

Abstracts

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COLUMBIA COLLEGE Columbia Engineering

Table of Contents

Sophia Ahmed CC'21: Sustainable Development
Brianna Alico CC'20: Biochemistry
Mika Aly CC'20: Biology
Paulina Babiak, SEAS'19: Chemical Engineering4
Annie Block CC'19: Sustainable Development5
Adam Block CC'19: Mathematics
Viggo Blomquist CC'21: Neuroscience and Behavior5
Heather Hsun Chang CC'21: Neuroscience
Ethan Chen CC'21: Biochemistry
Joshua Choe CC'20: Biology7
Mariya Delyakova CC'21: Mathematics Computer Science8
Matteo Di Bernardo CC'20: Biology Statistics
Vanessa Dippon CC'21: Chemistry9
Anastasia Dmitrienko CC'21: Statistics Computer Science9
Ailis Dooner CC'19: Neuroscience and Behavior10
Marcel Dupont CC'20: Biochemistry10
Micah Gay CC'20: Mathematics
Allison Ghuman CC'21: Mathematics Computer Science11
Midori Hosoda CC'21: Medicine, Literature and Society11
Allison Hung CC'20: Biochemistry
Linnie Jiang CC'19: Neuroscience and Behavior Computer Science
Benjamin Kepecs CC'20: Biochemistry13
Khrystofor Khokhlov CC'19: Chemistry14
Avik Laha CC'19: Physics, Computer Science14
Christina Lee CC'21: Biophysics14
Dimitri Leggas CC'19: Computer Science
Benjamin Lesea-Pringle GS'19: Biochemistry
Jenny Li CC'21: Computer Science
Leo Lo CC'22: Physics
Caroline Magalhaes de Toledo CC'21: Biochemistry17
Zachary Marcone CC'19: Mathematics Economics

Miguel Martinez CC'19: Astrophysics	18
Collins Mokua CC'21: Neuroscience and Behaviour	
Rose Orenbuch GS'19: Information Science	19
Cheryl Pan CC'21: Neuroscience and Behavior	19
Sohil Patel CC'20: Biology	20
John Monroe Pederson Jr. SEAS'19: Mechanical Engineering	21
Aunoy Poddar CC'19: Biology Computer Science	21
Eric Riesel CC'19: Chemistry	22
Helena Rios CC'20: Mathematics	22
Jaewook Ryu CC'19: Biochemistry Data Science	23
Kelly Ryu SEAS'19: Biomedical Engineering	23
Lorenzo Sampson CC'21: Sustainable Development	24
Abhishek Shah CC'21: Neuroscience and Behavior	24
Manasi Sharma CC'21: Physics Computer Science	25
Jihanne Shepherd CC'21: Biochemistry	25
Arjun Srivatsa CC'20: Statistics	26
Anna Sung CC'21: Biochemistry	26
Daiki Tagami CC'22: Statistics	26
Maya Talukdar CC'20: Computer Science Biology	27
Teresa Tseng BC'20: Computer Science	27
Lizka Vaintrob CC'21: Mathematics	28
Michelle Vancura CC'19: Biochemistry	28
John Wang CC'21: Computer Science Neuroscience and Behavior	29
Junho Won CC'19: Mathematics	29
Emily Zhang CC'21: Astrophysics	

Abstracts

Sophia Ahmed CC'21: Sustainable Development

sra2155@columbia.edu Faculty Mentor(s): Colin Nuckolls, professor of material science Title: Promising Perylene Diimide Electron Acceptor Oligomers with Methoxy Side Chains for Organic Photovoltaics

Abstract: Traditional solar cell semiconductors, electron donors and acceptors, are built with inorganic materials that have various production and environmental complications. Because of these complications, organic materials are increasingly being investigated as substitutes. A particular class of organic, non-fullerene electron acceptors are Perylene Diimide (PDI) derivatives, which have high electron mobility, tunability and strong absorption ability.

The properties of newly synthesized PDI polymers: trimers, tetramers, pentamer and hexamers consisting of trans-arranged methoxy peripheral groups are investigated here. Compared to single-unit PDI molecules, oligomer (multiunit) PDI derivatives (in this project: two, three, four, five and six) have been previously found to increase power-conversion-efficiency in solar cells. The methoxy peripheral groups were added because of their positive effects on performance due to their effects on PDI configuration. Moving out to the configurations of each PDI unit in relation to each other, the units were arranged in a helical confirmation to achieve lowest relative energy - such a confirmation is due to the steric congestion at the fusion bridges between PDI units.

UV-vis spectroscopy and cyclic voltammetry show that the electronic and charge-transport properties of the oligomers are promising candidates for OLED and photovoltaic applications.

Brianna Alico CC'20: Biochemistry

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Faculty Mentor(s): Keith Choate, professor of dermatology, Yale School of Medicine *Title:* Activity of ER stress response in cells expressing Cx43 mutants known to cause EKVP

Abstract: Erythrokeratodermia variabilis et progressive (EKVP) is a rare skin condition characterized by permanent, thickened layers and temporary red patches of skin. This disorder is known to be linked to mutations in DNA that encode connexins, proteins that come together in the cell membrane to form channels to communicate between the cell's internal and external environment. Because the symptoms of EKVP cause much discomfort to the affected individual, it is important to understand how the condition occurs on the cellular level to choose effective treatments. To better understand the effects of these mutations on cell health, normal and mutant connexin proteins were expressed in cells. The experiments aim to detect key players in the unfolded protein response (UPR) to cellular stress using immunofluorescence studies, which illuminates proteins and cellular structures with bright, colorful tags to make them more visible. The results show that this particular stress response is not utilized by the cell in response to mutant connexins. Future studies may look for different proteins of the UPR for stronger fluorescent signaling or may investigate different stress response mechanisms to link to EKVP.

Mika Aly CC'20: Biology

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Faculty Mentor(s): George Mentis, professor of pathology and cell biology in neurology *Title:* Characterization of central synaptic dysfunction in a mouse model of spinal muscular atrophy

Abstract: SMA is an autosomal recessive disease that occurs in about 1 in 6,000 human patients, mostly affecting babies. The disease is fatal and the mechanisms that cause dysfunction and death of spinal motor neurons — the hallmark of disease — are largely unknown. Previous work from the Mentis lab has identified that certain excitatory and neuromodulatory synapses are impaired and precede motor neuron death. These observations raised the possibility that SMA might be a disease of spinal motor circuits. My project involves the characterization of certain synapses that impinge on vulnerable SMA motor neurons at early and late stages of disease. Preliminary results revealed that SMA motor neurons receive fewer dopaminergic synapses. The basic question that I will be addressing is: what is the effect of synaptic dopaminergic reduction in motor neuron function. Dopamine has been implicated as one of the major neuromodulators involved in the generation of locomotor activity during normal behavior. By extension, we aim to characterize the involvement of dopaminergic synaptic dysfunction as a central component in the compromised motor neuron output, which ultimately may lead in muscle paralysis. Successful accomplishment of this project will provide potentially key insights into the cellular mechanisms responsible for the pathology in spinal motor neurons in SMA.

Paulina Babiak, SEAS'19: Chemical Engineering

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Faculty Mentor(s): Allie C. Obermeyer, assistant professor of chemical engineering *Title:* Purification of Negative Caspase-3 Mutants for Cellular Delivery through Complex Coacervate Core Micelles

Abstract: Since their emergence in the 1980s, protein therapeutics have climbed their way into the daily lives of millions, most notably through the use of insulin replacement for diabetes treatment. Protein therapeutics provide a wide range of non-intrusive medical treatments that cannot be easily replicated by traditional medicine; replenishing deficient protein, replacing protein that has lost its activity due to a mutation, augmenting existing pathway, and interfering with harmful molecules are only a few examples of the plethora of applications of protein therapies. However, vast majority of potential that protein therapies could offer is limited due to current inability to transport proteins inside the cell, leaving a large unexplored area in the field. The scope of this research is to explore possibility of intracellular transport of proteins using thermodynamically driven phenomena of complex coacervation, using apoptotic caspase-3 as a vehicle of study, delivery of which could be utilized for cancer treatment. Exploiting chemistry of block co-polymers enables for the formation of complex coacervate core micelles, size of which could be manipulated to be adequate for endocytosis. Over the course of the study, six negative caspase-3 mutants were successfully cloned, expressed, purified, and tested for activity. While the mutants show partial or complete loss of activity, the potential for micelle formation is still to be investigated with turbidity assays.

Annie Block CC'19: Sustainable Development

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Faculty Mentor(s): Jennifer Cherrier, professor of earth and environmental sciences, Brooklyn College *Title:* A New Green Infrastructure Approach for Addressing Water Quality Challenges

Abstract: Non-point source nutrient loading from surface and subsurface runoff is one of the leading causes of impairment to United States waterways. This nutrient loading directly impacts the health of aquatic ecosystems resulting in fish kills, dead zones and harmful algal blooms. In addition, these runoff related impacts also affect human health and local and national economies (i.e. commercial fishing and tourism). Green infrastructure (GI) has been gaining recognition as a cost effective approach for addressing runoff related pollutant loading. However, the design of many GI systems is passive and water retention and nutrient removal efficiencies have been shown to be highly variable. A new hybrid system (ecoWEIR) activates GI to control retention times and soil conditions and therefore minimizes this variability. The goal of this study was to gain background information about these two forms of GI by comparing ecoWEIR to current flow through system outflows in planted and non planted systems. Simulated rain events were carried out and outflow samples were collected to analyze phosphorus (PO4), dissolved organic carbon (DOC) and total nitrogen (TN) concentrations. Our results showed higher PO4 removal in both planted and non-planted ecoWEIR systems, but highest removal was observed in the planted systems. The addition of grass significantly increased the outflow concentrations of both DOC and TN, which we attribute to soil manure amendments. Despite these increases, we still observed slightly greater removal of both in ecoWEIR systems. While ecoWEIR appeared to be more effective at nutrient removal than flow through systems, further simulated rain event studies should be carried out once system plant/microbial communities have matured. With increased urbanization and projected climate change, non-point source runoff will be more acute. It is therefore important to find new technologies like ecoWEIR to enhance the performance of GI systems to address these challenges.

