

TAPPING INTO LOV DYNAMICS: TIME RESOLVED TRYPTOPHAN FLUORESCENCE OF LIGHT ACTIVATED EL222

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Department: Biophysics

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - Summer Research Experience - UC LEADS

Light-oxygen-voltage (LOV) domains are signaling modules found in photosensory proteins across Eukarya, Archea, and Bacteria. These blue light sensing domains have been characterized in higher plants by their functions of phototropism, stomatal opening, circadian rhythm, and gene expression. The engineered LOV domain EL222 presents itself as a possible genetic tool for controlled gene transcription with rapid activation (<10s) and deactivation (<50s) protein kinetics, making it a suitable for optogenetic control. Upon photoillumination (~450nm) EL222 has been observed to form a cysteine-flavin covalent adduct, a mechanical response within the protein leading to a dissociation of LOV domain's β -sheet surface interacting with the J α helix of the helix-turn-helix (HTH) domain. Using tryptophan as an endogenous fluorescent marker and Foster Resonance Energy Transfer (FRET) we demonstrate that EL222's unfolding may involve a two stage mechanism, an immediate stage (~1 sec.) and much slower one (~2 secs.) toward the end of its unfolding. We provide a addition to the understanding of EL222's photocycle, thus possibly expanding the utility of LOV domains as powerful light-gated gene encryption tools.

ENGINEERING AUTOCRINE/PARACRINE EXTRACELLULAR SIGNALING CIRCUITS TO RESHAPE COLLECTIVE CELL RESPONSES

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Summer Program: UCSF/UCB iGEM

We seek to understand how a group of cells can integrate their individual noisy responses to a stimulus into a robust community decision. In some cases, the decision reaches consensus, and all cells respond the same, a phenomenon seen in quorum sensing by some species of bacteria where gene expression is coordinated based on signals sensed at particular cell densities. Alternatively, decisions can favor the success of one individual in the group, such as in the human immune system where several T cells respond at varying levels to antigen stimulation, but only those with the strongest signals are "chosen" to proliferate and undergo clonal expansion. To study this, we are investigating cellular communication and signal processing using yeast as a model system. Taking cells that have variable/noisy response to a stimulus, we are engineering autocrine/paracrine extracellular signaling circuits to reshape collective cellular responses. One set of engineered cells will coordinate their behavior, achieving consensus or a narrower response distribution, using alpha factor as a messenger molecule. Another set of engineered cells will form divergent communities, where communication through alpha factor works to segregate cells into two or more distinct populations. "Post-cellular" processing is not well understood, and as a result of our

iGEM research program, we hope to provide novel insights about signal processing through this method of cell-to-cell communication.

HOW DOES ACCUMULATION OF PHOSPHATIDYLINOSITO 4 - PHOSPHATE (PI(4)P) IN THE YEAST SACCHAROMYCES CEREVISIAE AFFECT CELL SIZE?

Alejandro Anaya, María Alcaide, Doug Kellogg

Department: MCD Biology

Home Institution: Cabrillo College

Summer Program: ACCESS

The phosphoinositides (PIPs) are membrane bound lipids that function as structural components of membranes as well as regulators of many cellular processes in eukaryotes. In *Saccharomyces cerevisiae* there are several proteins that play a role in the regulation of the levels of the different phosphoinositides through phosphorylation and dephosphorylation. The *Sac1* gene encodes for a phosphatase that is responsible for the dephosphorylation of the PI(4)P lipid to form PI, and the *mss4* gene encodes for a kinase that phosphorylate PI(4)P to form PI(4,5)P₂. It has been previously shown that PIPs affect cell size. The main goal of this project is to analyze how the lack of function of *sac1* and/or *mss4* affects cell size and if this is related to the accumulation of the PI(4)P lipid. A *sac1* deletion in *S. cerevisiae* by PCR mutagenesis will be created. Four different strains of yeast will be analyzed: wild type, *mss4-ts* (temperature sensitive), *sac1* deletion, and *sac1* deletion combined with *mss4-ts*. It is expected that results will show that the accumulation of PI(4)P by either deletion of *sac1*, mutation of *mss4*, or both is making the cell smaller.

FUNCTIONAL ANALYSIS OF INDUCED LOCUS-SPECIFIC MUTATIONS OF LIN9 PROTEIN IN MUVB COMPLEX

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Summer Program: ACCESS

The LIN9 protein is one of the components of the multi-vulval class B (MuvB) complex which is responsible for repression of most, if not all, cell cycle gene expression during quiescence. Despite fruitful biochemical analyses of the MuvB complex, the LIN9 protein remains largely uncharacterized. One aspect of LIN9 that has been annotated is its central tudor domain, which is a plausible starting point to characterize LIN9. Tudor domains are generally responsible for protein-protein interactions, leading to the hypothesis that the LIN9 tudor domain mediates protein interactions within the MuvB complex and is necessary for complex formation. LIN9's tudor domain's direct involvement in protein interactions in MuvB complex can be checked through observing the overall ability of the mutant LIN9 proteins to bind with the four other main proteins (LIN37, LIN52, LIN54, and RBBP48) of the MuvB complex through immunoprecipitation assays. This can be achieved by inducing six locus-specific mutations (L230A, L237A, L272A, F238A, F256A, and R229E/R231E) within the tudor domain of LIN9 protein, via Polymerase Chain Reaction (PCR) with specifically-designed primers, cloning these

mutant constructs into mammalian cell vector, and transfecting these vectors into T98G mammalian cells. Further understanding of the roles played by LIN9's tudor domain and these specific LIN9 mutants in their interaction with the rest of the MuvB complex and how they affect MuvB complex's ability to repress cell cycle gene expression can help advance both cancer research and development of tumor suppression treatments.

ANALYSIS OF DIFFERENTIALLY EXPRESSED GENES FUNDAMENTAL IN THE SUSPENDED ANIMATION OF NON-HIBERNATING MICE

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Home Institution: UC Santa Cruz

Summer Program: NASA Advanced Studies Laboratory

Metabolic control presents an innovative approach to reduce the negative effects of space environmental factors on astronauts and to preserve their lives in the case of catastrophic events during a long-duration space mission. Induction of metabolic suppression in non-hibernating animals, during which mammals dramatically lower their metabolic rate and body temperature, remains a challenging problem. While suppression of metabolic rate in hibernating animals occurs in a regulated manner, this may be fatal in other (non-hibernating) mammalian species. Our objective is to understand detailed molecular mechanisms underlying metabolic suppression in non-hibernating animals (mice) and to identify genes and gene products that are uniquely expressed during hypometabolic states. Hibernating and non-hibernating animals have the same genes and therefore the phenotype (hibernation) results from the differential expression of the same existing genes, rather than the introduction of new genes. We will perform a comparative study that integrates differential gene expression during maintenance and recovery phases from intentionally induced hypometabolic states in non-hibernating mice. We will use both specific and general approaches to examine gene expression during metabolic suppression as well as to identify specific pathways involved in the process.

DETERMINING THE ROLE OF CASEIN KINASE 2 α IN MEDULLOBLASTOMAS

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Home Institution: UC Santa Cruz

Medulloblastomas are malignant pediatric brain tumors that comprise the majority of brain tumors in children. They have a relatively poor prognosis and no cure. Casein kinase 2 is an oncogenic kinase that consists of two catalytic subunits (CK2 α) and two regulatory subunits (CK2 β). CK2 α was recently shown to be involved in a variety of tumors, including adult brain carcinomas. Currently, there is no direct evidence linking CK2 α to medulloblastoma; however, preliminary findings suggest that medulloblastoma patients with high CK2 α expression have a worse prognosis than patients with low CK2 α expression, and that there are two naturally occurring mutations in patient tumors. To determine if CK2 α is involved in medulloblastoma tumorigenesis, we will study the tumorigenic effects of the wild-type and two discovered mutant forms of CK2 α in multiple immortalized medulloblastoma cell lines. We want to determine if there is a connection of CK2 α with medulloblastomas, and then, test how the two naturally occurring

mutations affect the tumorigenicity of medulloblastomas. After constructing the viral plasmid containing the wild-type and each mutant, the plasmids will be transduced into the medulloblastoma cell lines. Next, growth assays will be conducted to compare overexpressing the three different CK2 α proteins in the D283 cell line in comparison to the control protein, Y-Pet. We hypothesize that the cell lines expressing CK2 α and the two mutated forms will express increased tumorigenic effects in growth assays. This is first study exploring CK2 α in medulloblastomas, and results may pave the way for an additional therapeutic option to the current treatments for medulloblastomas.

IDENTIFICATION OF RESIDUES CRITICAL FOR THE FUNCTION OF TRANSCRIPTIONAL REGULATORS OSCR AND COSR

Patrick Bailey, Ana Gallego, Fitnat Yildiz

Department: METX

Home Institution: UCSC

Summer Program: STEM Diversity - Julie Packard Summer Scholar

Identification of residues critical for the function of transcriptional regulators OscR and CosR P. Bailey, A. Gallego, F.H. Yildiz. University of California Santa Cruz Seasonal outbreaks of the diarrheal disease cholera caused by the bacterium *Vibrio cholerae* continue to be a public problem in many developing countries. *V. cholerae*'s infectivity and transmission are linked to the physical and chemical fluctuations of its aquatic habitat. The transcriptional regulators OscR (Osmolarity controlled regulator) and CosR (Compatible solute regulator) have been shown to be involved in the bacteria's response to salinity and osmolarity changes in the environment by regulating motility and biofilm formation. We hypothesize that there are conserved regions responsible for activity in both of these proteins and that mutation of such residues will alter activity of these proteins. Using sequence alignment tools, we have found areas of complete and partial conservation among many bacterial species. We will randomly and selectively mutate OscR and CosR genes and transform them into their respective knockout strains of *V. cholerae*. We will then analyze biofilm and motility phenotypes to identify mutations that alter function of these proteins. Our studies will provide critical structure/function information that will contribute to future projects involving NMR and crystallography, as well as current projects involving understanding mechanisms of action of OscR and CosR.

SYNTHESIS OF HEXA-PEPTIDE ANALOGUES TO OPTIMIZE CELL DISRUPTION

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Home Institution: Hartnell College

Summer Program: ACCESS – Hartnell Title V CUSP Award

Cyclic peptides naturally occur in plants, fungi, and animals, and have the potential to treat diseases. The purpose of this project is to optimize the bioactivity of a cyclic hexa-peptide that is known to disrupt cell division in certain cells. A set of side chain analogues will be synthesized using solid phase peptide synthesis. The synthetic products will be analyzed by mass spectrometry and their biological activity will be assessed in HeLa cells. Based on these results, a strategy will be developed to improve cyclic peptides as drug candidates by changing non-essential side chain amino acids

and observing the effects on the disruption of the cell cycle. The outcomes will help future efforts towards improving this drug scaffold.

ESCAPE: GENERATING ENERGY FROM ANIMAL MOVEMENTS

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Summer Program: SURF-IT

Current conventional animal tracking collars have short battery lives that require recapturing and retagging animals frequently, which not only incurs several additional costs to researchers but also threatens to alter animal behaviors from capture-related stress. The Energy Scavenging Collar for Animal Physiology and Ecology (ESCAPE) aims to decrease the frequency of recapture by using alternators to generate energy from animal movements as a supplement to the collar's battery. At its best case, the energy generated may extend the collar's battery life for up to a year-and-a-half of additional operation time. As part of the project, we designed a testing rig set to mimic a wolf's canonical walk data to run preliminary tests on two different alternators, linear and rotary. Voltage increases over time were then measured for both alternators. With this information, we were able to measure their performance to determine which alternator we would like to continue to test further.

ETHNIC-RACIAL IDENTITY, SELF-ESTEEM, AND PERCEIVED DISCRIMINATION AMONG INDIGENOUS MEXICAN YOUNG ADULTS

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The formation of ethnic-racial identity is an important developmental task for ethnic-racial minorities and immigrant adolescents and young adults. Research has revealed that experiences of discrimination negatively impact youths' self-esteem and often prompt youth to explore their ethnic identity. While previous research has focused on the negative impact of between-group discrimination, there is little research examining the impact of within-group discrimination. The recent wave of immigration of Indigenous Mexican youth has highlighted the prevalence of within-group discrimination Indigenous Mexican youth experience from their non-Indigenous Mexican peers. This study will analyze the discriminatory experiences of Indigenous Mexican young adults in relation to their ethnic-racial identity and self-esteem. The following research questions will be addressed: (1) Is there a negative relationship between perceived within-group discrimination and self-esteem? If so, (2) does a strong ethnic-racial identity buffer the negative effects associated with perceived within-group discrimination? 60 online surveys will be collected from Indigenous Mexican young adults between the ages of 18 to 25 years old. Participants will complete Umana-Taylor's 17-item Ethnic Identity Scale, Rosenberg's 10-item Self-Esteem Scale, and a 14-item perceived discrimination scale. It is expected that perceived within-group discrimination will be negatively correlated with self-esteem. However, it is predicted that a strong ethnic-racial identity will buffer the negative effects of discrimination on self-esteem. The findings of this study will contribute to the understanding of the psychological experiences of within-group

discrimination, and the impact of such experiences on an individual's ethnic-racial identity and well-being.

PURIFYING MCHERRY PROTEIN USING AFFINITY CHROMATOGRAPHY

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Home Institution: UC Santa Cruz

Summer Program: STEM Diversity Summer Research Institute: 1. Julie Packard Summer Scholar 2. Maximizing Access to Research Careers

Determining a protein's function is critical to understanding cellular biology. In order to study a particular protein, we must first isolate it from a biological source. For our study we used affinity chromatography to purify mCherry, a pink fluorescent protein present in corals, which is usually used to visually tag other molecules. To obtain the protein, we transformed *Escherichia coli* with a plasmid containing the DNA sequence coding for mCherry and a six histidine-tag that aided the purification process. We grew *E. coli* overnight, allowing the bacteria to synthesize a large amount of the protein, and then broke the *E. coli* cell wall to free the protein. After constructing a column of beads that bound to the six-histidine tag, we used three different buffers: one bound mCherry to the beads, the other washed away unbound proteins, and the final one eluted mCherry. Taking the final elutant, we performed assays to confirm we had obtained mCherry. To do this, we ran the protein through an SDS PAGE and stained it to confirm its presence, expecting to see a band corresponding to the molecular weight of mCherry. We also ran a western blot and used an antibody that detected the six histidine-tag on the protein. Overall, our results were not what we had expected due to an error in buffer preparation. However, other groups that conducted the same experiment demonstrated that the protein could be purified when the buffers were made correctly.

X-RAY ANALYSIS OF ACTIVE GALACTIC NUCLEI IN CLUSTERS FROM THE DARK ENERGY SURVEY

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Summer Program: STEM Diversity - Julie Packard Summer Scholar

We use Chandra X-ray images combined with optical information from the red mapper catalogue on clusters of galaxies detected by the Dark Energy Survey to analyze the evolution of Active Galactic Nuclei (AGN) and their host galaxies in large scale structure. Recent research has shown that the presence of AGN in clusters is a function of redshift and cluster richness. Our purpose is to investigate these correlations and what this implies for the evolution of AGN in clusters. We accumulated a sample of 30 AGN in 17 clusters at $0.2 < z < 1$ using an IDL matching program that matches the optical positions of galaxies in clusters detected in early data from the Dark Energy Survey (DES) with the X-ray positions of detected point sources in Chandra X-ray observations. We identified each confirmed match with the imaging software Ds9 and calculated the X-Ray count rate, flux, and luminosity of the point sources. We compared the average number of AGN per cluster to the redshift and richness with appropriately sized bins. We find that there appears to be a positive correlation between average AGN per cluster and

redshift/richness, though the trend with richness appears weaker than claimed in the literature. A larger sample of cluster AGN is needed to be able to strengthen this claim and improve the associated error for which we will use the full DES survey as it becomes available.

ANALYZING MITOCHONDRIAL MOTILITY IN DROSOPHILA MOTOR NEURONS USING EOS2 PROTEIN

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Home Institution: University of California Santa Cruz

Summer Program: STEM Diversity - Julie Packard Summer Scholar

The vast size and asymmetry of neurons has raised questions about how their energy requirements are met by the ATP-producing mitochondria. The majority of mitochondria proteins are encoded by the genomic DNA, synthesized on cytoplasmic ribosomes and later imported into mitochondria. The classical mitochondria biogenesis hypothesis proposes that new mitochondria are made in the neuron cell body and must be transported great distances to reach energy requiring destinations in the axon. We will use a mitochondria-targeted photoconvertible fluorescent protein Eos2 that can be permanently converted with a 405nm laser from green to red which will help us uniquely mark and trace small groups of mitochondria in axons over prolonged time periods to test the classical hypothesis. This fluorescent protein will be expressed in motor neurons using a UAS-Gal4 system and will be imaged in real time, using live *Drosophila*, to give us a better understanding of the behavior of mitochondria. Based on the classical hypothesis we predict that the converted mitochondria will move anterograde the closer they are to the cell body and retrograde/stationary further away. After a period of being stationary we expect the mitochondria to move anterograde so that they can return to cell body where the recycling and degradation occurs.

