

Entry Number: 1 GB DISPLAY ONLY

ADOLESCENT TIME RELATION AND BULLYING DIFFERS BETWEEN GENDERS: A FEMALE EFFECT

By: Alyssa Youngquist

Psychology: Developmental Psychology

Faculty Advisor: Dr. Zena R. Mello

Abstract: Almost 30% of youth have indicated being involved in some form of bullying (i.e., bully, victim, both bully-victim; U.S. Department of Health and Human Services, 2014). This study sought to contribute toward this topic by examining its relationship with a new psychological construct--time perspective. Results from a self-reported survey indicated that adolescents who were oriented toward the past were significantly more likely to be either a victim or bully-victim than those who were oriented toward the present and the future. This research will be used to inform bully intervention programs.

Entry Number: 2 GB DISPLAY ONLY

PURCHASING HAPPINESS; IT'S WRITTEN ALL OVER YOUR FACE

By: Kristine Tom

Psychology

Faculty Advisors: Dr. Ryan Howell and Dr. Mark W. Geisler

Abstract: Psycho-physiological study assessing subjective, behavioral, and physiological measures of happiness in consumer spending habits.

Entry Number: 3 GB

EMOTIONAL AMBIVALENCE DURING THE PRODROMAL PHASE OF SCHIZOPHRENIA

By: Alen Tersakyan, Celena Valenzuela, and Josephine Keenan

Psychology

Faculty Advisor: Dr. David Gard

Abstract: Negative symptoms of schizophrenia (i.e., flat affect, anhedonia) often cause functional impairments in the daily lives of patients. Often, the effects of negative symptoms cause deficits in emotional processing such that patients may experience abnormal levels of negative emotions, and may not be able to inhibit them (Horan, Green, Kring, Nuechterlein, 2006). In schizophrenia there is evidence that negative symptoms may be partially driven by the experience of emotional ambivalence, the simultaneous experience of conflicting emotions (Cohen & Minor, 2010). If so, emotional ambivalence may be present in those who are at risk for developing schizophrenia as well and could provide an early indicator of risk for the disease, allowing for earlier interventions. The current study sought to examine the relationship between emotional ambivalence and individuals who are at risk of developing schizophrenia.

Entry Number: 4 GB

PLEASANT TO AVERSIVE: BRAINWAVE RESPONSES TO EATING CHOCOLATE PAST SATIATION

By: Alen Tersakyan, Erica Walker, Anar Salayev, and Alejandro Heredia

Psychology

Faculty Advisors: Dr. David Gard and Dr. Mark W. Geisler

Abstract: Recent neurobiological research has distinguished between the experience of "wanting" and "liking" pleasurable or rewarding stimuli, and these differences have been especially helpful in psychopathology research. However, the conscious self-reported discrimination of wanting and liking has been difficult to reliably measure. We sought to examine this distinction using frontal asymmetry with electroencephalography (EEG). We hypothesized that since EEG can reliably measure approach-withdrawal behaviors, it should also measure changes in "wanting" of pleasurable stimuli (Davidson et al., 1990). EEG was recorded while hungry participants ate chocolate until they were past satiation. Participants reported subjective ratings of: a) how much they liked the current piece, and b) how much they wanted the next piece. Results indicate no electrophysiological difference between "wanting" and "liking".

Entry Number: 5 GB

PSYCHOPATHOLOGICAL PREDICTORS OF PSYCHOLOGICAL INERTIA

By: Alen Tersakyan, Catherine Kircos, Bree Koenig, and Valerie La

Psychology

Faculty Advisor: Dr. David Gard

Abstract: Psychological inertia, or a failure to initiate goal directed behavior, often results in the tendency to stick with the default option (the Status Quo Bias) when making a decision, even if the default option is obviously inferior and results in harmful or undesirable consequences and the effort required to initiate the behavior is low. Negative Inertia occurs when an individual fails to avoid something negative (e.g., failure to take a necessary medication to avoid health consequences), whereas Positive Inertia occurs when an individual fails to pursue something positive (e.g., failure to sign up for a retirement savings plan). Abnormalities in motivation are common in a variety of psychopathologies. We hypothesized that these abnormalities may affect inertia in a valenced image task. Participants (N = 65) were shown a default image (either a negative or a neutral image) and were given the option of pressing a button to switch to viewing a more preferred, higher valenced image. Participants displayed considerable Negative and Positive Inertia, switching from a negative to a neutral image in only 56% of trials (Negative Inertia) and switching from a neutral to a positive image in 51% of trials (Positive Inertia). Furthermore, more severe depressive and prodromal symptoms significantly predicted increased Negative and Positive Inertia (less switching). Interestingly, more severe anxiety significantly predicted decreased Negative Inertia (more switching). Ambivalence (SAS), anticipatory and consummatory pleasure (TEPS), and prevention and promotion regulatory focus (RFQ) were not significant predictors of either Negative or Positive Inertia. These results indicate that depressive and prodromal symptoms are related to difficulty both avoiding negative consequences and pursuing positive rewards, whereas anxiety is associated with a decreased avoidance of negative consequences. Building on these findings, there is potential for the development of treatments aiming to decrease inertia and increase compliance and motivation in psychiatric patients.

Entry Number: 6 GB

POSTTRAUMATIC STRESS DISORDER: DESENSITIZATION TO NON-TRAUMA RELATED
NEGATIVE STIMULI

By: Callan R. Lujan, Rachel Gonzalez, and Jessica Mcmillin

Psychology

Faculty Advisor: Dr. Mark Geisler

Abstract: Negative expectations of one's self, others, or the world are a symptom of posttraumatic stress disorder (APA, 2013). To provide electrophysiological evidence for this symptom, and show that negative expectations are an automatic process rather than a product of rational thought, participants were given an adapted visual oddball paradigm with stimuli from the Reflexive Imagery Task. In order to measure an expectation violation, the stimuli were set up in valence-congruent and valence-incongruent trials, in which target images were preceded by three context images. We hypothesized that individuals with PTSD would have smaller P300 amplitudes to negative images when the images followed a positive context due to negative expectations. Additionally we hypothesized that those with symptoms would also have smaller P300 amplitudes in response to the negative targets when they followed a negative context due to desensitization to negative stimuli.

Entry Number: 7 GB

IMPLICATIONS OF EMOTION MINDFULNESS ON DEMAND-WITHDRAW COMMUNICATION

By: Ella Tarnate and Alina Belohlavek

Psychology

Faculty Advisor: Dr. Sarah Holley

Abstract: Demand-withdraw is a common, harmful communication pattern in which one partner nags or pressures while the other partner avoids or withdraws. Because demand-withdraw is strongly linked to relationship dissatisfaction, it is important to understand what individual factors can mitigate this conflict pattern. This study focused on the association between emotion mindfulness (i.e., paying attention to feelings that are presently occurring) and demand-withdraw behaviors. Undergraduate students and their romantic partners (N = 257 couples) completed an online survey. Hypotheses were evaluated using actor-partner interdependence modeling; the model controlled for relationship satisfaction and relationship length. Our findings suggest that emotion mindfulness is negatively correlated with the tendency to be in the withdrawing

role. This suggests that individual differences in being mindful of emotions have important implications for demand-withdraw behaviors during relationship conflict.

Entry Number: 8 GB

SUPPORTING CHINESE PRESCHOOLERS' SOCIAL AND EMOTIONAL DEVELOPMENT THROUGH A TECHNOLOGY-INTEGRATED PROGRAM

By: Jessica Dow

Psychology

Faculty Advisor: Dr. Jae H. Paik

Abstract: The purpose of this study is to examine the efficacy of using technologically-integrated programs as a way of teaching children emotion knowledge. Teacher's taught preschool children, in their regular classrooms, emotion knowledge by using an iPad application with various games that specifically targets emotional development. Children were measured on the Emotion Matching Task (EMT) before and after the iPad program. Data has already been collected in Chengdu, China at a preschool. A 2 (Test Session: pre- and post-test EMT score; within subjects) by 2 (Condition: experimental vs. control condition; between subjects) repeated measures ANOVA was conducted and results showed a significant main effect of Test Session, $F(1, 58) = 38.34, p < .001$ and a main effect of Condition, $F(1, 58) = 12.59, p = .001$. More importantly, there was a significant interaction, $F(1, 58) = 7.75, p = .007$.

Entry Number: 9 GB

WHY ARE SOME PEOPLE MORE CREATIVE THAN OTHERS? AN ELECTROPHYSIOLOGICAL APPROACH

By: Kristina Pfeifer, Nancy Garcia, Gavin Dowd, and Reza Gafur

Psychology

Faculty Advisor: Dr. Mark W. Geisler

Abstract: Why are some people more creative than others? Past research has suggested that creative people have unique associative abilities, which allows them to easily think originally when solving a creative problem. These unique associative abilities may be a product of atypically wired associative networks. To test this theory, we investigated the N400 ERP component and sustained negativity as measures of associative processing. Greater N400 amplitude may occur as a result from inability to easily access associative information about a concept (Kutas & Federmeier, 2000). A positive shift in sustained negativity may occur from successfully establishing a new association between remote concepts (Kröger et al., 2013) Since creative people may have more flexible associative networks, we hypothesized that the N400 and/or sustained negativity would show less amplitude to distantly related or unrelated word pairs.

Entry Number: 10 GB

"WHAT'S IN A NAME?" ON THE TENDENCY TO HOMOGENIZE WOMEN AND INDIVIDUATE MEN.

By: Lyndsey Wallace, Chirag Dalibar, Callan Lujan, and Kristina Pfeifer

Psychology

Faculty Advisor: Dr. Avi Ben-Zeev and Dr. Mark W. Geisler

Abstract: Simone de Beauvoir is famous for writing: "...men say 'women', and women use the same word in referring to themselves" (Beauvoir, 1949, p.8). The rationale is that a woman tends to be categorized by her gender, and as 'other', even by women. We ask whether de Beauvoir's theorizing captures a current social reality in which women are perceived more categorically (i.e., at a group level) are thus less individuated than men. // The basic level advantage (e.g., Mervis & Rosch, 1981) is central to categorization, such that people tend to categorize instances fastest at an intermediate/basic level of abstraction (e.g, dog) than at the subordinate (e.g., Chihuahua) or superordinate (e.g., animal) levels. The underlying theorizing is that basic levels afford the most essential information about a category without being too specific or too general (Rosch, Mervis, Gray, Johnson, & Boyes-Braem, 1976; Mervis & Rosch, 1981). However, a notable exception occurs when people develop expertise and are just as quick to categorize at the subordinate level, termed the subordinate-level shift (Johnson & Mervis, 1997; Tanaka, 2001). // D'Lauro, Tanaka, and Curran (2008) showed that even with acquired expertise, a homogenous set of stimuli, comprised of female celebrity faces, tends to produce a basic level advantage. Participants were first presented with a label for 255 ms, which was either a female celebrity's name, such as 'Jennifer Garner' (subordinate level) or 'human' (basic level). Then, participants were shown a

photograph for 255 ms and were asked to make a true/false judgment about whether the photograph matched the previously shown label (e.g., Is this Jennifer Garner?). D'Lauro et al. (2008) found that priming a female celebrity face with the basic level elicited faster reaction times than priming with the female celebrity's name. It is impossible to know however, whether this 'homogenous set effect' was due to the fact that the set of stimuli were comprised of only female faces without running an additional condition of male faces. / / Thus, to explore whether women are perceived more categorically than men, we replicated and extended D'Lauro et al.'s (2008) categorization paradigm by including a set of all male celebrity faces. We reasoned that if female faces would produce a basic level advantage, similar to D'Lauro et al., but male faces would elicit a subordinate-level shift instead, that this finding would imply that males tend to be more individuated than women. / / We used sets of both female and male celebrity faces; piloted to be equivalent on fame, likability, attractiveness, and age. 136 undergraduate students (81 female) participated for course credit. As expected, and consistent with D'Lauro et al.'s homogeneity hypothesis, the set of female faces produced a basic level advantage: Participants were slower to respond to a female face after being primed with a name ($M = 632$ ms, $SE = 19.61$) than with 'human' ($M = 517$ ms, $SE = 19.98$). However, the set of male faces produced a subordinate-level shift: Participants responded with equal ease to male faces after being primed with a name ($M = 567$, $SE = 20.5$) or with 'human' ($M = 557$, $SE = 20.89$), $F(2,264) = 5.64$, $p = .004$. There was no effect of participant gender. /

Entry Number: 11 GB

WORKING MEMORY-BASED ACTION CONTROL: AN INTERFERENCE PARADIGM FOR NEUROIMAGING

By: Sabrina Bhangal

Psychology

Faculty Advisor: Dr. Ezequiel Morsella and Dr. Mark W. Geisler

Abstract: Representations held in working memory can result in interference resembling that of distractors in response interference paradigms such as the classic flanker task (Eriksen & Eriksen, 1974; Hubbard et al., 2013). We developed a paradigm in which participants ($n = 16$) pressed certain buttons in response to certain visual stimuli (letters). At the beginning of each trial, participants were presented with a letter pair (the memoranda), with one letter presented over the other and with the two letters separated by a horizontal bar. Participants held the letter pair in mind over a delay (4 s). Afterward, participants were presented with only one of the two letters (the Letter Cueing condition). In the Congruent condition, participants responded to this letter; in the Incongruent condition, participants responded to the other letter of the pair, which was not presented visually but held in memory. In a separate, Spatial Cueing condition, a non-letter cue (a dot) replaced the letter stimuli and was presented either above or below the horizontal bar, indicating the correct response. In the Congruent condition, participants responded to the corresponding letter; in the Incongruent condition, participants responded to the other (un-cued) letter. Response latencies were longer for Spatial Cueing than Letter Cueing $F(1,15) = 10.95$, $p < .01$. In the Spatial Cueing condition, latencies in the Incongruent condition were longer than in the Congruent condition $t(15) = 3.52$, $p < .01$. This paradigm is amenable to neuroimaging techniques that can elucidate the neural aspects of working memory-based action control.

Entry Number: 12 GB

COGNITIVE BIASES AND INVOLUNTARY COGNITIONS IN AT-RISK POPULATIONS

By: Wei Dou, Hyein Cho, and Anthony G. Velasquez

Psychology

Faculty Advisors: Dr. Mark W. Geisler and Dr. Ezequiel Morsella

Abstract: Research suggests that individuals with elevated anxiety and depression tend to exhibit a bias toward threat-related or negatively valenced stimuli. Using a new paradigm, the Reflexive Imagery Task, we investigated how individuals with these characteristics suppress unintended thoughts (involuntary subvocalizations) toward valenced visual stimuli (e.g., image of a spider).

Entry Number: 13 GB

FATHER-CHILD RELATIONSHIP'S IMPACT ON FATHERING GOAL MEETING AND FATHER-CHILD INTERACTION IN ADOLESCENCE

By: Xiaoye Xu

psychology

Faculty Advisor: Dr. Jeff Cookston

Abstract: The quality of the parent-child relationship is socially constructed between parents and children. Parents who interact more with children are often regarded to have better parent-child relationship. To understand parent-child interaction and their relationship more concretely, we examined factors that influence the goals fathers set for themselves in their parenting. We found pathways from earlier father-child relationship quality predicting later father-child interaction through the mediation role of fathering goal meeting.

Entry Number: 14 GB

APPROACH, AVOID, OR BOUNCE-BACK: THE MEDIATING ROLE OF SELF-TALK

By: Zaviera Bonita Reyes

Psychology

Faculty Advisor: Dr. Seung Hee Yoo

Abstract: To date, this is the first study to examine self-talk as a mechanism contributing to resilient outcomes. Self-talk is a cognitive process that represents an individual's beliefs and thoughts about themselves, others and their world (Calvete & Cardeñoso, 2002). The following two studies examined self-talk or "inner speech" in the context of resilient outcomes in a general population to a recalled stressor and among college students experiencing an academic stressor (i.e., an exam or presentation). In the general population, self-talk partially mediated the relationship between approach (drive) sensitivity and avoidance sensitivity predicting resilience and the resilient outcomes (i.e., the experience of positive affect despite a stressor). Additionally, self-talk strategies and motivation styles showed a similar pattern across both samples whereby reassuring self-talk and approach sensitivity were associated with greater resilient outcomes; whereas critical self-talk and avoidance sensitivity were associated with less resilient outcomes.

Entry Number: 15 GB

"DEAR MOTHER OF THE TANTRUMING CHILD AT TARGET": MODERATORS OF PARENTAL DISTRESS TOLERANCE

By: Allie Morford

Developmental Psychology

Faculty Advisors: Dr. Jeff Cookston and Dr. Melissa Hagan

Abstract: Emotion regulation (ER) is essential to every day, normative functioning. One aspect of emotion regulation is distress tolerance (DT) - the ability to persist in goal-directed activities when experiencing aversive states. Although research on the normative trajectory of DT during middle adulthood is lacking, there is a need to focus specifically on parents for two reasons: Children depend on parents for skills necessary to successful development, and parenthood is an especially emotion provoking phase of adulthood. Theoretically, emotion regulation becomes less effortful over time due to long-term exposure and practice of dealing with emotion-evoking experiences. The purpose of the current study was to examine distress tolerance in a sample of parents who have children at three different developmental stages (i.e., infancy, toddlerhood, preadolescence), and evaluate potential moderators of this relationship. A total of 602 parents (66.3% female, Mage = 32.31 years, SD = 7.07) completed an online survey. The results indicated that although there was not a main effect of child's age and parent distress tolerance, there were successful moderation models. Children's negative affect and parents' feelings of social support were moderators of child age and parent distress tolerance. The implications of the current findings are discussed in the context of how the findings might contribute to future studies within developmental and clinical psychology.