Adam Block CC'19: Mathematics

adam.block@columbia.edu *Faculty Mentor(s):* Daniel Litt, postdoctoral research fellow and postdoctoral research scientist in the Department of Mathematics *Title:* Schur Functor Resolutions

Abstract: Certain nice vanishing theorems in algebraic geometry follow from the boundedness of a geometric quantity called Frobenius Amplitude. We attempt to bound this amplitude by the rank of a vector bundle over certain schemes in positive characteristic by analyzing the modular representation theory of Schur functors.

Viggo Blomquist CC'21: Neuroscience and Behavior

vb2446@columbia.edu *Faculty Mentor(s):* Robert Kass, professor of pharmacology *Title:* A Novel Suppression Technique of Premature Termination Codons and its Application to Congenital Long QT Syndrome 2

Abstract: The human ether-à-go-go related gene (hERG) codes for the pore-forming subunit of the voltage dependent potassium ion channel in cardiac cells known as Kv11.1. Potassium channels are voltage gated protein channels within the plasma membrane that allow potassium to move down the electrochemical gradient. The channel's central role is to initiate the repolarization of the cardiac action potential. Premature termination codons in hERG result in a hereditary and potentially deadly disease called Long QT Syndrome 2 (LQTS2). The purpose of this investigation was to test if novel codon edited human tRNAs would be able to recognize the premature termination codon within the mRNA strand and add the correct amino acid to the growing polypeptide chain, preventing premature termination and rescue of Kv11.1. In order to prove successful suppression, Western blotting, patch-clamp technique and flow cytometry were conducted on HEK293 cells transfected with DNA plasmids containing a gene for codon edited tRNA and the mutated hERG gene. I determined that codon edited tRNAs were capable of suppressing the W1001TGA premature stop in hERG, which causes LQTS2. Successful suppression of premature stops by using such tRNAs could lead to major medical advances in gene therapy for not only LQTS2, but also for other diseases caused by premature termination codons.

Heather Hsun Chang CC'21: Neuroscience

hhc2130@columbia.edu Faculty Mentor(s): Richard Axel, professor of neuroscience Title: Does Internal State Modulate the CO2 Avoidance Neuronal Pathway?

Abstract: Animals engage in innate behaviors from birth, without learning. These innate behaviors rely on genetically defined neural circuits, making them a great system to study the neural pathways from sensory input to behavioral output. Despite being hardwired, innate neural circuits can also be modulated by internal states. Drosophila melanogaster display innate avoidance to carbon dioxide (CO_2). Olfactory sensory neurons (OSNs) detect CO_2 and transfer information to the antennal lobe (AL) in the fly brain. Projection neurons (PNs) then convey information from the AL to the mushroom body (MB), a center for learning, and the lateral horn (LH), which is involved in innate behaviors. Previous research has shown that hunger states can affect the neural circuits that underlie CO_2 avoidance behavior. In starved flies the MB is necessary for CO₂ avoidance, but in fed flies it is not needed. Prior work in the Axel laboratory has demonstrated that a group of neurons in the LH, Split4, is necessary for CO₂ avoidance in fed flies. Based on this data, we wanted to determine whether Split4 neurons can be affected by internal states, similar to the MB. We silenced Split4 by expressing the inward-rectifying potassium channel, Kir, and compared CO_2 avoidance behavior between fed and starved flies. Starved flies displayed the same impaired CO_2 avoidance as the fed ones, suggesting that hunger does not influence these neurons. From this finding, our next step is to test all the identified neurons that are responsive to CO_2 to determine whether they can be modulated by a hunger state.

Ethan Chen CC'21: Biochemistry

eec2173@columbia.edu *Faculty Mentor(s):* Laura Kaufman, professor of chemistry *Title:* Studying the Mechanisms of Breast Cancer Cell Invasion Using 3D Culture of Spheroids

Abstract: My project studied breast cancer invasion using a multicellular spheroid model of invasion in collagen I matrices. Previously, spheroids generated from a mixture of cell lines have been employed to

explore heterogenous cell-cell interactions that may take place during cancerous invasion from a primary tumor. It has been reported that certain types of invasive cells can induce typically non-invasive cells to invade in collagen I when cultured together in a single spheroid. My project will instead focus on investigating this idea of co-invasion using a monoculture spheroid embedded in a matrix with dispersed invasive cells. Monoculture spheroids of non-invasive cells will be implanted in collagen I matrices containing different cell lines of varying invasive capacity. This research focuses on answering the questions: 1) Will invasive cell lines always induce non-invasive cell lines to invade? 2) In cases where invasion occurs, what are the co-invasion mechanisms adopted by each cell line? Spheroid invasion and collagen I matrix reorganization by cells will be monitored using confocal microscopy. Cell morphology during invasive spheroids and investigate co-invasion initiated by the dispersed cells using all invasive/non-invasive combinations of the cell lines being used. Characterizing co-invasion in cell lines with a diverse array of characteristics will give a broader perspective on co-invasion than currently exists in the literature. It will help to elucidate the range of invasive strategies potentially employed in vivo.

Joshua Choe CC'20: Biology

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Faculty Mentor(s): Carol Prives, professor of biology

Title: Hyperstability of a dimer-forming p53 mutant drives a distinct metabolic phenotype and altered chemotherapeutic sensitivity

Abstract: The tetramerization domain (TD) of tumor suppressor p53 facilitates its oligomerization, which is essential for efficient DNA binding, protein-protein interactions, and transactivation of downstream targets. Although the active conformation of tetrameric p53 has been extensively studied, dimeric p53 resulting from mutations within the TD still remains poorly characterized. Furthermore, mutations within the p53 TD have been linked to Li-Fraumeni Syndrome (LFS), a hereditary condition that predisposes individuals to various cancer types. We recently reported that Mdm2 preferentially binds to and degrades dimeric p53 through the ubiquitin-independent 20S proteasome pathway (Katz et al., Genes Dev 2018). Expanding on this study, we have characterized a representative LFS dimeric mutant p53 (A347D) in a physiologically relevant context. Specifically, CRISPR/Cas9 was used to generate clones of U2OS cells endogenously expressing either wild-type (WT) p53, no p53, heterozygous (WT/A347D) or homozygous (A347D/A347D) mutant p53. We discovered that mutant p53 (A347D) is unable to transactivate several known p53 target genes including Mdm2, leading to a highly stable protein that cannot be further increased by Nutlin treatment. By contrast, p53 in the heterozygous cells displays an intermediate transcriptional capacity and can be partly stabilized by Nutlin. Remarkably, cells expressing mutant p53 exhibit a dramatic glycolytic phenotype marked by extracellular metabolite secretion and enhanced ROS production. Interestingly as well, despite their attenuated transcriptional activity (including traditional pro-apoptotic p53 targets), A347D mutant cells display enhanced sensitivity to DNA damage response (DDR) inducer etoposide. Thus, the highly stable and transcriptionally impaired dimer forming mutant p53 (A347D) can drive a distinct metabolic and apoptotic phenotype, which may have significant potential for development of targeted therapeutic strategies for patients harboring tetramerization domain mutations.

Mariya Delyakova CC'21: Mathematics | Computer Science

mgd2140@columbia.edu Faculty Mentor(s): Jo Nelson, assistant professor of mathematics, Rice University Ila Varma, assistant professor of mathematics, University of California, San Diego Title: Knots and Integral Quadratic Forms

Abstract: In topology, knot theory is the study of mathematical knots. While inspired by knots, which appear in daily life in shoelaces and rope, a mathematical knot differs in that the ends are joined together so that it cannot be undone, the simplest knot being a ring. Studying knots is of great importance due to their applications in different fields. In the last several decades of the 20th century, scientists became interested in studying physical knots in order to understand knotting phenomena in DNA and other polymers. Knot theory may also be crucial in the construction of quantum computation (Collins 2006).

In this project, we study the structure of the sets \mathscr{P}_{Δ} of 4 X 4 Seifert matrices, which correspond to genus 2 knots, and give rise to the same Alexander polynomials $\Delta(x)$. More concretely, we give an explicit form of the 4 X 4 Seifert matrices and an explicit form of their characteristic and Alexander polynomials. Furthermore, we give a bijection between these 4 X 4 Seifert matrices and quaternary quadratic forms.

Matteo Di Bernardo CC'20: Biology | Statistics

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Faculty Mentor(s): Luis Parada, director of the Brain Tumor Center and American Cancer Society research professor, Gerstner Sloan Kettering School of Graduate Sciences *Title:* Preliminary study into tumorigenic potential of hypothalamic cells reveals expansion of oligodendrocyte lineage

Abstract: Glioblastoma Multiforme (GBM) is the most common form of primary brain tumor and has a median survival rate of fifteen months due to its aggressive nature. Previous research in the Parada Lab has identified neural stem and progenitor cells in the subventricular zone of mice models with human GBM-relevant mutations as potential cells of origin for glioma. We designed a transgenic mouse model that couples the diphtheria toxin receptor, H2B-GFP, and an inducible Cre recombinase under the control of the neural stem cell specific Nestin promoter/enhancer. This study focused on a population of GFP+ cells that we identified in the hypothalamus. We isolated GFP+ hypothalamic cells and grew them in vitro, where they gave rise to neurospheres that differentiated into multiple lineages. This is a common assay used to characterize neural stem cells. Pulse-chase studies revealed a proliferative subpopulation within the hypothalamus that was GFPlow and Olig2+. Our transgene places activation of Cre under the control of oral tamoxifen, which when bred into tumor suppressor floxed background (NF1, p53 and PTEN) leads to their subsequent homozygous ablation. Histological analyses following 1 month of tamoxifen treatment in these mice led to the preferential expansion of GFPlow and Olig2+ cells, which aligned with the proliferative potential seen in non recombined mice. Additional analysis suggested an expansion of Sox10+ oligodendrocyte precursor cells rather than APC+ mature oligodendrocytes. This data suggests the presence of a quiescent and proliferative stem/progenitor population in the adult hypothalamus that may progress via the oligodendrocyte lineage.