INVESTIGATING TISSUE SPECIFIC ALTERNATIVE SPLICING IN C.ELEGANS

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Summer Program: Visiting McNair Scholar

Introns are regions of genetic material that are removed by the spliceosome, a macromolecular complex consisting of hundreds of proteins and 5 RNAs. The 5' splice site and 3' splice site define the boundaries of an intron. Alternative splicing uses multiple 5' and 3' splice sites yielding a variety of proteins from the same gene. It may contribute to the development of specific tissues, and errors may lead to tissue specific diseases as well as developmental defects. In this study, we sought to identify genes that are responsible for tissue specific alternative splicing in *C. elegans*. Hundreds of genes have been identified in which tissue specific alternative 3' splice sites exist. In germline tissue, the 3' splice site closer to the 5' splice site is more often used, while in somatic tissue the 3' splice site further from the 5' splice site is preferred. These alternative 3' splice sites are generally a multiple of 3 nucleotides apart and no more than 18 nucleotides from one another. We hypothesized that splicing factor(s) may be contributing to this tissue specificity in alternative 3' splice sites. We constructed

plasmids containing the N-terminal portion of the *atx-2* gene, including alternative 3' splice sites that are 8nt apart and out-of-frame. We fused the somatic and germline isoforms to GFP and RFP, respectively, and expressed them in *C. elegans*. This expression will visually verify the alternative splicing difference in the tissue types and allow us to perform an RNAi screen to identify candidate splicing or RNA-binding factors that may contribute to tissue-specific splicing patterns.

PURIFICATION OF REVERSE TRANSCRIPTASE

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Summer Program: STEM Diversity Summer Research Experience – Initiative for Maximizing Student Development

The goal of our project is to purify the enzyme reverse transcriptase to use in RNA structure mapping of the spliceosome. Reverse transcriptase is an enzyme that uses an RNA template to create the complementary DNA strand. The spliceosome is an important molecule for eukaryotes because it is involved in the splicing of introns from the primary transcript. All genes in a eukaryotic cell require the removal of introns to complete the synthesis of proteins. The spliceosome is composed of many proteins and snRNAs, or small nuclear RNAs, and the arrangement of these components are unknown. The Jurica lab wants to know how splicing machinery works, focusing on the structure to determine function. We have reverse transcriptase cloned to express in *E. coli*, but we are using affinity chromatography to purify the recombinant version of the enzyme. Reverse transcriptase can be used with chemical probing to assay RNA structure, which will lead to determining how the various components of the spliceosome are integral to its functions.

THE CHALLENGES ANTIBIOTIC RESISTANT BACTERIA POSE: OBSERVED IN E. COLI WITH AMPICILLIN AND KANAMYCIN

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Summer Program: STEM Diversity - Summer Research Institute

1. UCSC MARC 2. PSci summer support 3. UC LEADS and Hartnell

Antibiotics have long been liberally used to treat infectious diseases. Overuse has allowed bacteria to develop resistance to most antibiotics, faster than the development of new therapies. Our objective was to analyze the growth of two antibiotic resistant *E. coli* strains, VA228 and VA264, in the presence of two distinct antibiotics. These strains carried a plasmid containing an ampicillin resistant gene, or a kanamycin resistant gene. Generation time was calculated by monitoring culture density using a spectrophotometer, or by counting colony forming units; they were found to be 45.68 and 47.13 minutes, and 42.67 and 50.8 minutes, respectively. This is longer than the maximal doubling time of *E. coli*, which suggested that growth of bacteria in the presence of an antibiotic, even when resistance is present, has a fitness cost. The degree of antibiotic susceptibility of the VA228 and VA264 strains was assessed using the Kirby-Bauer test. The VA228 strain yielded no zone of clearance surrounding a 10

µg disc of ampicillin due to its ampicillin resistance gene, and therefore should be considered fully resistant to the antibiotic. The VA264 strain produced zones of clearance averaging 21.56 mm in diameter, which indicated its susceptibility to ampicillin, as expected. Lastly, an eight-day course of antibiotics was modeled, inside a host organism, to demonstrate the impact of missing one or more doses of a prescribed antibiotic to a mixed population of bacteria that are susceptible, resistant, or have intermediate resistance. Results revealed that missing two or more doses failed to kill all antibiotic resistant bacteria.

CONVERSATIONAL DIALOGUE GENERATION FROM NARRATIVE

Kevin Doyle, Zhichao Hu, Marilyn Walker

Department: Computer Science

Home Institution: University of California Santa Cruz

Conversational storytelling has a long history in human culture and is an effective method for communicating ideas. This work describes an approach to automatically restructure a narrative into conversational dialogue. Here, conversational dialogue includes entrainment, acknowledgement, and co-telling of the story between interlocutors. Current conversions of narrative into conversational dialogue are handcrafted. A simple system has been constructed which performs a rough narrative-to-dialogue conversion automatically, using only the narrative's text. It serves as the prototype for a future system which takes a narrative's underlying syntactic structure as input. In this future system, conversational elements will be added to the syntactic structure, and then a natural language generation system will be used to realize the dialogue. The probability of occurrence for each conversational element will be varied throughout multiple generation cycles, in order to utilize a statistical selection method known as "overgenerate and rank". To get evaluative data on the output, human judges will rank each generated dialogue, and a handmade dialogue, for naturalness. Automatic generation of conversational dialogue from a narrative may facilitate education using virtual agents. A lot of available information is monologic. Presenting the same information as a conversation between two virtual agents may be more engaging, and improve information retention in students.

ENGINEERING HALOFERAX VOLANII FOR MICROBIAL SYNTHESIS OF BUTANOL

Wade Dugdall, Jazel Hernandez and David Bernick

Department: Biomolecular Engineering

Home Institution: UCSC

Summer Program: iGem

Partner Presentation. For abstract see Jazel Hernandez

ARGUMENT ANALYSIS AND PERSUASION IN ONLINE DISCUSSION

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Department: Computer Science

Home Institution: University of California Santa Cruz

Summer Program: Natural Language and Dialogue Systems (NLDS)

The wealth of online debate available today presents a valuable opportunity to learn about the persuasive techniques used in argumentation. In contrast to formal models of debate, online debate is often informal and participants offer few explicit indicators of any change in opinion. Because of this, some of our work currently focuses on analyzing the reliability of certain explicit discourse connectives as markers of attempts at persuasion. In particular, we are using a list of Penn Treebank discourse connectives that show promise in indicating argument to generate sets of data on which to analyze the development of two opposing opinions. Currently, argumentation between users is difficult to detect, and the time required to produce hand annotated sets of data makes training and evaluating models difficult. Such a system of automated argument extraction provides the necessary data to further our understanding of complex argumentation including what causes us to change our opinions, how readily we concede to an opposing view, and how our informal rhetorical exchanges differ from our traditional arguments.

ARE SOLUBLE PROTEASES IN THE UNIDENTIFIED FUNGAL ORGANELLE (UFO) IN *N. CRASSA*?

Carlos Alberto Espinosa, Cecilia Im, Marija Drašković, Barry Bowman

Department: MCD Biology

Home Institution: University of California Santa Cruz

Summer Program: STEM Diversity - Summer Research Experience – Initiative for Maximizing Student Development

We have recently observed what appears to be a new organelle in the fungus *N. crassa*, which we named Unidentified Fungal Organelle (UFO). The UFO was found to contain the vacuolar H⁺ ATPase pump, a protein that is present in the vacuolar membranes. We are trying to determine if the UFO contains other proteins that are also present in the vacuole; more specifically, we wanted to know whether the UFO contained soluble proteases in its interior. Looking for the presence of proteases within this organelle might give us an idea about the function that the UFO might have. Specifically, we are testing for the presence of 3 proteases: pep-4, prb-1, and lap-4. While pep-4 has been previously identified in *N. crassa*, homology search between *Saccharomyces cerevisiae* and *N. crassa* led us to two other proteases, lap-4 and prb-1. The protease genes are being inserted into pMF272, which contains a Green Fluorescent Protein gene. By transforming *N. crassa* cells with pMF272 + protease genes, we should be able to see whether any of these proteases are located inside the UFO. To do this, we designed the primers flanking the protease genes in *N. crassa*, while at the same time adding a restriction site on them. Then we amplified prb-1 and lap-4 using PCR. Subsequently, the protease genes were inserted into pJET, to make a stock of multiple clones of the gene. Our final step is to use restriction enzymes to cut out the protease genes and insert it in pMF272.

SYNTHESIS OF THE NATURAL PRODUCT CYCLIC DEPSIPEPTIDES ASPERGILICINS AND INVESTIGATION OF THEIR PHARMACOKINETIC PROPERTIES, BIOACTIVITY AND PERMEABILITY ON CELL MEMBRANE

Christian Etienne, Josh Schwochert, Scott Lokey

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Home Institution: University of California, Santa Cruz

Cyclic peptides are an important class of natural products that display a wide range of biological activities and are of interest in drug discovery. Many of these naturally derived compounds exhibit better than expected pharmacokinetic properties, and our goal is to understand why. In the Lokey Research group, we are interested specifically in understanding how cyclic peptides can achieve cell permeability, an important aspect of potential therapeutics. We also apply those studies to certain natural compounds that show similar characteristics and properties. Aspergilicins are natural product cyclic depsipeptides originally isolated from the marine fungus *Aspergillus Carneus*. The goal was to synthesize one analog, Aspergilicin A and use it as a model system to study the pharmacokinetic properties of cyclic peptides. Two different synthetic approaches were tried with the objective to compare the data on our synthetic material, which included HPLC and LCMS analysis as well as NMR results; to the literature. We performed a total synthesis of the natural product and developed new methods for the acyl rearrangement. The final goal of this project is to test our compounds for bioactivity and use them as a test case for the study of cell permeability. Testing for cell permeability will be achieved by running the compounds through parallel artificial membrane permeability assay (PAMPA). In addition, we hope to develop new synthetic methods for the synthesis of cyclic depsipeptides, which may be of use in the future synthesis of other natural products or drug-like compounds.

INFLUENCE OF DIETARY CHOLESTEROL AND COPPER ON LONGEVITY, BEHAVIOR, NEURODEGENERATION, LEARNING, AND MEMORY IN A DROSOPHILA MODEL OF ALZHEIMER'S DISEASE

Rebecca Pearson, Emmanuel Fonseca, Adrienne Maguire, Jeremy Lee

Department: Physically and Biological Sciences; Molecular, Cell, and Developmental Biology.

Home Institution: UCSC

Summer Program: Julie Packard Summer Scholar

*** Partner presentation. For abstract, see Rebecca Pearson ***

ATTACHMENT OF BORONIC ACID ONTO QUARTZ NANOPORES FOR NON-ENZYMATIC SACCHARIDE DETECTION

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Department: Biomolecular Engineering

Home Institution: UC Santa Cruz

Summer Program: STEM Diveristy - Summer Research Experience - MARC

The purpose of this research was to fabricate a “bench-top” method for the covalent attachment of boronic acid, which can be incorporated into miniature electrical sensors for saccharide detection. One device that can measure analyte-to-receptor interaction is a solid-state nanopore. Ion current through the device can be modulated by charge and physical blockage at the pore. The nanopores were fabricated utilizing quartz capillary tubes, which offer many practical properties that include reproducibility, low-cost, miniature size, and sensitivity. First, the nanopore surface is cleaned using a Piranha acid wash. Next, (3-aminopropyl) triethoxysilane (APTES) was utilized to modify the surface of the nanopore to yield an amine-terminated surface. The APTES-modified surface was then further reacted with 4-carboxyphenylboronic acid (4-CPBA), which results in a boronic acid-functionalized surface. After each modification process, linear sweep voltammetry was used to characterize the functionalized nanopore by measuring ionic current through the pore as a function of pH. Using the methods described in this work, a nanopore modified with boronic acid was able to detect 9 mg/dL of glucose at physiological pH. Principally, fabrication of such a device can further benefit bio-medical research regarding saccharide detection, protein-protein interactions, and intracellular sensing applications.

UNDERSTANDING THE STRUCTURE OF RELATIVISTIC JETS USING HYDRODYNAMICAL SIMULATIONS

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Home Institution: The University of Texas at El Paso

Summer Program: Lamat Summer Research Program on High Performance Computing in Astrophysics – Visiting MARC Scholar

Relativistic jets accelerated from compact objects, such as neutron stars or black holes, are thought to produce many of the observational signatures associated with high energy phenomena created from radio galaxies, quasars, microquasars and gamma ray bursts. Here, we present simulations of relativistic jets, calculated using the Mezcal special relativistic hydrodynamical code. We explore the effects of varying the pressure, density, and velocity of these jets, as well as the properties of the environment in which they propagate. The ratio of the density of the jet to the density of the medium has a marked effect on the dynamics and stability of the emanating jets, with lighter jets being more likely to be collimated and to develop prominent instabilities. Results are presented for jets propagating in a constant density medium, common for radio galaxies, and a wind stellar profile, common for microquasars.

MONITORING THE DISRUPTION OF ANAPHASE-PROMOTING COMPLEX LEADING TO APOPTOSIS IN CAENORHABDITIS ELEGANS

Rebecca Gonzalez and Needhi Bhalla

Department: MCD Biology

Home Institution: Hartnell College

Summer Program: ACCESS

In mitosis, the spindle assembly checkpoint (SAC) ensures proper chromosome segregation by preventing the progression of the cell cycle if all chromosomes are not attached to spindles. The SAC prevents the transition to anaphase by blocking the action of the anaphase-promoting complex (APC). In meiosis control of synapsis depends on SAC genes, such as MAD-1, MAD-2, and BUB-3. It has been shown that unsynapsed chromosomes lead to apoptosis and this apoptosis also depends on MAD-1, MAD-2, and BUB-3. The hypothesis is that the APC plays a role in the synapsis checkpoint in meiosis. Metaphase to anaphase in phase 3 (MAT-3) mutations in the APC will be tested to see if they lead to apoptosis in meiotic cells. The nematode *C. elegans* will be observed microscopically and apoptosis scoring will be done at the bend of the germ line. The outcome of this research may help prevent human infertility and birth defects.

PURIFYING MCHERRY PROTEIN USING AFFINITY CHROMATOGRAPHY

Sara Haile, Anissa Banabbas, Melissa Jurica

Department: MCD Biology

Home Institution: University of California Santa Cruz

Summer Program: STEM Diversity - Summer Research Institute –MARC

Partner presentation. For abstract, see Anissa Banabbas

ENGINEERING HALOPHERAX VOLCANII FOR MICROBIAL SYNTHESIS OF BUTANOL

Jazel Hernandez, Saumya Singh, Vinay Poodari, Dominic Schenone, Rolando Perez, Renee Jovic, Lenore Pafford, Max Genetti, Stas Fridland, Wade Dugdale, Kevin Sweeney, Chris Lee, Kaylee Walker, Charles Paine, Hoss Amiri, Logan Mulrone, Jeff Navala, Yat Li, David Bernick

Department: Bioengineering

Home Institution: Hartnell College

Summer Program: STEM Diversity - Hartnell Title V CUSP (Jazel), Maximizing Access to Research Careers (Rolando), Everyone: iGEM

In recent years, the burning of petroleum-based fuels has resulted in an increase in atmospheric greenhouse gas concentrations due to their long carbon cycles. As a result, there has been an increased interest in the development of short-cycle energy dense biofuels. One prominent biofuel is butanol, a four-carbon alcohol that can be metabolized naturally from glucose in many microorganisms and potentially from cellulose, a plant based polymer consisting of β -glucose subunits. Modern methods for extracting cellulose from plant material require ionic solutions that are inhospitable for conventional industrial micro organisms and their enzymes. The archaeon *Haloferax volcanii* is a salt

loving extremophile and well suited for these processing environments. The UCSC International Genetically Engineered Machine (iGEM) team is engineering *Haloferax volcanii* to produce the solar-based liquid biofuel butanol from glucose. Gene deletions in the fatty acid synthesis pathway will provide an increase in four-carbon substrate and drive the synthetic butanol pathway. Within this pathway bioinformatic investigations have identified seven possible paralogous Acyl-CoA dehydrogenase (ACD) genes. Each of the ACD genes are thought to favor activity on certain fatty-acid carbon chain lengths. By interrupting the ACD responsible for the four-carbon to six-carbon product we can accumulate butyryl-CoA, a product that may later be converted to butanol through the overexpression of certain aldehyde dehydrogenases. All synthetic DNA constructs will be shared with the Registry of Standard Biological Parts. The engineering of *Haloferax volcanii* will be achieved by utilizing synthetic biology techniques and butanol production quantified using analytic chemistry tools.