Entry Number: 16 GB

MECHANISMS OF MARITAL DISCORD SPILLOVER INTO YOUNG ADULT DATING VIOLENCE

By: Chase J. Boyer

Developmental Psychology

Faculty Advisor: Dr. Jeff Cookston and Dr. Sarah Holley

Abstract: It is widely accepted that violence in the family of origin predicts violence perpetration or victimization later in future relationships. However, the bulk of intergenerational violence investigations have relied upon cross-sectional methods and failed to account for the interdependent roles of both mothers and fathers. Guided by family systems theory and using structural equation modeling, we demonstrated the cascading effects of marital violence exposure during adolescence to dating violence in young adulthood as

explained by harsh parenting in late adolescence and emotional adjustment in young adulthood among a sample of target adolescents (N = 206), studied from age 12 to age 23, and their parents. The model accounts for the interdependence between mothers' and fathers' use of marital violence and harsh parenting. Our findings demonstrated a significant indirect path from fathers' use of marital violence to young adult dating violence and that this relationship was explained by mothers' harsh parenting when adolescents were age 16 years and young adult externalizing when target adolescents were 20-years-old. Implications for these findings are discussed.

Entry Number: 17 GB

WHO SHOULD I TALK TO ABOUT HIM? GUIDED COGNITIVE REFRAMING WITH NON-PARENTAL SOURCES ABOUT THE FATHER-CHILD RELATIONSHIP

By: Kenn Dela Cruz

Developmental Psychology

Faculty Advisor: Dr. Jeff Cookston

Abstract: Although conflict increases between parents and children in early adolescence, less is known about how adolescents interpret and cope with such conflict. Previously (Cookston et al., 2015), we found that adolescents commonly seek out non-parental figures to help them understand or reframe their relationships with their co-residential fathers/stepfathers, with mothers being the most commonly sought source. In the current study, we limited our sample to those adolescents (N = 129) who indicated they only spoke to one other reframing agent (versus multiple agents). We assessed two readily-categories along which the other sources varied: (1) age (i.e., younger sources such as siblings and friends versus older ones such as aunts and teacher) and (2) whether the source of reframing was related to the child (e.g., siblings, grandparents) or not (e.g., friends, school counselor). Both models followed a novel nine pathway solution that included a link between more frequent reframing and feeling worse about the father-child relationship after reframing. Contrary to our hypothesis, the age model did not show any differences in pathways between older and younger sources. The family relation model supported part of our second hypothesis where two pathways could not be fixed between the two categories, suggesting differences in guided cognitive reframing between related and unrelated sources.

Entry Number: 18 GB

POSITIVE AND NEGATIVE WELL-BEING AMONG ADOLESCENTS FROM THEOLOGICAL AND CONVENTIONAL SCHOOLS IN INDIA

By: Manpreet Kaur

Developmental Psychology

Faculty Advisor: Dr. Zena R. Mello

Abstract: In the study, we examined positive and negative well-being among 60 students from theological and conventional schools in India. Participants included 30 students (50% females) from each school, aged 16-18 years-old. Self-reported measures included life satisfaction and achievement motivation for positive well-being and stress and anxiety for negative well-being. Results indicated that theological school students reported much lower life satisfaction compared to students in conventional schools with a large effect size. Similar patterns were observed with stress and anxiety, although effects were small. There were no differences in achievement motivation between the two schools. Regarding gender, findings showed that males reported lower stress and anxiety than their female counterparts and these effects were large. Genders did not differ in life satisfaction and achievement motivation.

Entry Number: 19 GB

THE RELATIONS AMONG IMPLICIT THEORIES OF INTELLIGENCE, SELF-COMPASSION, AND MENTAL HEALTH AMONG CHINESE ADOLESCENTS

By: Riley Chu

Developmental Psychology

Faculty Advisor: Dr. Jae H. Paik

Abstract: Mental health among adolescents has become increasingly important as about 20% of the adolescents across the world experience a mental health problem, most commonly depression and anxiety [1]. / China is no exception to this concerning phenomenon, with some major Chinese cities surpassing the world's average such as Hunan reporting 22.2% and Hong Kong reporting 50% of the adolescents suffering from depressive symptoms [2]. / Given the substantial mental health crisis among Chinese adolescents, it is essential to identify

factors that might mitigate these deleterious effects. / Studies have shown links between self-compassion as well as implicit theories of intelligence with mental health among adults: / Self-compassion involves being kind and understanding to oneself when faced with personal failures [3]. / Self-compassion has been found to be negatively related to anxiety, personal distress, and depression while positively related to positive self-affect, positive coping, life satisfaction, and happiness [4]. / Implicit theories of intelligence (ITI) asserts that people have different mindsets in regards to the nature of intelligence [5]. / Entity Theorists: believes intelligence is a fixed, unchangeable trait; attribute success through innate abilities. / Incremental Theorists: believe that intelligence is a malleable trait; attribute success to hard work and effort / Entity theorists have been associated with greater levels of anxiety, anger, hopelessness, negative emotions, self-handicapping, emotional distress, aggressive and depressive symptoms [6]. / To date, no studies have examined the impact self-compassion and ITI have on mental health among Chinese adolescents. The present study examined the relations and the impact self-compassion and implicit theories of intelligence have on mental health among Chinese adolescents. / /

Entry Number: 20 GB

ELECTRONIC PROCEDURES FOR AUTONOMOUS CREWS IN SPACE: AN EXAMINATION OF INDIVIDUAL USE OF AUTOMATED PROCEDURE SUPPORT

By: Jessica Lam, Jessica Dow, David Mast, Laura Wayne, and Megan Winston

Industrial/Organizational Psychology

Faculty Advisor: Dr. Kathleen Mosier

Abstract: Astronauts on long-duration missions will lose the connection to ground support that enabled collaborative task performance. They will be on their own as they encounter and use new systems and perform unfamiliar tasks guided solely by electronic procedures. The quality of these electronic procedures in terms of the interface, level and adaptivity of automation, and attention to human-computer interaction and human-automation interaction principles will be critical for successful system management, as well as failure diagnosis and repair. The current study examines the impact of various levels and types of automated procedure support (i.e., different degrees of automation) on system learning and task performance.

Entry Number: 21 GB

APPRAISING VALUE STRENGTH: AN ANALYSIS OF STUDENT PERCEPTIONS OF SF STATE CORE VALUES

By: Emma Curran, Rebecca Ornellas, Laura Wayne, Michael King, Megan Winston, Darryl Hunter Jr., David W. Mast, Keith Chisholm, and Eric Nestingen

Industrial/Organizational Psychology

Faculty Advisor: Dr. Kevin Eschleman

Abstract: Data were collected from 832 San Francisco State (SF State) students to measure perceptions of how well the university is living up to its core values. We demonstrated convergent, divergent, and predictive validity for the SF State Value Strength scale. Value Strength was significantly associated with university outcomes (e.g., satisfaction, citizenship behaviors, willingness to donate). In addition, students in general share the values of the university, but perceive areas for improvement. Community demonstrated the weakest value strength. Comparisons between colleges were also evaluated. /

Entry Number: 22 GB

LONELINESS AND EXPRESSIVE SUPPRESSION: THE ROLE OF PESSIMISM ABOUT EXPRESSIVITY

By: Pooya Razavi

Social Psychology

Faculty Advisor: Dr. Seung Hee Yoo

Abstract: Loneliness triggers a state of hypervigilance to social threats. As a result, lonely individuals tend to form pessimistic views of the social world, and, choose prevention-focused interaction strategies in order to minimize the possibility of negative social evaluations. In the present research, the relationship between loneliness and suppressing emotions was investigated across three studies (N = 625). We hypothesized that (a) social isolation will lead to negative beliefs about expression of emotions (prevention-focused strategies); (b) such beliefs lead to the suppression of emotions. In Study 1, questionnaires were used to assess participants' loneliness, emotion regulation, and attitudes towards expressing emotions. In Study 2, participants were led to imagine a social interaction and report their expressivity, and beliefs about emotional expressivity. In Study 3,

loneliness (vs. connectedness vs. sadness) was induced, and participants' expressive suppression was measured. Overall, results supported our hypotheses, demonstrating that loneliness leads to the suppression of emotions, and this relationship is mediated by negative attitudes towards expressivity. These findings suggest that a pessimistic worldview leads lonely people to choose a costly regulatory strategy.

Entry Number: 23 GL1

L-ARGININE THROUGH NITRIC OXIDE SIGNALING MODULATES SOMITE DERMOMYOTOME GROWTH AND EXPANSION IN EARLY CHICK DEVELOPMENT

By: Fernando R Curiel and Gretchen Hazel Ford

Cell & Molecular Biology

Faculty Advisor: Dr. Wilfred Denetclaw

Abstract: During early embryo development the embryo is undergoing many morphological changes to form many different tissue structures. One of the first tissue structures to form is the somites (transient progenitor stem cells). In adult skeletal muscle NO is known to stimulate muscle stem cells called satellite cells for muscle regeneration. We have shown that NO is activated and signals strongly in the early chicken embryo. However, the role of NO signaling in early chick embryo development is not well known. Virtually nothing is known about NO's role in cervical level somite dermomyotome growth and expansion coupled with myogenesis. NO is a very potent signaling molecule, it is strongly expressed in the ectoderm (embryonic tissue). Nitric oxide is formed by a family of enzymes called nitric oxide synthase (NOS). By using L-arginine as its substrate it catalyzes redox reaction forming nitric oxide (NO). We hypothesize that ectoderm NO signals for growth and expansion of the dermomyotome. To study this, L-arginine the substrate for the NO canonical signaling pathway was used to stimulate NO signaling or to upregulate NO expression to demonstrate cause and effects for somite growth and expansion coupled with myogenesis. Primarily my assay for NO effects on dermomyotome growth is by immunofluorescence labeling of the myotome under various effects of regulating NO signaling. Here we show that NO activator compounds in HH 15-19 chick embryos such as L-arginine decrease dermomyome growth and expansion when compared to untreated. In, addition, DAF-2DA fluorescence showed high amounts of L-arginine like 25mM reduced NO expression in the ectoderm. These findings suggest that NO has regulatory control over early myogenic mechanisms in the chick embryo. Furthermore, these experiments for the first time assign a role of dynamic NO formation in the ectoderm layer and will provide additional insight into its role as a mediator functioning to activate activated dermomyotome growth and expansion coupled with myogenesis in somites.

Entry Number: 24 GL1

MATRIX METALLOPROTEINASE INHIBITION AFTER HEART ATTACK

By: Kimberly Spaulding

Cell & Molecular Biology

Faculty Advisors: Dr. Frank Bayliss and Dr. Mark Ratcliffe

Abstract: Myocardial infarction (MI) occurs when blood flow is blocked in the coronary artery (LAD, Fig. 1) and the downstream tissue dies, thereby causing a heart attack – a leading cause of heart failure in developed countries. Left ventricular (LV) cardiac remodeling is the process by which left ventricular size, shape, structure, and physiology of the heart undergoes rearrangement after a heart attack. LV remodeling is associated with the development of heart failure and patient mortality. / Decreased contractility in the area surrounding the MI which has normal blood flow (non-ischemic borderzone) is in part due to cleavage of myosin light chain 1 by intra-cellular matrix metalloproteinase (MMP)-2. MMP-2 is a biological molecule that usually degrades collagen in the matrix surrounding the cells in the heart. When cardiac cells are stressed, MMP-2 builds up inside the cell where it degrades structural proteins including those responsible for cardiac muscle contraction. / We recently showed that treatment with the broad spectrum MMP inhibitor, Doxycycline, for 2 weeks was associated with an improvement in borderzone contractile protein function in vitro. / / /

Entry Number: 25 GL1

LIVE CELL TRACKING OF RBM20-INDUCED CARDIOMYOPATHY IN HUMAN IPS-CARDIOMYOCYTES

By: Kristin Holmes

Cell & Molecular Biology

Faculty Advisor: Dr. Carmen Domingo

Abstract: Dilated cardiomyopathy (DCM) is one of the main causes of sudden cardiac death. Many genes have been linked to DCM, including many genes related to sarcomere structure or contractile function, and the heterogeneity of the disease makes finding clinically-relevant targets challenging. RBM20 is an RNA-binding protein that regulates RNA splicing and is essential for proper cardiac development and function. Recently, genome-wide association studies have identified a “hot spot” of human DCM-related single point mutations were found in RBM20 and animals studies have shown that RBM20 loss-of-function cause DCM. / My research focuses on utilizing CRISPR interference (CRISPRi) to inhibit RBM20 gene expression to investigate its role in cardiomyocyte function and pathology. I will generate induced pluripotent cell (iPSC) lines containing a tetracycline-inducible CRISPRi system for gene knockdown, and a fluorescent live cell reporter of for imaging sarcomeric architecture as a readout for sarcomeric disarray (a hallmark of DCM). One such reporter is a fusion protein of Lifeact—which marks filamentous actin f (F-actin)—and fluorescent protein, mEos4b, which will be used to label the sarcomeres in iPSC-derived cardiomyocytes (iPS-CM). I will knockdown RBM20 with CRISPRi to investigate its role in DCM. The result of this research will help to understand the exact cellular changes that occur in iPS-CMs due to RBM20 deficiency, and possibly use this knowledge to identify strong cellular markers and targets for clinical applications. /

Entry Number: 26 GL1

PP1 PHOSPHATASES GSP-3 AND GSP-4 AS KEY REGULATORS OF SEX-SPECIFIC CHROMOSOME SEGREGATION IN C. ELEGANS

By: Marco Monroy

Cell & Molecular Biology

Faculty Advisor: Dr. Diana Chu

Abstract: Complete sterility can arise due to defects in chromosome segregation. Much of the focus in trying to understand the mechanistic players of chromosome segregation has been on oocyte meiosis and mitosis. Sperm meiosis has received little attention. With one-third of infertility cases due to paternally sourced errors, there is a need for a better understanding of chromosome segregation in sperm. Using *C. elegans* our lab has shown that sperm-specific PP1 phosphatases GSP-3 and GSP-4 are key regulatory proteins for successful sperm meiosis. The deletion of these two genes results in a failure of sister chromatid separation during meiosis II and sperm aneuploidy. Additionally we have previously shown the characteristic lagging X-chromosome of sperm meiosis is disrupted in *gsp-3/4* mutants. The failure in segregation of the lagging X chromosome could be due to instability of mid-zone microtubule attachments. Characterization of central spindle proteins ZEN-4 and SPD-1, mid-zone microtubule stabilizing proteins will provide us a greater understanding of their role in microtubule stability and chromosome segregation. I hypothesize that the sperm specific PP1 phosphatases GSP-3 and GSP-4 regulate the localization of ZEN-4 and SPD-1 during *C. elegans* sperm meiosis. Through the use of immunohistochemistry and high resolution microscopy I aim to show that GSP-3/4 regulates the dynamics of these two key central spindle proteins. These mid-zone microtubule-stabilizing proteins have been found to be necessary for completion of oocyte meiosis. Confocal microscopy will be conducted in wild-type worms and in *gsp-3/4* mutant worms. Seeing as microtubule organization is unique during sperm meiosis, I expect to see different dynamics and localization of ZEN-4 and SPD-1. These finding will advance our understanding of important regulators and the mechanistic players of chromosome segregation that can lead to preventative treatments for genetic defects and male sterility.

