objective of this project is to study Aβ aggregation and cellular activity in different brain regions of mice with various APP mutations found in the familial forms of AD specifically knocked-in to the mouse genome (APP knock-in mice). Two different lines of APP knock-in mice at three different ages were created to examine the distribution of Aβ as the mice age and its effect on cellular activity in different brain regions over time. To evaluate the distribution and amount of Aβ in the APP knock-in mice, immunohistochemistry (IHC) with the monoclonal antibody (4G8) against Aβ is used. Additionally, the impact of Aβ on cellular activity is

determined by IHC using antibodies against phosphorylated ribosomal protein S6 (pS6) and the immediate early gene c-fos as proxies of cellular activity. For these IHC studies, three brain regions are examined: the hippocampus, amygdala, and hypothalamus. The results from this project once completed will elucidate how the distribution and accumulation of Aβ impacts basal cellular activity over time in these three brain regions.

Nicholas Herrera, Data Science

Contact: nh2473@columbia.edu
Faculty Mentor: Dr. Daniel Hsu, Department of Computer Science, Columbia University
Title: Efficient Algorithms for Active Learning with Seeds

Abstract: Active learning provides an algorithmic framework for statistically efficient learning with limited use of labeled data in domains where labeled data is hard to procure. A variety of other learning paradigms further generalizing this setting provide promise for even more efficient learning algorithms. We present a set of statistically and computationally efficient learning algorithms and their formal analysis in the active and (local) member query settings that demonstrate the power endowed by moving outside the standard setting of active learning or being given a set of helpful seed examples.

Ivy Huang, Chemical Engineering

Contact: ih2283@columbia.edu
Faculty Mentor: Dr. Xavier Roy, Department of Chemistry, Columbia University
Title: Exploring the Solid State Chemistry of Metal Chalcogenides

Abstract: Inorganic solid state compounds can be synthesized through molecule-based solution chemistry or solid state reactions. Molecules are attractive tunable building blocks for assembling materials but forming extended covalent solids with ordered structures from solution chemistry remains a daunting challenge. By contrast, solid state reactions that start from the pure elements and uses high temperatures to drive the reaction can form infinite crystalline arrays of covalently bonded atoms, which are solid state compounds.

The focus of the Roy Group has previously centered around molecular solids. This summer, my research involved developing the tools and methods to expand our expertise into solid state reactions, from the conventional high temperature synthesis to the hydrothermal. Depending on the quality of the material formed, powder x-ray diffraction or single crystal x-ray diffraction was employed, enabling a structural characterization of the compound.

One area of my research involves the synthesis of tunnel compounds to use as battery electrodes that may serve as intercalation anodes for Na, Mg and Al ion batteries. Molecular compounds have already been investigated by the Roy group, but the structure of their compounds do not stay intact as ions are cycled in and out of the structure. We believe that these tunnel compounds are promising materials because solid state reactions are known to form highly stable materials. High quality single crystals of AlV4S8, KV6S8, RbCr5Te8 have successfully been grown through the conventional solid state synthesis, and we are currently testing their performances as battery electrodes.

My main project focuses on the solid state chemistry of iron chalcogenides, a class of materials that was recently discovered to behave as high temperature unconventional superconductors. Unconventional superconductivity is particularly exciting because physicists have not yet been able to fully understand

and predict its occurrence. Below a certain critical temperature, the electrical resistivity of a superconductor goes to zero, enabling it to become a perfect conductor. As this occurs, the superconductor expels any magnetic field, leading to the well-known Meissner Effect. Normal superconductors have a critical temperature close to 0K, but iron chalcogenides have been reported to have a critical temperature as high as 56K. Motivated by theoretical works and literature precedents, we are currently working towards the synthesis of Ru-doped iron chalcogenides and iron chalcogenides with intergrown layers (e.g., PbOFeSe).

Ifeoma Irobunda, Environmental Biology

Contact: ii2154@columbia.edu
Faculty Mentor: Professor Mimi Shirasu-Hiza, Department of Genetics and Development, Columbia University Medical Center
Title: Paraquat sensitivity and the function of sleep in several mutants of Drosophila melanogaster

Abstract: Though sleep is conserved across virtually all animal species and thus considered an integral part of animal survival, its overarching function is poorly understood. In Drosophila melanogaster, mutants that sleep for shorter periods of time and/or lack multiple bouts of consolidated sleep are commonly known to display sickliness, shorter lifespans, an inability to handle oxidative stress, and reduced fitness in general, speaking to the importance of adequate sleep for overall organismal function. Mutations in a wide variety of genes all contribute to a short-sleeping phenotype in Drosophila, but an experimentally determined commonality among many different sleep mutants is sensitivity to the ROS-inducing neurotoxin paraquat. Here, we examine this common sensitivity to paraquat among several short-sleeping Drosophila mutants, and, in investigating the relationship between paraquat sensitivity and sleep disordered mutants, give more insight into the precise function of sleep.

Jacob Irwin, Computer Science

Contact: jai2128@columbia.edu
Faculty Mentor: Professor Stephen A. Edwards, Department of Computer Science, Columbia University
Title: Multi-LCD Display from a Single-Board Computer (SBC)

Abstract: Using a credit card-sized single-board computer (Raspberry Pi 3 Model B), 9 integrated LCDs displaying real-time data from the World Wide Web (via an application program interface). LCDs are embedded in a physical substrate to demonstrate practical application; simultaneous display of contextual information: worldwide markets data.

Maria Andrea Jurado, Biochemistry

Contact: mmj2146@columbia.edu
Faculty Mentor: Dr. Benjamin Fogelgren, Department of Anatomy, Biochemistry and Physiology, John A. Burns School of Medicine, University of Hawaii, Mānoa
Title: Investigating the role of exocyst in urothelial differentiation signaling in congenital obstructive nephropathy

Abstract: Congenital obstructive nephropathy (CON) is a common pediatric kidney disease that is the leading cause of renal failure in infants and children. A majority of CON cases result from an obstruction at the ureteropelvic junction (UPJ), the region where the renal pelvis transitions into the ureter. While

the underlying causes of most UPJ obstructions remain unknown, we know that many cases initiate during fetal development. We have recently described a unique transgenic mouse model of prenatal UPJ obstructions, where the Sec10 gene was deleted from the epithelial cells lining the ureters (urothelial cells). Sec10 is a subunit of the eight-protein exocyst complex that regulates the exocytosis of certain vesicles from the endomembrane system to the plasma membrane. Our previous work showed that without Sec10, the ureter's urothelial cells fail to form a barrier against urine between embryonic day 16.5 and 17.5, and the mice develop bilateral ureter blockages, severe hydronephrosis, anuria, and neonatal death. Here, we test the hypothesis that Sec10 inactivation causes defects in the essential signaling factors that control urothelial differentiation, particularly the epidermal growth factor receptor (EGFR).

EGFR belongs to an important family of tyrosine kinase receptors located on the surface of the epithelial cells, and aberrant EGFR signaling has been linked to a wide range of diseases. To investigate how the exocyst is involved in urothelial differentiation, we used quantitative real-time PCR to measure gene expression of epithelial signaling genes in E15.5-E17.5 mice. We also used immunohistochemistry to locate the proteins in the tissues, and compare levels and localizations between wild types and Sec10-mutant urothelial cells. RT-PCR analysis shows a significant decrease in EGFR expression in Cre-knockout mice compared to wild type mice from E15.5 to E17.5. In addition, ureteric explants from E16.5 were treated with EGFR inhibitor to compare the development of both wild type and Cre-knockout mice. With a better molecular understanding of the role of EGFR in urothelial differentiation, we may be able to better understand the pathways controlling ureter development and contributing to human CON.