COASTAL SEDIMENT-DERIVED GRAM-NEGATIVE BACTERIA AS A SOURCE OF NEW NATURAL PRODUCTS

Thalia Hernandez, Christine Theodore and Phil Crews

Department: Chemistry and Biochemistry

Home Institution: Transferring to UCSC from Hartnell College

Summer Program: STEM Diversity - Hartnell Title V CUSP

Natural Products (NPs) are the chemical compounds produced by natural sources such as animals, plants and microorganisms. NPs are a good choice for drug discovery since historically, some have a pharmacological or biological activity that can be used in drug discovery or design. The goal of this study was to identify bacteria that produce NPs. Our research group at University of California Santa Cruz collected sediment samples from the Northern California Coastlines such as Monterey Bay area beaches. Gram-negative bacteria (GNB), were isolated from these samples. The bacteria were then grown in liquid cultures, extracted and analyzed by liquid chromatography mass spectrometry (LCMS). Chemically prolific strains identified by the screening procedure were then grown in a large-scale bioreactor designed by the UCSC research group. Compounds from the large-scale culture were isolated through pre-fraction and chromatographic technique. Their structures elucidated through advanced spectroscopic methods, such as nuclear magnetic resonance (NMR), and mass spectrometry. Crude extracts were also evaluated for biological activity such as cancer cell cytotoxicity, through biomap screening at the UCSC screening center.

CLONING OF A SPT5 FRAGMENT USING MOLECULAR CLONING TECHNIQUES

Kendy Hoang, Joanna Perez, Grant Hartzog

Department: MCD Biology

Home Institution: UCSC

Summer Program: STEM Diversity - Summer Research Institute – Initiative for Maximizing Student Development

Spt5 is a universally conserved protein that binds RNA Polymerase II and regulates transcription elongation. In eukaryotes, Spt5 forms a complex with Spt4. In addition to transcription elongation, the Spt4-Spt5 complex has been proposed to regulate co-transcriptional RNA processing. Recently, we have discovered that Spt4-Spt5 binds

RNA. To investigate the role of this RNA-binding activity in Spt4-Spt5 function, we are working to create mutations in SPT5 that abolish RNA binding but preserve its ability to bind Spt4 and RNA polymerase II. Based upon structural modeling, we hypothesize that a triad of amino acids are responsible for RNA binding. To test this hypothesis, we are using site-directed mutagenesis to target these residues. Because SPT5 is a very large gene, our first step is to subclone a small fragment of the SPT5 gene into a plasmid, allowing for efficient mutagenesis. This mutated Spt5 fragment will then be reinserted fragment back into full length Spt5 and expressed in *Saccharomyces cerevisiae* for genetic analysis and in bacteria so that we can purify recombinant proteins and perform biochemical analyses of RNA binding.

SIMULATION OF PROPOSED SERIAL MANIPULATOR FOR INTERNATIONAL SPACE STATION'S MOBILE SERVICING SYSTEM

Nathanel Hooks, Mircea Teodorescu

Department: Computer Engineering

Home Institution: Arcadia University

Summer Program: SURF-IT

A simulated model of a proposed robotic serial manipulator to replace the CanadArm2 is presented. The simulation is crafted using Matlab/SimMechanics, and also is built using the concept of starting with a small, miniscule idea and then adding complexity on that idea until it becomes manifested. Using this approach, one of the simplest models for a serial manipulator, an inverted pendulum, is first presented. Following this, the different stages of the proposed serial manipulator model are presented, each with a few images and equations depicting the manipulator.

CHARACTERIZING INDUCED PLURIPOTENT DERIVED CHONDROCYTES BY COMPARING GENE EXPRESSION WITH PRIMARY CHONDROCYTES

Oarteze Hunter, Jieun Lee, Nidhi Bhutani

Department: Department of Orthopaedic Surgery, Stanford

Home Institution: University of California Santa Cruz

Summer Program: UCSC MARC and Stanford Summer Research

Osteoarthritis is a joint degeneration disorder that affects about 630 million people worldwide. A major cause of this condition is the loss of specialized cartilage cells called chondrocytes. Research in this area is currently investigating ways to regenerate and find new sources of chondrocytes. Implantation of these new chondrocytes into patients could lead to the eradication of this condition. Therapeutic remedies for osteoarthritis remain a challenging area of study, but research into stem cell based therapies show promising results in treating osteoarthritis. However, much about the behavior of induced pluripotent stem cell derived chondrocytes (iChondrocytes) in human models remains unsolved, specifically whether iChondrocytes are genetically and functionally similar to primary human chondrocytes. Here, we examined gene expression levels of iChondrocytes as well as patient-extracted chondrocytes from human patients. The chondrocyte samples used in this study came from 18 month old, 6 year old, 27 year old, and 41 year old individuals. Comparing gene expression of these two types of chondrocytes gives us insight into what genes iChondrocytes should be expressing in

vivo and therefore, how iChondrocytes would mimic characteristics of naturally occurring chondrocytes if surgical iChondrocyte implantation takes place in osteoarthritis patients. This research could potentially improve current therapeutic remedies for osteoarthritis, such as surgical joint replacements, which are expensive and time consuming.

PEROXYNITRITE-GENERATING PLATFORM

Sharon Idiga, Tara DeBoer, Pradip Mascharak

Department: Chemistry and Biochemistry

Home Institution: University of California Santa Cruz

Summer Program: STEM Diversity – Initiative for Maximizing Student Development

Peroxynitrite (PN) is a reactive nitrating and oxidative species that plays a key role in inflammation-mediated disease states, from neurodegenerative disorders to diabetes. PN is formed in the radical terminating reaction between nitric oxide (NO) and superoxide. It has been difficult to observe PN directly within cells due to its transient nature. With a photo-controlled peroxynitrite-generating platform, the Mascharak lab has developed a system that is able to release PN in situ, to better understand the dynamic chemistry of PN. Stable metal nitrosyl, [Mn(PaPy3)(NO)]ClO₄ (PaPy3=N,N-bis-(2-pyridylmethyl)amine-N-ethyl-2-pyridine-2-carboxamide), was used as the source of NO because it rapidly releases NO upon illumination with visible light. To match the rapid release of NO from the nitrosyl, the xanthine oxidase/hypoxanthine (XO/HX) system was employed as the source of superoxide. Both sources were encapsulated in a sol-gel matrix to avoid contamination. A multi-well plate was used to study the chemistry of the precursors as well as PN. Construction of the PN-generating platform was completed by layering both NO and XO sol-gels at the bottom of individual wells. Release of the precursor molecules is triggered with exposure to low powered visible light and the addition of HX. This light-activated platform allows the study of PN-mediated chemistry under varied flux ratios and pH conditions. We plan to utilize the multi-well platform to study the reactions of PN with various biomolecules such as amino acids, peptides, and lipids.

INDOOR LOCALIZATION WITH IBEACONS

Mark Idleman, Roberto Manduchi, Matthew Guthaus

Department: Computer Engineering

Home Institution: Amherst College

Summer Program: SURF-IT

Apple's recently introduced iBeacon technology allows for mobile developers to design applications that communicate with small, inexpensive beacons running on the Bluetooth Low Energy protocol. iBeacons have widespread applications in in-store product advertising and indoor localization, and their low cost and portability allows dense wireless networks to be setup with relative ease. We present an iOS application that tracks the walking paths of users using the iPhone's accelerometer and gyroscope, and correlates this directional data with iBeacon signal strength (RSSI) readings taken along each respective path from multiple beacons placed throughout the testing environment. The relationship between movement paths and iBeacon RSSI readings, which is clearly established in our collected data, is instrumental to the development of more sophisticated indoor localization systems that can locate and track users inside buildings with high accuracy. Through further analysis of our data, a mapping between observed

RSSI readings and a user's location indoors could be extracted for use in such a localization system.

UFO: THE SEARCH FOR AN UNIDENTIFIED FUNGAL ORGANELLE

Cecilia Im, Carlos Espinosa, Marija Draskovic, Barry Bowman

Department: MCD Biology

Home Institution: University of California Santa Cruz

Summer Program: STEM Diversity - Summer Research Experience - UC

LEADs

We are investigating the structure and distribution of organelles in eukaryotic cells, using *Neurospora crassa*, a filamentous fungus, as our model organism. About 50 to 100 μm from the growing tip of *N. crassa*, circular organelles were detected that appear to have enzymes commonly found in the vacuole. However, Oregon Green, a common stain for the vacuole, does not stain this organelle. These organelles have been named as UFOs, or Unidentified Fungal Organelles. These organelles were first observed by looking at the location of a major proton pump on the vacuolar membrane (*vma-1*) tagged with red fluorescent protein (*rfp*). To try to determine the identity of the organelles, *rab* genes, which are used to ensure that vesicles go to the correct place, were used to help specify which known organelles are involved. The *rab-7* protein, which is specific to the vacuole, was found on the UFOs. We are in the process of adding a new green fluorescent tag (*gfp*) to both *rab-7* and *vma-1*. We are investigating whether the level of expression of *rfp* or *gfp* tagged proteins affects the cellular location. In order to visualize the UFOs, *vma-1* and *rab-7* genes tagged with *gfp* will be used to replace the endogenous gene using homologous integration. We are also using a novel technique of tagging a gene on the 5' end while also using the endogenous promoter instead of the derepressible promoter that we currently use. Placing *gfp* or *rfp* between the promoter and the protein-coding region of a gene requires assembly of 5 different DNA fragments. We describe how this is done by combining Fusion PCR and cloning into a plasmid.

MODELING VARIANTS TO THE PYTHAGOREAN THREE-BODY PROBLEM

Mark Johnson, Greg Laughlin

Department: Astronomy & Astrophysics

Home Institution: Crafton Hills College

Summer Program: Lamat Summer Research Program on High Performance Computing in Astrophysics

We explore a sequence of variations to the classical Pythagorean three-body problem, wherein three bodies possessing masses equal in magnitude to their opposing sides located at the vertices of a 3, 4, 5 right-triangle, are acted upon exclusively via a modified version of Newtonian gravity. In the standard version of the problem, which uses a $1/r^x$ gravitational force law, where $x=2$, the solution is known not to be periodic. Utilizing Python-based numerical integration schemes, we solve the governing ordinary differential equations that describe the problem. We systematically vary the gravitational coupling through modification of the power-law index, x . Additionally, we examine the trajectories that immediately precede and follow the regions of deviation, the areas within the simulation where each body approaches its initial position, yet subsequently veers away. Using this information, we discover a range of power-law indices which

dictate the characteristics responsible for causing the specific occurrences of the critical transitions between orbital stability and chaos within each respective simulation. The significance of the Pythagorean three-body problem is not drawn preeminently from within an astronomically relevant framework however, comprehension of the associated variants to the problem, allow its presence to be expressed in a broader and richer context. The Pythagorean three-body problem consequently remains pertinently factual among the most simplistic systems exhibiting this variety of orbital chaos and the intricate complexities of nonlinear dynamics.

SINGLE MOLECULE SENSING WITH VOLTAGE DETECTION

Erik Jung, William Dunbar, Christopher O'Donnell, Noam Harel

Department: Computer Engineering

Home Institution: University of California Santa Cruz

Summer Program: SURF-IT

Too many lives have been lost by catching cancers and diseases far too late. Using solid-state nanopore technology we can help doctors diagnose patients by reading their genetic sequence. By repeatedly exercising these methods on how to approach this project, each and every experiment we do brings our research closer to a more efficient process. By using our solid-state nanopore technology, the costs of these diagnosis will hopefully be fairly cheap and all doctors will need to use is a drop of blood from their patients.

ANCIENT DNA EVIDENCE FOR THE EXTINCTION OF THE LAST NORTH AMERICAN MAMMOTHS

Josh Kapp, Ed Green, Beth Shapiro, Pete Heintzman

Department: Biomolecular Engineering

Home Institution: University of California Santa Cruz

The last mainland North American mammoths survived in Alaska until 10,500 years ago. In contrast, radiocarbon dating of fossils from St. Paul Island in the Bering Sea demonstrates that mammoths disappeared from North America around 6,500 years ago. When determining extinction time with high precision, however, fossils are not the best option because they are difficult to find, date, and generally the last surviving organism of a species is never found. On the other hand, lake sediment can resolve the precision issues as mammoths are expected to have used the lake throughout the history of the species on the island and they would likely leave behind DNA from skin, feces, and hair. For this study, a 13m sediment core was collected from a lake on the island. Two grams of sediment were taken from the core every 4cm and DNA was extracted from a selection of samples at varying depths in the core. We expected to see the presence of mammoth DNA in the deeper and older sections of the core and mammoth DNA to be absent from the younger sections. The presence-absence data was used to precisely determine when mammoths went extinct on St. Paul Island.

SIMULATION OF RED GIANT CLUSTER WINDS

Jose A Lopez, Melinda Soares-Furtado, Enrico Ramirez-Ruiz

Department: Astronomy and Astrophysics

Home Institution: University of California Santa Cruz

Summer Program: STEM Diversity - Summer Research Experience - Hartnell
Title V CUSP

Modern advances in technical sciences require sophisticated computer simulations to make further explorations possible. The simulations should be able to depict the various physical phenomena that are difficult to observe directly, either due to extremely large or small length scales, or across time scales ranging from microseconds and millions of years. Red giant stars present such a scenario, as they are difficult to observe directly and must be studied using simulations. The FLASH hydrodynamical physics simulator was used to evolve the structure of stellar winds from a cluster of red giants over time. FLASH produces a series of HDF5 files containing vast arrays of physical parameters, representing individual snapshots of these events over the desired time interval. For the sake of physical fidelity and to maintain comprehensiveness, the files were rendered and analyzed at different camera angles using Yt, a Python package tailored specially for visualization of astrophysics simulations. I employed Yt to demonstrate manipulations of the HDF5 files and stitched them together to create equally useful and aesthetic animations. The animation created for the star cluster simulation aptly shows how the winds expand over time. The ultimate goal of this project is to create a program which would allow the user to stop the animation at any point in time and manipulate the viewing angle in 3-space in any way desired by means of input more intuitive than keystrokes; doing this on a 3-D screen would be ideal.

UNDERSTANDING THE STREAM-DISK INTERACTION IN MASS-TRANSFERRING BINARY STAR SYSTEMS

Aaron Lopez, Phillip Macias, Enrico Ramirez-Ruiz

Department: Astronomy and Astrophysics

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - Summer Research Experience - Hartnell
Title V CUSP

Observations of a wide range of interacting binary stars show that accretion disks in these systems display pronounced deviations from axisymmetry, for which the most obvious agent is the impact of the gas stream from the mass-donating companion star onto the accreting star's disk due to Roche lobe overflow. The complexity of this stream-disk interaction mandates the use of sophisticated hydrodynamic simulations to fully explore its consequences. Here I use multi-dimensional, high-resolution simulations via the FLASH hydrodynamical physics code to provide quantitative estimates of the effects of the accretion stream's impact on disks in interacting binaries. I employ an expansive and open source Python package specialized for problems in astrophysics, yt 3.0, for visualization and analysis of said simulations. I focus particularly on the various mass ratios characteristic of known types of binaries as they pertain to the ensuing angle of impact, structure of the hotspot region, and other relationships overlooked in previous analyses.

THE EFFECTS OF MODELING CLOUDS IN TRANSIT TRANSMISSION SPECTRA OF EXTRA SOLAR PLANETS

Kyle L. Luther, Mike R. Line, Jonathan J. Fortney

Department: Department of Astronomy and Astrophysics

Home Institution: UC Berkeley

Summer Program: Lamat Summer Research Program on High Performance Computing in Astrophysics

In the past decade, several planets that transit across their parent star have been discovered. Statistical methods, known as atmospheric retrieval, in combination with models of radiative transfer have been used to analyze the observed spectra of these transiting exoplanets. These analyses seek to give information about the chemical composition and temperature structure of these planets which allows for a better understanding of the physical processes that govern the formation and evolution of planets. These analyses have already yielded several claims of molecular detections in these atmospheres. However, many of these claims are not in agreement with one another. Furthermore, the robustness of the radiative transfer models used to detect molecules has been called into question because of the inability of these models to account for the effects of clouds in an atmosphere. In this study, we perform a retrieval on two Hot Jupiters: HD189733b and HD209458b. We use the Markov chain Monte Carlo approach in combination with a forward model that accounts for clouds to retrieve these planets' temperatures and molecular abundances. We then compare the retrieval results to those produced by previous models that do not account for clouds. We find that the updated model yields noticeably different results for the retrieved temperatures and water abundances. As in previous studies, this model does not result in a statistically significant retrieval of any other molecular abundance.