Vanessa Dippon CC'21: Chemistry

vnd2105@columbia.edu Faculty Mentor(s): Tomislav Rovis, professor of chemistry Title: Using Monomeric Streptavidin (mSA2) to Enhance the Selectivity and Reactivity of Transition Metal Catalysis

Abstract: All chemical reactions involve the movement of positively charged nuclei and negatively charged electrons. All charged particles experience an electrical force within an electric field that causes them to accelerate and undergo a change in position. Therefore, it can be expected that an applied electric field can change the outcome of a chemical reaction, a concept supported by several theoretical studies. Electric field catalysis occurs when the dipole of a reacting solute's transition state is more stabilized than that of the ground state in the presence of an electric field.

It has been argued that nature utilizes this concept in enzymatic catalysis using the charges and dipoles of its amino-acid residues. The advancement of site-directed mutagenesis makes possible the engineering of a mutant enzyme capable of performing electric field catalysis. A modifiable catalyst that is capable of demonstrating this effect, accelerating bond formation and turning over product, would be demonstrably more useful and general. By taking advantage of nature's ability to express proteins and thus control an enzymes active pocket microenvironment, an engineered molecular electric field can be generated. This targeted electric field will be used to accelerate novel chemical reactions by direct manipulation of transition states revealing unprecedented reactivity. Monomeric streptavidin (mSA2) has been employed as a more efficient and modifiable protein scaffold to accelerate the Rh(III) coupling of acrylamides to styrenes via its enhanced electric field.

Anastasia Dmitrienko CC'21: Statistics | Computer Science

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Faculty Mentor(s): Todd Ogden, professor of biostatistics in psychiatry *Title:* Estimation of the Linearity Point in Graphical Analysis

Abstract: Graphical analysis offers a simplified alternative to kinetic modeling when quantifying Positron Emission Tomography (PET) brain images. Such analysis relies on selecting a time-point t*after which the relationship between the variables involved in the analysis is approximately linear. t* can be determined by visual inspection of the data, but this is subjective and impractical when quantifying many images. Automatic procedures for choosing t* require specification of an arbitrary threshold (e.g., a bound on the relative size of residuals). We propose an alternative fully automatic approach based on how well the graphical model fits the data. For each candidate t* value, we fit all data points for which t>t* according to a likelihood-based procedure for graphical analysis. The optimal t* is then automatically selected based on these residuals as the solution to a problem in change-point estimation, by applying an onset-of-trend change-point model to the estimates of the noise level. We apply this procedure to both simulated and clinical PET human data.

Ailis Dooner CC'19: Neuroscience and Behavior

acd2174@columbia.edu Faculty Mentor(s): Clare Kelly, assistant professor of psychology, Trinity College, Dublin Title: Social Cognition, Self Awareness, and Structural Language Use in Adults with Autism Spectrum Disorder

Abstract:

One research goal of the Imaging of Mind Architecture Lab at the Trinity College Institute of Neuroscience in Dublin, Ireland, is to understand the interplay between self-awareness, social cognition, executive and structural language use in adults with Autism Spectrum Disorder. Contributing to this line of research, I have transcribed and scored existing audio recordings of 20 participants' responses to the Strange Stories Film Task (SSFT), a way to gauge individuals' capacity for social cognition (Murray et al., 2017). All transcription and scoring is performed when blinded to each participant's diagnosis status. Sections of recording that are incomprehensible due to accent or audio quality have been, and continue to be, reviewed by additional listeners with native Irish accents (in progress). I have learned how to enter transcripts into Computerized Language Analysis as Codes for Human Analysis of Transcripts (CHAT) files, so I can analyze them for structural language features. Once transcription, scoring and structural language analysis are complete, the role of self-awareness will be considered as well, based on participants' scores on Self-Reflection and Insight Scale (Grant, Franklin, & Langford, 2002), a metric previously administered by the research team. Through this analysis, we can begin to understand how self-awareness and social cognition might be related in adults with Autism Spectrum Disorder. More participants will be needed for this line of research, and during my time in Dublin, I contributed to recruitment efforts by emailing organizations with information about the study.

Marcel Dupont CC'20: Biochemistry

mmd2221@columbia.edu Faculty Mentor(s): Brent Stockwell, professor of biological sciences and chemistry Title: A Live Cell Assay for Monitoring Protein-Protein Interactions

Abstract: Many diseases involve abnormal protein-protein interactions, and compounds that target these interactions are often promising therapeutic strategies. Here, we use the NanoBiT live cell assay to monitor protein-protein interactions, such as the interaction between oncoprotein MDM2 and tumor suppressor p53 in Glioblastoma multiforme (GBM). In the NanoBiT assay, MDM2 and p53 are fused to functional bits that luminesce when MDM2 and p53 bind. By adding compounds and detecting changes in luminescence, we can determine whether a compound is acting as an inhibitor and disrupting the protein-protein interaction. Although we concluded that MDM2 inhibition and BBB penetrability are largely incompatible, the assay worked as expected since known MDM2 inhibitor Nutlin-3a causes a large decrease in luminescence. We also expanded the assay into other contexts such as RAS-RAF interactions, and identified some compounds that inhibit that interaction. Together, these experiments demonstrate the utility of protein-protein interaction assays such as NanoBiT in the search for molecularly targeted drugs.

Micah Gay CC'20: Mathematics

mcg2194@columbia.edu Faculty Mentor(s): Gus Schrader, assistant professor of mathematics Alisa Knizel, postdoctoral research fellow and postdoctoral research scientist in the Department of Mathematics Title: Whittaker Vectors in Positive Representations of Non-Simply-Laced Quantum Groups

Abstract: In this work, we obtain explicit formulas for Whittaker vectors in positive representations of non-simply-laced quantum groups. Recently, a realization of these representations based on quantum cluster algebras has been given by Ip, and based on his construction it is natural to expect that Whittaker vectors in these representations should admit a factorized expression in terms of non-compact quantum dilogarithm functions. Finding such a description of the Whittaker vectors generalizes results of Gerasimov-Kharchev-Lebedev-Oblezin to the quantum group case, and allows one to obtain integral representations for the eigenfunctions of Coxeter-Toda systems in non-simply-laced type.

Allison Ghuman CC'21: Mathematics | Computer Science

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Faculty Mentor(s): Clark Barrett, associate professor (research) of computer science, Stanford University *Title:* Fuzzing and Debugging SMT Solvers

Abstract: While SAT solvers use Boolean logic, SMT solvers use first-order logic and combine SAT with theory reasoning. Using their logical modeling and solving capabilities, Satisfiability Modulo Theories (SMT) solvers are often key tools for program analysis and verification, security, synthesis and many other verification applications. For this reason, robustness and correctness are critical and solvers must be tested as rigorously and completely as possible. Due to their complexity however, full verification of SMT solvers remains an open question. Nevertheless, grammar based black-box input fuzzing has been previously shown to be a very effective strategy in debugging.

We have developed our own grammar-based blackbox fuzzer to test the lab's SMT solver, CVC4. Our fuzzer produces random valid SMT2 formulas, but also randomly enables/disables solver options with option fuzzing, a feature we added to maximize coverage of the solver's code when testing. Here, we discuss the functionality and utility of this fuzzer in generating input formulas and debugging our solver.

Midori Hosoda CC'21: Medicine, Literature and Society

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Faculty Mentor(s): Jeremy Veenstra-VanderWeele, professor for the implementation of science for child and adolescent mental health in psychiatry

Title: Relationship Between the Maternal Serotonin System and Neurodevelopment in an Animal Model of Autism Spectrum Disorder

Abstract: Serotonin (5-HT), a neurotransmitter, has been known to play a crucial role in ASD, but exactly how it contributes to the disorder remains unclear. Serotonin neurotransmission is modulated by the serotonin reuptake transporter (5-HTT or SERT). Mutations in SERT have been found in ASD patients,

including the Gly56Ala mutation that leads to enhanced SERT function. In a 2012 study conducted by the Veenstra-VanderWeele lab, male mice with the Gly56Ala variant of the serotonin transporter gene had hyperserotonemia – an unusually large amount of serotonin in the blood, altered central 5-HT system function and behavioral abnormalities related to ASD.

Midori's summer research examined the impact of the maternal SERT genotype on development and behavioral outcomes of offspring. Mothers with two Gly56Ala copies (AA) or normal copies (GG) of the SERT gene were mated with fathers of the opposite genotype. The resulting offspring were heterozygous (i.e. they have one copy of the Gly56Ala gene and a normal copy). The development and behavioral outcomes were investigated by 1) serotonergic labeling of mouse embryo brains and 2) analysis of experimental videos of the offspring's social behavior either as juveniles or adults.