This project was funded by NIH/NIDDK, along with the American Physiological Society.

Smriti Kanangat, Biology; Economics

Contact: sk3974@columbia.edu
Faculty Mentor: Dr. Kenneth Olive, Department of Pathology & Cell Biology; Department of Medicine, Irving Cancer Research Center /Columbia University Medical Center
Title: Gene Expression Analysis of Untreated KPC Mouse Pancreatic Tumors

Abstract: Pancreatic cancer has a very negative outlook and extremely low survival rates. Currently, there is a need to analyze gene expression profiling and transcriptional networks that operate in pancreatic cancer. The KrasLSL.G12D/+;p53R172H/+;PdxCretg/+ mouse model is widely used, but further investigation is needed to understand how well this model can approximate the human disease. To this end, the present study examined gene expression of epithelial and stromal cells from mouse pancreatic tumor samples. I screened untreated pancreatic cancer mouse tumor samples from the Olive lab mouse tumor bank for samples with epithelial and stromal cells suitable for cutting and collection using Laser Capture Microdissection. Samples of the eluted RNA from LCM-collected cells were submitted for quality control testing. High quality RNA samples were sent for RNA-sequencing. I used the DESeq2 package in the R software environment to analyze the resulting gene expression count data and existing results from this workflow carried out previously in the Olive lab. I generated a heat-map in R of the 50 most highly expressed genes in all the samples. Clustering showed clear distinction between epithelial and stromal cells. Additionally, a few genes of interest that were differentially expressed were identified for further, more rigorous, protein-based study.

Aaron Kennon, Physics; Mathamatics

Contact: amk2249@columbia.edu
Faculty Mentor: Professor Brian Metzger and Dr. Nicholas Stone, Department of Physics, Columbia University
Title: General Relativistic Analysis of Schwarzschild and Kerr TDEs

Abstract: Tidal Disruption Events (TDEs) occur when a star passes within the tidal radius of a Supermassive Black Hole. They can result in significant distortions in the structure and shape of the victim star. From a Newtonian standpoint, the effects of the Black Hole on the star are well understood: Analytical and numerical analysis suggests that the star is compressed in the direction normal to the orbital plane and in one direction in the orbital plane, and the star is stretched in the remaining direction. This research seeks to determine how General Relativistic considerations alter the results of the Newtonian case. To this end, the poster considers the effects that different black hole parameters, integrals of motion, and initial conditions have on the physical distortion of the star. The poster also displays results of a "toy model" that attempts to account for hydrodynamical forces involved in the compression, and as applications of the theory, attempts to characterize gravitational wave emission and energy dispersion at various heights within the compressed star. Understanding the nature of the gravitational waves signals and optical signals following from the energy dispersion will allow astronomers to potentially identify and characterize TDEs in reality.

Khrystofor Khokhlov, Chemistry

Contact: kk3106@columbia.edu
Faculty Mentor: Professor Colin Nuckolls, Department of Chemistry, Columbia University
Title: Toward efficient and scalable synthesis of graphene-derived molecular helical ribbons

Abstract: Organic photovoltaics (OPVs) have potential to become a widespread, low-cost energy source. However, although fullerene derivatives are used as electron acceptors in most of existing OPVs, their poor visible light absorption and complicated energy tuning limit power conversion efficiency (PCE) . This has fueled new research to explore alternative electron acceptors that could overcome limitations of fullerenes while retaining sufficient solubility and appropriate energy level for popular donor materials (e.g. PTB7). One class of molecules that fulfill all these requirements is perylene diimides (PDIs), with PDI tetramer showing PCE surpassing that of fullerenes.

In order to tune HOMO-LUMO gap of PDI tetramer and study relationship between graphene nanoribbons' tendency to self-aggregate through π-stacking and their molecular structure we attempted to flatten out PDI tetramer's helical ribbon by inserting carbon atoms between the proximal carbons in the cove region. Direct insertion turned out to be impossible, but we were able to develop synthesis of a reasonably close analogue through photocyclisation. Furthermore, we tried to develop scalable and efficient method to synthesize PDI oligomers that would be based on organotin-free Suzuki-Miyaura coupling and avoids using HPLC. Existing methods for synthesis of PDI-based graphene nanoribbons that show high PCE are low-yielding.

In the poster, we will present our efforts to prepare PDI oligomers by using boronic acids for introduction of ethylene residue and a completely new synthetic pathway that leads to synthesis of novel flattened graphene nanoribbons through PDI-based quinones. Use of MIDA-protected boronic acids greatly improved selectivity of couplings that are used for introduction of ethylene residue. Moreover, it led to synthesis of new PDI-based building blocks that will allow us to further investigate

structure-PCE and structure-aggregation relationship, possibly for a whole series of the flattened PDI-based graphene nanoribbons. Synthesis of flattened version of PDI tetramer is currently progressing towards completion. Once completed, we will test whether improved conjugation compensates for the aggregation of PDI molecules.

Young Joon Kim, Biology

Contact: yk2611@columbia.edu
Faculty Mentor: Dr. Omar Abdel-Wahab, Human Oncology & Pathogenesis Program (HOPP), Memorial Sloan-Kettering Cancer Center
Title: SRSF1 is Vital for Adult and Embryonic Hematopoiesis and has Non-Overlapping Functions from those of SRSF2

Abstract: Recent discoveries in cancer epigenetics have unveiled the significance of mutant splicing machinery in leukemic oncogenesis. For instance, SRSF2, a key splicing factor, is frequently mutated in myeloid leukemias, suggesting its significance in hematopoietic stem and progenitor cell (HSPC) function. SRSF1, another member of the SR family, has been suggested to have partially overlapping roles with SRSF2. Thus, the present study aims to reveal SRSF1's role in adult and fetal hematopoiesis, particularly in relation to that of SRSF2.

Srsf1, as with Srsf2, was found to be vital for adult murine hematopoiesis. Peripheral blood (PB) chimerism of transplant recipient mice showed that, while heterozygous deletion of Srsf1 had no significant effects, homozygous deletion of either Srsf1 or Srsf2 both resulted in compromised multi-lineage reconstitution. 20 weeks post-transplant, neither Srsf1 or Srsf2 homozygous knockout BM made any contribution to the hematopoietic organs. Simultaneously, HSPC counts were vastly reduced in mice transplanted with Srsf1- and Srsf2-deficient BM. Likewise, homozygous knockout fetuses for either splicing factor exhibited various functional defects in fetal hematopoiesis. Interestingly, Srsf1 homozygous knockout fetal livers exhibited comparable HSPC counts to that of control fetal livers. Nevertheless, Srsf1 and Srsf2 homozygous knockouts had significantly reduced colony-forming capacities in vitro. Ultimately, the study found that both Srsf1 and Srsf2 are both essential in a haplo-sufficient, non-overlapping manner for adult and fetal hematopoietic function.

Oh Sang Kweon, Chemistry

Contact: ok2227@columbia.edu
Faculty Mentor: Professor Laura J. Kaufman, Deparment of Chemistry, Columbia University
Title: ¬¬Integrin localization in bleb protrusions in disseminating breast cancer cells

Abstract: Integrins are involved in the crosstalk between different signaling proteins within focal adhesion sites that facilitate cell-cell or cell-ECM adhesion. The distribution of integrins as a function of cell morphology yields interesting observations. For example, it is well understood that for cells bearing sharp protrusions, integrins are clustered at the ends of these protrusions, pulling at the ligand primarily from these areas. For rounder cell protrusions known as blebs, however, integrin accumulation is generally assumed to be homogenous across the protrusion, and no significant clustering has been noted in these regions thus far. However, our study introduces new findings in which integrin clustering is evident in the base or neck regions of these blebby protrusions. These accumulations are further characterized by a narrow range of clustering.