SYNTHESIZING MUTANT ASiP FOR IMPROVED BINDING AFFINITY AND SPECIFICITY WITH MC1R IN ORDER TO INHIBIT MELANIN PRODUCTION

Andrew Martinez, Jillian Miller, Glenn Millhauser

Department: Department of Chemistry & Biochemistry

Home Institution: California State University of Los Angeles

Summer Program: Visiting MARC U*STAR Fellow

Melanocortin receptors serve the purpose regulating various physiological mechanisms, such as the production of melanin, sexual function, and proper metabolic function. Literature connects the ligand known as ASiP (Agouti Signaling Protein) with MC1R (Melanocortin 1 Receptor), a G-protein coupled receptor that is known to control skin pigmentation and coat color in mice. ASiP switches melanin production off when it binds to MC1R, which can aid in melanoma treatment as melanosomes interfere with chemotherapy. Using the known structure of ASiP, a more stable and efficient ASiP will be synthesized so that it can be used as an effective drug for melanoma treatment. Additionally, ligand affinity can then be monitored and manipulated in model organisms in order to improve therapeutic potential of not only melanoma treatment, but various other medical ailments associated with MC1R.

AN EXAFS ANALYSIS OF THE THERMOELECTRIC SKUTTERUDITE SMOS₄SB₁₂ CRYSTAL

Nathan D. Martinez, Trevor Keiber, Frank Bridges

Department: Physics

Home Institution: University of California Santa Cruz

Summer Program: Julie Packard Summer Scholar

Skutterudites are excellent thermoelectric materials with applications in which a temperature difference can be converted to electrical power. The SmOs₄Sb₁₂ skutterudite has unusual properties that are speculated to arise from unusual vibrations of the Sm “Rattler” atom, but the local structure has never been investigated. To do so we used the Extended X-rays Absorption Fine Structure (EXAFS) technique to analyze the local structure about the Sm atom; this technique requires the high intensity flux available at SLAC Synchrotron Radiation facility. The temperature dependence of the Sm-Sb and Sm-Os atom pairs as a function of temperature from 8-190 Kelvin was determined.

PURIFICATION OF SPLICING PROTEINS, INCLUDING MER1, TO IDENTIFY RNA SEQUENCES INVOLVED IN SPLICING

Britney Martinez, Manny Ares

Department: MCD Biology

Home Institution: University of California Santa Cruz

Summer Program: STEM Diversity - Summer Research Experience – Maximizing Access to Research Careers

Splicing is an essential step in gene expression that removes introns from pre-mRNA to make messenger RNA (mRNA). Pre-mRNA can be spliced in different ways to produce different mRNAs, a process known as alternative splicing. Splicing and alternative splicing is performed and controlled by the spliceosome and its protein regulators, many which bind RNA. To understand how the spliceosome works and how it is regulated, we need to know which parts of the snRNAs and pre-mRNA bind to which proteins. To ask this question we will employ ultraviolet light-induced RNA-protein crosslinking. Our main focus is Mer1, a yeast RNA binding protein that controls an alternative splicing event in four different yeast pre-mRNAs expressed during meiosis. To identify which RNAs are bound by Mer1 after UV exposure we added a “biotinylation-TEV site-6HIS tag” to the N-terminus of Mer1 in order to purify the protein and recover RNA that it binds. We are currently testing various steps in this process to ensure that we can purify Mer1. We are also working with yeast strains that express tagged versions of other known splicing proteins, for example Prp9, Hsh155 and Cus2. Ultimately we hope to identify which RNA sequences bind to each of these proteins in the working spliceosome.

PREPARATION OF A tRNA AMBER SUPPRESSOR FOR SITE-DIRECTED FLUOROPHORE INCORPORATION INTO RIBOSOME-BOUND NASCENT PROTEINS

Ramon Martinez, Arellys Rosado, Silvia Cavagnero, Ph.D

Department: Department of Chemistry, University of Wisconsin-Madison

Home Institution: University of California Santa Cruz

Summer Program: Integrated Biological Sciences Summer Research-University of Wisconsin-Madison

Deeper insights in the biophysical analysis of protein folding require incorporating fluorescent labels covalently bound to amino acids to integrate into proteins. These fluorescently labelled amino acids are used to understand protein conformation and the range of rotational motions as the protein exits out of the ribosome. In this study, we propose utilizing an engineered construct of the SupN gene (SupNmut) encoding for a stop codon-bearing suppressor tRNA, incorporating lysine at the place of the amber stop codon of the model protein apoHmpH (i.e. the N-terminal portion of E. coli flavohemoglobin). Utilizing an aminoacyl-tRNA synthetase that recognizes our engineered tRNA (as part of the S100 cell preparation from E. coli), I set out to in vitro transcribe a tRNA that can be aminoacylated with lysine for subsequent chemical modification with the fluorescent label Bodipy 576. Design of the tRNA amber suppressor will give us novel insight into how the core of our model protein folds at the ribosomal exit tunnel.

METHOD FOR IDENTIFICATION OF FUNCTIONAL PARTNERSHIPS USING TRANSCRIPTIONAL CO-REGULATION IN TUMORS

Duncan McColl, Jay Kim, Manel Camps

Department: Microbiology and Environmental Toxicology

Home Institution: University of California Santa Cruz

Transcriptional profiles can produce functional information, but lack the resolution to identify individual gene-gene interactions. We reasoned that for processes that require precise gene dosage, dysregulation of gene expression associated with tumor formation would lead to compensatory changes in the expression of functional partners which could be used to detect functional interactions. To test this hypothesis, we scored the transcriptional status for two sets of genes in each tumor available in the cbiportal site. The scoring method analyzes which genes are commonly upregulated together to identify functional networks. Our analysis scores gene-gene pairs, but more complex patterns of co-regulation are incorporated through a normalization index that increases exponentially with the number of genes upregulated in concert. Co-regulation between individual genes is visualized as a network. Modular structures within the network were identified using the Clauset-Newman-Moore community network analysis. Analysis of five base-excision repair genes and six tight-junction genes were correctly separated in to two distinct communities matching their function. We next ran two sets of ALKB-like (ALKBH) family genes and base-excision repair (BER) genes. Our network suggests that most ALKBH homologs interact functionally with BER, consistent with known substrate overlap between those ALKBH genes and some DNA glycosylases. FTO and ALKBH8, two ALKBH homologs that modify RNA targets, show no connections to BER, again consistent with their known functions. Our analysis represents a new procedure for

identifying functional partners between individual genes that may complement other approaches.

THE EFFECT ON VARIOUS CAPPING LIGANDS ON RHODIUM-GOLD ALLOY NANOPARTICLES FOR THE USE IN ELECTROCHEMICAL REDUCTION

Rene Mercado, Christopher Deming, Vamsi Gadiraju, Mohammad Khan, Shaowei Chen

Department: Chemistry and Biochemistry

Home Institution: University of California Santa Cruz

Summer Program: STEM Diversity - Summer Research Experience - CAMP

Many studies have shown platinum (single metal) to be an optimal catalyst for oxidation/reduction of Proton Exchange/Polymer Electrolyte Membrane Fuel Cell (PEMFC). However, platinum is scarce, which limits its use in commercial settings. Therefore, more cost-effective catalysts that show activity comparable to platinum for both oxidation and reduction reactions are being developed. Recent studies have shown that rhodium (Rh) nanoislands on gold (Au) increases the oxygen reduction reaction (ORR) when compared to pure Au. Hence, we synthesized Rh-Au alloy nanoparticles (NP's) using a modified Brust phase transfer method. Various ligands such as dodecylne, dodecanethiol, triphenylamine (TPA), and 4-ethylphenylacetylene (EPA) were used to cap the Rh-Au alloy NP's in order to examine the ligand effect on catalytic activity. Spectroscopic measurements including UV-Vis, FTIR, Transmission electronic microscope (TEM) and X-ray photoelectron microscopy (XPS) were utilized to characterize the Rh-Au nanoparticles. UV-Vis confirmed that nanosized Rh-Au alloy NP's were synthesized, and FTIR indicated all ligands are surface bound. Rh-Au catalyst were analyzed by cyclic voltammetry (CV) in nitrogen saturated, 0.1M NaOH. Results indicated both Rh and Au are active components of the metal core surface. Rotating ring disk electrode (RRDE) voltammetry in oxygen saturated 0.1M NaOH was used to evaluate the electro catalytic oxygen reduction activity. This activity will be dependent on choice of capping ligand due to different interfacial connection between ligands and metal core that will ultimately alter electronic structure of the metal core and consequently ORR activity.

DISTRIBUTION OF DARK MATTER HALOS IN THE COSMIC WEB

Christian Millan, Xavier Prochaska and Nicholas Tejos

Department: Astronomy and Astrophysics

Home Institution: Transferring to UCSC from Hartnell College

Summer Program: Lamat Summer Research Program on High Performance Computing in Astrophysics – Hartnell Title V CUSP Award

Galaxy clusters, groups of ~1000 galaxies or more, with dark matter halo (DMH) masses exceeding 10^{14} MSun, are the most massive structures in the universe. Current theory predicts that galaxy clusters are connected by cosmic webs, vast filaments and sheets of dark matter which carry DMHs through a large scale structure of the universe spanning distances beyond 100 Mpc. With the Bolshoi cosmological simulation, halo catalogs and merger trees were generated through an algorithm to obtain data and carefully understand the distribution of DMHs. By analyzing the velocity of the DMHs through their positions with masses less than 10^{14} MSun, data is plotted to understand the

properties of the cosmic web. First, 10,000 DMHs were graphed on a 2D plot with a scale of 50 Mpc across to help visualize the cosmic web. Then, ~1 million DMHs were graphed in 3D and with clusters identified separately. Cluster pairs were then located by distances less than 10 Mpc apart and defined by traces of cosmic filaments. A cylinder was then generated to connect each cluster pair to identify the DMHs inside and outside those filaments. The velocity of the DMHs inside the cosmic web and outside the cosmic web are analyzed and compared. An understanding of gravity on the DMHs is that the gravitational pull of the cluster increases velocity for almost all DMHs near that cluster. Another effect besides gravity inside the cosmic web is gradually increasing the DMHs to gain additional speed compared to DMHs outside the cosmic web.

SWEETCAM: SOLAR WI-FI ENERGY EFFICIENT TRACKING CAMERAS

Leland Miller, John Anthony Rinehart, Guilherme Porto, Kevin Abas, Katia Obraczka

Department: Computer Engineering

Home Institution: University of California Santa Cruz

Summer Program: SURF-IT

The SWEETcam system is a solar-powered smart camera network utilizing wireless networking for communication. The cameras are able to autonomously recognize and classify activity, which then allows for the selective recording of desired events. This allows us to create small, power efficient cameras that are completely self-contained and require no infrastructure outside of a wireless network. These cameras remove several of the limitations of traditional camera networks. Since they do not require wiring for data transmission or power, deployment location options are far greater than a traditional camera network, especially outdoors. The low cost of these cameras also means that it is possible to cover a greater area than would be possible with the same budget put toward a traditional camera network. In addition, the automated recognition of important events and selective recording means that a lesser amount of human intervention is required to find all of the important data contained in the increased amount of video footage that a wider deployment would create. The availability of a camera network with these characteristics opens up the possibility of monitoring wider and more remote areas than possible in the past. We hope that this research may open up possibilities in wildlife tracking, automated systems monitoring, and other areas with similar needs. In this spirit, the tools that we are developing are intended to be as flexible and open as possible, and we hope that these cameras can be used to enable data collection in previously inaccessible ways.

SYNTHETICALLY TESTING PARTS OF SPT5 PROTEIN FOR PRION-LIKE COMPLEXES

Pavel Morales, Grant Hartzog

Department: MCD Biology

Home Institution: Hartnell College

Summer Program: ACCESS

Nucleosomes control transcription by blocking transcription factors and RNA polymerase from binding underlying DNA sequences. The goal of the lab is to find out how nucleosomes position and structure are modulated to regulate transcription. Spt4 and Spt5 are conserved eukaryotic proteins that form a protein complex, which associates

with elongating RNA polymerase II and controls proteins that remove and reassemble nucleosomes over transcribed genes. The C-terminal domain of Spt5 contains multiple repeats of the sequence ST/AWGGA/Q, which are targeted by regulatory kinases and act to recruit regulators of chromatin structure. The hypothesis that will be tested is that this C-terminal region of Spt5 forms prion-like complexes. Prions are proteins that convert between two configurations, one of which is infectious. Prions in this transmissible configuration are self-templating, which allows them to convert other proteins into the infectious configuration by mere contact. A disease associated with the transmissible configuration of prions is mad cow disease. To test the hypothesis, full-length Spt5 and the C-terminus of Spt5 will be fused to green fluorescent protein. Fluorescent microscopy will be used to monitor the ability of these proteins to form aggregates. Kinase and phosphorylation site mutants will be used to determine if Spt5's phosphorylation state affects its ability to aggregate.

CLUSTERSLUG: INFERRING THE PROPERTIES OF STAR CLUSTERS FROM PHOTOMETRY WITH IMPLIED CONDITIONAL REGRESSION

Michelle Myers, Mark Krumholz

Department: Astronomy and Astrophysics

Home Institution: City College of San Francisco

Summer Program: Lamat Summer Research Program on High Performance Computing in Astrophysics

Photometry is a technique which measures the intensity of light produced by a star or a group of stars through one or more filters. Photometric observations can be used to infer many properties of stellar populations such as mass and age. However, in smaller star clusters (groups of stars that form together), the fact that stars form discretely introduces stochastic variations in the stars' photometric output. This in turn causes the mapping from luminosity to mass and age to become non-deterministic. To handle this problem, we simulated star clusters using Stochastically Lighting Up Galaxies (SLUG). We then performed implied conditional regression on these simulations in order to compute the probability distribution of mass and age given a set of observed luminosities. We are using this technique to develop a software tool that will provide the user with full joint probability distributions of mass and age given a set of observed photometric data. Future work will incorporate the effects of dust extinction on the observations.

EXAFS INVESTIGATION OF FILLED SKUTTERUDITE $\text{CePt}_4\text{Ge}_{12-X}\text{Sb}_X$

Patrick Nast, John Wilde, Frank Bridges

Department: Physics

Home Institution: University of California Santa Cruz

We investigated the structure of the filled Skutterudite $\text{CePt}_4\text{Ge}_{12-X}\text{Sb}_X$ using Extended X-Ray Absorption Fine Structure (EXAFS) analysis. $\text{CePt}_4\text{Ge}_{12-X}\text{Sb}_X$ belongs to a class of materials that are currently studied for their potential thermoelectric properties. Prior analysis of $\text{CePt}_4\text{Ge}_{12}$ suggests that Ce may behave like a "rattler" atom in a cage, leading to a lower thermal conductivity in the material. We present a comparison of EXAFS analyses at different Sb doping levels for the Ce LIII and Pt LIII edges over a temperature range of 5-300 K. Investigating how the EXAFS changes with different doping levels may shed light on their potential for thermoelectric applications.

EXAFS data is collected by directing a monochromatic X-ray beam at a sample and analyzing the absorption spectra as a function of X-ray energy for a particular atomic edge. Using diffraction data, we fit theoretical standards for neighboring atomic pairs to the data and extracted sigmas and their temperature dependencies for specific pairs of atoms. We found that the EXAFS for Ce LIII became significantly disordered with increasing Sb concentration. In the analysis of the X=1 concentration, we found higher static disorder in the Ce edge at low temperature. Further research may investigate whether Sb pushes the rattler off-center, and if the Ge rings and Ce atom vibrations are coupled in the plane formed by the ring and the rattler. More investigation is needed at the higher doping levels to study the behavior of atoms in this material, and its candidacy for thermoelectric applications.

THE RELEASE OF A TRACKABLE SILVER(D ANTIMICROBIAL AGENT FROM A CARBOXYMETHYLCELLULOSE HYDROCOLLOID DRESSING: FOR APPLICATION IN WOUND CARE

Kimberly Nguyen, Gustavo Chata, Tara Deboer, Pradip Mascharak *

Department: Chemistry & Biochemistry Department

Home Institution: University of California Merced

Summer Program: STEM Diversity - Summer Research Experience - UC

LEADs Visiting Scholar

Because open wounds are often susceptible to bacterial infection, silver impregnated wound dressings have been designed to reduce the bacterial bio-burden at these sites and facilitate proper healing. A silver complex, namely silver imidazole dansyl perchlorate ($[\text{Ag}(\text{ImDansyl})_2]\text{ClO}_4$), has been synthesized with the intent to build on the application of silver in wound dressings as an antimicrobial agent. $[\text{Ag}(\text{ImDansyl})_2]\text{ClO}_4$ is a fluorescent compound that will allow individuals to visually observe the delivery of Ag^+ to a wound site. In order to evaluate the antibacterial efficacy of the compound, $[\text{Ag}(\text{ImDansyl})_2]\text{ClO}_4$ was introduced into a hydrocolloid dressing composed of carboxymethylcellulose and polyethylene glycol. This formed a pliable bandage material whose polymer network affords controlled and sustained release of Ag^+ . The release of $[\text{Ag}(\text{ImDansyl})_2]\text{ClO}_4$ from the polymer was facilitated by the exposure of the dressing to a maximal recovery diluent (MRD) solution, which mimics wound moisture. The leaching of $[\text{Ag}(\text{ImDansyl})_2]\text{ClO}_4$ was first assessed through qualitatively evaluating the extent of fluorescence observed on an agar surfaces, and then quantitatively assessed using electronic absorption spectroscopy (UV-VIS). From our UV-VIS data, the rate of the release of the fluorescent compound was determined and analyzed to validate the use of the cellulose system as the mode of delivery for $[\text{Ag}(\text{ImDansyl})_2]\text{ClO}_4$. Future experiments are required to substantiate the antibacterial efficacy of the silver complex in comparison to standard silver antibacterial agents.