Allison Hung CC'20: Biochemistry

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Faculty Mentor(s): Alexander Johnson, professor of microbiology and immunology, University of California, San Francisco

Title: Characterizing white and opaque C. albicans interactions with macrophages

Abstract: Candida albicans is an opportunistic fungal pathogen which resides harmlessly in healthy individuals, but causes serious illness in immunocompromised patients. Previous studies have linked the pathogenesis of C. albicans to its morphological plasticity. C. albicans also exhibit distinct white and opaque cell types, although it is unclear how the white-opaque switch contributes to its pathogenesis. White and opaque cells are known to interact differently with the innate immune system – macrophages preferentially phagocytose white cells over opaque cells. Strains heterozygous at the mating type locus (a/α) are unable to switch due to inhibition of the regulatory protein WOR1. Yet, switching has recently been observed in clinical a/α isolates. We evaluated this phenomenon by measuring WOR1 in these strains. Although most strains had detectible WOR1, wide variation suggests that multiple mechanisms are used to override the canonical a/α block. We then used a murine macrophage infection model to determine how such strains interact with the host immune response. To evaluate whether these clinical strains induce different inflammatory responses, we measured secretion of cytokine TNF- α . A significant (p < .05) reduction in cytokine release was observed in macrophages co-cultured with opaque cells compared to white cells. Further, we assessed whether these strains are differentially phagocytosed by quantifying the phagocytic index following infection. We found that most opaque strains are phagocytosed at a lower rate than white strains. Finally, because C. albicans can survive in and rupture host macrophages, we monitored macrophage survival by measuring cytotoxicity following infection. We observed increased cytotoxicity following infections with white clinical strains compared to their opaque variants. Taken together, these results suggest that opaque C. albicans can evade the immune system during infection, possibly serving as a reservoir for subsequent infection.

Linnie Jiang CC'19: Neuroscience and Behavior | Computer Science

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Faculty Mentor(s): Larry Abbott, professor of theoretical neuroscience and professor of physiology and cellular biophysics in biological sciences

Ashok Litwin-Kumar, assistant professor of neuroscience Richard Axel, professor of neuroscience

Title: Circuit Mechanisms Underlying Expectation

Abstract: During learning, evidence contrary to current predictions must be used to modify expectations about the future. To examine how prior experience guides learning and behavior, we will focus on a circuit in a model organism: the fruit fly Drosophila melanogaster, which exhibits multiple forms of learning. Olfactory perception and learning in the fly require the mushroom body (MB). Kenyon cells (KCs) of the MB are sparsely activated by odors and synapse onto MB output neurons (MBONs) in compartments that play different roles in influencing behavioral output. Dopaminergic neurons (DANs) induce plasticity in the KC-to-MBON synapses. In typical models of classical conditioning, KCs represent the conditioned stimulus (odor), whereas DANs represent the unconditioned stimulus (US). Previous work has shown that learning in the MB involves depression of the KC-MBON synapses. We construct a model with few neuronal components wherein we propose connections between the MBONs and DANs that allow classical phenomena of learning (like extinction and second-order conditioning) to occur. This model is informed by EM data that can help characterize the flow of information between various classes of neurons in the MB. We will continue to conduct experiments to inform our working model of the MB network, which will then be revised to form new predictions about fly behavior. By first investigating the role of dopamine in a tractable invertebrate system, we will better understand how dopamine neurons in other animals govern their use of a rich array of past experiences to inform present and future actions.

Benjamin Kepecs CC'20: Biochemistry

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Faculty Mentor(s): Tal Danino, assistant professor of biomedical engineering *Title:* Design and characterization of a lactate-sensing genetic circuit for targeted bacterial cancer therapy

Abstract: Current cancer therapies such as chemotherapy and gene therapy are often limited in efficacy and safety by lack of tumor-targeting specificity. Often, a therapeutic agent administered to a patient systemically can fail to reach or penetrate a tumor, and indeed can cause harmful side-effects in healthy tissue. One exciting area of research within microbiology and synthetic biology is aimed at creating targeted cancer therapies by using bacteria to deliver therapeutics directly to tumors. Bacteria are well-poised for such, as studies have found that some bacteria administered to the body have a natural tendency to selectively target, penetrate and colonize cancerous tissue, to the exclusion of healthy tissue. While bacteria predominantly colonize tumors over healthy tissue in ratios of 100:1 to 1000:1, this colonization is not completely specific, and trace colonization of organs has been found. In this study, we built on previous efforts to engineer a genetic biocontainment circuit in bacteria, to ensure that they can only grow in the tumor microenvironment and will not cause off-target effects. Taking advantage of the high lactate levels that are a distinctive biomarker of cancer, we aimed to engineer a small gene regulatory network in bacteria that would allow them to grow only in the presence of high lactate concentrations. We designed and characterized a preliminary circuit based on lactate-sensing genetic

regulatory elements, and then made incremental adjustments and additions. We demonstrate a promising biocontainment strategy that restricts production of an essential bacterial gene to conditions of high external lactate.

Khrystofor Khokhlov CC'19: Chemistry

kk3106@columbia.edu Faculty Mentor(s): Colin Nuckolls, professor of material science Title: Functionalized helical graphene nanoribbons for nanoelectronics

Abstract: We have attempted to synthesize a series of antiaromatic oligomers of existing benzene-based rylene propeller-like scaffold, which displayed promising power conversion efficiencies (PCE ~8 percent) in organic solar cells. We have used the IBr/ICI-assisted radical cyclization of PDI-alkyne precursors to synthesize PDI-semicoronenes functionalized with bromine/chlorine and MIDA boronate/trimethylsilyl functional groups. Furthermore, we have synthesized a set of PDI-based helicenes regioselectively functionalized with 4-phenylamino substituents to study their single-molecule conductance. These molecules will be tested for single-molecule conductance in order to study orbital overlap between PDI units in the helicene scaffold. We will also use these PDI-helicene molecules to attempt to observe photocyclization of electrode-bound molecules in real time. Additionally, in order to make these molecules in the form of enantiopure helices, we have devised a scheme for separation of enantiomers of dihydroxy PDI-helicene through its functionalization with enantiopure chiral derivatization agent - (1S)-(-)-camphanic chloride. Diastereomers displayed distinct difference in retention times on conventional silica gel-covered chromatographic plates for preparatory TLC, though procedure is not yet feasible for large-scale separation of PDI-helicene enantiomers.

Avik Laha CC'19: Physics, Computer Science

al3510@columbia.edu *Faculty Mentor(s):* Greg L. Bryan, professor of astronomy *Title:* The Circumgalactic Medium of Dwarf Galaxies

Abstract: Dwarf galaxies (galaxies with masses significantly lower than the Milky Way) form the vast majority of the overall galaxy population, but much about them is still poorly understood, both theoretically and observationally. Some of the biggest outstanding issues in cosmology, like the nature of dark matter, are motivated by or may be solved by such low-mass galaxies. Recently, much attention has been focused on the circumgalactic medium (CGM), consisting of the gas which is not in a galaxy's disk but is still gravitationally associated with it. The CGM mediates a galaxy's interaction with its environment, giving it a central role in galactic evolution, and recent advances in computing power and in observations have afforded astrophysicists the opportunity to study it in much more depth. In this work, we simulate a small population of isolated dwarf galaxies (not near any significantly more massive galaxy) from the early universe down to the present day, and seek to characterize the emergent CGM, and how its properties scale with galactic properties.

Christina Lee CC'21: Biophysics

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Faculty Mentor(s): Anthony Fitzpatrick, assistant professor of biochemistry and molecular biophysics *Title:* Using Expansion Microscopy to Visualize Tau in Human Brain

Abstract: To overcome the resolution limits of a light microscope, expansion microscopy (ExM) was developed to achieve higher resolution imaging of biological samples through a process of sample expansion. ExM was used to visualize tau in samples of human brain tissue with Alzheimer's disease (AD). An expandable polymer web was formed within the tissue, causing it to expand approximately four to six times its original size. Along with staining for DNA, immunofluorescence (IF) staining labeled tau within the expanded tissue, allowing for the visualization of expanded tau. Methods to enhance IF staining in ExM were explored and compared with IF staining in standard tissue. Though AD is often characterized by the presence of tau aggregates, the precise relation between tau aggregates and the manifestation of AD is unknown. Further studies in ExM could elucidate the location of tau aggregates within the brain.

Dimitri Leggas CC'19: Computer Science

ddl2133@columbia.edu Faculty Mentor(s): Nakul Verma, lecturer in the discipline of computer science Title: Spatial Analysis of Graffiti in Exarcheia, Athens, Greece

Abstract: Dense graffiti covers most of the walls in Athens, Greece. In this study, we perform an exploratory analysis of the graffiti in one Athens neighborhood, Exarcheia. The data set consists of several thousand images taken over the course of three days in August 2018. Using techniques in computer vision, we attempt to understand the salient features of the neighborhood's visual landscape and how different surfaces prompt different styles of graffiti. From various spatial analyses, we gain insight into the variations of the graffiti between different important locations in the neighborhood. Of particular interest, given Exarcheia's leftist political history, are the characterizations of graffiti around sites of political action and community organization. In addition to using these analyses as a way to gain insight into recent local histories, we consider how statistical studies of graffiti distribution can contribute to an anthropology of the neighborhood. Because it is generally difficult to conduct anthropological studies on graffiti crews, this work greatly supplements our knowledge of the artists who paint on Exarcheia's walls.

Benjamin Lesea-Pringle GS'19: Biochemistry

bjl2148@columbia.edu Faculty Mentor(s): Ann McDermott, professor of biological chemistry and professor of biological sciences and chemical engineering Title: Pb Resistance in NYC Soil Bacteria

Abstract: Lead is a common, persistent environmental neurotoxin that particularly affects young children. Many urban environments have soil lead levels that are well above background levels, and even above Environmental Protection Agency limits. Children may be exposed to lead through urban dust or by playing in contaminated soils. How much lead gets taken up by children ingesting soil depends heavily on the bioavailability of the lead species present in the soil — that is, the solubility of a particular lead species in an acidic environment (the stomach). Soil bacteria develop resistance to lead through a

number of mechanisms, many of which can change the species of lead in the soil, and so the bioavailability. This study examined the relative lead resistance of four strains of soil bacteria isolated from a heavily contaminated site in Brooklyn, NY, in comparison with three strains presumed sensitive to lead due to their lack of selection (S. lividans WT, P. aeruginosa WT, competent E. coli), as well as a strain used as a model organism for heavy metal resistance containing a lead-selective operon (C. metallidurans CH34). Resistance levels were determined by the Minimum Inhibitory Concentration (MIC), the highest concentration of lead at which a particular strain still grew. One soil isolate, A. russicus BP10, showed strong growth even at twice the MIC of the known lead resistant strain. Further research will look for the mechanism of this resistance.