Ashley (Hyun Ah) Kwon, Biology

Contact: hk2875@columbia.edu
Faculty Mentor: Professor Angela Christiano, Department of Dermatology, Columbia University Medical Center
Title: Identifying Autoantigens in Alopecia Areata

Abstract: Alopecia Areata (AA) is considered a cell-mediated autoimmune hair loss disorder. Unknown autoantigen(s) attracts and induces an immune response from the T cells. Our work narrows down the potential autoantigen targets that can trigger high T cell responses in mouse models of AA. We have performed Co-Immunoprecipitation and Enzyme-Linked ImmunoSpot (ELISpot) assay on total proteins extracted from mouse skin samples to see if these approaches can be applied to studying the potential autoantigens involved in AA pathogenesis. We observed higher frequency of T cell activation when AA mouse lymph node cells (LNC) were stimulated with total skin protein compared to the control mouse in vitro. Thus, there were antigens in the AA mouse skin that can induce a T cell response. Potentially, the work here would further our understanding on the pathogenesis of AA and lead to developing more effective, targeted treatments for AA patients.

Avik Laha, Physics; Computer Science

Contact: al3510@columbia.edu
Faculty Mentor: Greg Bryan, Department of Astrophysics, Columbia University
Title: Supernova Feedback and Galactic Circular Velocities

Abstract: The Navarro-Frenk-White radial density profile, fitted to galactic dark matter simulations, fits many mass ranges of galaxies well. These profiles are measured through the proxy variable of the circular velocity as a function of radius. However, many dwarf galaxies appear to have less centrally-concentrated density distributions than theory predicts, known as the dwarf galaxy "inner-mass deficit" problem. We conjecture that a lack of effective treatment of heating and shocks of interstellar gas due to supernovae is the cause of models predicting more centrally-dense profiles of dwarf galaxies than observation shows, and seek to implement such feedback. We compare our results to the observed sample in order to validate the technique.

Daniel Lee, Mathematics-Statistics

Contact: djl2169@columbia.edu
Faculty Mentor: Professor Laura J. Kaufman, Deparment of Chemistry, Columbia University
Title: Correlating Extracellular Matrix Properties to Cell Morphology

Abstract: Breast cancer cell lines generally form aggregates with one of four distinct morphologies: round, mass, grape-like, and stellate. Recent studies have indicated that there is some correlation between the morphology and the invasiveness of the tumor cells. Although it is known that there are physical, chemical, and genetic factors that influence cell morphology, how the specific factors affect the overall morphology is poorly understood. We use two-dimensional Cellular Potts model simulations to determine the minimum physical factors needed to create the four major breast cancer cell aggregate shapes.

The Cellular Potts model is a lattice-based model in which each pixel can be part of a cell or part of the environment. It is designed allow cells or sets of cells to adopt shapes that are most thermodynamically

stable, having the lowest energy for a set of given parameters. The Hamiltonian equation – which calculates the total energy of the system – we are employing considers contact between cell and environment, contact between cells, deviation from an optimal cell volume, and deviation from an optimal cell perimeter. The model will be extended to consider the interaction between cells and collagen that is a critical component of the extracellular matrix in vivo in breast cancer. By optimizing the parameters, the research aims at reproducing the experimentally observed morphologies, thus determining a minimal set of parameters that may underpin the aggregate morphologies observed.

Hyunwook Lee, Biochemistry

Contact: hl2863@columbia.edu
Faculty Mentor: Professor Virginia Cornish, Department of Chemistry, Columbia College
Title: Development of a Yeast Three-Hybrid Screen for Tetracycline Derivatives

Abstract: The yeast three hybrid (Y3H) screen has been shown to be an important and valuable tool for investigating protein-protein interactions and discovering small molecules in a high-throughput manner. The aim of this study was to use the yeast Saccharomyces cerevisiae, as a heterologous host for TAN-1612, a fungal polycyclic polyketide and tetracycline derivative that has recently been discovered and characterized from Aspergillus niger. The detection of yeast cells that are genetically engineered to heterologously produce TAN-1612 can be achieved with a Y3H screen. For our Y3H system, two expression plasmids containing the LexA DNA binding domain fused to a tetracycline repressor protein (LexA-TetR) and the B42 activation domain fused to an E. coli dihydrofolate reductase (B42-eDHFR) were constructed, both located downstream of a GAL1 promoter. While TetR does not naturally have an affinity to bind to TAN-1612, there has been previous studies showing that its binding affinities to various tetracycline derivatives can be altered by single-site mutagenesis and rational design. The chemical inducer of dimerization (CID) is a minocycline-methotrexate (Min-Mtx), which bridges the two fusion protein components. A reporter gene, lacZ, were placed downstream of a GAL1 promoter and multiple LexA operons in a separate plasmid. In the presence of the CID, the two fusion proteins will be recruited and the reporter gene will be expressed. In the presence of a tetracycline derivative, the small molecule will outcompete the CID, disassembling the transcription complex and reducing the expression of the reporter gene. We demonstrate we have a working Y3H screen for tetracycline, doxycycline, and 9-amino-minocycline. We hope to ultimately develop a TetR that binds to TAN-1612 and use the Y3H screen as an assay to improve heterologous production of TAN-1612 in yeast.

Briley Lewis, Astrophysics

Contact: bll2124@columbia.edu
Faculty Mentor: Professor Rebecca Oppenheimer, Department of Astrophysics, American Museum of Natural History
Title: Direct Imaging of Exoplanets with Project 1640

Abstract: Project 1640 is a suite of instrumentation and software focused on high-contrast imaging of exoplanets, probing the parameter space of companion size > 1MJ and distance 5-50 AU around the host stars. The instrument consists of an apodized Lyot coronagraph, with a Mach-Zender interferometer and an integral field spectrograph, forming data cubes of dimensions right ascension, declination, and wavelength. P1640 is operated at Palomar Observatory in Southern California, in conjunction with their PALM-3000 adaptive optics system. Data reduction models out remaining speckle noise using principle component analysis and produces a residual cube, which can then be manually inspected for possible companions. For this summer project, data reduction using the Karhunen-Loève

Image Projection (KLIP) algorithm was completed on many of the survey stars and inspected, in an effort to search for more candidates. At this time, two possible candidates have been found, and are awaiting further confirmation.

Jessica Li, Applied Physics

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Faculty Mentor: Professor Francesco Volpe, Department of Applied Physics and Applied Mathematics, Columbia University
Title: Zero-plasma-current equilibria generated by tilted planar coils

Abstract: It is known that an axisymmetric arrangement of tilted planar coils, combined with vertical field coils, can generate a helical magnetic field. One question, though, is: is this coil-set a generator or an amplifier of rotational transform? In other words, is a finite plasma-current needed? A numerical scan of coil-currents shows that configurations exist, for which no plasma-current is needed, and yet torsatron plasmas of finite volume can be obtained. The case of six tilted circular coils has been examined in great detail because of its relevance to the CIRCUS device operated by Columbia. More axisymmetric configurations featuring a higher number of tilted circular coils are also being investigated. The calculations are performed with the aid of the VMEC field-line tracer and equilibrium solver, slightly modified to reflect the simplicity of the coil geometry: the coils are not discretized; instead, their field is evaluated by means of analytical expressions. This allows for faster calculations and rapid, fine scans of large parameter spaces.