VALSALVA DEVICE: NON-INVASIVE HEART FAILURE PREDICTION

Hunter Nichols, Matthew Guthaus, Liviu Klein

Department: Computer Engineering

Home Institution: University of California Santa Cruz

Summer Program: SURF-IT

Heart failure has become more common due to the increasing population of the elderly. However, heart failure can be predicted via the Valsalva maneuver which bases the prediction on the patient's breath pressure and blood pressure. Generally, devices that can measure this information are either bulky and expensive or require some type of invasive procedure, e.g. a sensor implanted with a pacemaker. The device that we created is small, non-invasive, and interacts with common, modern technologies such as smartphones. Our device, named the Valsalva board, is a printed circuit board that contains several sensors and micro controllers to predict heart failure using the Valsalva maneuver. While collecting this data, it is transferred over to a nearby phone using Bluetooth Low Energy to be displayed, analyzed in a meaningful way, and shared with a patient's physician remotely.

SUPER RESOLUTION THROUGH STRUCTURED ILLUMINATION

Rexavalmar M. Niduaza, Annie O, Mark Reinig, Xiadong Tao, Joel Kubby

Department: Electrical Engineering, Jack Baskin School of Engineering

Home Institution: Transferring this Fall from Hartnell College to the University of California Santa Cruz

Summer Program: STEM Diversity - UC LEADs – Hartnell Title V CUSP Award

In biology, substantial amounts of information are gathered through microscopy, and our understanding is limited by the observable plane. Standard microscopes are governed by the classical diffraction limit, restricting the resolution of its images to about 250 nm. In recent years, several methods have been developed in an effort to exceed this limit and achieve super-resolution; surpassing the previous amount of resolution achieved. One such method is with the use of structured illumination (SI). We illuminate the sample with a grating pattern set using a digital light processor (DLP) and take several images at different phases. In this process, variations in the tissue being observed introduce aberrations, reducing the actual resolution obtained. These aberrations increase as we look deeper. We measure the aberrations with a wavefront sensor (WFS) (a form of adaptive optics (AO)), and make corrections to the light to compensate for the aberrations that occur as light travels through the sample using deformable mirrors (DM). Given the specific patterns, multiple images are taken at specific offsets or shifts as calculated mathematically. Using mathematical inverse analysis, the images collected are then reconstructed creating a final image with approximately twice the resolution as compared to the previous classical limit. When we present our findings for this project, we will use two different SI patterns and discuss the results of the final images reconstructed.

LC-MS AND NMR CHEMICAL PROFILING OF THE INDONESIAN SPONGE ZYZZYA FULIGINOSA: CHEMICAL DEREPLICATION AND OVARIAN CANCER CELL (OVC-5) ANTICANCER ACTIVITY

Gerson Ortuño, Patrick Still, Phil Crews

Department: Chemistry and Biochemistry

Home Institution: Monterey Peninsula College

Summer Program: ACCESS

Natural products research is crucial to the discovery of potential treatments for cancer and other ailments. It is stated that nearly fifty percent of all cancer drugs are natural products or derived from natural products. The marine environment, in particular, has been shown to be a productive source of natural product lead compounds. In this study the Indonesian sponge *Zyzzya fuliginosa* was shown to have activity against human ovarian cancer (OVC-5) cells in vitro. This finding prompted the chemical investigation of this marine sponge to determine the chemical compounds responsible for the observed activity. Crude methanol extracts of *Z. fuliginosa* obtained from the National Cancer Institute were subjected to liquid chromatography-mass spectrometry to determine known molecular weights that have previously been isolated from this genus of sponge. This dereplication process allowed identification of two known pyrroloiminoquinone compounds, tentatively assigned as makaluvamine C and makaluvamine L, based on mass spectral characteristics. Nuclear magnetic resonance was utilized to confirm the presence of these compounds based on diagnostic chemical shift patterns. From these studies, the potential of marine organisms to produce bioactive compounds is illustrated.

SPATIAL AUDITORY DISPLAYS: SUBSTITUTION AND COMPLEMENTARY TO VISUAL DISPLAYS

Trisha N. Patel, Martine Godfroy, Elizabeth M. Wenzel

Department: NASA Ames Human Systems Integration Department

Home Institution: University of California Santa Cruz

Summer Program: Advanced Studies Laboratory Summer Internship

During extra vehicular exploration on surface, astronauts learn how to keep track of various "targets" (eg. team members, rovers, habitats, etc.). In most cases, these "targets" are out of their immediate field of view, making it difficult for them to be located efficiently. The goal of the current study was to delineate how and when different types of displays can influence orientation and localization of stationary target objects. Three types of displays were tested: a 3D spatial auditory display, a 2D North-up visual map, and a combination of both in a bimodal display. Performance was compared under different environmental conditions with low and high levels of visibility and ambiguity. Results showed a benefit of a bimodal display, especially when visual information was degraded. Using a similar method, the next experiment manipulated visual workload. Preliminary data shows that visual workload reduces performance in visual-only displays more than displays involving auditory cues. Together results demonstrate the importance of utilizing auditory cues in displays to aide in orientation and localization.

INFLUENCE OF DIETARY CHOLESTEROL AND COPPER ON LONGEVITY, BEHAVIOR, NEURODEGENERATION, LEARNING, AND MEMORY IN A DROSOPHILA MODEL OF ALZHEIMER'S DISEASE

Rebecca Pearson, Emmanuel Fonseca, Adrienne Mcguire, and Dr. Jeremy Lee

Department: Physical and Biological Sciences, Molecular, Cell and Developmental

Home Institution: University of California Santa Cruz

Summer Program: STEM Diversity - Summer Research Experience

With the global population increasing and living longer age-related cognitive decline, dementia, is an increasing concern. In 2013, Alzheimer's disease (AD), the most common form of dementia, was the sixth-leading cause of death in the U.S.; 5.2 million Americans had AD, as did 35 million individuals worldwide. Medical expenses related to AD are projected to surge from \$203 billion in 2013 to \$1.2 trillion per year by 2050. With no effective treatments, there is great need to understand this disease, improve therapies, and develop preventative treatments. While epidemiological studies have found correlations between AD and dietary cholesterol and copper, there are few studies that address the causal relationship between AD and high cholesterol and/or copper. Using a Drosophila model of AD, this study investigates the effects of dietary cholesterol, copper, and their interaction on AD pathology. Like mouse AD models, the Drosophila AD model exhibits decreased activity, decreased longevity, altered learning and memory, and neuronal accumulation of A-beta ($A\beta$), the key peptide involved in AD. We are feeding Drosophila AD models diets with differing levels of cholesterol and/or copper and observing the effects on $A\beta$ accumulation, longevity, activity level, neural degeneration, learning, and memory. It is hypothesized that high levels of cholesterol and copper will exacerbate AD-like pathology in Drosophila and will synergistically increase neurodegeneration and other aspects of AD-like pathology. If this hypothesis is supported, this study will provide an impetus for similar studies in the human population.

SURFACE MODIFICATION OF SOLID-STATE NANOPORES VIA (3-AMINOPROPYL) TRIETHOXY-SILANE: EARLY DEVELOPMENT OF A SACCHARIDE SENSOR

Edmundo Perez, Ace Galermo, Rifat Emrah Ozel, Nader Pourmand

Department: Biomolecular Engineering

Home Institution: Hartnell College

Summer Program: ACCESS, Hartnell Title V CUSP Award

The development of a reversible, miniature, and non-enzymatic, saccharide sensor can improve current glucose monitoring techniques for diabetic patients. One device that can be used to measure saccharide concentration is a solid-state nanopore. Ion current through the nanopore can be modulated by charge and/or physical blockage at the pore's orifice. The goal of this project was to create terminal amine functional groups

onto the surface of a quartz nanopore to serve as a “seat” for the covalent attachment of carboxyl-containing boronic acid saccharide receptors. A potential method to modify a quartz nanopore involves treatment with an organosilane. Organosilanes are known to serve as adhesives or bridges between inorganic and organic materials. In this experiment, quartz nanopores were prepared, treated with a solution of (3-aminopropyl) triethoxysilane (APTES) in different solvents: methanol, acetone, or absolute ethanol, and characterized for the presence of terminal amine functional groups via linear sweep voltammetry. The nanopores were fabricated utilizing quartz capillary tubes, which offer many practical properties that include fast production, low-cost, and sensitivity. Principally, the fabrication of such a device can further benefit bio-medical research.

CELL SIFTER: HIGH THROUGHPUT IMMOBILIZATION OF NON-ADHERENT SINGLE CELLS

Rolando Perez, Nader Pourmand

Department: Bioengineering

Home Institution: University of California Santa Cruz

Summer Program: STEM Diveristy - Summer Research Experience –
Maximizing Access to Research Careers

High throughput immobilization of non-adherent single cells allows automated manipulation of many single cells in parallel. This system consists of two main modules with accompanying software, the nanopipette biosensor and the cell sifter. The nanopipette, a capillary quartz tube with a nanometer sized pore, has shown great promise for single cell manipulation and analysis with high resolution. The cell sifter, a microfluidic device, is the focus of this research. The cell sifter was fabricated utilizing semiconductor processing techniques and consists of a sandwich structure with an optically transparent membrane window perforated by an array of micro holes. Coupled with a vacuum control system the cell sifter enables capture and release of cells in solution while maintaining cell viability. The cell sifter will capture cells in solution, immobilize the cells, and release the cells on demand. Adding the ability to manipulate non-adherent cells facilitates the expansion and capabilities of the nanopipette technology. The promise of the cell sifter device coupled with a nanopipette and custom software lies with the ability to assay a single cell at the nanometer scale, maintaining cell viability. Applications of this system include analysis of cellular micro environments, various omics analysis with sub cellular resolution, induction of single cells for induced pluripotent stem cell (iPSC) research, greatly increasing our understanding of these cells, and single cell aspirations that allow for transfer of biomaterial into and out of a single cell, known as single cell nanosurgery.

AIR BEARING TEST RIG FOR A CUBESAT ALTITUDE STABILIZATION SYSTEM

Tyler Eliot Peterson, Dmitry Rivkin, Gabriel Elkaim

Department: Computer Engineering, Jack Baskin School of Engineering

Home Institution: University of California Santa Cruz

Summer Program: SURF-IT

CubeSats are small satellites 10cm on a side that have been introduced to dramatically reduce the cost of space exploration. Typically, they are launched as "secondary" payloads on rockets in orbits and altitudes of convenience (mostly in LEO). Several have

been designed and flown by student groups, and CubeSats offer a manageable gateway to space. However, their small size, weight, and power introduces its own difficulties in terms of communications, payloads, and control. Most CubeSats use either no attitude stabilization or passive bar magnets to orient to the Earth's magnetic field. Active orientation control has been limited in the past. Current work is progressing on developing a small reaction wheel control system based on conservation of angular momentum. Testing such a system requires an extremely low friction test rig as the forces are very small. The project details the development, deployment, and refinement of a test rig suitable for CubeSat attitude control testing.

GENERATION OF SUMATRAN ORANGUTAN iPSC LINES FROM FIBROBLASTS

Alex Phillips, Andrea Reyes-Ortiz, Andrew Field, Sofie Salama, David Haussler

Department: Biomolecular Engineering

Home Institution: University of California Santa Cruz

We have generated 15 induced pluripotent stem cell (iPSC) clones from fibroblasts of a Sumatran Orangutan that show the characteristic colony morphology of PSCs using the CytoTune® 2.0 iPS Sendai Reprogramming Kit from Life Technologies™ and are in the process of characterizing the clones. Once they are determined to be karyotypically normal and truly pluripotent, they will be added to our cross-species developmental comparison studies, as well as investigations of retroviral elements in primate genomes, with other potential applications in genetic study, epigenetics, and conservation.

PERTURBING HEMATOPOIETIC STEM CELL MIGRATION THROUGH A VASCULAR ENDOTHELIAL BARRIER BY BLOCKING VCAM1 ADHESION

Javier Portillo, Stephanie Smith-Berdan, E. Camilla Forsberg

Department: Biomolecular Engineering

Home Institution: University of California Santa Cruz

Summer Program: STEM Diversity - Summer Research Experience - UC

LEADs

Hematopoietic stem cells (HSCs) have been utilized clinically for over half a century, however the mechanisms regulating HSC trafficking through vascular barriers remains unclear. We seek to further understand the intricate mechanisms of HSC binding to vascular endothelial cells (VECs) and the impact of blocking these mechanisms on HSC migration towards the chemokine CXCL12. One such mechanism involves vascular cell adhesion marker-1 (VCAM1) which is expressed both on the surface of HSCs and VECs. It is involved in binding of leukocytes to the VECs as an integral component in the migration of leukocytes through the vascular endothelial tissue in-vivo. Previous in-vitro data from our lab suggests that blocking integrin- α -4 (VLA-4), VCAM1's binding partner, on VECs blocks the migration of HSCs, progenitors, and B-cells through the VEC layer towards CXCL12. We next pursued whether the reciprocal is true; whether HSC migration through VECs is perturbed by blocking VCAM1 on VECs. We tested this by utilizing two different blocking antibodies targeting VCAM1 in an in vitro VEC migration assay. VECs were cultured on transwells and grown to confluency prior to adding anti-VCAM1 blocking antibodies to the VEC layer. Lineage-depleted bone marrow cells were then allowed to migrate towards CXCL12 for 2hrs. The effects of blocking VCAM1 were

quantitatively measured using flow-cytometry (BD LSRII). Our hypothesis was that by blocking VCAM1 on ECs, HSCs would have perturbed migration through VEC transmembranes as seen with the blockage of VLA-4 in previous studies. Understanding HSC migration mechanisms may lead to innovations in HSC transplants.

INVESTIGATING THE RELATIONSHIP BETWEEN INTRON BRANCH SEQUENCE AND SPLICING INHIBITION BY PLADIENOLIDE B

Crystal Prado, Kerstin Effenberger, Melissa Jurica

Department: Molecular, Cell, and Developmental Biology

Home Institution: Cabrillo College

Summer Program: ACCESS

An essential step in gene expression is RNA splicing: the removal of non-coding intron sequences and ligation of the remaining exon sequences in pre-mRNA gene transcripts to produce a mature mRNA. This process is catalyzed by a complex macromolecular machine called the spliceosome. Understanding spliceosome activity is important because changes in splicing are associated with several human diseases. For example, mutations of the core splicing factor, SF3B1, are associated with cancer. A key role of SF3B1 is to stabilize U2 snRNP, a small nuclear ribonucleoprotein, in the spliceosome and identify the intron branch sequence. The anti-tumor drug, pladienolide B (PB) targets SF3B1 and inhibits splicing of some, but surprisingly not all, pre-mRNA transcripts. Therefore, it is hypothesized that splicing inhibition by PB depends on the strength of intron branch sequences and it is predicted that, compared with stronger intron branch sequences, weaker intron branch sequences will be inhibited more easily by PB. To test this hypothesis, an in vitro splicing assay with a pre-mRNA containing different intron branch sequences will be used, and PB inhibition will be compared. Results will be helpful to future studies in understanding the effect of SF3B1 and PB on splicing of introns in cancer cells. These studies will also impact efforts to use PB as a chemotherapeutic.

INTERACTIONS BETWEEN MANZANITAS AND COAST LIVE OAK AND THEIR EFFECT ON HERBIVORY BY DEER AND WOODRATS IN MARITIME CHAPARRAL

Mizael Preza, Laurel R. Fox

Department: Ecology and Evolutionary Biology

Home Institution: University of California, Santa Cruz

Summer Program: STEM Diversity - Summer Research Experience

Work in maritime chaparral at Fort Ord, in coastal California, shows that biotic interactions, including herbivory, competition and facilitation affect the community. We investigated how interactions between manzanita shrubs and coast live oak affected browsing by black-tailed and Monterey dusky-footed woodrats. We hypothesized that 1) oak saplings are less browsed by deer when they grow inside dense manzanita mounds compared to growing on their own; 2) oak saplings are negatively affected by competition from the manzanitas; and 3) young oaks may eventually outcompete the manzanitas when they become taller than the manzanitas. To assess these interactions we measured the structure of manzanita clumps (e.g., height, intactness, distance from oak to manzanitas, age of manzanita stems growing next to the oaks), and assessed

browsing damage and the age of oaks from wood samples. Deer browsing is much higher in oaks growing outside compared to inside manzanita clumps, but woodrat damage did not change at all. Also, the average height with respect to age was higher in oaks growing inside a clump, showing that dense clumps of manzanita can benefit oak growth by making a “natural fence” that shelters young oaks from browsing, despite likely strong competition from the manzanita. Furthermore, browsing on oaks increases as clumps become less intact. Finally, oaks within a clump are in average 7 years younger than nearby manzanitas, but manzanita growing immediately beneath taller, older oaks eventually die. These interactions potentially determine community composition of marine chaparral where oak trees might eventually become the dominant species.