Jenny Li CC'21: Computer Science

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Faculty Mentor(s): Gil Zussman, associate professor of electrical engineering *Title:* Experimental Evaluation of Throughput and Fairness in Heterogeneous Half-Duplex and Full-Duplex Networks

Abstract: Full-duplex wireless is an emerging communication paradigm with high potential for improving network capacity and reducing delay in wireless networks. In this research project, we seek to address the problem that introducing full-duplex users into existing half-duplex networks might impair the throughput of legacy half-duplex users. We developed an experimental framework leveraging the WiFi nodes in the ORBIT testbed (orbit-lab.org), which were used to evaluate our proposed algorithms tailored for such heterogeneous networks where full-duplex and half-duplex users co-exist. The framework is built on the Wi-Fi Multimedia (WMM), which is a certification providing quality of service to 802.11 networks. In particular, we investigated different access categories and contention window settings and evaluated their effects on network throughput and fairness. Lastly, we developed methods to label traffic packets to be assigned to different access categories to adaptively adjust the throughput. The project is part of the ongoing Columbia FlexICoN project (flexicon.ee.columbia.edu).

Leo Lo CC'22: Physics

Cl3815@coluimbia.edu Faculty Mentor(s): Dmitri N. Basov, professor of physics Title: Temperature-dependent optical constants of highly p-doped silicon wafer

Abstract: Scattering-type scanning near-field optical microscopy (s-SNOM) provides nanoscale-resolution imaging based on local dielectric properties of materials, allowing for 2D imaging and "fingerprint" spectra of diverse materials such as photonic devices, biological molecules for virus imaging, and chemicals for trace explosive detection. Silicon wafer is widely used as a substrate for nano-optical devices, yet a recent s-SNOM measurement of a highly-p-doped silicon wafer exhibited thermal behavior that remained to be clarified using numerical simulation method. Electromagnetically, highly-p-doped silicon dioxide exhibits metallic behaviors such as a low resistivity of ~0.01-0.02 Ω cm; however, thermally, highly-p-doped silicon wafer's near-field signal increases with increasing temperature, a characteristic semiconductor behavior. To elucidate the incongruent electromagnetic and thermal behavior of the highly-p-doped silicon wafer, a numerical simulation method was employed. The temperature-dependent carrier concentration was calculated using Fermi-Dirac statistics. Permittivity,

far-field reflectivity, near-field reflectivity, and near-field signal were calculated based on the lightning rod model. An improved understanding on the thermal and the near-field electromagnetic responses of SiO2 provides more parameters to adjust the properties of SiO2, and hence a wider range of control in nano-devices for chemical sensing and photovoltaics applications.

Caroline Magalhaes de Toledo CC'21: Biochemistry

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Faculty Mentor(s): Clarissa Waites, associate research scientist in the Ddepartment of Pathology and Cell Biology

Title: The role of Rab GTPases in alpha-synuclein mediated alterations in vesicle reuptake

Abstract: It is well established that in Parkinson's Disease, the neurons present elevated levels of the protein alpha-synuclein that leads to the formation of protein clumps. One of the effects of this increase in alpha-synuclein is alterations in vesicle reuptake, which occurs after the neuron releases vesicles with neurotransmitter in the synapse. However, the specific mechanism that leads to these alterations is still unclear. In this project, we studied the role of Rab GTPases, an important class of proteins that are fundamental to transporting vesicles within the cell, in the alterations in synapses caused by alphasynuclein. These changes were studied using live cell fluorescence microscopy of mice neurons with a pH sensitive fluorescent marker, which allows for tracking whether the vesicles were released and reuptaken by the cells. A comparative analysis was then performed with cells in which the expression of alphasynuclein and different Rab GTPases was induced using transfections, a method of inserting external DNA sequence in a cell.

Zachary Marcone CC'19: Mathematics | Economics

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Faculty Mentor(s): David Weinstein, professor of Japanese economics *Title:* A Measurement of the Gains from Variety of the Opening of Japan from 1858-1900

Abstract: In 1853, Commodore Matthew Perry of the United States sailed into Tokyo bay and demanded that Japan open its ports to international trade. Five years later, Japanese ports opened for business. For nearly 250 years Japan had maintained limited economic trade with the outside world. Thus, in just a few short years Japanese economic system faced one of the biggest shocks any economy has faced in history. Such a sudden shock provides a perfect opportunity to investigate economies in transition and measure the effect of trade on consumer well-being. Previous studies have measured aggregate changes in consumer happiness due to the opening of Japan to trade. This research attempted to refine this measurement and elucidate the contribution of increased product variety. When consumers are presented with greater product choice due to an influx in imports then there is an increase in well-being. This change was measured by constructing mathematical models of well-being (utility functions) with empirical import data from the late 19th century. It was found that the increase in consumer well-being from new imports amounted to 10 percent of Japanese gross national product in 1900 (the sum total of all goods produced by Japanese citizens).

Miguel Martinez CC'19: Astrophysics

mm4767@columbia.edu Faculty Mentor(s): Brian Metzger, associate professor of physics Title: Orbital Evolution of Tidally Detached Exomoons

Abstract: The irregular and sometimes deep transits of Boyajian's star (KIC 8462852) are an intriguing astrophysical mystery, particularly in combination with the long-term secular dimming of the star. One proposed solution is that the secular dimming is due to the aftermath of a planetary collision, which heated the outer layers of Boyajian's star; in this scenario, the transits are caused by tidally stripped, icy exomoons that have been detached onto highly eccentric orbits and are now rapidly outgassing (Metzger et al. 2017). We have been investigating this scenario further by running large ensembles of orbital integrations, to quantify the orbital elements of moons tidally detached in the leadup to a planet-star collision. In our numerical integrations, a distant brown dwarf companion excites the eccentricity of a gas giant with semimajor axis of 30 AU through the eccentric Kozai-Lidov effect. We show that there is a large parameter space conducive to planet-star collisions (even in the presence of general relativistic precession). Next, we focus on one particular planet-perturber configuration, and run followup simulations examining the fate of tidally detached exomoons. In general, exomoons on initially wider orbits are more likely to survive the dynamical blender of the planet-star-perturber system, while those on tighter orbits are more likely to be perturbed into a collision with their host star.

Collins Mokua CC'21: Neuroscience and Behaviour

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Faculty Mentor(s): Ahluwalia Kavita, associate professor of dental medicine *Title:* Building Capacity to Address Oral Health in Lea Toto Clinics, Nairobi, Kenya

Abstract:

Research Question: How can existing care networks be leveraged to address oral health?

Background: Kenya has one dentist per 44,500 Kenyans. Lea Toto is a network of eight clinics located in informal settlements in Nairobi, Kenya, that target children (and families) living with HIV. Although oral health is central to nutrition and wellness in people living with HIV, it is not routinely addressed by healthcare workers targeting underserved populations living with HIV.

Methods: Survey methodology was used to assess Lea Toto nurses', clinical officers' and nutritionists' oral health-related knowledge, opinions and practices. The information collected was used to develop and implement an oral health intervention.

Results: Survey data (N=21) suggest that 80.9 percent of workers report toothaches as the most frequent dental or oral problem of their patients, and 76 percent of workers indicate that patients complained about difficulty chewing. All participants requested oral health training but clinical officers and nurses requested training on oral examination, while nutritionists requested more information on the relationship between oral health and nutrition.

Conclusion: Although oral problems are prevalent among Lea Toto patients, oral health is not systematically addressed. Healthcare workers are willing to seek additional training to integrate oral health into their care systems.

Rose Orenbuch GS'19: Information Science

rao2128@columbia.edu *Faculty Mentor(s):* Itsik Pe'er, associate professor of computer science Raul Rabadan, professor of biomedical informatics in systems biology *Title:* ArcasHLA: human leukocyte antigen typing from RNA sequencing

Abstract: Human leukocyte antigens (HLAs) encode the proteins that make up the major compatibility complex whose role is to present antigens to specialized immune cells as a part of innate and adaptive immune response. HLA typing is necessary for determining tissue compatibility as well as facilitating the study of associations with the outcome of a plethora of diseases.

Wet lab methods specialized for HLA typing are prohibitively expensive. However, the increasing quality and use of next-generation sequencing (NGS) has enabled efficient HLA-typing from standard sequencing data. NGS-based typers must be able to predict an individual's genotype from short reads out of thousands of known alleles, a challenging task given the high level of polymorphism and homology between the HLA genes.

We present arcasHLA, a fast, accurate in-silico tool that predicts HLA genotypes from RNA sequencing. Reads are aligned to an HLA reference with Kallisto which determines the set of transcripts compatible with each read using a graph-based alignment. Next, arcasHLA probabilistically quantifies the abundance of allele transcripts for each gene, finding the assignment of reads to alleles that best explains the observed reads. Low-support alleles are dropped from consideration. If more than two alleles remain, the most abundant alleles are compared pairwise to find the pair which maximizes the proportion of aligned reads. Our tool outperforms the established HLA typers on the gold-standard benchmark dataset for HLA typing.

Cheryl Pan CC'21: Neuroscience and Behavior

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Faculty Mentor(s): Brent Stockwell, professor of biological sciences and chemistry *Title:* Purines & Polyamines: Understanding the Role of their Metabolic Pathways in Ferroptosis

Abstract: Elucidating the underlying mechanisms of ferroptosis, a form of regulated cell death characterized by iron-dependent accumulation of lipid peroxides, will facilitate the development of new treatments for various cancers, as well as further understanding of neurodegenerative disease pathology. Based on a metabolomics screen of ferroptosis, changes in specific molecules involved in the purine and polyamine pathways were identified. While previous studies have demonstrated correlations between ferroptosis and changes in intracellular levels of purines and polyamines, the exact metabolic role of polyamines remains undefined. This project explored the in vitro effects of these metabolites on ferroptotic cell death. Cell viability assays demonstrated that the delivery of the polyamines spermine and spermidine sensitized cells to ferroptosis and increased the lethality of the ferroptosis inducer erastin.