Gabrielle Lubitz, Neuroscience and Behavior

Contact: gl2401@barnard.edu
Faculty Mentor: Professor John I. Glendinning, Department of Biological Sciences, Program in Neuroscience and Behavior, Barnard College
Title: Taste is Just the Beginning: Functional Analysis of a Novel Sweet Taste Pathway

Abstract: The ability of mammals to taste sugars involves at least two signaling pathways in taste cells. The T1r2+T1r3 receptor mediates a pathway responsible for behavioral attraction to sugars. K(ATP) signaling is thought to mediate another pathway that elicits cephalic-phase insulin release (CPIR), a preemptive response that limits the post-meal spike in blood sugar. Mice lacking T1r2+T1r3 signaling show no behavioral attraction to sugars but normal CPIR. We hypothesized that mice lacking K(ATP) signaling would show no CPIR but normal behavioral attraction to sugars. To this end, we measured taste-mediated licking for sugars and blood glucose levels following sugar intake in two strains of mice, one with K(ATP) signaling (wild-type, WT), and one without (Sur1 knockout, KO). In behavioral experiments, we examined whether licking behavior for sugars differed between the two genotypes. Overall, the behavioral data show no impact of KATP signaling on attraction to sugars. We then tested the blood glucose and insulin levels in both groups of mice after sugar intake. We found impaired glucose regulation and no CPIR in Sur1 KO mice, exhibiting the importance of K(ATP) signaling for glucose tolerance. Together, these results indicate that the T1r2+T1r3 and K(ATP) pathways function independently of one another, and that K(ATP) signaling is necessary for CPIR but not behavioral attraction to sugars.

Tatini Mal-Sarkar, Psychology and Sociology

Contact: tm2680@columbia.edu
Faculty Mentor: Dr. Tory Higgins, Department of Psychology, Columbia University
Title: Effects of Communication and Shared Reality on Memory Construction

Abstract: In the concept of shared reality, individuals experience a commonality of inner states about an external stimulus. This tie can bind both strangers and close partners alike. Strangers who experience a shared reality may feel instant attraction, while close partners with shared reality may affect each others' very sensations. On a base level, shared reality is contingent upon external verification by others. Shared realities can be constructed through audience-tuning, namely the idea of adapting one's position so as to better fit that of the audience. Further, memory can be changed through the context of interaction. For example, if the audience thinks favorably of the subject, the speaker may acquire a more positive stance. The work will primarily entail running subjects, designing surveys, and coding participants. This research will explore the role of communication and shared reality in the co-construction of memory and interpersonal closeness.

Zachary Marcone, Mathematics

Contact: zm2252@columbia.edu
Faculty Mentor: Dr. Eunsoo Kim, Department of Ecology, Evolution and Environmental Biology, Columbia University and the American Museum of Natural History
Title: Palpitonomas bilix and Crocosphaera in a Nitrogen-Deprived Media: A Preliminary Step to Endosymbiosis

Abstract: In this study Palpitomonas bilix and Crocosphaera were grown in two separate media: SN-SSW and SN -N. The former is a saltwater media collected from an American Museum of Natural History expedition to the Solomon Islands. The SN -N is a media similar in composition though deprived of all major nitrogen containing solutes. The purpose of this study was to attempt to induce the cyanobacteria to migrate towards the protist species and develop a mutualistic relationship, ideally an endosymbiotic relationship. Samples of pure Palpitomonas and Crocosphaera were grown separately as controls. The results indicate predictable patterns of growth for most samples. Observations under the microscope failed to yield any indication of endosymbiosis. In future studies similar methods will be employed in an oxygen deficient environment.

Rachel Mikofsky, Neuroscience and Behavior

Contact: rmm2234@columbia.edu
Faculty Mentor: Dr. David Sulzer, Department of Psychiatry, Neurology, Pharmacology, Columbia University
Title: Acute amphetamine administration increases locomotion and enhances activation of D1-expressing medium spiny neurons in the mouse dorsal striatum

Abstract: Amphetamine (administered as Dexedrine or Adderall) is a stimulant with therapeutic value for treating ADHD. Amphetamine also has a high potential for abuse and addiction. There is much evidence supporting the role of the nucleus accumbens (ventral striatum) in addiction-like behaviors. However, less is known about amphetamine's effect on the dorsal striatum. We used time correlated single photon counting (TCSPC) (ChiSquare Bioimaging) to optically record fluorescence changes in GCaMP6f in D1-expressing medium spiny neurons (D1MSN) in the dorsal striatum. These neurons

project to the substantia nigra pars reticulata and the internal segment of the globus pallidus (termed the direct pathway). We injected AAV9 FLEX GCaMP6f virus into the dorsal striatum of mice expressing cre recombinase in D1MSNs. We then implanted imaging fibers into the same location and recorded calcium transients in mice treated with acute amphetamine or saline in their home cage. We found that amphetamine produced and enhancement of locomotion that correlated with increases in calcium transients in the D1MSNs suggesting that amphetamine may modulate the direct path in the dorsal striatum.

Noah Miller, Physics; Mathamatics

Contact: nmm2166@columbia.edu
Faculty Mentor: Dr. effrey Kuan, Department of Mathmatics, Columbia University
Title: Interacting particle systems and representations of quantized Lie Algebras

Abstract: We investigate the asymmetric simple exclusion process (ASEP), a simple model of interacting particle systems, through algebraic means. By constructing ASEP through quantized Lie algebras, we can easily investigate variants of ASEP, which all have Stochastic Duality. Specifically, we investigate what processes arise from taking higher powers of the energy, which allows particles to interact across multiple sites.

Rachel Mintz, Biomedical Engineering

Contact: rlm2187@columbia.edu
Faculty Mentor: Professor Harris Wang, Department of Pathology and Cell Biology, Division of Systems Biology, Columbia University Medical Center
Title: Mos(Quit)o rhamnoshield: An alternative to DEET-based repellents

Abstract: Every year 2.6 million people die from mosquito borne illnesses (MBI). Since there are no vaccines for many MBIs, the best option for avoidance is preventing bites. The project aims to engineer a repellent in which the bacterial species Pseudomonas putida (P.P.) and Staphylococcus epidermidis (S.E.) synthesize rhamnolipids, a compound known to repel mosquitos. The following objectives were established: clone rhamnolipid-producing strains, test the safety/efficacy of bacteria producing rhamnolipids, and develop the product. The operon (RhlAB and RhlC) that produces enzymes in the rhamnolipid synthesis pathway from Pseudomonas aeruginosa was cloned into P.P. and S.E. Mosquito experiments will confirm the quantity of rhamnolipids needed for full protection. Safety will be assessed using human skin cells and mouse models. The product will be maintained in a bottle with freeze-dried strains, rehydration media, and lotion suitable for human skin.

Osman Moneer, Chemical Physics

Contact: owm2102@columbia.edu
Faculty Mentor: Dr. Xiaoyang Zhu, Department of Chemistry, Columbia University
Title: Interlayer Excitons in Two-Dimensional Transition Metal Dichalcogenide Heterostructures

Abstract: Because two-dimensional transition metal dichalcogenides (TMDC) are atomically thin semiconducting materials, TMDC heterostructures provide a great model system to study charge transfer across a simple interface. In the long term, TMDC heterostructures are a viable option for incorporation into ultrathin electronic systems. We are interested in understanding the physical nature of momentum conservation of interlayer excitons across a TMDC heterostructure. The aim of this

research is to understand momentum conservation as a function of the orientation of the two layers of TMDCs. We fabricated TMDC heterostructure devices, which consisted of two layers of TMDCs—specifically MoSe2 and WSe2—on top of a layer of hexagonal Boron Nitride (hBN). Using an atomic force microscope tip, we have managed to move TMDC monolayers on top of the atomically smooth surface of hBN; however, we are still attempting to rotate TMDC monolayers relative to each other. Currently, we are exploring the effects of relative crystal dimension with respect to rotation of the monolayers. We will optical study the heterostructures to probe the nature of momentum conservation across the interface as a function of crystal angle orientation using pump probe spectroscopy.