Entry Number: 27 GL1

EXPLORING THE ROLES OF HISTONE VARIANTS HTZ-1 AND HTAS-1 DURING SPERMATOGENESIS

By: Monet Jimenez

Cell & Molecular Biology

Faculty Advisor: Dr. Diana Chu

Abstract: During development, it is imperative that the right genes are accessible at a precise time and place; thus, regulation of chromatin is a highly complex process. Histones, which package DNA into nucleosomes composed of the canonical histones H2A, H2B, H3, and H4, play an important role in maintaining chromatin accessibility. Canonical histones are only expressed in S-phase and replaced by histone variants at differing times throughout the cell-cycle. Histone variants are often highly conserved across species, indicating they have evolved to sustain tissue-specific functions that cannot be done by canonical histones. In *C.elegans*, the evolutionarily conserved HTZ-1 is 54% identical to H2A and ubiquitously expressed. Staining experiments exhibit that HTZ-1 is present throughout meiosis, and without its expression mutants are sterile. In embryogenesis, it is required to activate certain developmental promoters, however whether this is also true during spermatogenesis has yet to be explored. Distinctively, HTAS-1 is sperm specific, and 48% identical to H2A. It localizes to sperm chromatin, and when absent, mutants are sub-fertile. We speculate these two variants have key roles in spermatogenesis; however, how histone variants are specialized to function distinctly, remains unclear. When compared, these histone variants differ the most in their N- and C-terminal domains, sites where histone modification typically occurs. We hypothesize that these differing domains are responsible for the unique function that characterizes the role of each variant. To address this, chimeric histones will be expressed using the CRISPR/Cas-9 genome editing system. These chimeras will be mostly H2A, and each will have a different histone variant domain swapped in. For example, one chimera will have the N-terminus and core domain of H2A, but the C-terminus sequence for HTZ-1. We expect that the N-term and C-term domains of HTZ-1 and HTAS-1 will be major determinants for rescue in the respective mutants, since these regions are most accessible to cell-type specific players that are involved in regulating chromatin during development. It is also possible that the core regions maintain important DNA interactions, since each variant also differs from each other in this domain. These results will elucidate the amino acid sequences that uniquely corresponds to their function in different cell types, and help define broad features of histone variants important to their function across species. These regions will also grant insight to cell-type specific regulation of genes.

Entry Number: 28 GL1

EXAMINING THE INNER AND EXTRINSIC CUES OF ER PARTITIONING PRIOR TO ASYMMETRIC CELL DIVISION

By: Norma Gaytan

Cell & Molecular Biology

Faculty Advisor: Dr. Blake Riggs

Abstract: Asymmetric cell division is a key mechanism to generate cell diversity. To establish cell diversity in the brain, a precursor cell, also known as a proneural cells will asymmetrically divide and generate a self-renewing neuroblast (stem cell). There are two proposed mechanisms in *Drosophila melanogaster* that can explain asymmetric proneural cell divisions: the extrinsic or intrinsic signaling cues. The intrinsic signaling cues allow microtubule (MT) spindle to align parallel to the embryonic surface. The extrinsic cues rotate the MT spindle perpendicularly to the embryonic surface with the help of centrosomes. Previous studies have shown the Endoplasmic Reticulum (ER) to cluster around the centrosomes, associate with the MT spindle, and to asymmetrically divide in proneural cells. Nevertheless, the initial signaling cue and changes that occur that drive asymmetric proneural cell divisions remains unknown. I will determine the preferred signaling cues of asymmetric proneural cells by using this ER to MT to centrosome relationship. To test this, I will be using confocal imaging on asymmetric proneural cell divisions of *Drosophila* embryos. I expect to find the spindle rotating itself into an axis perpendicular to the fly's cortical membrane and the majority of the ER material accumulating towards the centrosome that is inherited to the neuroblast. Allowing the ER to be properly partitioned, the cell will avoid an accumulation of misfolded proteins that later cause human diseases. These results will provide a model for conserved asymmetric cell divisions that give rise to brain development.

Entry Number: 29 GL1

EVOLUTION OF A MODERN RETROGENE

By: Gerid Ollison

Cell & Molecular Biology

Faculty Advisor: Dr. Scott Roy

Abstract: Splicing factors are proteins responsible for binding pre-mRNA transcripts, causing changes through the inclusion or exclusion of target exons. It has been shown that splicing networks minimally require: 1) a

functional splicing factor to affect expression of target genes, 2) tissue-specific expression, 3) the presence of genes to be regulated with targeted exons, and 4) the sensitivity of targets to the regulatory molecule, in the form of a binding motif.

LS2 is a retroduplicated paralog of the highly conserved ubiquitously expressed splicing factor U2AF50. LS2 has evolved sufficiently to having its own specificity, function, and expression in *Drosophila*. It is unknown how LS2 was able to acquire a distinct function given the fact that it requires an assembled network to function. To this end I am taking a systematic approach to elucidating the evolutionary history of each requirement of the LS2 regulated splicing network.

While LS2 has been shown to be enriched in the testes of *D. melanogaster*, we conducted a study across several *Drosophila* species that revealed a more complex situation; varying and absent levels of testes enrichment. A comparative genomic study in diptera revealed conservation of genes and exons targeted by LS2. Furthermore, we bioinformatically determined the progenitor of LS2 to be *Scaptodrosophila*, a close relative of *Drosophila*. We will conclude by testing the protein functional equivalency and binding affinity of *Scaptodrosophila* LS2 (*Scapto_LS2*) compared to the known functional *Drosophila melanogaster* LS2.

By studying these splicing network requirements independently, my goal is to uncover the evolutionary steps in which this splicing network was created.

Entry Number: 30 GL1

STRESS RESPONSES OF TALBOTIA ELEGANS AT EXTREME TEMPERATURES

By: Thuy Tran and Elias M. Duarte

Cell & Molecular Biology

Faculty Advisor: Dr. Zheng-Hui He

Abstract: My research is focused on the extreme conditions *Talbotia Elegans* can survive in. These plants from South Africa are known for to withstand long periods of draught. These plants maintain their chlorophyll during desiccation periods and go through a resurrection process when water is made available. For my research, I will be focusing on the morphological changes and resurrection process at extreme low temperatures and high temperature of dehydrated and hydrated plants. The significance of this research, is to observe the resurrection process of these plants and survivability when the hydrated (control) and dehydrated are submerged in liquid nitrogen and in a conventional oven. These plants will be video recorded during the resurrection process. These plants have never been video recorded during the resurrection process.

Entry Number: 31 GL1

THE EEG EFFECTS OF COMBINING EMOTIONAL MUSIC AND VERBAL ATTENTION DURING THE COLD PRESSOR TASK

By: Liana Bruggemann, Trevor Jackson, and Jason Soares

Cognitive Neuroscience

Faculty Advisors: Dr. Mark Geisler and Dr. Ezekiel Morsella

Abstract: The purpose of this study is to investigate the neural mechanisms underlying the emotional and cognitive processing of pain. We measured this by comparing Alpha frequencies in the left fronto-temporal cortex, and inter-hemispheric coherence between Alpha and Beta frequencies between the control conditions and experimental conditions. Previous research has shown that emotion and cognitive load have been established as part of the method behind the processing of painful stimuli (Silvestrini, Piguet, Cedraschi, and Zentner, 2011, Price, 2000). Silvestrini et al. (2011) showed that subjects increased pain tolerance of the cold pressor task after listening to pleasant music, and decreased pain tolerance for the cold pressor task after listening to unpleasant music. For our analyses we used a 2 (emotional music vs neutral music) by 2 (cognitive distraction vs no cognitive distraction) design.

Entry Number: 32 GL1

TRACKING THE EVOLUTION OF HIV-1 IN PATIENTS ON PrEP TREATMENT

By: Dwayne Evans

Microbiology

Faculty Advisor: Dr. Pleuni S. Pennings

Abstract: HIV-1's rapid mutation rate allows it to be efficient at producing a diverse viral genome. The diversity of HIV's genome allows it to evade drug treatments. PrEP is a relatively new drug treatment that has not been as extensively studied as current antiretroviral drugs, such as Lamuvidine. Thus, it is not known of significant resistance to PrEP will develop in HIV-1 to the extent that it should be discontinued in patients. My research proposes that HIV's total resistance to PrEP can be determined by creating mathematical simulations to model how the virus evolves resistance to PrEP in an HIV infected patient on PrEP treatment. The models are based on infected patient data that show how the virus mutates when exposed to the drug. These mathematical models will allow me to discover which amino acid mutations, such as K70E, contribute the greatest resistance to PrEP. Identifying these key mutations in PrEP resistance will inform future vaccine designs and drug therapies to target those mutations for the most effective HIV-1 treatment. Targeting these key amino acid mutations will prevent the transmittance of PrEP resistant HIV-1 viral particles and the loss of already effective PrEP treatments for patients. Identifying amino acids essential for significant PrEP resistance involves testing a novel statistical approach that can be used for identifying key amino acid mutations in other diseases already exhibiting significant drug resistance, such as Hepatitis B, Gonorrhea, and Chlamydia, for which there are fewer drug treatments than HIV-1.

Entry Number: 33 GL1

ELUCIDATING THE JOINT ROLES OF A PROTEASE AND A LIPOPROTEIN IN SINORHIZOBIUM MELILOTI DURING SYMBIOTIC INFECTION OF PLANT HOST

By: Hector Ramirez

Microbiology

Faculty Advisor: Dr. Joseph Chen

Abstract: Sinorhizobium meliloti establishes symbiotic relationship with compatible leguminous plants by inducing root nodule formation and fixing molecular nitrogen for the host in exchange for carbon compounds. This mutualistic process requires complex communication to allow the beneficial infection of specific tissues by S. meliloti. A critical symbiotic factor, exopolysaccharide-I (EPS-I), enables S. meliloti to begin inducing root nodule formation in the plant host via infection threads. Regulators of EPS-I production include the essential ExoR-ExoS signaling pathway, which controls expression of genes that encode enzymes involved in EPS-I synthesis. Recently, two previously uncharacterized genes, jspA (encoding a protease) and lppA (encoding a lipoprotein), were identified as modulators of EPS-I production. Strains lacking either gene exhibit a competitive disadvantage compared to the wild type during initial symbiosis stages. We aim to use transcriptional reporter assays to demonstrate that lppA and jspA require each other to induce EPS-I expression. We will also aim to explore the effects of lppA and jspA on the ExoR-ExoS pathway. By investigating the molecular mechanisms underlying host colonization in our model system, we hope to uncover the roles that different signaling molecules may play during key stages of symbiosis in similar symbiotic interactions.

Entry Number: 34 GL1

SURVIVAL OF THE FITTEST: DETERMINE THE RATE AT WHICH MUTATIONS ARE MOVING THROUGH AN HIV POPULATION.

By: Kadie-Ann Williams

Microbiology

Faculty Advisor: Dr. Pleuni S. Pennings

Abstract: According to the World Health Organization, Human immunodeficiency virus (HIV) has infected almost 78 million people and is responsible for the death of about 39 million people worldwide. The continuous development of new and improved drugs to treat HIV has led to a major improvement of patients' survival rates. However, there is still no cure for HIV and the evolution of drug resistance is still a challenge to the treatment of HIV. Evolution of drug resistance in pathogens such as HIV can lead to treatment failure. Therefore, understanding the process of how drug resistance evolves in a viral population is an important goal in the field of evolutionary biology. My aim is to study how drug resistance mutations evolve in a viral population using existing sequence data from HIV patients on various treatments. This study is important to reach a better understanding of the evolution of drug resistance in a viral population which, in turn, can help us understand how to prevent the evolution of resistance and to develop better ways to treat HIV.

Entry Number: 35 GL1

IMMUNE RESPONSES DURING TISSUE REGENERATION OF IMAGINAL DISCS IN *MANDUCA SEXTA*

By: Rachel Bhaskar

Microbiology

Faculty Advisors: Dr. Megumi Fuse, Dr. Steven Weinstein, and Dr. Lily Chen

Abstract: Immunological processes influence the overall development and vitality of every organism. In Lepidopteran insects, phagocytic cells and antimicrobial peptides trigger a cascade of signaling pathways that elicit antimicrobial defense. The tobacco hornworm, *Manduca sexta*, is one such organism that is also a common agricultural pest feeding on Solanaceous plants such as tobacco leaves and tomatoes. It is known that *M. sexta* hemocytes play a role in phagocytosis and encapsulation when triggered by foreign molecules or when they encounter damaged tissue. // After damage to the regenerative imaginal discs, developmental delays are noted that putatively arise from signals released from the discs. However, it is unclear as to whether hemocytes, and other immune signals play a role in these delays. Immune responses upon irradiation have been characterized in *Drosophila melanogaster* (Zhang et al. 2015), however, they have not yet been looked at in *M. sexta*. Irradiation triggers *Drosophila* hemocytes to aggregate near damaged tissue after wounding and during development. These hemocytes also mediate a systemic metabolic and growth response to localized DNA damage in the eye imaginal disc (Kelsey et al. 2012). Similarly, pattern recognition receptors alter the antimicrobial peptide levels when *M. sexta* are challenged with bacterial infection, while irradiation alters the plasmatocytes, which is part of the cellular system (Eleftherianos et al., 2007; Lavine et al., 2002). Thus, it will be an interesting comparative study to assess the effects of radiation and infection during imaginal discs regeneration in *M. sexta*. *Manduca* is less studied as a molecular model that allows us to discover its physiological characteristics and qualify it as a representative of the invertebrate immune system. // Moreover, the model organism, *M. sexta*, is an innovative model that allows us to compare the immune responses under different conditions without the effect of adaptive immunity, because most invertebrates only have the innate immune system. This allows us to confer the effects that radiative therapy or opportunistic infections have on immunocompromised humans. /

Entry Number: 36 GL1

INVESTIGATING UNIQUELY CONSERVED GENES ACROSS ARCHAEAL AMMONIA OXIDIZERS AS CANDIDATES FOR GENETIC DETERMINANTS OF THE AMMONIA OXIDATION PATHWAY

By: Roxanne Bantay

Microbiology

Faculty Advisor: Dr. José R. de la Torre

Abstract: One consequence of increased anthropogenic nitrogen deposition is the increase in greenhouse gas production by nitrifying organisms. The recently discovered ammonia-oxidizing archaea are producers of nitrous oxide, yet the mechanisms behind their use of nitrogen for energy production remains unresolved. Genomic comparisons with ammonia-oxidizing bacteria (AOB) showed limited similarities. Both oxidize ammonia to hydroxylamine with an ammonia monooxygenase (AMO) but AOA lack homologues for key components present in the bacterial pathway, such as hydroxylamine oxidoreductase (HAO), which catalyzes the conversion of the hydroxylamine intermediate to nitrite. We hypothesize that genetic determinants of archaeal ammonia oxidation are genes that are conserved across and specific to all AOA. To find these genes, we compared the genomes of 18 AOA from terrestrial, marine, and geothermal environments against outgroup genomes consisting of representatives from Crenarchaeota, Euryarchaeota, and closely related archaea that do not oxidize ammonia. Protein coding genes for all sequences were compared against each other using all-vs-all BLASTP with an E-value cutoff of $1e-05$, minimum sequence identity of 50%, and minimum coverage of 75%. Results were then clustered using OrthoMCL with an inflation parameter of 1.5. The resulting clusters represent ortholog families containing orthologous and paralogous genes from the genomes analyzed. To identify conserved and unique genes, we searched for ortholog families that are present in 90% of the AOA taxa examined (in order to account for potential mistakes in gene calling and annotation between the different genomes) and absent in all of the outgroup genomes. We have identified 242 ortholog families that are conserved and unique across all AOA. arCOG functional classification indicate that the majority of these conserved, unique genes are involved in energy production and conversion (14%), amino acid metabolism and transport (12%), coenzyme metabolism (12%), and translation, ribosomal structure and biogenesis (12%) although a considerable number of families have unknown functions (18%). These conserved and unique

ortholog families represent candidate genes that may be involved in ammonia oxidation. Further studies will examine the genomic context of these genes as well as co-expression with AMO genes known to be involved in the ammonia oxidation pathway. /

Entry Number: 37 GL1

IDENTIFICATION OF THE GUT MICROBIOME OF MANDUCA SEXTA AND NATIVE INVASION PATHOGENESIS

By: Ryan Marder

Microbiology

Faculty Advisors: Dr. Lily Chen and Dr. Megumi Fuse

Abstract: Microbiota plays an important role in a host's healthy and diseased states and may be altered by exposure to antibiotics. Streptomycin is a broad-spectrum antibiotic that inhibits the growth of both Gram-positive and Gram-negative bacteria. The focus of our study is to use the tobacco hornworm, *Manduca sexta* to identify its gut microbiota throughout development as well as analyze the microbial and developmental effects of streptomycin on the organism. Previous studies have used mouse models to study the adverse effects of antibiotics on the developing gut microbiome, but a cheaper and simpler alternative is to use the invertebrate model, *M. sexta*, to study these host-microbial developmental effects. Because *M. sexta* larvae have been exposed to the broad-spectrum antibiotic streptomycin, initial characterization tests were conducted to observe the differences in streptomycin positive and streptomycin negative *M. sexta* gut microbiota in order to determine which larval colony to use for the host-microbial interaction assays. Hatchlings were divided into two groups: an experimental group fed a diet without streptomycin and a control group with streptomycin. Frass samples were collected at the L4 instar and inoculated for isolated bacterial culture. Colony PCR and biochemical assays, including catalase, oxidase, hemolysis, and anaerobic tests were performed to identify isolated bacteria from its larval gut. The results indicate larvae fed with streptomycin contained microorganisms including *Bacillus* and *Pseudomonas* spp. However, larvae fed without streptomycin consisted of *Staphylococcus*, *Bacillus*, and *Peptostreptococcus* spp. In addition, larvae reared without streptomycin were found to have higher average larval weights, a shorter developmental period, as well as a consistent hemocyte population throughout development. These immunological and developmental abnormalities resulted from the loss of microbial diversity in those larvae fed a diet with streptomycin. When *M. sexta* larvae were force fed their own gut microbiota after being isolated from their feces, specifically *Bacillus*, *Staphylococcus*, and *Pseudomonas* spp., those fed with streptomycin, had a change in hemocyte populations and decreased survivability compared to those on a diet without streptomycin. /

Entry Number: 38 GL2 DISPLAY ONLY

CHARACTERIZING ADAP/VE GENE/C VARIATION IN THE SALT MARSH HARVEST MOUSE, REITHRODONTOMYS RAVIVENTRIS

By: Anastasia Ennis

Ecology, Evolution & Conservation Biology

Faculty Advisor: Dr. C. Sarah Cohen

Abstract: This study seeks to characterize baseline levels of adaptive genetic diversity in populations of the endangered salt marsh harvest mouse. This species is only found in marshes of the San Francisco Estuary, and its survival is dependent on the effective management, conservation, and restoration of its wetland habitat. Adaptive immune system variation is frequently characterized in endangered species to assess the potential of limited populations to respond to disease. We have isolated the first adaptive immune system locus from the salt marsh harvest mouse in the major histocompatibility complex (MHC, Class II DRB).