Surprisingly, ferrostatin-1, a specific inhibitor of ferroptosis, was unable to rescue cells exposed to a combination of erastin and the polyamines. This result suggests that spermine and spermidine may interfere with the protective effect of ferrostatin-1, or may be inducing cell death through a mechanism that ferrostatin-1 cannot inhibit. Ultimately, these findings offer greater insight into the connections between ferroptosis and polyamines, and the possibility of polyamines being used as novel targets for drug development.

Sohil Patel CC'20: Biology

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Faculty Mentor(s): John F. Hunt, professor of biological sciences *Title:* Coupling between translational blockages and premature transcription termination in E. coli characterized using bicyclomycin, an antibiotic that inhibits Rho-dependent transcription termination

Abstract: The genetic code is degenerate, allowing a single amino acid to be encoded by several different synonymous codons. Many studies of the effects of synonymous codons on protein expression in E. coli have focused on the influence of AGG and AGA, which are the rarest codons in E. coli. Here, we test the effects of tandem AGG codons on protein expression levels under a variety of expression conditions. Prior studies have demonstrated that placing five AGG codons in tandem significantly attenuates translation of overexpressed proteins. We qualitatively measured protein expression levels from a gene with five tandem AGG codons added at the N-terminus of the XcR50 gene, which is known to express well in E. coli strains without these added residues. Consistent with results in prior literature, we show that addition of this AGG repeat creates a "codon block" that strongly attenuates expression of protein from this gene when a bacteriophage T7 promoter and polymerase are used to drive high-level transcription. Expression of this protein is greatly increased when tRNAArgU, which is cognate to AGG, is overexpressed simultaneously with induction of the AGG5-XcR50 gene. Interpreting these results in conjunction with prior studies, we conclude that both a global overexpression of the mRNA for the gene containing the codon block combined with the local tRNAArgU depletion due to the tandem codon repeat itself are jointly responsible for the low protein expression levels. In contrast to these results, when we drive highlevel transcription of the same AGG5-XcR50 gene using an endogenous promoter (pTrc or pBAD) employing the native E. coli RNA polymerase, we observe only low-level protein expression either with or without tRNAArgU overexpression. These data suggest that the transcription by E. coli RNA polymerase, which as opposed to T7 RNA polymerase can be coupled to translating ribosomes, is somehow attenuated by the five tandem AGG codons for some reason unrelated to tRNA supply. We hypothesize that this effect is caused by difficulties translating the five consecutive arginine residues that are encoded by the tandem AGG repeat. Furthermore, in the presence of bicyclomycin, an antibiotic known to inhibit the Rho in the transcription-termination factor, protein expression levels were significantly boosted when complemented with tRNAargU. These results suggest that translational obstacles in E. coli genes under endogenous promoter control may frequently cause premature transcription termination due to transcription-translation coupling via a mechanism upon Rho that is suppressed upon addition of bicyclomycin.

John Monroe Pederson Jr. SEAS'19: Mechanical Engineering

jmp2252@columbia.edu Faculty Mentor(s): David Mascareñas, research and development engineer, Los Alamos National Laboratory's Engineering Institute Title: Interactive Robotic Control with Augmented Reality

Abstract: As robots become ever more commonplace in industry and manufacturing, the need for easy and precise robotic control is growing. Current robotic operators must use complicated manual controllers and receive hours of training to perform simple tasks; in addition, such tasks are hindered by the lack of force feedback, which can cause undesired dropping or crushing of objects. At the same time, augmented reality (AR) devices, such as Google Glass and the Microsoft HoloLens, are becoming cheaper and easier to develop.

Our goal was to develop an AR application that would allow a user to intuitively control and manipulate a robotic arm with ease. In addition, a means to display the forces on each arm component would further assist the user. Using the game engine Unity and Microsoft Visual Studio, we created an AR application to run on a Microsoft HoloLens; the app included an interactive robotic arm and a button-based user interface. We then used libraries in the Robot Operating System (ROS) to connect to the HoloLens, relay the instructions to motion planning libraries and control a Yaskawa Motoman SIA5D robotic arm. We also used a MATLAB Simulink program to calculate the torque on each robot joint in near-realtime.

Our final result is an AR application that successfully allows a user to control and manipulate a robotic arm with little training. By manipulating an AR hologram of the robotic arm, the user can "click and drag" the robotic arm into a new position. In addition, the user can choose to "preview" the impending motion of the robot; in this mode, the torques on each joint are calculated and displayed as colors, giving force feedback to the user.

The application represents a proof-of-concept means of robotic control that surpasses current control methods in ease of use and training requirements. Further work would include 3D mesh-based obstacle avoidance and adjustment of holographic scale for precision maneuvering.

Aunoy Poddar CC'19: Biology | Computer Science

ap3441@columbia.edu *Faculty Mentor(s):* C. Daniel Salzman, professor of psychiatry and neuroscience *Title:* Learning and Reasoning in Complex Environments: You Sunk My Battleship!

Abstract: How do animals reason? In a complex environment, animals must be able to forage for information efficiently. We hypothesize that animals reason by searching for information in internal or external environments. To investigate, we created a visuospatial reasoning task for monkeys. In this task, monkeys search for the location of a hidden shape, uncovering the shape piece-by-piece. As the pieces are discovered, more of the shape is revealed and the monkey receives a reward, much like the board game Battleship. We found that monkeys were able to learn the task very rapidly, and we attempted to characterize their learning and efficiency. We observed their choice patterns and calculated the optimality of their decisions along with the response times of the monkeys. We conclude that the

monkeys are learning both the task and the shapes based on the distribution of their choice patterns and continually evolving response times. We continue to investigate the model by which these monkeys learn.

Eric Riesel CC'19: Chemistry

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Title: Understanding InP Synthesis with Microwave Heating and Ionic Liquid Additives

Abstract: The field of nanocrystal chemistry has turned to indium phosphide quantum dots (InP QDs) because of their relatively low toxicity compared to that of cadmium or lead-based alternatives. This study focuses on optimizing the synthesis of InP QDs for brightness or quantum yield (QY) and size distribution in the presence of tetrafluoroborate anion, hypothesized to be a source of fluoride. This study also aims to understand the mechanism by which this additive increases QY of InP QDs by postsynthetically treating with indium fluoride. Solvents that readily dissolve InP magic-sized clusters (MSCs) and are also miscible with the tetrafluoroborate ionic liquid are hypothesized to yield narrower size distributions because the ionic liquid will be more homogeneously dispersed and it is the chemical that inductively couples to the microwave which heats it directly. Diphenyl ether (DPE) was found to make a relatively narrow size distribution of small particles, whereas octadec-1-ene (1-ODE) made particles with a very broad size distribution. Addition of volumes of water 5µL or less were found to narrow size distribution at a cost of quantum yield. The best quantum yield in DPE was 6 percent, while particles made in 1-ODE had a quantum yield of 35 percent. Post-synthetic treatment of conventionally synthesized InP QDs with indium fluoride increased quantum yield of these crystals from less than 1 percent to 22 percent while maintaining a narrow size distribution of a full width half max (FWHM) less than 67nm. This data suggests that surface indium fluoride plays a large role in increasing QY.

Helena Rios CC'20: Mathematics

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Faculty Mentor(s): Adam Sobel, professor of applied physics and applied mathematics and professor of earth and environmental sciences

Suzana Camargo, research professor in the Lamont-Doherty Earth Observatory *Title:* Tropical Cyclone Genesis in the North Indian Ocean

Abstract: In this study, we examined the roles of several climatological variables in the formation of tropical cyclones in the Arabian Sea and in the Bay of Bengal. We also investigated how the available Poisson Regression indices, which measure storm genesis probability, and which are fit globally, captured the tropical cyclone genesis phenomena in the North Indian Ocean.

Before conducting a more thorough analysis, we hypothesized that the vertical wind shear was the most deterministic variable in the process of storm genesis in the North Indian Ocean, because of the high vertical shear and the low storm count in the monsoon months. However, by analyzing June storms, which aren't well predicted by the different indices and which occur mostly in the Arabian Sea, we concluded that storms still form under high vertical shear, if the Saturation Deficit or Relative Humidity is

high enough. We also concluded that the available Tropical Cyclone indices largely underestimate the numbers of storms formed in the pre-monsoon and post-monsoon periods in both basins.

Furthermore, we concluded that the distributions of Saturation Deficit and Relative Humidity, averaged across a small area around each storm genesis, are different in the Arabian Sea and in the Bay of Bengal. This means that, while the physics behind cyclone genesis is universal, since there are many variables that influence the formation of storms and since each locality has its own uniqueness, the weight and preferable values of each variable changes from one basin to the other, the weight and preferable changes from one basin to the other.

Jaewook Ryu CC'19: Biochemistry | Data Science

jr3576@columbia.edu Faculty Mentor(s): Ruben L. Gonzalez Jr., professor of chemistry Title: Characterization of the allosteric positioning of initiation factor 2 for rapid subunit joining during translation initiation

Abstract: Translation Initiation is a crucial regulatory step of translation that involves three translational initiation factors (IF1, 2, 3) bound on the 30S ribosomal subunit selectively incorporating the initiator tRNA (fMet-tRNAfMet) as well as regulating rate of 50S ribosomal subunit joining to form the 70S elongation complex. In particular, translation initiation factor 2 (IF2) is known to modulate initiation fidelity by directly interacting with the initiator tRNA and selectively accelerating 50S subunit joining to initiator tRNA bound 30S ribosomes (Caban et al. 2017). Currently, IF2 is also known to undergo multiple conformational changes with respect to the initiator tRNA during initiator tRNA selection, for which a specific conformation of IF2 promotes 50S subunit joining (Caban et al. 2017). To further investigate how conformation dynamics of IF2 regulate translation initiation, we will utilize single-molecule Fluorescence Resonance Energy Transfer (smFRET) with a newly developed internal IF2 FRET signal to better understand the conformational dynamics of IF2 during translational initiation. Collectively, our results have allowed us to develop a detailed, structure-based mechanism describing how allosterically regulated conformational changes of IF2 are used to tightly control the fidelity of initiator tRNA selection during translation initiation.