MUTAGENESIS OF HELICOBACTER PYLORI'S CHEMORECEPTOR TLPD IN CONSERVED CZB DOMAIN

Sindy Ramirez, Kieran Collins and Dr. Karen Ottemann

Department: Microbiology and Environmental Toxicology

Home Institution: University of California Santa Cruz

Summer Program: STEM Diversity - Summer Research Experience - IMSD

Mutagenesis of Helicobacter Pylori's Chemoreceptor TlpD in Conserved CZB Domain by Sindy Ramirez, Kieran Collins and Dr. Karen Ottemann Helicobacter Pylori is a gram-negative bacteria that colonizes the stomachs of approximately 50% of the world's population. H. pylori infection can lead to the development of gastric pathologies including gastric ulcers and certain gastric cancers. This bacterium employs chemotaxis to sense its environment and alter motility to concentrate around beneficial molecules and avoid detrimental chemicals. Chemotaxis appears to be important for H. pylori infection during the colonization of the gastric epithelium, particularly in the antrum. TlpD is a soluble chemoreceptor which appears to be responsible for driving colonization in the antrum of the mouse stomach. This chemoreceptor binds zinc through the Chemoreceptor zinc-binding (CZB) domain. This domain contains three conserved histidines and a cysteine, suspected to coordinate zinc. It is currently unclear what role this domain plays in TlpD function, although the CZB is found in other chemoreceptor proteins, as well as other protein architectures. The purpose of my research is to assess the contribution of the CZB to TlpD function by creating point mutants at conserved residues in this domain, and analyze the swimming behavior of these mutant H. pylori in comparison to a wildtype genetic background.

POLYMERASE CHAIN REACTION (PCR) USED TO DETECT WOLBACHIA IN DROSOPHILA COLLECTED FROM BIG CREEK RESERVE

Mayra Rios¹, Juan Orantes², Maryam Toma³, Bill Sullivan

Department: MCD Biology

Home Institution: University of California Santa Cruz

Summer Program: STEM Diversity - Summer Research Institute –

1. UCSC-MARC 2. VCR summer support 3. PBSci summer support

Wolbachia is a gram-negative intracellular bacteria that infects organisms through maternal inheritance and spreads to wild populations through Cytoplasmic Incompatibility (CI) in arthropods. Wolbachia is known to cause high

CI, viral protection, and a parasitic relationship with its host. CI is the process used by Wolbachia to ensure its transmission to progeny by favoring infected *Drosophila* females due to their ability to mate with infected or uninfected males. Though, when an uninfected female mates with an infected male, it results in death of the progeny. We were unable to generate mutants since Wolbachia live inside the female germline. Our goal was to find variants that are rarely found in nature. Variants are highly infected with Wolbachia and can be used to help us understand the biological relationship between host and bacteria to further assist in preventing insect-borne human diseases. At Big Creek Reserve, *Drosophila*, twenty water striders, one grasshopper, and one moth were collected to detect Wolbachia. In the lab, we used one organism per eppendorf tube and added a genomic prep buffer that contained Protease K to dissolve proteins and keep the DNA intact. Consequently, PCR mix was added to allow the amplification of the Wolbachia gene. Agarose Gel electrophoresis was the technique used to separate the bands of DNA that would tell us which organisms contained Wolbachia. Our results show that only one fruit fly was infected. In conclusion, furthers studies are needed to determine whether or not we have a variant.

MOTB PROTEIN LOCALIZATION IN RELATION TO MOTILITY IN *H. PYLORI* BACTERIA

Ygnacia Rivas, Daniela Keilberg, Karen Ottemann

Department: Microbiology and Environmental Toxicology

Home Institution: Gavilan

Summer Program: ACCESS

Helicobacter pylori (*H. pylori*) is a gram negative, spiral-shaped bacterium which possesses 6-8 flagella for movement. It has been determined that these bacteria play an important role in causing stomach ulcers and stomach cancer. In order for pathogenicity to occur under the mucus lining of the stomach, motility is essential. This project focuses on MotB, a protein which is part of the flagella motor powering motility in *H. pylori*. A strain lacking MotB has been generated in the lab previously. However, a deeper analyzation of MotB is required. A complementation construct expressing MotB from a plasmid will be constructed to restore motility in the *H. pylori* strain lacking the MotB gene. To test motility, the activity will be analyzed by soft agar motility assays. A second plasmid will be generated, expressing Mcherry only, which can be used to fluorescently label the cells. Additionally, a construct will be made of a functional fusion plasmid expressing MotB-Mcherry to determine localization of MotB in *H. pylori* cells. Cloning and PCR techniques will be used for this approach. This work will aid further research regarding mutations in MotB and their ability to affect motility in *H. pylori* cells.

BABY RESUSCITATION ENHANCED: A TECH HELPER (BREATH) DEVICE

Adrienne Saludades, Matthew Guthaus

Department: Computer Engineering

Home Institution: Smith College

Summer Program: SURF-IT

According to the World Health Organization, 99% of all neonatal deaths occur in low- and middle-income countries. Several factors influence this high neonatal mortality rate,

such as the distance between patients and healthcare facilities, lack of adequately trained medical personnel, and outdated health informatics systems. Inexpensive, multifunctional smart devices can be used to monitor neonatal health post-delivery and inform clinical procedures to mitigate health disparities in developing areas. The Baby Resuscitation Enhanced: A Tech Helper (BREATH) is a device that aims to improve the identification of live babies suffering from respiratory distress and to assist neonatal practitioners in timely and accurate neonatal resuscitation decision-making. In collaboration with neonatologist Holly Martin MD from UCSF Medical Center, Professor Guthaus's lab has been developing this hands-free Android application that will coach the birth attendant through the resuscitation algorithm. The heart rate is transmitted via Bluetooth LE from a noninvasive umbilical cord sensor and helps guide the algorithm. The current prototype aims to utilize the TI CC2541 Sensor Tag to remotely control the changes in heart rate of a simulation baby for training personnel and testing the functionality of the device. For this project, we focused on programming the user interface of the android application and ensuring ease of use of the device for users of various technological backgrounds.

SIZE BIAS DURING PRESERVATION OF INSECTS IN AMBER

Thooba Samimi, Matthew Clapham

Department: Earth and Planetary Sciences

Home Institution: University of California Santa Cruz

Summer Program: Julie Packard Summer Scholar

Amber is valued for its inclusions that are ensnared by the organic resin. Because the life trapped in amber is preserved better than ones buried in sedimentary rock, insect inclusions in amber are crucial for reconstructing the insect fossil record. Resin's sticky and viscous nature allows entrapment of a variety of insect species, but the size of insects may bias their preservation in amber. Our objective was to understand why most of insects in amber tend to be smaller. I entered previously-published measurements of wing and body size of specimens preserved in amber into the Paleobiology Database and compared wing length of insects preserved in amber to insects preserved as compressions in rock. The mean wing size in amber is 3.18mm, whereas the mean size is 11.82mm in rock. Comparing the sizes between families in amber to the same family preserved in rock provided more evidence that amber is biased toward smaller insects. Out of the 111 families on record, 91 or 82 percent are classified smaller in amber. In addition, we used logistic regression to calculate the probability of an insect being trapped in resin. It revealed that for every millimeter decrease in wing length, there is a fifty percent greater chance of the insect being preservation in amber. This explains why amber contains predominantly small insects ranging from a millimeter to two millimeters in size and not many with wing lengths greater than ten millimeters. The abundance of small insects in amber indicates that organic resin is more likely to trap smaller insects, so the relative abundance of a family in amber may not completely indicate its true abundance in the geological record.

A DEEPER SLEEP AND A BRIGHTER DAY: DETERMINING THE STRUCTURE OF THE BMAL1 PROTEIN SWITCHING REGION

Michael Sanchez, Chelsea L. Gustafson, Carrie L. Partch

Department: Department of Chemistry and Biochemistry

Home Institution: Cabrillo College

Summer Program: ACCESS

Mammalian circadian rhythms control the body's 24 hour cycle. Sleeping and waking, anabolic and catabolic processes, all rely on the cellular mechanisms that keep them in alignment with each other and the external environment. The proteins CLOCK and BMAL1 form a heterodimeric transcription factor that promotes proper circadian function. The transcription activation domain (TAD) of BMAL1 contains a region critical to both activation and repression of circadian driven transcription. The goal of this project is to understand how the BMAL1 TAD controls this balance of activation and repression to generate the molecular circadian clock. BMAL1 has a region at the end of the TAD with two different conformations that act like a switch (e.g. cis and trans) to control interactions with transcriptional regulators. In order to crystallize this protein, a trans-locked TAD will be used. A section of the BMAL1 gene containing the TAD will be mutated to the trans form of the molecule, and the recombinant protein will be purified. The structure of the protein will be determined through x-ray crystallography in complex with the KIX domain of the transcriptional activator CBP. The structural determination of BMAL's TAD region will be a step forward in the quest for a mechanistic understanding of the circadian clock and towards the development of therapeutic agents to modulate circadian function in individuals.

OBSERVATION OF CYGNUS X-1 WITH A HIGH- PRECISION OPTICAL POLARIMETER

Melody Sanchez, Sloane J. Wiktorowicz, Larissa Nofi, Nikki Ridder, Enrico Ramirez

Department: Astronomy Department

Home Institution: Hartnell College

Summer Program: Lamat Summer Research Program on High Performance Computing in Astrophysics, Hartnell Title V CUSP

Cygnus X-1 (Cyg X-1) is a black hole located 6,070 light-years away in our Milky Way galaxy, its proximity to Earth allows for a closer observation comparison to other known black holes. Since its discovery in 1964, Cyg X-1 has been essential in furthering the understanding of black holes. However, the angle of inclination of Cyg X-1 relative to our line of sight remains a mystery. While there are numerous data on the radial velocity of Cyg X-1, the mass of the black-hole remains unknown because the inclination has yet to be determined. Our observation combined with known radial velocity can offer an estimate for the unknown mass. The orbital inclination is vital because the object must be a black hole if it is found to be above a certain mass. The purpose of this project is to measure the inclination of Cyg X-1 using POLISH2, an optical polarimeter with an 0.01% accuracy simultaneously in linear and circular observations. The accuracy of this instrument is vital because Cyg X-1 changes every night. The ongoing data collected from multiple nights of observation will be used to shed light on the matter by observing the change in polarization as a function of orbital phase of the binary system.

MODIFICATION OF HEMATOPOIETIC STEM CELL DIFFERENTIATION USING INHIBITORS OF HISTONE MODIFYING ENZYMES

Gabriela Sanchez, Rebekah Sousae, Fernando Ugarte, Camilla Forsberg

Department: Biomolecular Engineering

Home Institution: University of California Santa Cruz

Hematopoietic Stem Cells (HSCs) uniquely possess the ability to self-renew and produce all blood lineages. During differentiation, key changes in chromatin occur. As HSCs differentiate towards final mature lineages, their relatively open chromatin converts to increasingly more closed heterochromatin. To identify the role of specific chromatin modifiers during HSC differentiation, we used inhibitors of histone and DNA methylation enzymes. We focused on four chromatin-modifying inhibitors: SGI-1027, EPZ-5676, Decitabine, and DZNEP. None of these four inhibitors had an effect on HSC differentiation under the conditions tested. In contrast; in vitro treatment of HSCs with the inhibitor UNC0638 resulted in an increase in hematopoietic stem/progenitor cells, defined as ckit+lin-Sca1+ (KLS) cells. UNC0638 targets the G9a histone methyl transferase. G9a-mediated methylation of histone H3 promotes gene silencing and heterochromatin formation. Each of the other four inhibitors was combined with UNC0638 to investigate whether they enhanced or counteracted the effects of G9a. Inhibitor combinations did not affect the numbers of KLS cells compared with G9a alone, showing that our observed accumulation of KLS cells is specific to G9a inhibition. To test whether the accumulated KLS cells were functional hematopoietic stem/progenitor cells, we transplanted these populations into irradiated mice and analyzed their ability to reconstitute mature blood lineages. These transplantation data confirmed that the KLS cells that accumulate upon UNC0638 inhibition are, in fact, functional hematopoietic progenitor cells. These results highlight the importance of G9a in the transition of HSCs to more mature lineages and emphasize the role of chromatin condensation during stem cell differentiation.

SEXUAL SUBJECTS: QUEER LATINO MIGRANT YOUTH IN HIGHER EDUCATION

Chris E. Sanchez, Adrian Felix, Elizabeth Gonzalez

Department: Latin American & Latino Studies

Home Institution: University of California Santa Cruz

While the experiences of Latino students in academic institutions has received more attention in recent years, the experiences of Lesbian, Gay, Bisexual, Transgender and Queer (LGBTQ) Latino/a students in higher education remain largely overlooked. Nearly three-quarters of LGBTQ Latino youth report that their school is accepting of LGBTQ people, and more than 8 in 10 report that their peers are accepting. Given the relevance of this topic, this study focuses on migrant LGBTQ Latino/a youth in higher education. It analyzes how LGBTQ students negotiate their multiple identities as sexual and ethnic minorities while navigating heteronormativity at the university. Through the scholarship of Juana Rodriguez and her theory of Queer Latinidad; Lionel Cantu and his analysis of sexuality of migration, and Gloria Anzaldua and her theory of Nepantla, we argue that these theories relate to daily lives of LGBTQ Latino youth students. Most participants report identities of being Latin@s, migrants, queer, first generation attending college and transfer student. LGBTQ Latino students at the University of California, Santa Cruz, share their experiences with faculty, staff, and administrators and the importance of their mentorship. This study highlights the importance of educators being aware of the

intersectionality of race, class, gender, sexuality, citizenship, and language in order to understand how these factors impact students' academic success. This study makes use of focus groups, one-to-one interviews, and online surveys to analyze the differences and similarities between documented and undocumented queer Latino students. Lastly, students share which support systems have helped their retention and graduation goal.

PHOTOVOLTAIC DEMONSTRATION SYSTEM: MAXIMIZING POWER GENERATION

Anna Serova, Michelle Shi, Michael Oye

Department: Electrical Engineering

Home Institution: University of California Santa Cruz

Summer Program: Advanced Studies Laboratory Summer Internship

Our goal in this project is to build a demonstration version of a solar array and tracker system, and analyze its effectiveness with variable characteristics, such as light intensity and angles of exposure to the light source. The main focus is to show the difference in power generation between the two systems.

EXPRESSION PROFILE OF PERINEURONAL NETS IN ADULT CEREBRAL CORTEX AND HIPPOCAMPUS FOLLOWING STRESS

Fernando Serrano, Chia-Chien Chen, Yi Zuo

Department: Department of Molecular, Cell, and Developmental Biology

Home Institution: University of California, Santa Cruz

Summer Program: Julie Packard Summer Scholar

Perineuronal nets are aggregates of extracellular matrix (ECM) proteins predominantly surrounding inhibitory neurons which were discovered more than one hundred years ago. Despite detailed descriptions of their morphology and location, little is known about their functions in developing animals. Recently, it has been suggested that ECM maturation is both age- and activity-dependent. Furthermore, very recent evidence has posited that ECM plays a protective role against oxidative stress and memory erasure. Additionally, the presence of chondroitin sulfate proteoglycans (CSPGs), a critical component of the ECM plays a crucial role in stabilizing synaptic plasticity in the brain after postnatal development. Its functionality in the context of psychological stress and their presumed contribution to the development of depression, however, remains unclear. Exposure to psychological stress has been observed to reduce the degree of synaptic plasticity in several regions of the brain, including the cerebral cortex, amygdala, and hippocampus in mice. However, what is not entirely understood are the effects of stress on perineuronal net content in the cortex and hippocampus. To investigate this, we stressed 1-month mice for 2 weeks, transcardially perfused and extracted their brains at postnatal day 44/45, followed by vibratome sectioning. Perineuronal nets and parvalbumin interneurons were visualized by Wisteria Floribunda agglutinin and immunofluorescent staining. Stained sections will be inspected on a Keyence BZ-9000 fluorescent microscope for dual-channel imaging. Obtained data will be imported into the Neurolucida 9.0 program and CSPG+ neurons will be quantified. We expect to see reduction of CSPGs following stress due to their protective properties.