Entry Number: 39 GL2

HIGH THROUGHPUT SEQUENCING PROVIDES NOVEL INSIGHT INTO THE CALIFORNIA DELTA FOOD WEB

By: Ann Holmes

Ecology, Evolution & Conservation Biology

Faculty Advisor: Dr. Wim Kimmerer

Abstract: Food web interactions are fundamental characteristics of ecosystems. In the California Delta, an endangered fish (delta smelt) eats plankton called copepods. Copepods, in turn, eat a diverse assemblage of

microplankton. However, copepod feeding patterns are poorly understood; traditional food web studies provide too little taxonomic resolution. We use high-throughput sequencing (HTS) to describe copepod feeding patterns. Our results provide new insights into the food web that supports delta smelt and other fish species in the Delta. /

Entry Number: 40 GL2

CLOSE TO DEATH: TRANSCRIPTOME COMPARISON BETWEEN PLASMODIUM GALLINACEUM AND HAEMOPROTEUS COLUMBAE

By: Jasper Toscani Field

Ecology, Evolution & Conservation Biology

Faculty Advisor: Dr. Ravinder Sehgal

Abstract: Malaria is one of the most devastating diseases on the planet, killing more people than any other parasitic infection. Malaria is caused by parasites of the Plasmodium genus. Plasmodium is a member of the order Haemosporidia as are two other genera, Haemoproteus and Leucocytozoon. All three genera are widespread in birds and provide ideal systems for studying host-switching and parasite epidemiology. Little is known about how closely the members of Haemosporidia resemble one another in terms of gene expression. This is particularly interesting as there are two subgenera of Haemoproteus: Parahaemoproteus and Haemoproteus. Parahaemoproteus is found in the majority of birds and is transmitted by biting midges. Haemoproteus is found in pigeons and doves and is transmitted by louse flies. Almost no information is available on erythrocyte invasion gene expression in Haemoproteus species. Using next generation sequencing technology, I will assemble the transcriptome of a Haemoproteus species for the first time. A whole transcriptome approach will allow me to identify genes involved in erythrocyte invasion and host specific determination. I will then compare the new expression data to the transcriptome of human malaria parasites, and *P. gallinaceum*. The host specificity of *P. gallinaceum* to chickens makes it an excellent choice to compare to *H. columbae*. I will employ bioinformatics techniques to search for orthologous genes expressed by both parasites. The findings of this study could provide new treatment opportunities and methods to study avian malaria.

Entry Number: 41 GL2

UNDERSTANDING MICROALGAL SPECIES COMPOSITION AND CONTRIBUTIONS IN ANTARCTIC GLACIAL MELT WATER THROUGH RBCL HIGH THROUGHPUT SEQUENCING

By: Kathryn Barretto and Andrew Kalmbach

Ecology, Evolution & Conservation Biology

Faculty Advisors: Dr. Edward Carpenter, Dr. José R. de la Torre, and Dr. Luisa Falcon

Abstract: The McMurdo Dry Valleys (MDV) in Antarctica present unique research opportunities, both because of the understudied biogeochemical impact of their microbial communities, and their sensitivity to climate change. Despite harsh desiccation, pH, and salinity stress, summer glacial melt water supports life in the MDV in the form of algal mats. These mat communities are complex in structure, with a network of dominant cyanobacteria interspersed with heterotrophic diazotrophs, smaller photoautotrophs, and thick extracellular polymeric substances. Due to their complexity, standard microscopy yields a limited understanding of community assemblages. Our previous high throughput sequencing (HTS) approaches focusing on 16S rRNA have profiled communities with understudied photosynthetic phyla such as Acidobacteria, Gemmatimonadetes, and Chloroflexi. To characterize these phototrophic communities, we are interested in (1) understanding their temporal dynamics and how the dominant cyanobacterial species influence community composition, (2) modeling how pH, nutrients, soil wetness, and temperature act as multivariate drivers of community composition, and (3) establishing a pipeline for HTS of the *rbcL* gene – which encodes the large subunit of the ubiquitous photosynthetic protein RuBisCO. Our initial screening of community DNA from MDV algal mats has shown the presence of Form IA, IB, and IC *cbbL* (an *rbcL* ortholog), and Form ID *rbcL* – indicating a relatively high degree of photoautotrophic diversity. Soil wetness drives anoxic conditions and we see that it shifts overall microbial composition – we expect photoautotrophs to respond similarly. We also expect photoautotrophic assemblages to shift with pH and soil nutrients. Our deep sequencing efforts suggest an inconsistency between indexing primers and algal DNA that could underestimate cyanobacterial and overestimate eukaryotic abundance. Resolving these issues with new approaches will allow us to more fully understand the dynamics of the MDV.

Entry Number: 42 GL2

INVESTIGATING UNDERGRADUATE STUDENTS' USE OF INTUITIVE REASONING AND EVOLUTION KNOWLEDGE IN EXPLANATIONS OF ANTIBIOTIC RESISTANCE

By: Melissa Richard

Ecology, Evolution & Conservation Biology

Faculty Advisor: Dr. Kimberly Tanner

Abstract: Natural selection is a central and critical concept throughout biology; however, it is also a process frequently misunderstood. Bacterial resistance to antibiotic medications provides a contextual example of the relevance of evolutionary theory outside of a biology classroom and is also commonly poorly understood. While research has shed light on common student misconceptions of natural selection, minimal research has focused on the degree to which misconceptions may be based in intuitive, deep-seated cognitive patterns rather than in the complexity of evolutionary concepts themselves. These intuitive patterns are studied in the field of cognitive psychology as informal assumptions developed at an early age to make sense of the world (Coley and Tanner 2015). In this study, we investigated undergraduate students' application of three modes of intuitive reasoning — teleological, essentialist, and anthropocentric thinking — to the concept of antibiotic resistance. To what extent do students embrace misconceptions, and to what extent is intuitive thinking evident in student responses? Does acceptance of misconceptions correlate with intuitive reasoning? To investigate these questions, we created a novel assessment tool designed to probe students' understanding of natural selection and application of intuitive reasoning framed in the context of antibiotic resistance. Responses were collected from 484 students representing non-biology majors (n=58), entering biology majors (n=319), and advanced biology majors (n=107), as well as from biology faculty (n=14). Participants were asked to provide a written explanation of antibiotic resistance and then agree or disagree with three misconception statements, explaining their reasoning. Presented here are four key findings: 1) Approximately 50% of students in all populations produced misconceptions and language evidencing intuitive reasoning unprompted. 2) When presented with misconceptions hypothesized to be rooted in intuitive thinking, over 94% of all students agreed with one or more of these misconceptions. 3) Over 90% of students used at least one instance of intuitive thinking in their written responses to misconceptions. 4) Most strikingly, chi-squared analyses showed significant associations in all student populations between acceptance of a misconception and production of the hypothesized form of intuitive thinking (all $p \leq 0.05$). The associations between intuitive thinking and misconceptions elucidate ways in which inaccurate biological ideas may persist even throughout formal biology education. Since the language of intuitive thinking may represent a subtle but innately appealing verbal shorthand in conveying concepts, instructor awareness of how intuitive thinking could fuel student misunderstandings can inform evolution educators' addressing of persistent misconceptions.

Entry Number: 43 GL2

OCEAN ACIDIFICATION EFFECTS ON PHOTOSYNTHETIC SYMBIONTS IN THE SEA ANEMONE ANTHOPLEURA XANTHOGRAMMICA

By: Alison Fisher

Marine Biology

Faculty Advisor: Dr. Edward Carpenter

Abstract: In a world facing climate change, it is vital that we understand how ecologically significant marine species will be impacted by increasing temperatures and decreasing seawater pH. One ecologically important species in California is the giant green anemone (*Anthopleura xanthogrammica*), which has two photosynthetic algal symbionts that make these anemones important primary producers in the intertidal zone. This research will investigate the effects of changes in temperature and pH on anemones and their symbionts over a natural gradient along the coast of California and Oregon. Algal cell counts, chlorophyll a measurements, and mitotic index, and anemone oral disk diameter will be used to evaluate abundance of symbionts and health of both symbionts and anemones. This study will test the hypothesis that symbiont amount and animal size will both increase under conditions of higher temperature and lower pH. These results will help inform environmental policies, since there is the potential for radical ecological shifts if anemones are able to outcompete other ecologically important intertidal species.

Entry Number: 44 GL2

DISSOLVED AND PARTICULATE PRIMARY PRODUCTION BY COMMUNITIES IN THE AMAZON RIVER PLUME

By: Andrew Kalmbach

Marine Biology

Faculty Advisors: Dr. Edward J. Carpenter, Dr. Ina Benner, and Dr. William P. Cochlan

Abstract: The Amazon River Plume is a dynamic region in the tropical Atlantic Ocean, where riverine nutrients drive high rates of primary productivity and subsequent carbon sequestration by phytoplankton. Although the majority of carbon fixed by phytoplankton is retained in the cell, a portion is released to the environment as dissolved organic carbon. This research seeks to identify the effects of phytoplankton taxa and size on extracellular release of DOC in the Amazon river plume, and help to further describe the carbon cycle in this unique region.

Entry Number: 45 GL2

IMMUNOGENETIC VARIATION IN X-CELL DISEASED FISH ACROSS AN ESTUARINE GRADIENT OF CONTAMINANTS

By: Calvin Lee

Marine Biology

Faculty Advisor: Dr. C. Sarah Cohen

Abstract: Juvenile English sole (*Parophrys vetulus*) use the San Francisco Bay Estuary (SFBE) as a nursery but are subject to environments with different sediment contaminant loads. Juveniles are susceptible to parasitic protozoans that cause skin tumors. We used molecular methods to confirm the presence of the causative pathogen, known in fish pathology literature as X-cell disease. In other regions higher incidences of skin tumors have been seen in urbanized estuaries. Contaminants in urbanized estuaries can alter adaptive immune response in flatfish. Habitat in San Pablo Bay (SPB) is less impacted by contaminants than regions in the South Bay (SB). We examine variation in Major Histocompatibility Complex (MHC) genes, which recognize parasites and diseases. We isolated the exon 2 region of the MHC class IIB genes from infected and uninfected English sole caught in the two differentially impacted regions. In other studies, contaminants and disease have been shown to be important influences on variation in the MHC. By examining fish from these two contrasting environments in SFBE, we assess how contaminants may be influencing relationships between population genetics and disease. We compare differences in the antigen binding region of the MHC protein from infected and uninfected fish in contaminated and less contaminated areas. Preliminary data from 50 individuals (27 from SPB and 23 from SB) shows high levels of allelic diversity and substitutions concentrated on inferred antigen binding sites of the protein. Selection tests using confirmed alleles show a signal of positive selection in samples from both regions of the bay combined ($dN/dS = 2.35$ $p = 0.010$, $n = 14$ confirmed alleles) and each separately (SPB: $dN/dS = 2.28$ $p = 0.012$, $n = 13$, SB: $dN/dS = 2.32$ $p = 0.011$, $n = 10$). This study will provide information on immunogenetic diversity in juvenile fish in SFBE in relation to contaminant distribution patterns.

Entry Number: 46 GL2

THERMAL PREFERENCE AND AVOIDANCE BEHAVIORS IN THE PORCELAIN CRAB, PETROLISTHES CINCTIPES

By: Emily Lam

Marine Biology

Faculty Advisor: Dr. Jonathon Stillman

Abstract: Small scale vertical shifts are expected to occur in the rocky intertidal zone under future climate scenarios and will produce ecological consequences such as local extinction and loss of biodiversity. The upper intertidal zone porcelain crab, *Petrolisthes cinctipes*, inhabits a narrow range that exhibits extreme thermal fluctuation that can reach lethal levels, but at what temperature the crabs migrate to the cooler low intertidal zone is unknown. *Petrolisthes manimaculis* is a closely related species or congener of *P. cinctipes* that inhabits the cool and stable low intertidal zone where warming is less imminent. If *P. cinctipes* moves down the shore, the two species' boundaries will increasingly overlap and both species will face increased competition and aggressive interactions that may be risky for egg carrying females and success of their broods. This research aims to determine if reproductively active females are most vulnerable to climate change. Porcelain crabs have different thermal tolerances at each life-cycle stage and mobile ectotherms are known to regulate their body temperature behaviorally. Brooding females may behaviorally regulate their temperature to increase

reproductive fitness. I will investigate if maternal provisioning occurs via thermoregulation to buffer the effects of warming and determine the associated costs due to increased behavioral interactions between species. /

Entry Number: 47 GL2

BIOFILM AS A MECHANISM FOR METAL SORPTION ON PLASTIC DEBRIS

By: Heather Richard

Marine Biology

Faculty Advisor: Dr. Edward Carpenter

Abstract: Heavy metals from the water column accumulate onto weathered plastic debris to a greater extent than onto virgin plastic. Hypothesized mechanisms that drive this process include oxidation by ultraviolet light, precipitation of metal ions onto the surface of the plastic, and biofilm growth. We provide the first example of research quantifying how biofilms influence metal sorption onto plastic debris. We conducted laboratory experiments to find out whether or not the presence of biofilms increases the sorption capacity of plastic debris, and also performed in situ experiments in the San Francisco Bay to compare low-density polyethylene, polylactic acid, and glass as substrates for fouling and metal sorption. This research reveals the potential for plastic debris to act as a vector bringing heavy metals into aquatic food webs relative to other debris materials.

Entry Number: 48 GL2

CHANGES IN DEMOGRAPHY ALONG A THERMAL GRADIENT IN THE INTERTIDAL CRAB PETROLISTHES CINCTIPES

By: Metadel Abegaz

Marine Biology

Faculty Advisors: Dr. Alex R. Gunderson and Dr. Jonathon Stillman

Abstract: Different demographic groups within a population (i.e., males/females, small/large individuals) are often distributed differently along environmental gradients, suggesting different ecological or physiological needs. The intertidal zone porcelain crab *Petrolisthes cinctipes* is distributed along a vertical thermal gradient within the intertidal, though it is currently unknown how individuals are distributed along this gradient. We monitored under-rock temperature and crab demographics (size, sex) over summer and autumn months in fixed transects along the species' vertical distribution boundaries. In the upper intertidal, under-rock temperatures were strongly size dependent, with smaller rocks reaching temperatures up to 37°C but larger rocks never exceeding 20°C. Lower in the intertidal, rock size was less important and no rocks exceeded 17°C. Results show mean crab density much lower in the warm high intertidal (83 crabs/m²) compared to the cooler low intertidal (171 crabs/m²). In addition, we found male-skewed sex ratios in the upper and lower intertidal zones where male crabs were 25% and 21% more abundant than female crabs respectively. From these data we can conclude that under-rock temperatures influence demographic parameters of *P. cinctipes* within the intertidal.

Entry Number: 49 GL2

MODELING THE DISTRIBUTION OF PETROLISTHES CINCTIPES IN NORTHERN CALIFORNIA

By: Alma Y. Ceja

Marine Science

Faculty Advisor: Dr. Jonathon Stillman

Abstract: In this project, I will model the distribution of the porcelain crab, *Petrolisthes cinctipes*, inhabiting the rocky intertidal zone of northern California.

Entry Number: 50 GL2 DISPLAY ONLY

EXPLORATORY EXERCISE IN GIS: ZOOPLANKTON HABITAT SUITABILITY MAPS IN THE GULF OF THE FARALLONES REGION

By: Ryan Hartnett

Marine Science

Faculty Advisor: Dr. Karina Nielsen

Abstract: Zooplankton aggregation patterns in the Gulf of the Farallones region is key to understanding planktivorous predator abundances. Utilizing species distribution models to elucidate these patterns may be advantageous when observational data of zooplankton is not available. I created habitat suitability maps using

Marine Geospatial Ecology Tools in ArcGIS to predict where zooplankton aggregate based upon environmental variables.