Kelly Ryu SEAS'19: Biomedical Engineering

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Faculty Mentor(s): Alberto Ciccia, assistant professor of genetics and development *Title:* Identification of stimulators of CRISPR-mediated precision base editing

Abstract: The substitution of C-G base pairs with T-A in the human genome accounts for approximately half of the mutations in human inherited diseases, such as Duchenne Muscular Dystrophy and several types of cancer. Therefore, efficiently converting specific T-A base pairs to C-G or vice versa could enhance the study and treatment of genetic diseases. While the modification of genomes has been accomplished with standard CRISPR-Cas9 technology, novel CRISPR-based precision genome editing tools have been developed to circumvent the generation of toxic double strand breaks (DSB) and overcome the random nature of mutations involved with standard CRISPR. However, current precision genome editing shows limited efficiency, as DNA repair mechanisms can lead to undesired byproducts. The present study

aimed to identify DNA repair factors that increase the efficiency of precision genome editing and mutants that cause loss of their stimulatory function. Various cell types with a blue fluorescent protein (BFP) reporter were transfected with the wild type (WT)/mutated gene, base editor and gRNA that induced conversion of the BFP into a GFP reporter to indicate base editing efficiency. Four factors (SNM1B, TIPIN, RPA2, USP1) enhanced base editing in both HeLa and K562 cells. Among mutants, TIPIN del185-218, RPA2 del187-270, and USP1 G670A G671A increased efficiency relative to respective WT factors in HeLa, while TIPIN del66-131, RPA2 T21A S23A S29A S31A, and SNM1B del 219-299 decreased the efficiency. In addition, the enhancement of efficiency observed for USP1 G670A G671A was reproduced in K562 cells. The genetically encoded WT stimulators and their mutants that further improve base editing efficiency will contribute to generating a highly precise genome editing system for human disease research and treatment.

Lorenzo Sampson CC'21: Sustainable Development

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Faculty Mentor(s): Jerry McManus, professor of earth and environmental sciences *Title:* Reconstructing Past Climate Using Deep Sea Sediment Cores

Abstract: During this project, data was collected from sediment cores from the Juan de Fuca Ridge, a divergent plate boundary in the Pacific off the coast of the Pacific Northwest, in an effort to date this core and eventually provide useful proxies which can be used to reconstruct the paleoclimate. These cores were severely bent as sediment was being collected, making the data less reliable and harder to extract. However, these cores were some of the oldest collected on that cruise. Proxies such as density, magnetic susceptibility, x-ray fluorescence, calcium carbonate and microfossils called foraminifera were collected and processed. These proxies point to several different climatic events which are used as time markers and assist in understanding and dating the core. By cross-referencing the data collected from this core with data collected from past cores, the core is contextualized in time and can be used to demonstrate glacial and interglacial periods throughout Earth's history.

Abhishek Shah CC'21: Neuroscience and Behavior

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Faculty Mentor(s): Christine Denny, assistant professor of clinical neurobiology in psychiatry *Title:* Ketamine, Sex, and Stress Jointly Modulate HCN1 Expression

Abstract: Major depressive disorder (MDD) affects nearly 300 million people worldwide. While present in all populations, women are twice as likely as men to fall victim to MDD. As such, it is important to analyze this disparity, especially in the context of treatment. Current approaches to treating depression have largely centered on treating symptoms and responding to depression after its incidence. However, the drug ketamine has shown promising results in preventing the onset of depression, acting prophylactically, or before the incidence of symptoms. Research has shown that an important component of ketamine's action as an antidepressant are HCN1 protein channels. In this work, I find that ketamine, stress and sex modulate expression of HCN1 as well as depressive-like behavior in mice models. Specifically, I find that ketamine acts to reduce depressive-like behavior when administered both before and after stress, and that HCN1 expression levels decrease upon administration of ketamine. However, female mice that have had their hormones removed do not show this decrease, suggesting that female sex hormones play an

important role in regulating depressive-like behavior in females. Altogether, these results suggest that HCN1 may play an important role in ketamine's action as both typical and prophylactic antidepressant and that HCN1 may be a future target for understanding disparities in MDD.

Manasi Sharma CC'21: Physics | Computer Science

manasi.sharma@columbia.edu Faculty Mentor(s): Charles Hailey, professor of physics Title: Investigating Polars

Abstract: The cause of Galactic Ridge X-ray Emission (GRXE), a stream of X-rays coming from the galactic center, has been a mystery for years, and one proposed solution for what causes it is the notion of polars, which are binaries of a white dwarf and a star. To test this, six selected polars will be observed by the NuSTAR telescope. However, polars change in brightness over time, so we can only observe them when they are at a sufficient level of brightness (>1,000 counts in our detector). In order to determine whether polars can be observed by the telescope, we use the online NASA tool WebSpec and the analysis software xspec to predict how many counts would appear in the detector from the different polar sources. We show that we can successfully decide which polar sources would be optimal to observe and approximately when they should be viewed.

Jihanne Shepherd CC'21: Biochemistry

jjs2273@columbia.edu *Faculty Mentor(s):* Virginia W.Cornish, professor of chemistry in systems biology *Title:* Promoter Characterization in GIT Conditions

Abstract: Saccharomyces cerevisiae (baker's yeast) a widely used GRAS (generally regarded as safe) biological factory whose complete genome sequence has been mapped. S. cerevisiae var boulardii maintains these advantages and has also been reported to be able to survive in the human gut and in many other animal models; thus, studying the probiotic capabilities of both species is of great importance.

In this study we have attempted promoter characterization in in vitro GIT (gastro-intestinal) conditions, in strains of S. cerevisiae and S. boulardii, using mCherry, a red fluorescent protein, as a reporter. While many factors may affect the titers of a final product of an enzyme pathway, efficiency of these pathways are often improved by altering the promoter sequences which precede each gene and testing the system's responses to external conditions. We intended to characterize the activity of promoters in YPD (yeast-peptone-dextrose) and GIT media for future use. To do so, we used a plasmid system: transferring circular DNA containing genetic information into the yeast hosts without integration into its chromosome. However, this approach resulted as unreliable in our promoter characterization experiments. Before attempting chromosomal integration of our promoter system, we decided to screen for the ability of yeast lab strains to survive under GIT conditions. None withstanding, all of the lab strains tested were unable to grow in GIT conditions. Our preliminary results provide further insight to how our methods can be improved, such as employing a different GIT media recipe or screening for new lab strains resistant to GIT conditions.

Arjun Srivatsa CC'20: Statistics

arjunsrivatsa11@gmail.com Faculty Mentor(s): Liam Paninski, professor of statistics and neuroscience Title: Encoding and Decoding of Color Images within Retinal Ganglion Cells

Abstract: The neural coding problem is a statistics problem that involves two processes: encoding and decoding. Encoding is the process by which external environmental variables are encoded into neural signals, whereas decoding is the process by which neural spike trains are converted into external inputs (like images, auditory signals, etc.). In this project, we attempted to create accurate statistical models for both encoding and decoding processes within the monkey retina. We collected data from around 35 small bistratified cells within a macaque retina by presenting random RGB stimulus to the retina for around 30 minutes. From this data we created encoding models which were mostly generalized linear models. We used these encoding models to generate neural spiking responses from images. Finally, we plan to use the encoding models to generate a decoding model, that is we will pass images through the encoding model to generate neural spikes for a dataset. We plan to then train a neural network to decode the image presented from the set of neural spikes.

Anna Sung CC'21: Biochemistry

daeun.sung@gmail.com Faculty Mentor(s): Oliver Hobert, professor of biological sciences and biochemistry and molecular biophysics Title: Specification of neuronal identity in the C. elegans pharyngeal nervous system

Abstract: The nervous system is composed of a network of neurons each with different functions and characteristics. We are interested in how these neurons develop and what molecular mechanisms differentiate each type from another, specifically which transcription factors are unique to a neuronal type. Here we use the simple model organism C. elegans to study neuron type specification in vivo as its cell lineage is fully described, it's easy to genetically manipulate and its genome is very compact, so we have a lot of entry points to understand how this nervous system is built. In this study we focus on a group of these neurons called the pharyngeal nervous system in the head of the worm.

Within the pharyngeal nervous system, it has been discovered that a transcription factor called Ceh34 acts as a master regulator and potential terminal selector of pharyngeal neuronal fate. Furthermore, by analyzing ceh34 mutants, it has been discovered that the identity of pharyngeal neurons is broadly affected in a mutant background.

Daiki Tagami CC'22: Statistics

dt2631@columbia.edu Faculty Mentor(s): Minoree Kohwi, assistant professor of neuroscience Title: How to make Drosophila neural stem cells produce early born neurons

Abstract: A wide variety of our neural cells are being produced by a relatively small pool of neural stem cells, which determine when and what type of cells to produce. However, as the neural stem cells divide

to produce a variety of neural cells, they lose the ability to produce the earlier-born cells. It is therefore important for us to completely understand how neural stem cells can produce cells from different stages to harness stem cells for brain tissue repair.

We used Drosophila in our research, since it is a model organism suited to understand the nature of neural stem cells. Individual neural stem cells, or neuroblasts, can be individually identified, and they have different cell lineages to produce a wide variety of neurons and glia. Neuroblasts sequentially express the transcription factors Hunchback (Hb) > Kruppel > Pdm1/2 > Castor > Grainyhead, and generate specific neural cells during each window of gene expression.