WHY DO PEOPLE LOOK AT THE RIGHT SIDE OF OTHERS' FACES?

Cameron Smith, Bruce Bridgeman

Department: Psychology

Home Institution: UC Santa Cruz

The Left Gaze Bias (LGB) is a phenomenon that occurs when subjects tend to look at the right side of faces (the left side of observers' visual space). The LGB occurs in faces but not other kinds of stimuli, and is exhibited in the direction of an observer's first eye movement as well as their overall looking time. The LGB is interesting as it is hypothesized to be a consequence of the Fusiform Face Area (FFA), which exists in the right cerebral hemisphere (contralateral to the direction of the LGB). In this experiment, we tested to see whether the LGB was a product of cortical bias that might be a consequence of the FFA, or whether the LGB was produced by some external property of faces. If faces possess some property that causes subjects to look first to the right side of the face, then mirroring faces should reverse the direction of the LGB. Across two study conditions we tested this hypothesis by flipping faces, and found no evidence of the LGB following the direction that faces were flipped. This indicates that the LGB is produced by a cortical bias rather than a bias in face stimuli as they exist external to the brain.

COLLABORATIVE INCLUSIVENESS AMONG NOVICE COMPUTER PROGRAMMERS VARIES WITH GENDER

Inez Amada Solis, Madelyn Low, Omar Ruvalcaba & Linda Werner

Department: Psychology

Home Institution: University of California Santa Cruz

Pair programming, a collaborative approach to computer programming, has been shown to increase girls' interest and retention in the field of computer science. Many girls are discouraged from pursuing computer science because of the perception that computer science is socially isolating and competitive. Middle school has been found to be a pivotal time during which many girls decide whether or not to pursue the study of computer science. We researched middle school students' collaboration while learning to program using pair programming. The present study includes four same gender dyads, two girl dyads and two boy dyads, by using video recordings of pair programming sessions. We examined inclusiveness during collaboration by coding four types of interactions between the pairs. By comparing 4 aspects of collaboration, we were able to characterize the inclusiveness of each pair. We concluded that collaboration in girl dyads was more inclusive as defined by our study, but we did not find any clear patterns to explain differences in the inclusive collaboration of different gender partnerships. By investigating collaborative styles in same gender dyads, we hoped to understand potential gender differences in inclusiveness that could lead to understanding of effective computer science education for all young students.

SHAPES AND ORIENTATIONS OF DARK MATTER HALOS IN GALAXY SIMULATIONS WITH AND WITHOUT RADIATIVE PRESSURE FEEDBACK

Teresa Spix, Miguel Rocha, and Joel Primack

Department: Physics

Home Institution: University of California Santa Cruz

Summer Program: Lamat Summer Research Program on High Performance Computing in Astrophysics

Utilizing 4 pairs of high resolution galaxy simulations at $1.8 < z < 3$ with and without radiative pressure feedback, we analyze the ellipsoidal shape and orientation of dark matter halos as a function of increasing radii from the center of a halo to its virial radius. We identify the host halo using a HOP halo finding algorithm, and shapes and axis orientations are calculated by iteratively computing the moment of inertia tensor of dark matter particles in concentric ellipsoidal shells of approximately equal particle number. Shells extend to the virial radius of the host halo unless a portion of the halo is contaminated by lower resolution particles, in which case the analysis concludes before contamination is introduced. Preliminary results show that the inclusion of radiative pressure in the simulation noticeably affects halo shapes and orientations as a function of radius. In the absence of radiative pressure feedback, we find halo shapes are triaxial at smaller radii with c/a ratios of 0.75 ± 0.09 near the center, decreasing to 0.58 ± 0.12 near the virial radius. We also find a strong tendency for the long axes of the halo at different radii to be well aligned with $\cos\theta = 0.998 \pm 0.001$. In contrast, halos formed in simulations with radiative pressure feedback remain predominantly triaxial from the center out to the virial radius, with c/a ratios 0.55 ± 0.1 , and we show that long axes alignment decreases to $\cos\theta = 0.93 \pm 0.14$. Keywords: cosmology – dark matter – galaxies: halos – methods: numerical – simulations

MODELING THE EXPECTED SYNCHROTRON EMISSION FROM DARK MATTER ANNIHILATION

Megan Splettstoesser, Emma Storm, Tesla Jeltama

Department: Santa Cruz Institute for Particle Physics

Home Institution: University of California Santa Cruz

Summer Program: Julie Packard Summer Scholar

Dark matter accounts for ~25% of the mass in the universe. However, dark matter does not interact electromagnetically, which means it does not emit light. Although dark matter itself cannot be detected directly, products of its annihilation may be observed. Weakly Interacting Massive Particles (WIMPs)—a convincing class of proposed dark matter particles—annihilate into electrons and positrons, among other things. These charged particles move at relativistic velocities, and if they travel through a sufficiently strong magnetic field, the electrons and positrons undergo synchrotron radiation, which is observable at radio frequencies. Galaxy clusters are typical astrophysical objects to use in the study of dark matter; clusters are dark matter dominated and host the magnetic field strength required for synchrotron radiation. We use the magnetic field of the Coma cluster, as well as the Navarro-Frenk-White (NFW) profile, to model the synchrotron emission of a Coma-like cluster at various frequencies. We want to examine the strength of synchrotron emission to see how existing and expected telescopes, such as LOFAR, ASKAP, and the JVLA, which operate at different frequency ranges, fare in detecting synchrotron emission, and by extension, dark matter content.

ONLINE REVIEW SYSTEM FOR PEOPLE WITH DEVELOPMENTAL AND COGNITIVE DISABILITIES

Mike Tan, Luke Buschmann, Lourdes M. Morales, Sonya Pita

Department: Computer Engineering

Home Institution: Arcadia University

Summer Program: SURF-IT

Developmental Cognitive Disability (DCD) is a condition that results in intellectual functioning significantly below average and is associated with concurrent deficits in adaptive behavior that require special education and related services. The current tools aimed to help people with DCD were designed for young children. Thus, older people with DCD are still heavily relying on one-to-one tutorial sessions with caregivers, which is inefficient and time consuming. We have developed a program aimed to help people of ten and older learn basic skills through an online review system that improves the process of administering and taking the reviews. It is a web-base project that provides reviews of numbers, uppercase and lowercase letters, shapes, colors, US currencies, and money additions. We work closely with an organization that provides services to these patients to get feedback on how to improve our system to optimize the effectiveness for patients.

STRUCTURAL EVOLUTION OF GALAXIES FROM COSMIC ASSEMBLY NEAR-INFRARED DEEP EXTRAGALACTIC LEGACY SURVEY AND COSMOLOGICAL SIMULATIONS

Vivian Tang, Yicheng Guo, Joel Primack

Department: Physics

Home Institution: University of California Santa Cruz

Summer Program: Julie Packard Summer Scholar

We determine intrinsic shapes of simulated galaxies in the early universe at redshifts between 1 and 3 by analyzing cosmological galaxy simulations with and without radiative pressure (RP) feedback from massive short-lived stars. We systematically compare our results to images of galaxies taken by the near infrared Wide-Field Camera 3 and the visible-light Advanced Camera for Surveys on the Hubble Space Telescope (HST) as part of the Cosmic Assembly Near-Infrared Deep Extragalactic Legacy Survey (CANDELS), the largest-ever HST program. From statistical analysis, we obtain axis-ratio distributions as a function of redshift, effective radius, and Sersic index (radial distribution of light) from simulations with the same resolution of HST images. We then compare this to the axis-ratio distributions of the same types of galaxies from CANDELS analyzed previously to determine two things. First, we search for discrepancies in axis ratios distributions between simulations and observations. Second, by comparing results with and without RP, we can see how much RP changes the substructure and morphology of galaxies. In particular, we want to see whether the lower-mass simulated galaxies at these redshifts are elongated rather than disk-like or spheroidal, as the CANDELS indicate. Axis ratios, effective radii, and Sersic indexes of CANDELized galaxies are measured with GALFIT fit using single-component. Analysis of galaxies without RP is currently underway, and analysis of galaxies with RP is required before conclusion can be drawn.

SYNTHESIS OF RHENIUM CARBONYL COMPLEXES AS PHOTOCORMS: CONTRAST IN DENTICITY DEPENDING ON THE FLEXIBILITY OF LIGAND

Jennyfer Teña, Indrinil Chakraborty, Pradip Masharak

Department: Chemistry and Biochemistry Department

Home Institution: University of California Santa Cruz

Summer Program: STEM Diversity - Summer Research Experience - CAMP

Although CO (carbon monoxide) has been known as the “silent killer” our body naturally produces CO in small amounts during the degradation of heme by the enzyme called heme oxygenase (HO). This has prompted researchers to utilize CO in various therapeutic settings. However, application of CO in gaseous form suffers from controlled and safe delivery. Therefore certain metal-carbonyl complexes have been proposed as carbon monoxide releasing molecules (CORMs), which are expected to show CO release in a more controlled manner to the biological targets. The major downside of CORMs is associated with sustainable delivery. Thus, the photoCORMs (photo induced carbon monoxide releasing molecules) have emerged as credible alternatives where the CO release process can be triggered upon light illumination. In our laboratory we are interested in the synthesis of photoCORMs with suitable design principle. Herein we have synthesized and characterized a rhenium carbonyl complexes, $[\text{ReCl}(\text{CO})_3(\text{qmtpm})]$ incorporating qmtpm ligand (qmtpm = 2-quinoline-N-(2'-methyltiophenyl)-methyleneimine). This complex is structurally characterized. The next step in this project is to reduce the qmtpm ligand with NaBH_4 to obtain the corresponding amine (qmtpa). The main aim is to determine whether the flexibility of qmtpa ligand (compare to qmtpm) can lead to a tridentate binding mode in contrast to the qmtpm which shows a bidentate chelation with a -SMe appendage. All the complexes synthesized are (or will be) characterized by ^1H NMR, IR, UV-Vis spectroscopy and wherever possible with single crystal X-ray crystallography.

THE SEMANTICS OF NOTHING IF NOT CONSTRUCTIONS

Michael Titone, Adrian Brasoveanu

Department: Linguistics

Home Institution: University of California Santa Cruz

Nothing if not (NIN) constructions are constructions such as "Phil is nothing if not deliberate." Our goal is to elucidate the basic truth conditions and core semantic properties of these constructions. Although these constructions contain an "if" clause, they do not license the same patterns of inference as normal conditional constructions. We conduct an acceptability study that motivates treating "nothing if not" instead as a modifier of the predicate with which it is syntactically associated. The results reveal that NIN constructions are sensitive to the aspectual nature of their main predicates, which is not predicted when analyzing them as conditionals. A formal account of NIN construction truth conditions is introduced using a paraconsistent logical framework in combination with a special modal accessibility relation, the function of which is to rule out borderline cases of the main predicate from the predicate's denotation. According to this analysis, a NIN construction affirms that the subject is in its predicate's strict, non-borderline denotation in all possible worlds. The modal analysis allows us to transition to an account of the relationship between the utterance and speakers' beliefs in terms of a model system. This theoretical component distinguishes the meaning of "Phil is nothing

if not deliberate" from its non-NIN construction counterpart, "Phil is deliberate." The success of a modal analysis shows that even if NIN constructions do not behave like conditional constructions in all respects, they are still modalized like conditional constructions and thus seem to retain an important aspect of the compositional constructions upon which they are based.

INVESTIGATION OF SEN1 IN TRNA GENE

Hanh Truong, Johnathan Nguyen, Omar Handani, Misty Peterson, Ro Kamakaka

Department: Molecular, Cell, and Developmental Biology

Home Institution: University of California Santa Cruz

Summer Program: STEM Diversity - Summer Research Experience - UC

LEADs

Only a subset of genes in any organism are active at any given time while the rest are silenced. Insulators are DNA sequence elements that recruit proteins that help separate silenced regions from highly transcribed regions. Many things are still not known about the mechanism of boundary function of insulators. The purpose of this study is to elucidate the role of Sen 1 in insulation and to determine if Sen1 interacts with other repair proteins (Srs2, Rad51, and Xrs2) in this process. Sen1 is a highly conserved gene, which codes for a DNA helicase that prevents malfunctions that happen during DNA replication. In eukaryotes, DNA strands can be replicated and transcribed at the same time. However often this leads to problems such as collisions between the RNA and DNA polymerases. This result in the formation of DNA-RNA hybrids (called R loops). Sen1 interacts with other DNA repair proteins to resolve such issues. Since R-loops are often found at or near insulator elements, we hypothesize that Sen1 functions as an insulator function. In order to test this hypothesis, we will create a yeast strain that is mutated for Sen1 using PCR products. After we create the mutant strain, we will cross it with a strain containing reporter genes that will allow us to monitor function of the barrier insulator. We will then do an assay on whether the Sen1 mutant has an effect on barrier function.

SYNTHETIC BIOLOGY ETHICS: CASE STUDY

UCSC IGEM 2014

Matthew Waldron, Breeann MacDonald, Arlene Parra, Manuel Avalos

Department: Philosophy, Biomedical Engineering

Home Institution: University of California Santa Cruz

Summer Program: iGEM

Synthetic Biology Ethics is a developing field and presents unique challenges to contemporary applied ethics. Our UCSC Ethics iGem team has developed a unique approach by integrating ethics into synthetic biology research practices.

EXPRESSION ON EBF3 IN INTRINSICALLY PHOTSENSITIVE RETINAL GANGLION CELLS

Marissa Valenzuela, Neal Sweeney, David A. Feldheim

Department: MCD Biology

Home Institution: University of California Santa Cruz

Summer Program: Summer Undergraduate Research Award Recipient

Previous work in the Feldheim lab has found that about 10% of retinal ganglion cells (RGCs), the output cells of the retina to the brain, express the transcription factor Tbr2 and that these control a set of related subconscious visual behaviors such as circadian rhythms and the pupillary light reflex. Tbr2-expressing RGCs comprise a heterogeneous population that project to multiple brain areas. Different Tbr2-positive subsets likely express unique sets of transcription factors that in turn control the formation of connections in the brain via axon guidance and cell-cell adhesion genes. Using immunohistochemistry, we found that an antibody against the transcription factor Early B-Cell Factor 3 (EBF3) co-labels 8% of Tbr2. We then stained EBF3 in combination with a panel of markers that label Tbr2 subsets including Unc5d, Cadherin-3-GFP, and Melanopsin. 82% of the Melanopsin-positive RGCs, were EBF3-positive, compared to only 13% of Cadherin-3-GFP RGCs and 4% of Unc5d-positive RGCs. In further experiments, we found that 67% of RGCs that expressed both Tbr2 and EBF3 also expressed Melanopsin, the photopigment in intrinsically-sensitive RGCs (ipRGCs). As both Tbr2 and EBF3 have established roles in fate specification in the visual system, this expression pattern suggests that these two transcription factors participate in a combinatorial code that specifies ipRGCs from progenitor cells.

CHARACTERIZATION OF FACTORS THAT CONTRIBUTE TO ALTERNATIVE SPLICE SITE SELECTION

Ernesto E. Vasquez, Zach Neeb, Alan M. Zahler

Department: MCD

Home Institution: University of California Santa Cruz

Summer Program: STEM Diversity - Summer Research Experience – Initiative for Maximizing Student Development

Alternative splicing is a nuclear process in eukaryotic cells which allows multiple isoforms of proteins to be generated from a single gene. Mutations in the pre-mRNA 5' consensus sequence activates cryptic splicing of the pre-mRNA splicing substrate. Cryptic splice sites arising from mutations in 5' splice sites lead to dysfunction among expressing genes causing genetic diseases in humans. Proteins suppressing cryptic splicing have been identified and have been shown to stimulate wild-type splicing despite the mutant 5' consensus sequence still being present. The nematode SNRP-27 is an allele specific suppressor shown to suppress a 5' splice site mutation and identified to be a homolog of the mammalian tri-snRNP 27K protein associated with the spliceosomal U4/U6•U5 tri-snRNP complex. SNRP-27 and tri-snRNP 27K share 54% amino acid identity and interestingly tri-snRNP 27K shares a 100% sequence identity within the C-terminal region characterized to act as an allele dominant suppressor. We aim to study the dominant allele characterized by homology of tri-snRNP 27K. Currently, tri-snRNP 27K's function is unknown. Using alternative splicing assays we are probing whether the function of the dominant mutant tri-snRNP 27K will affect splice site choice of mutant 5' splice sites. Various constructs of radio labeled splicing substrates will be

used to determine splice site selection in nuclear HeLa cell extract containing the dominant allele of tri-snRNP 27K versus the wild type allele.