Entry Number: 51 GL2

HOW DOES *MANDUCA SEXTA*, (TOBACCO HORNWORM) COMMUNICATE LOCAL CELL DAMAGE IN THE IMAGINAL DISCS AND CAUSE SYSTEMIC RESYNCHRONIZATION OF ORGAN DEVELOPMENT?

By: Shams Janna Bashar

Physiology

Faculty Advisors: Dr. Megumi Fuse, Dr. Kimberley Tanner, and Dr. Laura W. Burrus

Abstract: A fundamental question in biology is how organisms sense and assess organ health and development in proportion to the growth of the whole body. Growth delays during metamorphosis, the “puberty” phase in insects, are observed during development when there is local damage to juvenile organs. An unexpected benefit of the delay is a time frame for damaged cells to regenerate and minimize organ injury. How local cell damage to organs causes systemic changes in developmental timing is still poorly understood. My goal is to identify the mechanism of communication between damaged tissue and the endocrine centers that regulate development, using the model organism *Manduca sexta* (*M. sexta*). I hypothesize that in response to damage, the tissues upregulate insulin-like growth factors, which are delivered by hemolymph (blood) to the endocrine centers and resynchronize hormone regulation of growth. I aim to identify the intrinsic signal by selectively damaging *M. sexta* imaginal discs and then screening their hemolymph for upregulated delay factors. I am assessing changes to protein profile in hemolymph before and after damage through SDS-PAGE gel electrophoresis, as well as Western blots using general insulin-like antisera. Identifying the developmental resynchronization mechanism in *M. sexta* will provide insight into how organisms synchronize growth in response to tissue injury and may help us understand similar puberty delays that arise in response to human inflammatory diseases.

Entry Number: 52 GL2

INVESTIGATING INSTRUCTOR TALK IN COMMUNITY COLLEGE BIOLOGY CLASSROOMS

By: Tiffy Nguyen

Physiology

Faculty Advisors: Dr. Kimberly Tanner, Dr. Laura Burrus, and Dr. Shannon Seidel

Abstract: Instructors have the significant responsibility of not only teaching coursework, but also structuring a safe and accessible learning environment. Evidence shows that how an instructor frames an assessment can affect student performance, and evidence also suggests that student learning can be affected by instructor immediacy, the perceived closeness a student feels to their instructor. One previous study has investigated and characterized Instructor Talk, the non-content related language instructors use to shape learning environment, in one 4-year university introductory biology classroom (Seidel et al, 2015). Although Instructor Talk was utilized in this classroom, to what extent is it utilized in other classrooms? We aimed to investigate the prevalence of Instructor Talk in community college biology classrooms and to discover whether new categories of Instructor Talk arose from this dataset compared to the previously described study. // To accomplish this, eight community college biology instructors recorded audio from every class session for the span of one term, averaging 27.4 ± 2.1 hours (16.5-33.9) of recording. Audio was analyzed for instances of Instructor Talk, then coded into categories and subcategories characterized by previous research. If a statement did not fall into one of the previously described subcategories, new subcategories were developed using a grounded-theory approach similar to the former framework. // Strikingly, all eight instructors utilized Instructor Talk, with an average of 15 ± 3 (1.3-18.8) quotes/hour. First day of instruction had the highest or second-highest rate of Instructor Talk. Building the Instructor/Student Relationship was the most prevalent category found, present in $87 \pm 8\%$ (36-100%) of class sessions, and Unmasking Science was the least prevalent category found, only in $23 \pm 8\%$ (0-74%) of class sessions. A new subcategory of Instructor Talk was discovered: Fostering Wonder in Science. In addition, non-productive Instructor Talk emerged, including quotes that could be perceived as disrespecting students, discouraging community among students, or using convenience to drive pedagogical choices. All instructors used non-productive Instructor Talk, with an average of 1.2 ± 0.5 (0.2-4.1) quotes/hour. We observed a trend that instructors with higher rates of productive Instructor Talk were also more likely to have higher rates of non-productive Instructor Talk. // These findings demonstrate that Instructor Talk is widely present in community college biology courses and describe first instances of non-productive Instructor Talk. Instructor

Talk is a specific tool instructors can use to structure classroom environments. It may potentially mitigate Stereotype Threat, increase Instructor Immediacy, and/or decrease Student Resistance to active learning techniques. /

Entry Number: 53 GL2

NOCTURNAL BEHAVIOR IN HONEY BEES PARASITIZED BY THE PHORID FLY APOCEPHALUS BOREALIS

By: Erika Bueno

Zoology

Faculty Advisor: Dr. Christopher Moffatt

Abstract: With one-third of our fruits and vegetables pollinated by honey bees (*Apis mellifera*), recent colony declines pose a threat to food availability. One possible driver of colony declines is an increasing prevalence of parasitic organisms. The phorid fly, *Apocephalus borealis*, is parasitoid that infects bumble bees, paper wasps, and honey bees. Many parasitized honey bees appear to abandon the hive at night and die around outdoor lights, at least in urban areas. To further understand the nature of *A. borealis* infections, we measured parasitism rates of bees collected from the ground in front of hives from Winter 2014 to Fall 2015. The highest rates of infected bees peaked in the Fall season and drastically declined thereafter. To determine infection frequencies between day active foragers and nocturnally active bees we used standard PCR to identify infections in samples. We found a significant difference between the proportion of infected bees collected during the day and night; however, infections were not exclusive to nocturnal activity. Future work will focus on examining the expression of clock genes within the brains of parasitized and unparasitized bees in order to determine the physiological mechanism driving this change in behavior. /

Entry Number: 54 GL2

COMPUTATIONAL CHARACTERIZATION OF HUMAN ALKYLADENINE GLYCOSYLASE: IMPLICATION FOR PROTEIN-DNA COMPLEX ASSEMBLY

By: Gabrielle Marie Garcia

Biochemistry

Faculty Advisor: Dr. Anton Guliaev

Abstract: Exposure to environmental pollutants produces adenine mutations within DNA. These mutations are repaired by human alkyladenine glycosylase (hAAG) via base excision repair (BER). There is little known about the behavior of unbound hAAG and how base excision repair is initiated when DNA and hAAG come into contact followed by the formation of the protein-DNA complex. This piece of information is vital to cancer studies because hAAG is an enzyme which excises carcinogenic lesions within DNA. In this project, conformational dynamics and behavior of free hAAG were examined by explicit solvent molecular dynamics simulations with AMBER force field. Data accumulated from 2 microseconds of the production run of hAAG demonstrated macromolecular reorganization between bound and unbound enzyme, indicating a possible clamping mechanism by which hAAG recognizes and binds modified DNA to excise the carcinogenic adenine lesion. This work provides important structural insight into the protein complex formation and could also benefit future therapeutic approaches.

Entry Number: 55 GL2

STRUCTURAL FRAMEWORK OF PYRIDOXAL 5'-PHOSPHATE BINDING TO HUMAN GLUTAMATE-OXALOACETATE TRANSAMINASE (hGOT1)

By: Jesi Lee

Biochemistry

Faculty Advisors: Dr. Anton Guliaev and Dr. Zheng-Hui He

Abstract: The active form of Vitamin B6, pyridoxal 5'-phosphate (PLP), plays an essential role in the catalytic mechanism for various proteins, including human glutamate-oxaloacetate transaminase (GOT1), an enzyme in amino acid metabolism. Recent molecular and cellular study showed that E266K, R267H, and P300L substitutions in aspartate aminotransferase, the Arabidopsis analog of GOT1, genetically suppress a developmentally arrested Arabidopsis *rus1* mutant and the mass spectrometry analyses suggest that the variants exist as apoproteins. In this work, we assessed the stability of PLP in the GOT1 PLP-binding pocket for the variants and wild type (WT) using combined 4 μ s molecular dynamics (MD) simulations. For all variants and

WT in the holo form, the MD simulations reproduced the “close-to-open” transition needed for substrate binding. This conformational transition was associated with the rearrangement of the P15- R32 small domain loop providing a substrate access to the R387/R293 binding motif. The position of PLP in the WT binding site was stabilized by a unique hydrogen bond network including the phosphate group binding cup, which positioned the coenzyme for a formation of the covalent Schiff-base linkage with K259 for catalysis. Nevertheless, amino acid substitutions at positions 266, 267, and 300 significantly reduced the structural correlation between PLP and the GOT1 active site. Also, weaker PLP binding energies were observed for E266K and R267H variants. The low affinity of PLP in the GOT1 variants observed in our simulations provides structural rational for both the apoprotein and vitamin B6 in regulating metabolic pathways.

Entry Number: 56 GL2

CONFORMATIONAL ANALYSIS OF THE FRUCTOSE-SPECIFIC TRANSPORTER GLUT5 VIA STEERED MOLECULAR DYNAMICS

By: Trevor Gokey

Biochemistry

Faculty Advisor: Dr. Anton Guliaev

Abstract: GLUT5 is a member of the GLUT sugar transporter family and is unique in that it passes fructose but not glucose through lipid membranes. Other GLUT transporters are known to switch between two states during glucose passage, however recent crystallographic data suggests GLUT5 utilizes four states during fructose passage. The mechanisms which account for fructose specificity and drive GLUT5 between the four conformational states are unclear. To address this, we utilized steered molecular dynamics to model fructose permeation through GLUT5. This method revealed several energy barriers that fructose must overcome to pass through GLUT5. Each barrier was associated with disruption of specific hydrogen bonds between fructose and residues lining the channel. A cavity in the center of the channel provided a stable binding site with five hydrogen bonds with fructose, and moving fructose away from this position produced the highest energy barrier during passage. The multiple barriers calculated in this work identified key residues which account for GLUT5 substrate specificity.

Entry Number: 57 GP1 DISPLAY ONLY

A MULTIFACETED DATA MINING APPROACH TO ANALYZING COLLEGE STUDENTS' PERSISTENCE AND GRADUATION

By: Aparna Gopalakrishnan

Computer Science

Faculty Advisor: Dr. Hui Yang

Abstract: This study describes a host of generalizable and data mining-based approaches to identify factors that contribute towards student persistence and graduation, using data from an academic program named Metro College Success Program at San Francisco State University, California. These approaches include (1) a visual analysis to identify bivariate relationships and to understand the flow of students in an educational institute, (2) an ensemble feature selection method to recognize factors that have a significant impact on a student's persistence and graduation, (3) classification and prediction algorithms to predict whether a student will persist in a given semester and ultimately graduate, and (4) a variety of association patterns to help education practitioners gain further insights into factors that affect persistence and graduation. Our analysis reveals the following main insights: (1) most students who dropout do so in the fourth and seventh terms, (2) the educational level of a student's mother, the ELM (Entry Level Mathematics) score and race are identified as the most influential factors in predicting a student's third-term persistence, (3) Naïve Bayesian is the most suitable model for predicting graduation while AdaBoost and SVM models are most suited for predicting persistence (4) a student's low ELM score and Pell eligibility (an indicator of socioeconomic status) together predict a lower rate of graduation. By collaborating with practitioners and focusing on generating human-interpretable results, the study helped identify bottlenecks to a student's path towards graduation.

Entry Number: 58 GP1

SMART IRRIGATION SYSTEM

By: Ammar Naqvi, Abhilash Shrivastava, Swati Patel, Rujoota Shah, and Pooja Kanchan

Computer Science

Faculty Advisor: Dr. William Hsu

Abstract: The application optimizes the water consumption required for irrigation. Our application uses weather apis and GE's Predix Cloud services to calculate the soil's evaporation rate to determine the best time and duration for water-sprinklers on the SFSU lawns to be turned on. In addition, based on the weather prediction, the application adjusts the irrigation system accordingly, e.g. if there's going to be rain, the system will decrease the duration or completely turn off the system depending on plant types that exist in the environment. /

Entry Number: 59 GP1

TUNETUTOR: AN AUDIO PLAYER FOR LEARNING MUSIC BY EAR

By: Ben Saylor

Computer Science

Faculty Advisor: Dr. Bill Hsu

Abstract: TuneTutor is an audio player designed to help musicians learn music by ear. / / In many forms of traditional folk music, pieces of music are passed from musician to musician and / from generation to generation orally. In traditional dance music in particular, tunes are usually played / at a tempos that are too fast for easy learning. Therefore, tunes are usually taught by breaking them into / short phrases and playing each one slowly for the student to mimic. This is repeated until the student / can play the phrase correctly. Then, phrases are joined, the tempo is slowly increased, and the student / can eventually play the entire tune from memory. / / Recording technology has provided an alternative to live person-to-person tune learning, but not all / media and playback systems allow slowing down the playback rate. If they do, pitch and tempo are / lowered together, and the music sounds in the wrong key. Some digital audio applications have helped / improve the situation by allowing independent control of pitch and tempo using time stretching and / pitch shifting algorithms. / / TuneTutor provides a new, convenient feature set and user interface for learning tunes by ear from / recordings. It provides time stretching and transposition with high sound quality, as well as / visualization and annotation capabilities that make it easy to locate sections of the recording.

Entry Number: 60 GP1

SOLAR SIMULATOR AT SCALE

By: Jason Burmark, Omar Shaikh, and Moses Lee

Computer Science

Faculty Advisor: Dr. Arno Puder and Dr. William Hsu

Abstract: An Augmented Reality application that shows the relative scale of the solar system viscerally, by opening a window into the solar system at your fingertips. Developed using Unity and Google's Project Tango technology to allow you to experience the scale of the Solar System by walking among the planets. See the Sun, planets, moons, dwarf-planets, and major asteroids in their relative sizes. Observe the orbits of those bodies, and their apparent paths from the perspective of another body.

Entry Number: 61 GP1

WORLD OF BALANCE

By: Jens Vanderhaeghe

Computer Science

Faculty Advisor: Dr. Ilmi Yoon

Abstract: World of Balance is an ecology simulation game project that has been in development for almost a year. It provides a different, yet interesting approach to the way we analyze the changes of species population in an ecosystem, specifically the Serengeti ecosystem. The combination with game elements allows us to create a virtual ecosystem where users can interact with the environment by introducing different species into the mix to see how it affects the current ecosystem. /

Entry Number: 62 GP1

TRACKING BEES USING IMAGING ANALYSIS TECHNIQUES

By: Kay Choi

Computer Science

Faculty Advisor: Dr. William Hsu

Abstract: Bees play an important ecological and agricultural role as pollinators, Bee colonies are large, well-organized systems; monitoring the health of colonies is likewise important. Video footage is often used to monitor bee activity. However, one of the difficulties in tracking bee activity over an extended period is the monotonous nature of the task. Human attention will naturally wander during the duration of a lengthy video. / Automatic software based tracking using computer vision techniques may be useful for monitoring bee activity in extended collections of video footage. Image analysis techniques can even extract useful information from video footage in real-time, greatly automating the normally time-consuming process of scanning footage for objects and events of interest. Software using these techniques can then annotate footage with the extracted information for later review, without having to extract information again. / This project introduces the BeeTracker program, a cross-platform application that uses image analysis techniques to track bee activity. We focus on two types of bee activity that may be correlated with the health of a bee colony: hive entries and exits, and waggle dances. BeeTracker is easy to use, and able to accurately identify these two types of bee activity; hence, it may be a useful tool for monitoring the health of colonies.

Entry Number: 63 GP1

AUTOMATIC QUESTION ANSWERING SYSTEM FOR FACTOID AND NON-FACTOID OPEN-DOMAIN QUESTIONS

By: Mariia Khvalchik

Computer Science

Faculty Advisor: Dr. Anagha Kulkarni

Abstract: Automatic question answering is a problem at the intersection of multiple disciplines - Natural Language Processing, Information Retrieval and Machine Learning. Although the problem of answering factoid questions (e.g. "What is the capital of the US?") has been investigated extensively, answering open-domain non-factoid questions (e.g. "What is the best way to cook fish?") remains a challenging problem. We focus on the latter type of questions, with the added constraint of keeping the response time to 1 minute at most per question. / / A typical question answering system is structured as a pipeline of three components: query formulation, document retrieval, passage retrieval/ranking. In this work we focus on the first and the last component. Specifically, we perform linguistic analysis of the question to transform it into a boolean query with conjunction and disjunction operators. This query is executed against the Web-as-a-corpus using a popular search engine, and the top results are used to compile the answer for the question. The performance of the system is evaluated using Yahoo answers dataset which consists of large set of questions along with the best answers, given and voted by users. We also plan to participate in the LiveQA track at TREC 2016 which will provide additional evaluation of the system, and also comparison with other participant systems.

Entry Number: 64 GP1

VIRTUAL MARINE ECOSYSTEM

By: Robert Moon

Computer Science

Faculty Advisor: Dr. Ilmi Yoon

Abstract: This project is a computer simulated fish tank inhabited by artificially intelligent fish. The fishes swim around as autonomous agents. They move around influenced by the stimulus of their environment as individuals or as flocks, and avoid immobile obstacles, aquatic plants, and other fishes. The fishes also reason about their environment. Using fuzzy logic, the fishes follow their strongest desire to either mate, search for food, flee from predators, spawn babies, die, or flock with other fishes. There is basic physics to the fish tank and fishes collide with other fishes, aquatic plants, or the fish tank walls. The design decisions of this project have been made to make the simulated fish tank look as close as possible to nature.