Gayathri Muthukumar, Biology

Contact: gayathri.muthukumar@columbia.edu
Faculty Mentor: Dr. Joseph Gogos, Department of Physiology and Cellular Biophysics, Neuroscience, Columbia University Medical Center
Title: The Role of microRNA Dysregulation in Psychiatric Disorders, Particularly Schizophrenia

Abstract: Humans with 22q11.2 microdeletion syndrome show behavioral and cognitive deficits, and are at a high risk of developing schizophrenia. In order to study this syndrome further, the Gogos lab engineered a mouse strain named Df(16)A+/-, created by hemizygous chromosomal deficiency on mouse chromosome 16, spanning a segment syntenic to the 22q11.2 microdeletion. This mouse model has haploinsufficiency of the Dgcr8 gene, which is a part of the complex involved in microRNA processing. As a result, 19% of all the mature microRNA forms were downregulated in the pre-frontal cortex and 10% in the hippocampus of the Df(16)A+/-mice. Expression of mir-185 (a specific microRNA) is downregulated by 70-80% in both the hippocampus and the pre-frontal cortex. The major downregulation in mir-185 levels in Df(16)A+/- mice results in the upregulation of its target gene, Mirta22 (miRNA target of the 22q11.2 microdeletion).

Understanding how Mirta22 affects neuronal connectivity and eventually behavior and cognition is likely to provide more general insights into the contribution of miRNAs in psychiatric and neurodevelopmental disorders, and facilitate development of new treatments. Furthermore, normalizing Mirta22 levels in the Df(16)A+/- mice could reverse several of the behavioral and physiological abnormalities previously found in these mice. Here, we sought to investigate the role and function of Mirta22 in multiple levels. At first, cytoplasmic and nuclear extraction of samples for wild-type mice, Mirta22 knockout mice, Df(16)A+/- mice and Df(16)A+/-Mirta22+/- mice was performed, followed by a Bradford assay and western blots with the Mirta22 primary antibody in order to study the Mirta22 protein levels in these mice. Our results could confirm its upregulation in the Df(16)A+/- mice and normalization in the Df(16)A+/-Mirta22+/- mice. In addition, results from prior RNAseq tests indicate a difference in the levels of certain genes between wild-type mice and the Mirta22+/- knockout (KO) mice.

Quantitative PCR (qPCR) was used to validate these differences. More specifically, qPCRs were done for 14 samples, 7 wild-type and 7 knockout, with the gene probes of interest: Kcnj11, Penk, Rtn4rl2, Chrm1, Sod3 and Bmp6. We were able to confirm changes in expression in Penk and Kcnj11. In a parallel investigation on proteomic analysis of the Df(16)A+/- mice, another potential target of the mir185 target, Ogt1 was found upregulated in a study done earlier this year in the protein level. Here, we sought to show that Ogt1 is overexpressed in the Df(16)A+/- mice at the mRNA level, as well. qPCR in Df(16)A+/- and WT confirmed this upregulation. Lastly, we set up a strategy to study Mirta22 protein function. To this end, HEK-293 cells were grown to study interaction of Mirta22 protein with other proteins. Mirta22 has two isoforms, a transmembrane form and a secreted form. Tagged ORF cDNA

Clones were designed for both isoforms, using the FLAG-HA tag for the transmembrane isoform and the 6-His tag for the secreted isoform, to transfect the HEK cells. Assays performed after transfection, such as pull-down and tandem affinity purification, will help characterize the interaction partners of Mirta22.

Richard Nederlander, Astrophysics

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Faculty Mentor: Dr. Reshmi Mukherjee, Department of Physics and Astronomy, Barnard College
Title: Prospects for the detection of hard Galactic Fermi sources with the Cherenkov Telescope Array

Abstract: The Large Area Telescope (LAT) onboard the Fermi satellite provides a wide-field view of the gamma-ray sky in the energy range between 50 MeV and 300 GeV. The 1FHL and 2FHL catalogs consist of gamma-ray sources detected by the LAT at energies above 10 GeV and 50 GeV, respectively. Current-generation air Cherenkov telescopes such as VERITAS, sensitive to very-high-energy (VHE) gamma rays above 80 GeV, have detected a significant fraction of the FHL sources extending these measurements to the TeV energy range. However, VHE counterparts to many of the FHL sources remain to be identified. We here concentrate on FHL sources observed by Fermi within 5° of the Galactic plane and provide prospects for the detection of additional Galactic sources using the Cherenkov Telescope Array (CTA), a next-generation VHE instrument.

Ilina Odouard, Neuroscience and Behavior

Contact: ico2108@barnard.edu
Faculty Mentor: Professor John I. Glendinning, Department of Biological Sciences, Program in Neuroscience and Behavior, Barnard College
Title: Functional Analysis of a Novel Sweet Taste Pathway

Abstract: The ability of mammals to taste sugars involves at least two signaling pathways in taste cells. The T1r2+T1r3 receptor mediates a pathway responsible for behavioral attraction to sugars. KATP signaling is thought to mediate another pathway that elicits cephalic-phase insulin release (CPIR), a preemptive response that limits the post-meal spike in blood sugar. Mice lacking T1r2+T1r3 signaling show no behavioral attraction to sugars but normal CPIR. We hypothesized that mice lacking KATP signaling would show no CPIR but normal behavioral attraction to sugars. To this end, we measured taste-mediated licking for sugars and blood glucose levels following sugar intake in two strains of mice, one with KATP signaling (wild-type, WT), and one without (Sur1 knockout, KO). In behavioral experiments, we examined whether licking behavior for sugars differed between the two genotypes. Overall, the behavioral data show no impact of KATP signaling on attraction to sugar. We then tested the blood glucose and insulin levels in both groups of mice after sugar intake. We found impaired glucose regulation and no CPIR in Sur1 KO mice, exhibiting the importance of KATP signaling for glucose tolerance. Together, these results indicate that the T1r2+T1r3 and KATP pathways function independently of one another, and that KATP signaling is necessary for CPIR but not behavioral attraction to sugars.

Lia Parkin, Biology

Contact: lap2184@barnard.edu
Faculty Mentor: Professor Ann McDermott, Department of Chemistry, Columbia University
Title: Development of Methods for Liposome Degradation Quantification

Abstract: Cell membranes and membrane proteins are important to study, as they are the targets of most pharmaceuticals. However, cell membrane proteins are often difficult to study using traditional methods, such as x-ray crystallography, since crystallography requires removing the protein from the membrane. However, membrane proteins must be studied in a native-like environment to obtain biologically relevant information. Solid- state NMR (ssNMR) spectroscopy can study the cell membrane protein in cell membranes or similar structures, such as liposomes. Liposomes are made by dialyzing synthetic phospholipids to create an empty membrane vesicle. Proteins can also be added to the synthetic lipids to create proteoliposomes. The McDermott group uses liposomes to examine the cell membrane potassium channel, KcsA, with ssNMR spectroscopy to conduct structural, dynamic and thermodynamic studies. Liposomes, therefore, are an important model to investigate cell membrane proteins in. However, the liposome will only provide relevant information if it is stable and it mimics the natural membrane the protein originates from. The stability of the lipids used to create the proteoliposomes was previously examined and hydrolysis was observed. Additionally, the lipid structure was correlated with NMR resonances. In this study, lipids and liposomes were investigated with different NMR spectroscopy methods to investigate hydrolysis marker peaks to be able to quantify hydrolysis of aged liposome samples. In addition, the natural bacterial membrane of KcsA was examined to try to characterize the different lipid components present in the cell membrane.