LOCATING REGULATORY GENES FOR ARSENIC RESPIRATION IN SHEWANELLA SP. ANA-3

April Villarreal, Pamela Watson, Chad Saltikov

Department: Microbiology and Environmental Toxicology

Home Institution: Monterey Peninsula College

Summer Program: ACCESS

Shewanella sp. ANA-3 is one microorganism that can live in an arsenic-contaminated environment and uses arsenic as its alternate electron acceptor in the absence of oxygen. Shewanella sp. ANA-3 can reduce arsenate, a less water soluble form, to arsenite, a water soluble form. It is known that Shewanella sp. ANA-3's arrAB genes convert arsenate to arsenite. The regulatory gene for arrAB is still unknown. Locating Shewanella sp. ANA-3 regulatory genes can potentially lead to the direction of cleaner water. One method used to locate the regulatory gene of arrAB is by transposon mutagenesis to generate random mutants in Shewanella sp. ANA-3; the aim is for the transposon to land on a regulatory gene. Samples of Shewanella sp. ANA-3 with the transposon are then grown with either oxygen or arsenic; the absence of growth in arsenic will possibly suggest that the mutation was in a gene that regulates arsenic respiration. After mutation is visible, the mutant colony will be sequenced to determine if the mutation is in a regulatory gene.

APPLYING A HYDRODYNAMICAL TREATMENT OF STREAM FLOW AND ACCRETION DISK FORMATION IN THE WASP 12/B EXOPLANETARY SYSTEM

Ian Weaver, Phil Macias, Enrico Ramirez-Ruiz

Department: Astronomy and Astrophysics

Home Institution: University of California Santa Cruz

Summer Program: Lamat Summer Research Program on High Performance Computing in Astrophysics and UC LEADS

WASP-12b is a hot Jupiter that orbits dangerously close to its parent star WASP-12 at a proximity of about 1/44th the distance the Earth stands from the Sun, or roughly 16 times closer than Mercury. Due to tidal forces from the gravitational influence of WASP-12 and their incredibly close proximity, WASP-12b gets distorted into an egg-like shape, causing it to expand beyond its Roche lobe, allowing mass to be transferred onto its host star through the first Lagrangian Point (the point between two binary objects where the net force is zero) at a rate of 270 million metric tonnes per second. This mass transferring stream forms an accretion disk which orbits the parent star and whose presence might be unveiled by examining the periodic dimming of light absorbed by disk material. This mass transferring stream forms an accretion disk that transits the parent star, which aids sensitive instruments such as the Kepler spacecraft, whose role is to examine the periodic dimming of main sequence stars in order to detect ones with orbiting planets. By implementing the hydrodynamical code, FLASH, we

apply a comprehensive fluid treatment of the behavior of mass transfer under the influence of the system's Roche Potential in a non-inertial reference frame and subsequent disk formation. We hope to use this model in the future to generate virtual spectroscopy signatures to compare to observations from the Hubble space telescope's Cosmic Origins Spectrograph (COS).

DEVELOPING EFFECTIVE DATA ANALYSIS FOR SPEECH PATHOLOGIST

Michael Weber, Zachary Rubin, Sri Kurniawan

Department: Computer Engineering

Home Institution: DePauw University

Summer Program: SURF-IT

The Center for Disease Control (CDC) estimates that each year around 7000 children are born with cleft palates. These children often go through reconstructive surgery, yet still suffer setbacks in their verbal development due to the nature of their condition. Failure to develop proper speech skills can lead to the development of social and emotional issues later in life. The mobile application Speech Adventure seeks to provide a supplement to speech therapy following surgical correction of cleft palates through a speech therapy game, and collection and processing of diagnostic data. Current development of Speech Adventure, through the implementation of data visualization, seeks to provide robust and easy to use statistical analysis tools to speech pathologist for use in treating individuals with cleft palates.

FILLING IN THE EDGE PIECES OF THE SPLICEOSOME: STRUCTURE THROUGH PROBING

Conor Williams, Andrew Macrae, Melissa Jurica

Department: Molecular, Cell, and Developmental Biology

Home Institution: University of California Santa Cruz

To understand the structure of the human spliceosome, the Jurica lab is taking a chemical probing approach to determine the relative positions of the over 100 individual protein components. The highly dynamic nature of the spliceosome and the fact that there are many associated proteins has made structural elucidation of the spliceosome incredibly challenging. As such, a high-resolution structure of the spliceosome does not exist. Electron microscopy has provided lower resolution models of the spliceosome; however, structural details regarding individual protein position cannot be obtained from these models. The specific goal of my project is to validate the chemical probing methods and to provide a "gold" standard for interpreting the resulting data. For this, we chose the ribosome, another large RNA-protein complex for which the structure is known. We hypothesized that residues located on the surface of ribosome crystal structure will be reactive with a chemical probing reagent, while those that are buried in the complex will not. Initial results indicate that this is indeed the case. We are also working to identify a parameter by which we can quantitatively relate reactivity to the position of the residue. Our results with the ribosome show that probing techniques can be used to gain insight into the location of individual spliceosome protein components in the complex. This information will be crucial for interpreting lower resolution EM models of the spliceosome.

FULLY EVOLVED MODELS OF 0.20-0.45M_⊙ HELIUM WHITE DWARFS WITH HYDROGEN ENVELOPES

Monique Windju, Phillip Macias, Enrico Ramirez-Ruiz

Department: Astronomy and Astrophysics

Home Institution: UCSC

Summer Program: Lamat Summer Research Program on High Performance Computing in Astrophysics

We developed stellar evolution models aimed at understanding the structure of these systems at the onset of mass transfer. We are interested in the evolution of double white dwarf binary systems where the donor star is composed of a pure helium core layered with a pure hydrogen envelope. Using a stellar evolution code MESA we evolved this donor in isolation to study the effects of composition on the long-term structure of the donor and the retainment of a pure hydrogen envelope. To explore this we prescribed a range of initial helium mass fractions ($Y=0.85-0.97$) to a desired core mass in our range. We found that for the desired white dwarf mass we could predict simply the mass of the resulting envelope. Once the envelope was constructed we cooled the model as a method to deplete the hydrogen through burning at the base of the envelope. We show that the depletion time depends only on the mass of the envelope and the luminosity provided by hydrogen burning. We also investigated how the mass of the hydrogen envelope affects the mass radius relationship of the post-depletion pure helium white dwarf. For a given mass helium white dwarf in our range we produced various hydrogen envelope masses and the mass radius relationship was shown to dependent only on the mass of the degenerate helium core.

MICROBIOTA PROBING AND IDENTIFICATION IN DAPHNIA MAGNA ADULT, EGGS, AND GUT

Aigbe Woghiren, Marilou Sison-Mangus

Department: Ocean Sciences

Home Institution: UCSC

Summer Program: Julie Packard Summer Scholar

Species of the fresh water crustacean *Daphnia* are commonly used as model systems in environmental genomics, host-parasite interactions and ecotoxicity. A recent study reported that microbiota or the community of bacteria associating with *Daphnia* greatly influences the host's fitness and reproductive success. Understanding the contribution of each microbiota members to the evolutionary and ecological adaptations of the daphnid host is therefore essential and needs to be assessed. To address these questions, we isolated and cultured different bacteria from the *Daphnia* hosts and did a pilot test of probing bacteria by Fluorescent In Situ Hybridization (FISH) using oligonucleotide probes. Bacteria isolates were obtained from 3 adult *Daphnia* animals and cultured on Luria broth agar. Six bacterial clones were isolated and genotyped by DNA extraction using modified hotshot method, amplification and sequencing of the bacterial 16s rDNA gene marker. Sequences were identified by Basic Local Alignment Search Tool (BLAST) and have homologous sequences to *Pseudomonas anguilliseptica*, *Pseudomonas peli*, and *Pseudomonas gessardii*. Furthermore, FISH probing using EUB555 (a universal bacterial probe) and BET647 (Betaproteobacteria probe), were tested on a *Pseudomonas* (Gammaproteobacteria) isolate. The EUB555 oligonucleotide probe successfully binds to *Pseudomonas* while BET647 did not bind to the bacterial DNA, suggesting that the FISH method can be effectively used to distinguish the locations of different microbiota in *Daphnia* animals. The FISH method will greatly facilitate studies

that address questions on the transmission of microbiota in *Daphnia*. Bacterial isolates will be used in experimentally manipulating *Daphnia*- bacteria association to answer ecological and evolutionary questions in this crustacean model.

SYSTEMS THINKING AND CODING STUDENTS RESPONSES

Dominga Xirum, Dr. Hee-Sun Lee, Zoe Buck

Department: Physics Department

Home Institution: Hartnell College

Summer Program: STEM Diversity - Summer Research Experience - Hartnell Title V CUSP Award

Systems thinking is way to better understand systems that are complex. Systems thinking allows students to understand problems as part of an overall system that has stocks, flows, connections and mechanisms. In this project 358 students participated in an online module about land management, including topics like soil quality, erosion and food production. After doing the module, students were given an online activity with questions about the systems involved in land management. My role was to give students a score based on the level of their systems thinking in their answers (0-3), which is called coding. The scores were based on a rubric that allowed students to be scored more accurately. Those students who correctly identified stocks, flows, connections, and mechanisms were given the highest score. This was done on an Excel spreadsheet.

STRUCTURAL DETERMINATION OF AN AVIAN ASTROVIRUS CAPSID CORE

Royce York, Rebecca DuBois

Department: Biomedical Engineering

Home Institution: UC Santa Cruz

Astroviruses are non-enveloped, small RNA viruses that cause diarrhea in a wide range of species. Human astroviruses infect children less than 3 years, the elderly, and immunocompromised individuals, and are particularly problematic in pediatric and elderly care centers. Avian astroviruses cause disease, growth defects, and mortality in young poultry that is needed for food. The 'core' domain of the capsid protein forms a protective shell for this non-enveloped virus, safeguarding the RNA genome inside. Unfortunately, astrovirus is relatively under-studied, and so little is known about the molecular mechanisms of the capsid protein in virus assembly and disassembly. We are in the process of solving the crystal structure of the core domain of the Turkey Astrovirus serotype 2 (TAsTV-2). Upon determining the structure, we will better understand the role of the core domain in astrovirus particle formation. This study will also advance the knowledge of astrovirus function and evolution. Novel treatments and therapies could also be developed as a result of this experiment, increasing the health of our children and the yields of our food industry.

THE CHALLENGES ANTIBIOTIC RESISTANT BACTERIA POSE: E. COLI GROWTH IN THE PRESENCE OF AMPICILLIN AND KANAMYCIN

Anh Nguyen, Anthony Del Cid, Carolina Zamora and Victoria Auerbuch Stone

Department: Microbiology and Environmental Toxicology

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - Summer Research Institute -Hartnell Title V CUSP

*** Group Presentation. For Abstract, see Anthony Del Cid ***

SLIT/ROBO1 SIGNALING REGULATES THE ASYMMETRIC SELF-RENEWAL OF MAMMARY STEM CELLS BY CONTROLLING THE LEVELS OF INSCUTEABLE THROUGH SNAIL

Anna Zhu, Mimmi Ballard, Lindsay Hinck

Department: Molecular, Cell, and Developmental Biology

Home Institution: UC Santa Cruz

Summer Program: STEM Diversity - Summer Research Experience – Maximizing Access to Research Careers

Mammary gland regeneration following each estrus cycle and pregnancy relies on the self-renewal of a population of mammary stem cells (MaSCs). Stem cells self-renew either through an asymmetric cell division (ACD), which also generates a progenitor cell, or through a symmetric cell division (SCD) that expands the stem cell population. Disruption of the balance between ACD and SCD can lead to tissue dysfunction. Therefore, understanding how these divisions are regulated is critical, but the mechanisms involved remain poorly understood. Research from the Hinck laboratory has shown that Inscuteable (mINSC), a regulator of mitotic spindle orientation, is critical in determining whether a cell divides asymmetrically or symmetrically. Furthermore, the lab has discovered that the extracellular cue, SLIT, signaling through its ROBO1 receptor, regulates mINSC expression. Assessing the levels of mINSC in mammary epithelial cells by immunoblotting, we have found that loss of Robo1 leads to increased SNAIL expression. We further determined that cells over-expressing the transcription factor SNAIL express higher mINSC levels. Thus, given these collective data, we hypothesize that SLIT signaling regulates the asymmetric self-renewal of MaSCs by controlling the levels of mINSC through the transcription factor SNAIL. Future research will include identifying if SNAIL regulates mINSC expression directly, by binding to the mINSC promoter region, or indirectly, by interacting with secondary factors. The balance between ACD and SCD of MaSCs is often disrupted in cancer. Thus, understanding the mechanisms that regulate this delicate balance is crucial for identifying new targets for anti-cancer therapeutics.

PURSUIT OF SELECTIVITY AND SENSITIVITY FOR SACCHARIDE RECOGNITION BY A TWO-COMPONENT BORONIC ACID-BASED FLUORESCENT SYSTEM

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The application of boronic acids as synthetic receptors for sugar recognition has been previously demonstrated to be a successful method. Boronic acid groups are effective synthetic receptors due to their ability to reversibly bind 1,2- and 1,3- cis-diols. Based on the properties of boronic acids, a two-component saccharide sensing system was previously developed, comprised of a bipyridyl (viologen) unit substituted with boronic acid groups that acts dually as a quencher and receptor, and a fluorescent pyranine dye (HPTS) as the reporter unit. The fluorescence sensing mechanism is dependent on the formation of a ground state charge-transfer complex between the HPTS dye and the viologen quencher. This two-component system allows identification of mono, di-saccharides, and sugar alcohols in aqueous solution at physiological conditions. Three quenchers, mono or bis-boronic appended viologens (o-monoalkyl, o-MBV, and o-BBV) were synthesized to test the selectivity and sensitivity of achieving a fluorescence signal. The quenched fluorescence for the three quenchers was measured at a concentration of 400 μ M to 4 μ M HPTS, yielding 43.9%, 87.9%, and 94.4% fluorescence decrease, respectively. Stern-Volmer (S-V) plots were generated to examine the quenching properties of mono or bis-boronic substituted viologens. Results demonstrate that the bis-substituted viologen receptor has a greater fluorescence recovery than the mono-substituted viologen.

DETERMINATION OF IC₅₀: INHIBITION OF THE SOYBEAN LIPOXYGENASE USING NORDIHYDROGUAIARETIC ACID

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Lipoxygenases are a family of iron containing enzymes that are involved in a diverse range of cell function in both plants and animals. There is evidence linking mammalian lipoxygenases to several common biological dysfunctions such as asthma, heart disease, cancer, and stroke. As a result, it has become important to develop effective inhibitors to lipoxygenases. The effectiveness of nordihydroguaiaretic acid (NDGA) as an inhibitor toward soybean lipoxygenase-1 (sLOX-1) was measured by quantifying the IC₅₀, which is the NDGA concentration at which the enzyme activity is reduced by exactly 50%. A spectrophotometer was used to measure the change of absorbance of the product formed by the enzyme-substrate reaction. This data was subsequently used to calculate the maximum rate of the reaction. Taking into consideration the fact that methanol has a slight inhibitory effect on sLOX-1, a control assay with only methanol was measured (1.8 mL CHES (pH 9.2), 10 μ M linoleic acid (LA), 10 μ L methanol, and 200 μ L sLOX-1). The same procedure was used to determine the sLOX-1 rate in the presence of various concentrations of NDGA and the percentage of inhibition was

calculated for each assay. We determined that NDGA has an IC₅₀ of 0.5 μ M which suggests sufficient inhibitory properties to warrant further investigation. The next step will be to test the compound for important pharmaceutical properties such as bioavailability, target specificity and its effectiveness on human LOX before drug development can occur.

THE QUANTIFICATION OF FREE METAL IONS USING TITRIMETRIC AND SPECTROPHOTOMETRIC ANALYSIS

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Metals such as calcium, magnesium, and iron play essential roles in many biological processes such as sites for redox activity and assistance in the binding of ligands. Due to their reactive nature, these metals must be constantly regulated in the body in order to maintain optimal concentrations otherwise an overdose or deficiency of these ions could result in disease. Given this sensitivity, careful maintenance of metal content in water is extremely important. Quantification of metal ions in water is possible using titrimetric and spectrophotometric analysis. Hence, the main objective of our experiment was to determine the concentrations of free metal ions in solutions with the aid of ligands utilizing these two techniques. Determination of the collective concentration of Mg²⁺ and Ca²⁺ ions in an unknown solution was determined through titrimetric analysis using Ethylenediaminetetraacetic acid (EDTA) and Eriochrome Black T (EBT) as the titrant and indicator, respectively. EDTA is a much stronger ligand than EBT and once it has bound all the ions in solution, the conjugated form of EBT will be present and thus a color change will be observed, signifying the endpoint. After the endpoint is achieved, dilution calculations were executed in order to determine the collective concentration. Finally, to determine the concentration of iron in an unknown solution, spectrophotometry was employed. A standard curve for iron was then established which used the ligand 1,10-Phenanthroline as a colorimetric tool. Collected absorbance data allowed for the extrapolation of an extinction coefficient using Beer's Law that could then be used to back calculate the concentration of an unknown Fe²⁺ solution.