Entry Number: 65 GP1

COMPUTATIONAL PREDICTION OF ATC CODES OF DRUG-LIKE COMPOUNDS USING TIERED LEARNING

By: Thomas Olson

Computer Science

Faculty Advisor: Dr. Rahul Singh

Abstract: The Anatomical Therapeutic Chemical (ATC) Code System is a World Health Organization (WHO) proposed classification that assigns codes to compounds based on their therapeutic, pharmacological and chemical characteristics as well as the in-vivo site of activity. The ability to predict the ATC code of an arbitrary compound with high accuracy can go a long way in selecting molecules for lead identification. We propose a computational approach to this problem that utilizes a natural pharmacological constraint, namely, that anatomical-therapeutic biological activity of certain types must preclude activities of many other types. The method proposed here utilizes machine learning in a tiered architecture; prediction of the ATC code at a certain level is constrained by the ATC code at the higher levels. Using this learning architecture, we have built classifiers that incorporate information from a compound's structure, as well as its chemical and protein interactions. The proposed approach has been validated using 2335 drugs from the ChEMBL database in both cross-validation and test setting. The prediction accuracy obtained with this approach is 78.72% and is comparable or better than the prediction accuracy of other methods at the state of the art.

Entry Number: 66 GP1

ALGORITHMIC MAPPING AND CHARACTERIZATION OF THE DRUG-INDUCED PHENOTYPIC-RESPONSE SPACE OF PARASITES CAUSING SCHISTOSOMIASIS

By: Rachel Beasley

Computer Science

Faculty Advisor: Dr. Rahul Singh

Abstract: Neglected tropical diseases, especially those caused by helminths, constitute some of the most common infections of the world's poorest people. Amongst these, schistosomiasis (bilharzia or 'snail fever'), caused by blood flukes of the genus *Schistosoma*, ranks second only to malaria in terms of human impact: two hundred million people are infected and close to 800 million are at risk of infection. Drug screening against helminths poses unique challenges: the parasite cannot be cloned and is difficult to target using gene knockouts or RNAi. Consequently, both lead identification and validation involve phenotypic screening, where parasites are exposed to compounds whose effects are determined through the analysis of the ensuing phenotypic responses. The efficacy of leads thus identified derives from one or more or even unknown molecular mechanisms of action. The two most immediate and significant challenges that confront the state-of-the-art in this area are: the development of automated and quantitative phenotypic screening techniques and the mapping and quantitative characterization of the totality of phenotypic responses of the parasite. In this paper we investigate and propose solutions for the latter problem in terms of the following: (1) mathematical formulation and algorithms that allow rigorous representation of the phenotypic response space of the parasite, (2) application of graph-theoretic and network analysis techniques for quantitative modeling and characterization of the phenotypic space, and (3) application of the aforementioned methodology to analyze the phenotypic space of *S. mansoni* – one of the etiological agents of schistosomiasis, induced by compounds that target its polo-like kinase 1 (PLK 1) gene – a recently validated drug target. In our approach, first, bio-image analysis algorithms are used to quantify the phenotypic responses of different drugs. Next, these responses are linearly mapped into a low-dimensional space using Principle Component Analysis (PCA). The phenotype space is modeled using neighborhood graphs which are used to represent the similarity amongst the phenotypes. These graphs are characterized and explored using network analysis algorithms. We present a number of results related to both the nature of the phenotypic space of the *S. mansoni* parasite as well as algorithmic issues encountered in constructing and analyzing the phenotypic-response space. In particular, the phenotype distribution of the parasite was found to have a distinct shape and topology. We have also quantitatively characterized the phenotypic space by varying critical model parameters. Finally, these maps of the phenotype space allows visualization and reasoning about complex relationships between putative drugs and their system-wide effects and can serve as a highly efficient paradigm for assimilating and unifying information from phenotypic screens both during lead identification and lead optimization.

Entry Number: 67 GP1

TOWARDS ANTI-STUTTERING: UNDERSTAND RELATION BETWEEN STRESS AND STUTTERING

By: Sarah Shamsi

Computer Engineering

Faculty Advisor: Dr. Xiaorong Zhang

Abstract: This project aims to determine the relation between stuttering and stress using ECG, GSR and other physiological signals. These physiological signals are collected from stutters and non-stutters over similar speaking tasks. The useful physiological markers and features have been determined to compare and study the stress variations in stutters and non-stutters. The suitable machine learning classification techniques have been implemented to classify stress patterns for stutters while speaking. This study uses biomedical sensing device called Shimmer. This research will provide the subjective role of the stress behind causing stuttering.

Entry Number: 68 GP1

CITIZEN SENSOR NETWORK - CLIENT SIDE APPLICATION

By: Asaf Weinberg

Electrical Engineering

Faculty Advisor: Dr. Xiaorong Zhang

Abstract: The main aim of the project is to develop and implement an iOS mobile application that captures seismic events and their previous data and transmits these to a backend server for further analysis. In addition, this project will set the guidelines for the next step in the development of the server side application of the citizen sensor network. / For this purpose, readings from the mobile device's accelerometer are used. Existing research has confirmed that the smartphone sensors are capable of accurately measuring sinusoidal vibration in a frequency range relevant to most civil engineering structures. Test have demonstrated the capabilities of smartphone sensors in measuring structural responses to a variety of dynamic loads with different amplitudes as well as frequency characteristics. / In order to determine a seismic event, accelerometer readings are sampled and compared to an average of previous samples, using a Short-term-average over Long-term-average (STA/LTA) calculation. The STA/LTA analysis starts once the previous samples' buffer is full. / In order to filter out false readings, gyroscope readings are sampled in order to detect a lift movement. If a lift movement has been detected, all previous data is erased and buffering restarts. The same principle applies if the device has been lifted during a seismic event. /

Entry Number: 69 GP1

PULSE WIDTH MODULATION GENERATOR USING FPGA

By: Saurabh Marulkar

Electrical Engineering

Faculty Advisor: Dr. Hao Jiang

Abstract: The project will cover the analysis and design of the pulse width modulation generator circuit using FPGA board. The design goal of this project is to develop digital pulse width modulation which will able to change the frequency and duty cycle of given signal to it. Altera DE2-115 cyclone IV FPGA kit is used to accomplish this project. The objective is to design and implement a system, capable of producing user defined digital waveform. The output of system is to generate digital square wave of any frequency ranging from 1.5 Hz to 200 MHz and also to amend duty cycle of generating wave. This project will be digital replacement of existing analog signal driver circuit which used to driver Low-input-voltage Wireless Power Transfer. I certify that the Abstract is a correct representation of the content of this thesis.

Entry Number: 70 GP1

A WIDE DYNAMIC RANGE CURRENT AMPLIFIER FOR NEUROMORPHIC COMPUTING SYSTEM

By: Chi Zhang

Embedded Electrical & Computer Systems

Faculty Advisor: Dr. Hao Jiang

Abstract: A wide dynamic range current amplifier used in the Current Sensing Scheme Neuromorphic Computing System. In the neuromorphic computing system, to ensure the current that generated from DAC circuit can drive the IFC circuit in a large dynamic range, a current amplifier is required to be a buffer, which can duplicated the current and also provide a high driving voltage. The challenge of the current amplifier is that the voltage at the input node has to be fixed and low, so that the large sensing current can keep in linearity even

the driving voltage is low. In addition, the accuracy of current amplifier is another critical factor. The proposed current amplifier meets above requirements by using OP-AMP to create negative feedback virtual short. /

Entry Number: 71 GP1

A FLEXIBLE PLATFORM FOR DEVELOPING REAL-TIME HUMAN MACHINE INTERFACE FOR MYOELECTRIC CONTROLLED PROSTHETIC ARMS

By: Ian Donovan, Kevin Valenzuela, Alejandro Ortiz, Sergey Dusheyko, and Kartik Bholla

Embedded Electrical & Computer Systems

Faculty Advisor: Dr. Xiaorong Zhang and Dr. Kazunori Okada

Abstract: Electromyography (EMG) analysis interprets the electrical signals produced by muscles to be used as inputs for human machine interfaces (HMI). Presented here is a modular system centered around a PC based graphical user interface (GUI) and analysis program developed in the San Francisco State University Intelligent Computing & Embedded Systems (ICE) laboratory. The analysis program (referred to as HMI) collects EMG data from commercial hardware, extracts features, and performs classification of static gestures. These gesture decisions are then past to either a prosthetic arm mock up or a virtual reality based arm. Though the HMI can be used to optimize classification accuracies by testing different features and classification methods, the testing of the usability of these methods require the tangible real-time control of the prosthetic or virtual arm. The HMI is built to be expended and to allow different methods to be explored.

Entry Number: 72 GP1

EFFICIENT ANALOG-TO-DIGITAL CONVERTER FOR SYNAPSE-BASED NEUROMORPHIC SYSTEM

By: Kang Jun Bai

Embedded Electrical & Computer Systems

Faculty Advisor: Dr. Hao Jiang

Abstract: Bio-inspired neuromorphic computing system that emulates human brains has gained great interests due to its high-efficiency computation. Meanwhile, the recently developed memristor-crossbar-array technology, which is able to efficiently emulate the plasticity of biological synapses and accommodate matrix multiplication, has been demonstrated its potential for synapse based neuromorphic computing. The hardware implementation of a bio-inspired system has always been a research focus. In this research, a analog-to-digital converter (ADC) using IBM 130nm CMOS technology was developed. The circuit efficiently and accurately facilitates memristor-crossbar-array matrix multiplication. The performance of the described ADC is evaluated with a 32x32 memristor-crossbar-array.

Entry Number: 73 GP1

POWER/AREA EFFICIENT INTEGRATE-AND-FIRE CIRCUIT FOR NEUROMORPHIC COMPUTING SYSTEM

By: Weijie Zhu

Embedded Electrical & Computer Systems

Faculty Advisor: Dr. Hao Jiang

Abstract: Bio-inspired neuromorphic computing system that emulates human brains has gained great interests due to its high-efficiency computation. Meanwhile, the recently developed memristor-crossbar-array technology, which is able to efficiently emulate the plasticity of biological synapses and accommodate matrix multiplication, has been demonstrated its potential for synapse based neuromorphic computing. The hardware implementation of a bio-inspired system has always been a research focus. In this research, a cyclical-sensing integrate-and-fire circuit scheme (C-IFC) using IBM 130nm CMOS technology was developed. The circuit efficiently and accurately facilitates memristor-crossbar-array matrix multiplication. The performance of the described C-IFC is evaluated with a 32x32 memristor-crossbar-array. With the optimized memristor-crossbar-array structure, the described C-IFC has shown great promise in accelerating matrix multiplication in a bio-inspired synapse-based neuromorphic computing system.

Entry Number: 74 GP1

ROBUST DESIGN OF SPIN TRANSFER TORQUE LOOK-UP TABLE MEMORY UNDER PROCESS VARIATIONS IN NANO-SCALE

By: Ali Attaran

Energy System Engineering

Faculty Advisor: Dr. Hamid Mahmoodi

Abstract: Hardware security and reliability are becoming an increasing threat to fabless semiconductor industries due to split between fabless design businesses and IC fabrication foundries that are globally distributed all over the world. In this research a new design scheme for reconfigurable digital logic Look-Up Table (LUT) is proposed by utilizing Spin Transfer Torque (STT) technology instead of traditional CMOS as storage units. STT technology brings non-volatility, ease of programming, almost zero leakage power and high scalability into main memory of CPUs. Magnetic Tunnel Junction (MTJ) is the storage units of a STTRAM, which are consist of two ferromagnetic layers and one insulator layer in-between. This technology uses magnetic orientation to storage information as traditional SRAM electron charges are used to store information.

Entry Number: 75 GP1 DISPLAY ONLY

APPLICATION OF FANO RESONANCE EFFECTS IN OPTICAL ANTENNAS FORMED BY REGULAR CLUSTERS OF NANOSPHERES

By: Ali Attaran

Energy System Engineering

Faculty Advisor: Dr. Zhigang Chen (Physics)

Abstract: In this paper an analytical model is developed to study the Fano resonance effect in clusters of spherical plasmonic nanoparticles under local excitation using an emitter dipole. According to analytical results and numerical simulations, the optimum transmission directivity, intensity and polarization is obtained when the emitter distance from cluster is 200nm and its geometrical structure is designed to operate at 520nm wavelength. Spatial polarization and field distributions of the optical states and resonance spectra are observed in pentamer and heptamer cluster configurations. In order to qualify the redirection of emission, the directivity calculation is studied. It has been found that subradiant mode effects are apparent in the heptamer and pentamer models, due to the fact that the interference of the polarization between the nanoparticles results in the formation of a second peak in the directivity spectra at 690nm. The angular emission of the cluster is highly directed and determined by antenna mode. The high directive feature of such antenna makes it a promising candidate for compact easy-to-address sensors.

Entry Number: 76 GP2

FUNDAMENTAL PERIOD PREDICTION OF STEEL PLATE SHEAR WALL STRUCTURES

By: Benjamin Kean

Structural & Earthquake Engineering

Faculty Advisor: Dr. Cheng Chen

Abstract: The Steel Plate Shear Wall (SPSW) is a structural system used today in design for the primary Lateral Force Resisting System (LFRS) of a building. In the initial design stage the fundamental period of the structure is used to calculate the seismic forces using the Equivalent Lateral Force Procedure (ELFP). The American Society of Civil Engineers (ASCE) allows for the approximation of the fundamental period to be performed using a general formula using two coefficients whose values are dependent on the type of LFRS. The SPSW uses a general value for the fundamental period coefficients and it has been shown that the current procedure for approximating the fundamental period of an SPSW produces overly conservative estimations. This study evaluates the fundamental period of a large population of SPSW prototypes. A formula for better approximation of the fundamental period coefficients is derived and then verified on code-designed SPSW prototypes.

Entry Number: 77 GP2

DELAY EFFECT ON MODEL UNCERTAINTY IN REAL-TIME HYBRID SIMULATION

By: Kai Chen

Structural & Earthquake Engineering

Faculty Advisor: Dr. Cheng Chen

Abstract: Uncertainties in numerical substructure can result in different responses for the same model in hybrid simulation. This problem is more serious in real-time hybrid simulation since the influence of the time delay. Polynomial chaos expansion (PCE) projects the model output on a basis of orthogonal stochastic polynomials, and utilizes polynomial as metamodel to represent the complicated model. From the polynomial chaos

expansion, the influence of the uncertainties in numerical model can be reflected. In this paper, the polynomial chaos is utilized to evaluate the delay effect on the maximum structure responses when numerical substructure contains uncertainty parameters in real-time hybrid simulation using delay differential equation (DDE) model. The polynomial chaos expansion for the system without delay is first discussed, and then applied to the systems under different time delay. The mean, variance and Sobol index based on polynomial chaos expansions are compared. Results show that the mean and variance of the maximum displacement increase with time delay linearly and exponentially, respectively. Sensitivity analysis also indicates the influence of the single random variable is decreasing while the coupling effect is increasing with the time delay. Also, time delay can change the variable which has the most influence on the variance of the maximum displacement in DDE model.

Entry Number: 78 GP2

LATERAL BRACING OF MOMENT FRAME BEAMS

By: Nadia Makoor and Charles Cao

Structural & Earthquake Engineering

Faculty Advisor: Dr. Cheng Chen

Abstract: Current code has two requirements for the strength and stiffness of lateral bracing of moment frame beams. These requirements can be easily achieved for a concrete diaphragm, however the stiffness requirement is difficult to satisfy in a light-framed wood diaphragm. The objective of this research is to explore the threshold when the beam will be engaged into lateral torsional buckling, and if the diaphragm in a light-framed wood building can deliver forces large enough to induce that. The expected findings from this research will improve current practice in the seismic retrofit of light-framed wood buildings and enable professional engineers to determine whether this lateral bracing is necessary or not.

Entry Number: 79 GP2 DISPLAY ONLY

SYNTHESIS AND TRAPPING OF ACYLFULVENES

By: Ariel Kuhn

Chemistry

Faculty Advisor: Dr. Ihsan Erden

Abstract: Fulvenes are cyclic cross-conjugated polyolefins that exhibit unique physical and chemical / properties. In addition to the diverse modes of reactions of these colorful compounds, certain / members of the fulvene family are found in nature, and more recently, 1-acylfulvenes have been / shown to exhibit considerable anticancer activity against a variety of solid tumors. However, these compounds are highly unstable, thus we have developed a method to trap 6-acylfulvene at low temperatures with cyclopentadiene in an intermolecular Diels-Alder reaction.