Aunoy Poddar, Biology

Contact: ap3441@columbia.edu
Faculty Mentor: Dr. Brent Stockwell, Department of Biological Sciences, Columbia University
Title: Design of allele-selective inhibitor for an engineered KRAS protein

Abstract: The KRAS GTPase isoform is known to be highly mutated in a significant proportion of cancers and be essential to tumor maintenance. Due to the nature of small GTPases, finding potent inhibitors for KRAS have eluded research attempts for a number of decades. We aimed to solve this problem by mutating KRAS to have an enlarged binding pocket and design a small inhibitor to selectively bind to this protein. This small molecule inhibitor will act as a competitive inhibitor to GTP, which binds selectively in the enlarged pocket. We were successful in creating a small molecule that binds successfully in protein protein interaction assays but we yet have yet to see success in viability assays. We are modifying our small molecule in order to alter its binding affinity and therefore increase its potency in living cell culture. After this endeavor, we seek to evaluate the therapeutic and toxic effects of inhibiting this KRAS mutant in the adult mouse. Hopefully, the inhibition of the KRAS mutant with the designed drug will demonstrate cancer-suppressing effects, which would indicate that KRAS is a valid cancer drug target.

Danielle Rowland, Astrophysics

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Faculty Mentor: Professor Steve Finkelstein, Department of Astronomy, University of Texas at Austin
Title: An Investigation of the Initial Mass Function with Increased Redshift

Abstract: The Initial Mass Function (IMF) is generally thought, among astronomers, to be universal but this is not well understood. Understanding the IMF is crucial because inferred results for distant galaxies tend to be heavily dependant on this assumption. There are several factors that could alter the IMF as redshift increases, one being that lower metallicities could lead to an increased production of higher mass stars. In this study I seek to find any top-heavy variations of the IMF from a sample of 3,958 galaxies with redshift $0.7 < z < 1.5$ when compared to the commonly used Salpeter IMF. To do this I use data from the 3D HST Survey to compare H-alpha emission to total UV emission to get a handle of the amount of high mass stars being produced. So far this has yielded 8 galaxies above the maximum production explainable by a Salpeter IMF. Although this result is still undergoing a complete analysis it is still an interesting implication the IMF isn't entirely universal.

Jaewook Ryu, Biochemistry

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Faculty Mentor: Professor Ruben Gonzalez, Department of Chemistry, Columbia University
Title: Identification of the role and mechanism of bacterial elongation factor P (EF-P)

Abstract: Bacterial elongation factor P (EF-P) was recently identified as a protein factor for bacterial translation elongation that relieves ribosomal stalling at stretches of multiple prolines (Jung, Science 2013). To achieve full biological activity, EF-P requires a post-translational modification that is catalyzed by three separate enzymes (Rodnina, Science 2013). Poly-proline stretches also frequently occur in eukaryotic proteins, and eIF5A has been identified as a eukaryotic EF-P homolog that exhibits the same biological activity as EF-P (Valentini, Wiley 2014). Therefore, identifying the role and mechanism of EF-P is crucial for our understanding of prokaryotic translation as well as the mechanism of its analog, eIF5A, in eukaryotic translation.

The detailed molecular mechanism of EF-P still needs to be identified. Since only a sub-population of ribosomes interacts with EF-P due to ribosome stall, a single-molecule approach will be more effective than conventional bulk assay methods. Therefore, this summer I began investigating the mechanism through which Escherichia coli EF-P relieves poly-proline-mediated ribosomal stalling by performing elementary molecular genetics and biochemistry experiments that are essential prerequisites for single molecule FRET (smFRET) experiments.

To begin with, I optimized the purification conditions for over-expressed His-tagged EF-P, where a combination of His-tag affinity chromatography and size-exclusion chromatography yielded mostly pure EF-P. In parallel with the approach of obtaining EF-P from an over-expressing strain, I pursued an alternative approach of developing a strain that would enable the purification of natively expressed EF-P by tagging the native efp gene with a His-tag. Even though the latter approach is still an ongoing project, it is anticipated that it will allow us to purify mostly fully-modified EF-P, which will serve as a source of fully-modified EF-P for further experiments such as smFRET experiments and as a reference to cellular EF-P modification status.

Simona Sarafinovska, Biochemistry

Contact: ss4758@columbia.edu
Faculty Mentor: Professor Frances Champagne, Department of Psychology, Columbia University
Title: Effects of Maternal Separation on Expression of Depression Candidate Genes in B6 Mice

Abstract: Early-life adversity has been linked to depression, particularly through enduring modifications of the epigenome. Maternal separation is used as a model of early-life stress to induce depressive-like behaviors in mice. Genes implicated in the pathophysiology of depression include growth factors, such as the brain-derived neurotrophic growth factor (Bdnf) and nerve growth factor (Ngf) genes. Genes within the stress response pathway, especially the corticotrophin-releasing hormone (Crh) and glucocorticoid receptor (Nr3c1) genes, have been linked to stress-related disorders. The serotonin system is a key research area, with the tryptophan hydroxylase 2 (Tph2) gene, a key to the synthesis of serotonin, and the brain serotonin receptors, including 5-HTr1a, as mediators of depression. Finally, the oxytocin system is fundamental for social behaviors, including maternal care behavior, and has demonstrated anxiolytic effects mediated through the oxytocin receptor (Otr).

This paper aims to determine whether daily maternal separation affects levels of Bdnf, Ngf, Crh, Nr3c1, Otr, 5-HTr1a and Tph2 expression in the hypothalamus, hippocampus and prefrontal cortex of male and female B6 mice. A daily separation between dams and litters from postnatal days (1–14), was implemented in B6 mice and compared to a control rearing condition (standard laboratory rearing with no separation).

None of the results were statistically significant, although there was a near significant rearing group effect for Otr expression in the PFC of male pups; a significant sex effect in Bdnf hypothalamic expression and litter effect in the hypothalamic Bdnf, Crh, and Ngf expression, as well as PFC Nr3c1 expression. Further epigenetic analysis, including determining DNA methylation of the gene promoters, combined with behavioral analysis of the mice, and supplemental analyses of receptor binding and blood peptide levels, should be a further course of study to shed more light on the pathways of depression and early-life adversity.

Amelia Sawyers, Biology

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Faculty Mentor: Dr. Liza Pon, Department of Pathology and Cell Biology, Columbia University Medical Center
Title: The Mitochondrial DNA Checkpoint in S. Cerevisiae: The Role of the MICOS Complex

Abstract: Yeast lacking mtDNA, which are referred to as rho0 cells, typically arrest at the mtDNA inheritance checkpoint, between G1 and S phase, which relies on the classical DNA damage proteins Rad53p and Pif1p. The MICOS complex is known for maintaining the architecture of the mitochondrial inner membrane and forming mitochondrial contact sites between the inner and outer membranes. Due to this role in contact sites, it is also possible that MICOS acts as a sensor for mtDNA loss and can communicate this message outside the mitochondria. If so, MICOS could communicate loss of mtDNA to the DNA damage response pathway, thus activating it. By measuring the level of Pif1p phosphorylation, we can determine mtDNA checkpoint activation and investigate this potential role for MICOS. We deleted genes that code for MICOS components and YPR010C-A, an uncharacterized protein that physically interacts with MICOS, in Saccharomyces cerevisiae to observe the effects on Pif1p phosphorylation in rho0 cells. We find that Pif1p is phosphorylated in YPR010C-AΔ, mic60Δ and mic26Δ

rho0 cells. However, we also find that Pif1p is phosphorylation in the wild-type cells that contain mtDNA. Thus, the DNA damage checkpoint was activated under our experimental conditions in a mtDNA-independent manner. Although our results are inconclusive, they nonetheless provide exciting insight into potential functions for MICOS.