We have examined the roles of several proteins, including nuclear receptor and polycomb complex, toward regulating neuroblasts' ability to produce early born neurons (Hb+ neurons). Under the mutant background of these proteins, Drosophila neuroblasts were capable of producing more Hb+ neurons than anticipated. We therefore concluded that these proteins play a vital role in regulating neural stem cells' ability to produce early-born neurons.

Maya Talukdar CC'20: Computer Science | Biology

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Faculty Mentor(s): Jesse Gillis, associate professor of quantitative biology, Cold Spring Harbor Laboratory *Title:* Shaping Our Understanding of Transcriptional Network Re-wiring via V-Shaped Relationships

Abstract: Transcriptional analyses of sequencing data typically analyze genes independently (i.e. via differential expression) in order to better understand the genetic underpinnings of various physiological and disease states; however, such analyses can be extended with the use of differential co-expression studies, which center on gene-gene relationships. Specifically, differential co-expression analyses can be used to both detect the sets of genes whose expression patterns change across various cell states and to infer functional relationships between genes based on similar expression profiles (guilt by association). Furthermore, of particular interest in such analyses are V-shaped co-expression relationships, which occur between a pair of genes that are correlated in certain cellular conditions and anti-correlated in others, providing evidence for transcriptional network re-wiring. Consequently, my summer project centered on the analysis of V-shaped relationships in primary motor area single-cell RNA-sequencing datasets in the hopes of addressing the following questions: 1) Between which genes can V-shaped relationships be found, and what do these genes have in common?, 2) What physiological changes and/or technical artifacts cause a change in co-expression? and 3) How can we find V-shaped relationships in sequencing datasets in an efficient and biologically valid manner that reflects information about molecular pathways and disease?

Teresa Tseng BC'20: Computer Science

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Faculty Mentor(s): Henning G. Schulzrinne, professor of mathematical methods and computer science and professor of electrical engineering

Title: Alexa, How Secure Are You? Reverse Engineering and Protocol Analysis of the Amazon Echo

Abstract: The use of cloud infrastructure in the Internet-of-Things (IoT) raises significant privacy and security questions regarding the security of user data. How secure are the network communication protocols and cloud infrastructure? Who has access to the data? Smart voice assistants, a subset of IoT devices, are becoming increasingly popular in the American household, and pose potential privacy concerns due to their always-on microphones. We focused on the Amazon Echo (first generation) in this project due to its widespread deployment— around 11 percent of the American population owns this device. We aimed to gain an understanding of the mechanisms and protocols by which the Amazon Echo communicates with local devices as well as Amazon cloud services. We rooted the Amazon Echo and ran a man-in-the-middle (MITM) proxy by diverting Echo traffic using IPtables and policy routing in order to capture Echo traffic. After analyzing the Echo traffic (both inbound and outgoing packets) using Wireshark, we determined that the Echo does not use certificate pinning during the cloud connection, meaning that it could potentially be vulnerable against nation-state actors if physical access to the device is granted. All Echo communications are encrypted, and the device only sends voice data to the cloud upon activation by the user-selected wake word. We examined three main functionalities of the Amazon Echo: voice assistant, IoT device control and intercom. For the voice assistant and device control functionalities, the Echo uses the SPDY protocol. For the intercom functionality, the Echo uses open protocols including SIP, RTP, STUN, and ICE. We were able to successfully decrypt all TLS/SSL traffic generated by the Amazon Echo. These findings will enable us to further analyze the authentication mechanisms used by the Echo in the future.

Lizka Vaintrob CC'21: Mathematics

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Faculty Mentor(s): Jérôme Germoni, lecturer in the discipline of mathematics, Université Claude Bernard Lyon 1

Title: Visualizing Kleinian Groups

Abstract: When M.C. Escher created his famous lizard tessellation, he demonstrated how simple transformations acting on a single lizard can create a remarkably symmetric and satisfying image. In fact, Escher's motions (90-degree rotation and a translation) generate a mathematical object called a transformation group. When certain groups act on things like points and disks, their trajectories form intricate pictures. The goal of this project was to study how properties of Kleinian groups are reflected in the delicate images of their limit sets (the regions where trajectories accumulate). Where Escher's print Lizards is produced by motions of the standard Euclidean plane, Kleinian groups include unorthodox transformations that can send a straight line to a circle. The study of Kleinian groups, started at the end of the 19th century by Poincaré and Klein, remains an active area of mathematics research lying at the crossroads of several distinct subfields. The project looked at ways to modify limit sets of these groups by tweaking parameters of their generators. It used techniques from different areas of mathematics: in particular, complex geometry, group theory and number theory. Tools from theoretical computer science such as tree-searching algorithms and computer graphics were used for producing visualizations.

Michelle Vancura CC'19: Biochemistry

mv2433@columbia.edu *Faculty Mentor(s):* Laura Kaufman, professor of chemistry *Title:* Gelatin Hydrogels as a Model to Study Breast Cancer Cell Mechanosensitivity Abstract: Breast cancer is the most common cancer in women worldwide, with fatalities primarily resulting from metastasis to other vital organs. To become metastatic, cells must invade the extracellular matrix, a process that is coupled with cell mechanosensitivity and mechanoresponsivity to the extracellular environment. As the extracellular matrix of breast tissue is primarily composed of collagen-I, cellular response to the mechanical properties of the extracellular environment is often studied in vitro using collagen-I matrices. However, the mechanical stiffness of collagen-I hydrogels is typically ≈ 10 Pa, which is below that of both healthy and cancerous breast tissue. Modified gelatin hydrogels, such as photo cross-linked gelatin-methacrylate (gel-MA), are alternatives to collagen-I matrices that can be prepared over a much wider range of stiffness, from 10 Pa to 100 kPa. Here, we use gel-MA as extracellular matrix models to study the relative mechanosensitivity of two breast cancer cell lines (MDA-MB-231 and MDA-MB-468) that utilize different migratory modes and are hypothesized to have different degrees of mechanosensitivity.

John Wang CC'21: Computer Science | Neuroscience and Behavior

zw2356@columbia.edu *Faculty Mentor(s):* Rafael Yuste, professor of biological sciences *Title:* Patterned Exploratory Behaviors of Hydra vulgaris in the Absence of External Stimuli

Abstract: Animals' exploratory behaviors are critical to maximizing their chances of survival. Specifically, extrinsic exploration in which the organism seeks information from its surrounding environment in search of food or predators is present across the Animalia kingdom. Exploratory behaviors require complex coordination between motor and decision-making systems; while this complex circuitry is actively studied in mammals, such coordination is carried out by rudimentary organisms via simple nerve nets with far fewer neurons. Hydra vulgaris, a freshwater polyp, is known for its complex behavioral repertoire while having a simple nervous system; however, its extrinsic exploratory behaviors remain uncharacterized. Therefore we examined the circular exploratory behavior of Hydra vulgaris in a uniform environment by tracking its body swaying. The results of this study provide evidence on Hydra executing exploration in an organized manner with robust patterns being displayed across all individuals (n=10). In a 4,000-second recording, Hydras' head positions are randomly distributed, however their angular velocities are relatively similar (p>0.05). Binning the circular area under Hydra's exploration into 12 regions shows that unique Hydras take similar amounts of time to revisit a region (p>0.05). Without clear evidences on Hydra's parenting behaviors, these robust exploration patterns could suggest hardcoded decision-making circuits embedded in its nerve net. Future studies may examine the efficacy of Hydra's exploration strategy by introducing favorable situations near Hydra to incentivize somersaulting or climbing, while employ neuroimaging techniques to inspect the circuitry that's responsible for coordinating the observed exploratory patterns.

Junho Won CC'19: Mathematics

jw3145@columbia.edu *Faculty Mentor(s):* Robert Friedman, professor of mathematics *Title:* Non-Kahler deformations of varieties and limiting mixed Hodge structures

Abstract: A result of Friedman considers Clemens manifolds, which are small smoothings of a certain family of compact complex threefolds X_0 obtained by contracting curves on a smooth threefold. These varieties have ordinary double points and a trivial dualizing sheaf. It turns out, surprisingly, that the smoothings are non-K\"{a}hler and yet still satisfy the ddbar lemma (equivalent to existence of strong Hodge decomposition), at least away from a proper real analytic sub-variety in the deformation space of X_0. Among the main technical tools are (limiting) mixed Hodge structures and deformation theory, in particular a precise unobstructedness theorem for Calabi-Yau threefolds with ordinary double points due independently to Tian, Kawamata, and Ran (and in the special case used in this paper, to Friedman). My research extends this study in a couple directions. We prove that the blowup of a compact ddbar manifold along a ddbar submanifold again satisfy the ddbar lemma. We also investigate compact complex manifolds where the weaker property of degeneration of Hodge-de Rham spectral sequence at E1 holds, but it is unclear whether the ddbar lemma holds. I also indicate other directions of study I am pursuing.

Emily Zhang CC'21: Astrophysics

zhang.emily@columbia.edu *Faculty Mentor(s):* Pat Slane, lecture in the discipline of astronomy, Havard University *Title:* Investigating the Composite Supernova Remnant G21.5-0.9

Abstract: Composite supernova remnants like G21.5-0.9 consist of a shell of material being driven into the interstellar medium by the ejecta from a supernova explosion, accompanied by a central pulsar that inflates a nebula of energetic particles and magnetic flux in the remnant's center. For this study, we applied models for the evolution of such systems to help constrain the properties of the progenitor star and the energetics of the explosion for G21.5-0.9, using data from the Chandra X-ray Observatory. We also reviewed these models in the context of observational results from across the electromagnetic spectrum. Our resulting parameters included a younger-than-expected age, new values for physical quantities such as the ejecta mass and magnetic field, and a high infrared photon energy density relative to the CMB (consistent with previous studies on G21.5-0.9). We were also able to recreate the observed flattened shell morphology at the top of the supernova remnant by modeling density jumps.