Entry Number: 80 GP2

THE EFFECT OF STRUCTURE AND MORPHOLOGY ON PHOTOOXIDATION IN EPITAXIAL TiO₂(001) THIN FILMS

By: Marissa Martinez

Chemistry

Faculty Advisor: Dr. Andrew Ichimura

Abstract: / / In this study, anatase TiO₂ films with strong [001] orientation and ~100% {001} facets at the surface were prepared and their photoactivity was measured via photooxidation of terephthalic acid. Anatase TiO₂ is well known for its ability to perform environmental remediation by photooxidation of organics, yet it is still unclear which structural and chemical features are best for optimizing its photooxidative power. The goal of this work is to determine the photooxidative power of anatase films with [001] orientation favorable for charge diffusion, and {001} facets favorable for charge transfer. The films were prepared on sapphire substrates using a one-pot hydrothermal synthesis. To compare the photocatalytic activity as a function of defect concentration in the bulk and surface, anatase films were processed by annealing in air at 400, 600, and 800 °C, annealing in H₂ atmosphere at 600 °C, and washing in NaOH. Each film was characterized with X-ray diffraction (XRD), field-emission scanning electron microscopy, electron dispersive spectroscopy (EDS), photoluminescence (PL) spectroscopy, and UV/Vis absorbance spectroscopy. The photoactivity determined by the photooxidation of terephthalic acid by •OH, where the photooxidation by the films was compared to both P25 and TiO₂ powders produced by the same method as the films. The XRD θ -2 θ and rocking curve scans

show that each film is pure anatase with strong [001] orientation and a rocking curve FWHM of $<2^\circ$. The films have {001} facets at the surface, as shown by SEM. EDS shows that the films as-synthesized films have annealed in air have fewer oxygen vacancies and little to no fluorine. The photooxidation and PL results show that TiO₂ films annealed at 400 and 600°C generate the most •OH and give the greatest PL intensity compared to as-synthesized and reduced films. This implies that bulk defects and surface composition play a major role in the photooxidation achieved by anatase (001), and that TiO₂ can be optimized by controlling both the orientation and morphology of the films. This study shows that [001] orientated anatase films with {001} facets at the surface have great potential for photocatalysis. /

Entry Number: 81 GP2 DISPLAY ONLY

TERRAIN-BASED PREDICTIVE MODELING OF FUNCTIONAL RIPARIAN CORRIDORS IN A COASTAL NORTHERN CALIFORNIA WATERSHED

By: Tom Robinson

Geographic Information Science

Faculty Advisors: Dr. Jerry Davis and Dr. Nancy Wilkinson

Abstract: Loss of floodplain habitat is a major factor in the decline of Pacific salmonid (*Oncorhynchus* spp.) populations. Current riparian protection policies and practices suffer from a lack of spatial data that represents the space required to allow natural, dynamic floodplain processes to maintain habitat function over time. This research aims to test new methods of mapping functional alluvial riparian corridors using high-resolution terrain data and hydraulic geometry relationships in stream reaches characteristic of coastal California. Field surveys of channel and upland morphology, soil and sediment character, and vegetation composition will be used to delineate and characterize the riparian zone of a salmon-bearing stream reach in a coastal watershed in Sonoma County, California. This study will demonstrate the efficacy of GIS-based modeling to estimate the full functional alluvial riparian zone for use in conservation planning by land conservation organizations.

Entry Number: 82 GP2

CLIMATE VARIABILITY AND VADOSE ZONE CONTROLS ON DAMPING OF TRANSIENT RECHARGE FLUXES

By: Claudia Corona

Applied Geoscience

Faculty Advisor: Dr. Jason J. Gurdak

Abstract: We investigate the effects of interannual to multidecadal climate variability on groundwater resources by exploring the physical processes in the vadose zone that partially control transient infiltration and recharge fluxes. Infiltration events become time-varying water flux through the vadose zone and are controlled by highly nonlinear, complex interactions between mean infiltration flux, infiltration period, soil textures, and depth to water table. We focus on the behavior and damping depth of water flux in the vadose zone. The depth at which the flux variation damps to 5% of its initial variation at land surface is defined as the damping depth. When the damping depth is above the water table, recharge may be considered steady; when the damping depth is below the water table, recharge may be considered transient. We examine controls on the damping depth by modeling transient water fluxes from land surface to the water table, using the Gardner-Kozeny soil model for diffuse unsaturated flow in HYDRUS 1-D. Results for homogeneous profiles show that shorter-period oscillations, smaller mean fluxes, and finer-grained soil textures with poor sorting, cause water flux to dampen at shallower depths. Modeling two-layered systems show similar, but more complicated responses. In two-layered systems, coarse-grained soils cause the greatest deviations from homogeneous damping depths, most evidently if they are the bottom soil in the profile. Flow simulations show that coupled finer-grained soil profiles result in damping depths closer to land surface, and are more similar to their homogeneous counterparts, than are coupled fine-grained/coarse-grained profiles. Linear superposition is observed in simulations of short periods and finer-grained soils. Longer periods and coarser-grained soils fail to provide evidence for linear superposition. Findings from this study will enhance understanding of the vadose zones influence on transient water flux and improve the simulation of recharge processes and climate variability effects in groundwater models.

Entry Number: 83 GP2 DISPLAY ONLY

DETECTING GLOBAL HYDROLOGICAL CYCLE INTENSIFICATION ON GLOBAL OCEAN SALINITY ANOMALIES

By: Jason Poague
Geosciences
Faculty Advisor: Dr. Alexander Stine
Abstract:

Entry Number: 84 GP2

A TALE OF TWO ISLANDS: CAN ATOLL ISLANDS ADAPT TO CLIMATE CHANGE BY REMOVING VEGETATION AND MANAGING AQUIFER RECHARGE?

By: Mehrdad Hejazian

Applied Geoscience

Faculty Advisors: Dr. Jason J. Gurdak and Dr. Mary Leech

Abstract: Groundwater resources on low lying atoll islands are extremely vulnerable to climate change and sea-level rise because they are typically less than 3 m above mean sea level and are composed of permeable rock that drains vital groundwater resources. Because thick, tropical vegetation covers large amounts of the landscape, evapotranspiration is high and recharge to aquifers is limited. The most recent IPCC report indicates sea level rise of 0.26 to 0.82 m and increased climate change related drought by the end of the century. Since atoll Islands are isolated from any mainlands, they rely heavily on groundwater resources, especially during times of drought. Landscape/Land-use (LULC) change and managed aquifer recharge (MAR) have shown promise in increasing groundwater supply on Roi-Namur Island, Republic of the Marshall Islands. Roi-Namur has two separate lobes with contrasting island settings and aquifers. Roi is estimated to have 226 million gallons of potable groundwater, compared to only 4.2 million gallons on Namur. This is mostly attributed to the removal of vegetation and MAR on Roi, which were implemented as result of a U.S. military base installation. A suite of monitoring wells were sampled on Roi-Namur and a statistical analysis of groundwater quality was performed to determine if LULC and MAR has a significant effect on natural geochemical processes on atoll islands. Dissolution of carbonate rock has been reduced by seven-fold as a result of LULC and MAR. Increased recharge on Roi has significantly increased the freshwater lens volume and altered natural geochemical processes. The dominant geochemical processes on Namur are equilibrium reactions, whereas on Roi, mixing processes are more dominant as a result of increased recharge and flushing of the aquifer. Results indicate that this is a viable groundwater management plan to increase groundwater storage on atoll islands. Groundwater managers can increase groundwater supply by using strategic MAR but must balance the need for vegetation and crops on atolls while limiting evapotranspiration. /

Entry Number: 85 GP2

TESTING THE INFLUENCE OF LIGHT AVAILABILITY ON A TREE-RING RECONSTRUCTED TEMPERATURE RECORD AT SONORA PASS, CA

By: Lan Ma

Earth & Climate Sciences

Faculty Advisor: Dr. Alexander Stine

Abstract: Tree-ring width near treeline tend to covary with local interannual temperature, motivating the use of such records to reconstruct past temperature variability. However, recent work has introduced the possibility of multiple environmental factors contributing to tree growth in cold environments. We investigate the influence of small-scale light variability on tree-ring based temperature reconstructions from a treeline ecotone near Sonora Pass in the California Sierra Nevada. Dominated by whitebark pine (*Pinus albicaulis*) growing as individuals and in stands, this site provides an opportunity to test the sensitivity of growth history and the variability to light environment. For this preliminary analysis, we use increment cores from ten trees: five growing in open areas of edge of a stand (sunny trees) and five growing in middle of stands (shaded trees). The correlation of ring width time series suggests a moderate significant difference between sunny and shaded trees, providing direction for further work to include detailed light environment measurements and greater core sample size.

Entry Number: 86 GP2

SEDIMENTARY CONTROLS ON FORAMINIFERA DEPOSITION IN THE BAY OF BENGAL

By: Theresa Fritz-Endres

Earth & Climate Sciences

Faculty Advisor: Dr. Petra Dekens

Abstract: IODP Expedition 354 drilled sites in the Bay of Bengal to improve our understanding of the links between tectonics, monsoon strength, and oceanographic conditions. The Bengal Fan contains complex depositional environments, which vary from sequences of turbidites that reflects channel activity to intervals of hemipelagic clay. Foraminifera are commonly used to reconstruct past oceanographic conditions, but the complex depositional environments raises the possibility that foraminifera in the cores were transported from the northern Bay of Bengal by turbidity currents rather than settling out from the overlying water column. The goal of the project is to determine if foraminifera in the modern sediments at IODP Exp 354 sites record the overlying water conditions or water conditions of the northern Bay of Bengal. / / Today sea surface salinity (SSS) and sea surface temperature (SST) has a larger seasonal range in the northern bay (3.0 psu and 5°C, respectively) compared to Exp 354 core sites at 8°N (0.7 psu and 1.4°C, respectively). We present Mg/Ca and $\delta^{18}\text{O}$ data of individual Globigerinoides sacculifer in the mud-line samples of site U1454 (8.4°N, 85.5°E, 3721 m water depth), which is near the modern active channel, and site U1449 (8.4°N, 88.7°E, 3653 m water depth), which is farthest from the active channel. Because foraminifera live ~2-4 weeks, each analysis reflects a short period of time. Taken together, the distribution of 70 to 80 data points reflect the seasonal SST and SSS distribution of the southern Bay of Bengal where the foraminifera likely calcified. /

Entry Number: 87 GP2 DISPLAY ONLY

SPECTRA OF TROPICAL LAPLACIANS OF BALANCED GRAPHS

By: Anna Schindler

Mathematics

Faculty Advisor: Dr. Federico Ardila

Abstract: Spectral graph theory seeks to understand graphs by using methods from linear algebra. Specifically, it is the study of the spectra (eigenvalues) of matrices that encode the combinatorial structure of graphs. This research is focused on a balanced graphs, and a matrix called the tropical Laplacian, which contains both geometric and combinatorial information about those graphs.

Entry Number: 88 GP2

MAXIMUM LIKELIHOOD ESTIMATION AND EM FIXED POINT IDEALS FOR BINARY TENSORS

By: Daniel Lemke

Mathematics

Faculty Advisor: Dr. Serkan Hosten

Abstract: A tensor is a multidimensional array. As such, they are objects in multilinear algebra with which we can identify certain properties similar to that of matrices, including rank, and eigenconfigurations. In statistics there is a well-known nonlinear optimization problem called maximum likelihood estimation. Given data in the form of tensors, our research utilizes tools from computational algebraic geometry to capture solutions to these problems. We also analyze the boundary strata of the 7-dimensional space of $2 \times 2 \times 2$ -tensors of nonnegative rank less than or equal to 2. Our methods provide a near comprehensive solution to the maximum likelihood estimation problem for this class of tensors.

Entry Number: 89 GP2

GENERALIZED EULERIAN NUMBERS AND THE DELTA-POLYNOMIAL FOR HALF-OPEN LATTICE PARALLELEPIPEDS: A GEOMETRIC PERSPECTIVE

By: Emily McCullough

Mathematics

Faculty Advisor: Dr. Matthias Beck

Abstract: The coefficients of the delta-polynomial of a lattice polytope P encode information about the lattice point counts in positive integer dilates of P . We consider the relationship between the (B, l) -Eulerian numbers, a refined descent statistic on the set of signed permutations on $\{1, 2, \dots, d\}$, and the delta-polynomial for the d -dimensional half-open ± 1 cube with l non-translate facets removed. Using the interplay of geometry and combinatorics, we improve upon known inequality relations on the coefficients of the delta-polynomials for specific families of half-open parallelepipeds. Our results extend naturally to the delta-polynomials for closed lattice zonotopes.

Entry Number: 90 GP2

THE DEHN--SOMMERVILLE RELATIONS AND THE CATALAN MATROID

By: Nicole Yamzon

Mathematics

Faculty Advisors: Dr. Federico Ardila and Dr. Matthias Beck

Abstract: The f -vector of a d -dimensional polytope P stores the number of faces of each dimension. When P is simplicial the Dehn--Sommerville relations condense the f -vector into the g -vector, which has length $\lceil \frac{d+1}{2} \rceil$. Thus, to determine the f -vector of P , we only need to know approximately half of its entries. This raises the question: Which $\lceil \frac{d+1}{2} \rceil$ -subsets of the f -vector of a general simplicial polytope are sufficient to determine the whole f -vector? We prove that the answer is given by the bases of the Catalan matroid.

Entry Number: 91 GP2

MAXIMUM LIKELIHOOD DEGREE OF VARIOUS TORIC VARIETIES

By: Radoslav Vuchkov

Mathematics

Faculty Advisor: Dr. Serkan Hosten

Abstract: Maximum likelihood estimation in statistics leads to the problem of maximizing a product of powers of polynomials, which gave rise to the maximum likelihood degree (ML degree). We will observe specific cases of the rational normal curve and the second hypersimplex, calculating their ML degree as well as introducing conjectures for Hirzebruch surfaces

Entry Number: 92 GP2

BIVARIATE ORDER POLYNOMIALS

By: Sandra Zuniga Ruiz

Mathematics

Faculty Advisors: Dr. Matthias Beck and Dr. Federico Ardila

Abstract: In the early 1900s, in an attempt to prove the 4-coloring theorem Birkhoff discovered the number of ways to color a graph, this is known as the chromatic polynomial. In 1970, Richard Stanley introduced a decomposition of the chromatic polynomial using order polynomials. We extend these results using bivariate polynomials. In 2003, Klaus Dohmen, Andre Pönitz, and Peter Tittman introduced a two variable generalization of the chromatic polynomial. Using the generalized bivariate chromatic polynomial we introduce a decomposition using bivariate order polynomials.

Entry Number: 93 GP2

KINEMATICAL EVIDENCE FOR TWO-ZONE EARLY-TYPE GALAXY FORMATION

By: Justin A. Kader

Astronomy

Faculty Advisor: Dr. Ron Marzke

Abstract: Kinematic measurements of nearby elliptical and lenticular galaxies reveal a conspicuous two-zone pattern in almost the entire sample. Almost all of the observed galaxies show rapid disk-like rotation in their central regions, and slowly rotating outer regions. In this project we have created the very first 2-D kinematic maps extending from center to halo, using field starlight in the inner regions and spatially resolved globular clusters and PNe in the outer parts. These observations are compared with state of the art simulations of galaxy formation, which include idealized major mergers and also "violent disk" systems found in cosmological simulations. From the comparisons we infer that most early-type galaxies were assembled in two zones: the inner region formed early in a violent-disk phase, and the outer part was assembled gradually from minor mergers and accretion. Different combinations of these processes may explain the full range of present-day galaxy morphology.

Entry Number: 94 GP2

STELLAR COMPANIONS TO THE EXOPLANET HOST STARS HD 2638 AND HD 164509

By: Justin Wittrock

Astronomy

Faculty Advisor: Dr. Stephen Kane

Abstract: An important aspect of searching for exoplanets is understanding the binarity of the host stars. It is particularly important because nearly half of the solar-like stars within our own Milky Way may be part of binary or multiple systems. Moreover, the presence of two or more stars within a system can place further constraints on planetary formation, evolution, and orbital dynamics. As part of our survey of almost a hundred host stars, we obtained images at 692 and 880-nm bands using the Differential Speckle Survey Instrument (DSSI) at the Gemini Observatory. Of those, we detect stellar companions to HD 2638 and HD 164509. The stellar companion to HD 2638 has been previously detected, but the companion to HD 164509 is a newly discovered companion. The angular separation for HD 2638 is 0.512 ± 0.002 arcsec and for HD 164509 is 0.697 ± 0.002 arcsec. This corresponds to a physical separation of 25.6 ± 1.9 AU and 36.5 ± 1.9 AU respectively. By employing stellar isochrone models, we estimate the mass of the stellar companions to HD 2638 and HD 164509 to be $0.482547 \pm 0.006716 M_{\odot}$ and $0.415811 \pm 0.007007 M_{\odot}$ respectively and their effective temperature to be 3570 ± 8 K and 3450 ± 7 K respectively. These results are consistent with late-type M dwarf spectral types.

Entry Number: 95 GP2

DISORDERED PHOTONIC STRUCTURES: MANIPULATING THE FLOW OF LIGHT

By: Shervin Sahba

Physics

Faculty Advisor: Dr. Weining Man

Abstract: Photonic structures are dielectric media in differing geometries that can be used to manipulate light. In designer highly-uniform disordered structures, as opposed to periodic arrangements, we can observe frequency ranges where light is fundamentally and isotropically prohibited. We investigate such structures and possibilities for waveguiding. Such advancements pave the way for photonic circuits in modern devices.