Shannon C. Shipley, Neuroscience and Behavior

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Faculty Mentor: Dr. Robert Pollack, ArchCare; Biology; Psychology, Terence Cardinal Cooke Health Care Center; Columbia University; Barnard College
Title: Internal and External Assessment of Psychotropic Drug Treatment in Vulnerable Patient Populations

Abstract: Psychotropic drugs have been shown to be tremendously helpful in treating mental illness; however, they have also been shown to cause serious and harmful side effects, especially when prescribed inappropriately. Certain populations - such as the elderly, those with dementia and/or psychosis, and children - are especially vulnerable to these harmful side effects. Health agencies around the world have issued warnings about the risks of prescribing such medications to frail individuals, and current guidelines recommend their use only in cases where the benefits clearly outweigh the risks. Despite these warnings, an estimated 20%+ of all adults in the United States, and an estimated 87% of older adults with dementia in acute care geriatric units, are taking at least one psychotropic medication. Needless to say, the provision of safe psychotropic drug therapy is one of the greatest challenges in health care; it is important for practitioners to thoroughly consider benefits and risks before administering these medications and to thoroughly assess efficacy after their administration.

To address these issues, the use and implications of psychotropic drugs were assessed in a sample of patients at Terence Cardinal Cooke Health Care Center (TCC), which included several vulnerable populations, such as patients with Huntington's disease, patients with dementia and/or psychosis, elderly patients, adolescents with developmental disorders, and patients with HIV/AIDS. Data on psychotropic drug use and its incidence with mental disorders were gathered and analyzed via retrospective chart reviews. Assessments of drug treatment efficacy from the perspective of the medical practitioner and the patient were recorded via interview.

We found that guideline recommendations were not always being met. Among identified barriers, we found: poor regularity in medication follow-up consultations; poor drug monitoring and inter-healthcare-provider communication; misconceptions about mental health illnesses and treatment options; discrepancies in opinion on the efficacy and appropriate prescription of psychotropics; and few alternative treatment options. We looked to specifically identify changes that can be made to improve patient outcomes. These prospective quality improvements target (1) improving inter-staff communication via patient behavioral mapping; (2) modifying and requiring relevant healthcare provider training; (3) implementing alternative treatments; (4) hiring more trained psychiatric healthcare providers; and (5) reforming insurance coverage. These results, and likewise these quality improvement studies, will lead to improvements in treatment practices and assessments, general management of mental disorders, and ultimately psychotropic-drug- and mental-disorder-related care and outcomes for vulnerable patients.

Amrita Singh, Biology; Data Science

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Faculty Mentor: Dr. Linus Sun, Department of Ophthalmology, Columabia University Medical Center
Title: Role of oculomotor proprioception in spatial processing by the parietal cortex

Abstract: Execution of spatially accurate eye movements requires the brain to represent visually guided saccade targets despite a constantly moving eye. The multi-step task is a laboratory metaphor for this problem: macaques and humans can make two or more sequentially accurate saccades to recently vanished stimuli despite the changing retinal position of the stimuli during intervening saccades. Two model theories have been proposed to solve the problem of the multi-step task: the gain field theory and the perisaccadic remapping theory. In this study, we explore evidence of both, and explore the source of oculomotor proprioception. Eye position modulates firing rate of parietal neurons linearly, increasing monotonically with orbital eccentricity. These gain fields can be used to calculate absolute position of a visual signal in supra-retinal coordinates. Preliminary results show that reversible cooling of area 3a in macaques eliminates gain fields. Eye position modulation of gain fields may only have an effect on spatial processing a short time after a saccade. The retinal mechanism of perisaccadic remapping with corollary discharge may contribute to spatial precision more rapidly, and we explore the idea that both perisaccadic remapping and proprioception have a differential contribution to spatial localization. Preliminary results show that due to the slow response of gain fields, the macaque can solve the multi-step task without gain fields but not visual responses.

Emily Sun, Biology; English

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Faculty Mentor: Dr. Yunglin (Elaine) Gazes, Taub Institute for Research on Alzheimer's Disease and the Aging Brain, Columbia University Medical Center
Title: Dendritic and axonal density as a form of reserve in aging

Abstract: Reserve theory hypothesizes that individual differences in various lifestyle factors contribute to individual differences in the aging process of the brain. So far, most research on cognitive and brain reserve has been macroscopic in nature, and has not yet found a measure that is sensitive to more rapid changes in the brain. This summer, I examined dendritic and axonal density as a potential of neuronal basis of reserve, using an innovative, non-invasive neuroimaging technology called neurite orientation dispersion and density imaging (NODDI), in order to measure neurite density. I recruited the first 12 subjects of the pilot study, between 50-80 years old, and supervised their MRI scans at the New York State Psychiatric Institute. All subjects were recruited from a previous study (Reference Ability Neural Networks study – RANN). Each participant received half an hour of scans in a 3T GE scanner, consisting of a T1-weighted image and two sets of 2x2x2 mm^3 diffusion weighted images using the HARDI sequence with (1) 30 gradient directions and b=700 s/mm^2 and (2) 60 gradient directions and b=2400 s/mm^2. I then performed preprocessing of the DWI data in FSL for eddy current correction and EPI distortion correction. The data was then input into the NODDI toolbox in Matlab to calculate neurite density and produce models for intracellular, extracellular, and cortical spinal fluid (CSF). We encountered many technical difficulties with the FSL preprocessing steps, and so were only able to finish running the data of the 12 subjects through NODDI during my 11-week research period. The next step is to recruit more subjects in order to collect at least 38 more sets of usable data. Then, we propose to use the intracellular model estimation of neurite density calculated by NODDI to conduct voxel-wise analyses with FSL FLAME. We then aim to relate neurite density to age, various reserve variables, and functional activation network usage. The reserve variables were previously collected in the RANN study,

which included a neuropsychological battery, questionnaires for reserve proxies, and structural and functional MRI scans.

Sahityasri Thapi, Biology; South Asian Studies

Contact: st2852@columbia.edu
Faculty Mentor: Dr. Kenneth Olive, Department of Medicine, Division of Digestive and Liver Diseases, Columbia University Medical Center
Title: Role of MCM2, MCM7, and CDC7 in DNA Replication of Pancreatic Cancer Cells

Abstract: CDC7 kinase phosphorylates the MCM2-7 helicase complex and thereby initiates DNA replication. A CDC7 kinase inhibitor molecule, MSK777, has been identified for efficient cytotoxic effects in tumor cells. MCM2 and MCM7 have been identified as master regulatory genes of pancreatic cancer. The present study investigates the role of MCM2 and MCM7 subunits in DNA replication in pancreatic cancer cells. Genetic and pharmacological inhibition of CDC7, MCM2, and MCM7 will be achieved. Various dose response assays with MSK777 were conducted on human pancreatic cell lines and the optimal treatment regimen in PANC1 cells was identified as 24 hours of drug exposure followed by 48 hours without exposure. Immunohistochemistry was conducted to observe the expression of CDC7, MCM2, p-MCM2, and MCM7 in KPC tumor sections. MCM2, p-MCM2, and MCM-7 IHC staining was localized in the nucleus. CDC7 staining was sparse and generally cytoplasmic. shRNA silencing of the CDC7, MCM2, and MCM7 genes will be achieved in further experimentation. Cell cycle analyses and western blot analyses of both the genetically and pharmacologically inhibited cells will be observed.

Michelle Vancura, Chemistry

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Faculty Mentor: Professor Laura J. Kaufman, Deparment of Chemistry, Columbia University
Title: Optimizing Synthesis and Chemical Cross-linking Conditions of Gelatin-Methacrylate Gels

Abstract: Biopolymer gels can be used to study the extracellular environment in vivo; specifically, gelatin is a biocompatible and highly modifiable material, which makes it of particular interest in cellular studies. However, gelatin is not a physically stable gel at physiological temperatures. Previous studies have shown gelatin modified with methacrylic anhydride produces a photo-polymerizable material, gelatin-methcrylate (Gel-MA), that forms stable gels at physiological temperatures. Here, we tried repeating and optimizing previously reported Gel-MA synthesis and cross-linking conditions. We tuned the methacrylic anhydride feed ratio and buffer pH during synthesis, reaction product purification conditions, and cross-linking conditions. We probed gel stability with rheological measurements of storage moduli. In accordance with literature, we found high-pH synthesis increased reaction efficiency. However, we were not able to achieve storage moduli as large as those previously reported, which have shown an order of magnitude increase after chemical cross-linking. We were able to show, at maximum, a three to five times increase after chemical cross-linking. We plan on continuing to optimize Gel-MA synthesis and cross-linking conditions and to further characterize previously studied Gel-MA properties, such as pore-size, that are important in developing materials that can be used in cellular studies.

Neyanel Vasquez, Chemistry

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Faculty Mentor: Professor Michael Dickey, Department of Chemical and Biomolecular Engineering, North Carolina State University
Title: Vacuum Fillings of Microchannels with Liquid Metals

Abstract: Eutectic gallium- indium (EGaIn) is a liquid metal at room temperature with a low toxicity and 1/15th the electric conductivity of cooper. Consequently better understanding which conditions best facilitates EGaIn to complete different patterns via vacuum filling allows for more electronic device possibilities with soft materials. This project explores the level of complexity of different patterns and sizes of patterns that can be accomplished through vacuum filling while investigating the kinetics of the delivery of EGaIn into the different patterns.

Shreyas Vissapragada, Astrophysics; Computer Science

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Faculty Mentor: Dr. Catherine Walsh, Leiden Observatory, University of Leiden
Title: Tracing the complex organic ice reservoir of TW Hya

Abstract: The complex organic ice reservoir in protoplanetary disks is thought to be the origin of comets. These comets may carry complex organic molecules (COMs) to planetary surfaces; thus, it is of crucial importance to understand the physics and chemistry of the COM ice reservoir for prebiotic astrochemistry. Both CH3OH (methanol) and CH3CN (methyl cyanide) have been proposed as candidates to observationally trace the COM ice reservoir, but no full modeling study has confirmed either possibility. We have updated a protoplanetary disk chemical network with new laboratory data on COM synthesis and destruction mechanisms, and have run that network on a physical model of the protoplanetary disk TW Hya. Here, we report that methanol is predicted to be more spatially coincident with the ice reservoir than is methyl cyanide in TW Hya, making it a good tracer candidate for COM ices in this disk.

Oliver Wang, Physics

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Faculty Mentor: John Parsons, Department of Physics, Nevis Laboratories , Columbia Univeristy
Title: Truth-level analysis of W/Higgs boson and Z/Higgs boson decays

Abstract: The purpose of this project is to investigate the properties of the decays of the elusive W' and Z' particles into the W/Higgs bosons and the Z/Higgs bosons, respectively. The subsequent decays of the W, Z, and Higgs bosons into leptons, neutrinos and quarks are modelled by 'jets', which are artificially-defined physical structures encapsulating various properties of decay products such as transverse momentum (GeV) and mass (GeV). The hypothetical mother particle masses of W' and Z' particles were assumed at different values and for each, Monte Carlo simulations were run on these truth-level (predetermined) data samples (2015, 13 TeV). Applying cuts to transverse momentum, mass and pseudorapidity (η) revealed graphical evidence of consistencies between the properties of decay products and mother particles.

Justin Whitehouse, Mathematics; Computer Science

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Faculty Mentor: Dr. Eamon Duede, Computation Institute, University of Chicago
Title: Developing a Research Analytics Institutional Lookup (RAIL) platform for the University of Chicago

Abstract: There is a wealth of information within an institution that can deliver powerful insights on institution structure, dynamics, and professional connections. In particular, the text of scientific publications and grants can provide information about unseen or undocumented similarities amongst various researchers. We generated an interactive tool to visualize these potentially unseen relationships between University of Chicago faculty members and even between researchers and grant calls through manipulating well-known topic modeling techniques such latent Dirichlet allocation on large sets of scientific abstracts, wiki-labeling these generated topics, and even designing novel topic contribution measures. Through exploring these unseen relationships, we can ultimately make predictions and recommend research collaborations to improve grant funding and increase the rate of scientific discovery.

Junho Won, Mathematics

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Faculty Mentor: Dr. effrey Kuan, Department of Mathmatics, Columbia University
Title: Interacting Particle Systems and Quantized Lie Algebras

Abstract: We explore the Asymmetric Simple Exclusion Process introduced by Spitzer in 1970. This is an interacting particle system on the one-dimensional lattice Z, where at most 1 particle is allowed to occupy a lattice site. Each particle has 2 exponential clocks, one for left jumps and one for right jumps. The clock for left jumps has rate q and the clock for right jumps has rate q^−1, where q ∈ (0, 1) is the asymmetry parameter, and all clocks are independent of each other. When the clock rings, the particle makes the corresponding jump to the adjacent site unless that site is occupied, in which case the jump is blocked. Carinci et al. [2014] gave a procedure to construct a interacting particle system with self-duality given a finite-dimensional Lie algebra g and a representation V . This is done for the spin 2j representation of gl2, and the resulting interacting particle system is named ASEP(q, j). Recently, Kuan [2016] obtained explicit formulas for the Markov process generator L obtained from the Gould-Zhang-Bracken central element C of gln, for any highest weight representation (d, 0, 0, · · · , 0) and arbitrary number L of lattice sites. This process is described by having n classes of particles and d particles at a given site. We investigate the process L(2) generated by C^2, which corresponds to speeding up the clock and allowing 2 jumps at a time. We obtain explicit forms for representations parametrized by d = 1, 2, 3, describe blocks in L corresponding to communicating classes of the Markov process, and try to generalize it for arbitrary d. Finally, we investigate the difference between the processes L and L(2) measured by the maximum α such that L(2) − αL is a generator of a Markov process.

Catherine Zhang, Biology and Environmental Science

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Faculty Mentor: Dr. Phong Tran, Cytoskeletal Architecture and Cellular Morphogenesis, Institut Curie
Title: Novel Role of Efr3 in Fission Yeast Mitosis

Abstract: Localized to the cell cortex, the evolutionarily conserved Efr3 is primarily known for its role in facilitating lipid modifications essential for membrane trafficking. Here, we identify an additional role for

Efr3 in the fission yeast S. pombe. Efr3-deletion (efr3Δ) results in chromosome segregation defects. Phenotypes of efr3Δ chromosome segregation defects include: lagging chromosomes, aneuploidy, micronuclei, collapsing spindles, and buckling spindles. efr3Δ cells also exhibit metaphase spindle delay, indicating activation of the Mad2-dependent spindle assembly checkpoint. Consistently, the double-deletion mad2Δ efr3Δ shows a significant increase in the frequency of chromosome segregation defects compared to single erf3Δ. Future work will determine how Efr3 maintain proper spindle dynamics and chromosome segregation.