Entry Number: 96 UI

A POTENTIALLY INTRIGUING TRIANGLE: COOPERATION, COMPETITION AND PREJUDICE

By: Reza Deiss Ghafur

Psychology

Faculty Advisor: Dr. Charlotte Tate

Abstract: Previous literature supports the hypothesis of their being an inverse relationship between cooperativeness, at a state level, and levels of prejudice (most literature pertains to ethnic based prejudice). For this study, we sought to establish negative correlations between cooperation, and prejudice pertaining to African Americans, Asian Americans, Lesbians and Gay men, and gender. Further, we sought to establish positive correlations between competitiveness and the aforementioned forms of prejudice. Additionally, we examined cooperativeness and competitiveness, at trait levels, as two distinct constructs as opposed to opposite ends of a spectrum. As expected we found positive correlations between several forms of prejudice and competition, though interestingly we did not find any significant correlations between cooperation and aforementioned forms of prejudice. Studies are currently underway to address if cooperation correlates with prejudice only at a state level, and if these results are unique to using cooperation and competition as two distinct constructs.

Entry Number: 97 UI

AGING FACES: GUESSING AGE AND ASCRIBING AGING STEREOTYPES

By: Hannah Lee

Psychology

Faculty Advisor: Dr. Sarah J. Barber

Abstract: As the number of older adults in the world is projected to increase by 135% between the years 2000 and 2050, it is important to understand and support the older population. However, from a young age we are conditioned through prominent negative representations of elders in the media to resent aging and to treat those who have grown old as less capable than they may actually be. These preconceived notions, either positive or negative, about aging may affect how we judge an older adult in a real world setting. This research examined how just the facial expression of an older adult can affect the way older adults and younger adults judge age, mental and physical capabilities, as well as social involvement and satisfaction with one's life. This study included male and female older adults smiling, frowning or displaying a neutral expression. It was hypothesized

that because smiling is associated with positive personality traits, smiling target photos would be categorized as younger and therefore more positively stereotyped (i.e., the perfect grandparent). Those photos with frowning faces were predicted to be as older and more negatively stereotyped. Participants were shown a single photo and asked to rate the older adult's on the aforementioned categories. We predict that younger adults will be less affected by the older adult's facial expression than older adult participants. This means that younger adults made similar judgments regardless of all facial expressions. Older adults showed more diverse judgments across the three facial expressions. This may show evidence of a black sheep effect: distancing yourself from unfavorable representation of your own group. These results demonstrate that younger adults lump together all older adults in an overall more negative way overall than older adults, who recognize that there may be differences in abilities for different people.

Entry Number: 98 UI

EVALUATING THE BOND BETWEEN HUMANS AND THEIR COMPANION ANIMALS

By: Meghan Quan

Psychology

Faculty Advisor: Dr. Caran Colvin

Abstract: Animal-Assisted Therapy (AAT) has been previously shown to be beneficial to humans. Past research has indicated that individuals can benefit socially, psychologically, and physiologically from AAT. As a majority of research has been focused on the human-canine experience, this research seeks to investigate the value of other companion animals, namely birds. This study will replicate a past study on how comfort is perceived by dog and cat owners on an emotional level (Zasloff, 1996), but will also include bird owners as a third category. Results from this research may indicate that avian therapy could be beneficial to humans. We hope to demonstrate that bird owners receive the same amount of emotional comfort from their pets as do dog and cat owners. Such findings may indicate that avian therapy can be as beneficial as dog therapy, which currently dominates the animal-therapy domain.

Entry Number: 99 UI

TIME ORIENTATION AND SELF-ESTEEM IN YOUNG ADULTS

By: Erica Walker

Psychology

Faculty Advisor: Dr. Zena R. Mello

Abstract: Time perspective is a multidimensional, cognitive, and motivational construct that comprises thoughts and feelings about the past, present, and future (Mello & Worrell, 2015). Time orientation is a dimension of time perspective that refers to the emphasis an individual places on each time period. Prior research has found that time orientation is associated with behavioral outcomes, such as risky behavior, academic achievement, and self-esteem in adolescents (Mello, Finan, & Worrell, 2013). However, research has not yet examined these relationships in young adults. Examining how time perspective is associated with self-esteem in young adults could inform future directions of research. To contribute toward research in this area, this study asked the following questions: (a) what are the time orientations among young adults, and (b) what is the relationship between time orientations and self-esteem? / / The sample consisted of 470 participants, 76% female with an average age of 23 (SDage = 5.89). Time orientation was measured using the Adolescent Time Inventory (ATI; Mello & Worrell, 2007). This measure assesses time orientation with varying circle sizes that emphasize the importance placed on each time period. The Rosenberg Self-Esteem Scale (RSE; Rosenberg, 1965) was used to measure global self-esteem. Results showed a present-future orientation was most commonly reported (n = 224, %?). A one-way ANOVA indicated a significant relationship between time orientation and self-esteem ($F[6,469] = 7.78, p < .001, r^2 = .08$). Post-hoc Tukey analyses indicated that self-esteem varied between present-future (M = 3.23, SD = .51) and past (M = 2.53, SD = .75) orientations, and present-future and past-present orientations (M = 2.6, SD = .51). / / These findings suggest that individuals with a present-future orientation have higher levels of self-esteem. Those who selected any orientation with a focus on the past showed the lowest levels of self-esteem. These results are consistent with previous literature with studies of adolescents (Mello et al., 2013). This study indicates that individual variation in time orientation and its relationship with self-esteem is similar in adolescence and young adulthood. These findings have implications for interventions that incorporate time perspective as a means of increasing self-esteem. Future studies would benefit from examining these topics among middle and older adults. /

Entry Number: 100 UI

THE EFFECT OF MEDIA AND MESSAGE TYPE ON PUBLIC PERCEPTION OF POLICE MISCONDUCT

By: Jessica G. Burgos Pimentel

Psychology

Faculty Advisor: Dr. Caran Colvin

Abstract: Traditional forms media such as newspapers have permeated society for years. However, social media has become an ever-present part of everyday life whose influence is relatively unexplored. In our current society, different types of media have covered officer involved shootings but their effect on public perception of police misconduct is relatively unexplored. In order to assess the relationship between media type and message type on the perception of police misconduct, participants participated in an online computer study. Participants were asked to read either a negative or neutral message formatted as a newspaper article or as a series of Twitter “tweets”. After reading, participants answered questions adapted from Weitzer and Tuch (2004, 2005a, 2005b) perception of police misconduct scale. This study will help to start the dialogue about social media’s influence on our perceptions. /

Entry Number: 101 UI

COASTAL COMMUNITY VULNERABILITY: A PROJECT DESIGN ON THE EFFECTS OF RECIPROCITY ON RESILIENCE AND ADAPTABILITY

By: Adrielle B. Cailipan

Marine Biology

Faculty Advisors: Dr. Tendai Chitewere and Dr. Shannon L. Watkins

Abstract: With the onset of climate change, the vulnerability of coastal communities is rapidly increasing and there is a growing need for adaptive technologies such as building structures like floodwalls to combat sea level rise (a “hard” technique) or wetland restoration (a “soft” technique). While these techniques have been discussed thoroughly, I ask whether a social value such as reciprocity can be considered an adaptive technique which also utilizes ecologically responsible habits. While people might not have their own means to utilize adaptive technologies, can reciprocity function as some kind of insurance? / Can norms of reciprocity be considered a form of an adaptive technology? With the increase of information dissemination, can sustainable adaptive techniques be more easily adopted and promoted by the people living in their communities? I speculate higher levels of reciprocity will lead to an increased desire to make a community adaptable, which will in turn lead to dissemination of information. I hope to understand whether or not this increase in information exchange will increase the likelihood a community adapts (and uses sustainable adaptive practices after a climate-related extreme event and have designed a research project to test this.

Entry Number: 102 UI

OBOT: HEALTH, CLIMATE CHANGE, AND ENVIRONMENTAL INJUSTICE IN WEST OAKLAND

By: Agustina Cartagena

Geography

Faculty Advisor: Dr. Tendai Chitewere

Abstract: Environmental injustice is the disproportionate exposure of people, generally minorities, low-income households, or recent immigrants, to environmental pollution and toxic environments. West Oakland is one of many communities grappling with environmental injustice, with a history of being marginalized in politics through a combination of five decades of historical racism that includes redlining and persistent poverty (Alameda County Department of Public Health). As a result, heavily polluting industries have resided within the boundaries of West Oakland, including a now closed Federal Superfund site and the Red Star Yeast factory (closed in 2003) that released acetaldehyde, a carcinogen that can cause abnormal muscle development in humans. This history of neglect and disproportionate exposure to what are known as locally unwanted land uses (LULU) has resulted in double the lung cancer rates when compared to the rest of Alameda County, higher childhood asthma rates, and life expectancy lowered by approximately 10 years. (Oakland Unified School District and Alameda County of Public Health) The dismal health outcomes are a result of many issues, including the fact that West Oakland is surrounded by major highways carry over 2,000 diesel trucks per day. On surface streets within the neighborhood, 7,000 diesel trucks travel through per day carrying goods to and from the 5th largest port in the United States (Bay Area Air Quality Management District). The Oakland Bulk

and Oversized Terminal (OBOT) will add at least 500 diesel trucks to the already congested roads, increasing resident's exposure to diesel particulate and add even more stress to these people's negative health outcomes, such as cancer and asthma. / Adding to these significant health concerns, OBOT received approximately 10% of its funding from major coal producing counties in Utah (LA Times, Oakland Global). Shipping coal in open rail cars from this terminal will make Oakland's Energy and Climate Action Plan (ECAP) to lower greenhouse gas emissions seem like nothing more than shallow political talk. The City of Oakland will be affected by rising sea levels, along with the rest of the world. Oakland must commit to the goals that we have set for ourselves in Paris in order to mitigate climate disaster that will be compounded by the already socially and environmentally stressed community /

Entry Number: 103 UI

CLIMATE CHANGE AND THE SACRAMENTO-SAN JOAQUIN DELTA: A CASE STUDY OF BETHEL ISLAND

By: J. Javier Padilla Reyes

Geography

Faculty Advisor: Dr. Nancy Wilkinson

Abstract: Bethel is a small (5.5 sq miles) island that is home to 2,137 people. It is located in the Sacramento-San Joaquin Delta (Delta) estuary. At the confluence of the Sacramento and San Joaquin River lies the Delta, carrying freshwater from the snow-coated Sierras, through the Central Valley, and out beyond the Golden Gate. As such, the tides from the Pacific Ocean and the outflow of freshwater directly affect the region. / / The entire Delta region is characterized by 1,100 miles of man-made levees and waterways that protect tracts of land, known as "islands" used primarily for farming, and delivers two-thirds of the State with freshwater. Most islands, including Bethel, have experienced several feet of subsidence due to the intense agriculture, with some sinking 10-25 feet below sea level, and are only protected by the levees surrounding them. / / With the projected estimates of sea level rise (SLR) ranging from a max. of 2 ft increase by 2050, to a max. 5.47 ft by 2100, and the increased drought conditions threaten the resilience of the Delta as a place to inhabit and transport water for California. Bethel Island was chosen as study area because it was one of the few islands with a high resolution digital elevation model (DEM) from USGS, it has a large population, still retains agriculture, and has experienced similar subsidence as other islands. By using Bethel Island as a case study for the effects on SLR, I can extrapolate these results for the rest of the Delta.

Entry Number: 104 UI

REFRIGERATION SYSTEMS AND CLIMATE CHANGE

By: Jose "Polo" Chavez

Mechanical Engineering

Faculty Advisor: Dr. Ed Cheng

Abstract: This project encompasses an initiative to reduce greenhouse gas emissions. Our goal of this research is to determine the feasibility, cost, and green house gas reduction benefit of using low-global warming potential refrigeration systems in super markets.

Entry Number: 105 UI

STATISTICAL EVALUATION OF HIGH-RESOLUTION PRECIPITATION FORECASTS IN THE BAY AREA AND CALIFORNIA

By: Nicholas Christen

Earth Sciences

Faculty Advisor: Dr. David Dempsey

Abstract: "Using high-resolution model data from three nested WRF-ARW domains across California, as well as two networks of surface weather stations, we statistically evaluate high-resolution WRF-ARW precipitation forecasts in the San Francisco Bay Area to obtain a variety of quantitative measures of forecast accuracy. This project addresses topics including whether model grid resolution has a significant effect on forecast accuracy, whether 48-hour precipitation forecasts are more accurate within the first 24 hours after initialization, whether there are notable diurnal variations in model performance, and the degree to which the model is likely to satisfy various categorical statistical criteria. Our categorical and continuous statistical calculations are made from the distance-weighted mean value of 24-hour forecast precipitation accumulations of the nine model grid points

nearest each of the set of core observation stations that lie within the inner-most WRF subdomain. From these forecast-observation matched pairs, we calculate Mean Absolute Errors for each station, as well as for the aggregate of matched pairs across the three WRF subdomains over the course of the 2015-2016 rainfall season (early October - early April)."

Entry Number: 106 UI

EFFECTS OF VEGETATION OF THE URBAN HEAT ISLAND

By: Robert Shortt

Geography

Faculty Advisor: Dr. Andrew Oliphant

Abstract: This project seeks to quantify the local cooling effect of vegetation in and urban area. Focus is placed on Street trees and differences between astroturf and natural grass.

Entry Number: 107 UI

THE EFFECT OF CLIMATE CHANGE ON THE DISTRIBUTION OF THE LYME DISEASE VECTOR IXODES PACIFICUS AND THEIR HOST SCELOPORUS OCCIDENTALIS

By: William O'Neill

Zoology

Faculty Advisor: Dr. Andrea Swei

Abstract: As part of the Climate Change Scholars Program, I studied the effect of climate change on habitable ranges for two species involved in Lyme Disease Ecology. Using QGIS, Maxent and species location data, I modeled how the next 50 years of climate change will effect where the Ixodes pacificus (western black-legged tick) and Sceloporus occidentalis (western fence lizard) will be able to find areas which meet there fundamental niche requirements.

Entry Number: 108 UI DISPLAY ONLY

THE HEALTH OF VULNERABLE COMMUNITIES AND CLIMATE CHANGE: EXAMINING THE ROLE OF PUBLIC POLICY AND NURSING

By: Zahra Hamidi, Dr. Shannon Lea Watkins, and Dr. Tendai Chitewere

Nursing

Faculty Advisor: Dr. Shannon Lea Watkins, and Dr. Tendai Chitewere

Abstract: Global climate change is causing extreme weather events which negatively affect the health of our communities by / increasing allergy seasons and respiratory diseases like asthma¹. The location of homes, low-income status, and / race/ethnicity, are among the factors that make some people more vulnerable to the effects of climate change than others. / Public policy can provide useful tools for mitigating and adapting to the effects of climate change and thereby supporting the / health of our communities. At the same time, nursing professionals are essential to addressing the health effects of climate / change because they provide members of vulnerable communities with immediate care in the short-term. Knowing how / climate change contributes to individual and community poor health and health disparities can deepen the contextual / knowledge of increases in illness, and widen the perspective of illness, empathy and compassion.

Entry Number: 109 UI

ESTIMATING ERROR RATES IN FORENSIC GENETICS

By: Kristine Roque

Applied Mathematics

Faculty Advisors: Dr. Rori Rohlf and Dr. Tao He

Abstract: The purpose of this project was to quantify error rates in DNA identification within a forensic genetics context by examining genotypes of non-contributors, computing the likelihood ratios (LRs) of each non-contributor having contributed to a given DNA mixture based on true and false assumptions about the person of interest's (POI's) ethnicity. The following five population groups were used: African-American, Caucasian, Latino, Navajo and African-American. Several sets of non-contributors and DNA mixtures with a varying number of contributors were simulated across these population groups. The LR function applied over each genotype, across all loci, and finally across each population group. The forensim package in R statistical software was used for data analysis.

Entry Number: 110 UI

CELESTA: A CATALOG OF EARTH-LIKE EXOPLANET SURVEY TARGETS

By: Colin Chandler

Astrophysics

Faculty Advisor: Dr. Stephen Kane

Abstract: Locating planets in circumstellar Habitable Zones is a priority for many exoplanet surveys. Space-based and ground-based / surveys alike require robust toolsets to aid in target selection and mission planning. We present the Catalog of Earth-Like / Exoplanet Survey Targets (CELESTA), a database of Habitable Zones around 36,000 nearby stars. We calculated stellar / parameters, including effective temperatures, masses, and radii, and we quantified the orbital distances and periods / corresponding to the circumstellar Habitable Zones. We gauged the accuracy of our predictions by contrasting CELESTA's / computed parameters to observational data. We ascertain a potential return on investment by computing the number of / Habitable Zones probed for a given survey duration. A versatile framework for extending the functionality of CELESTA into the / future enables ongoing comparisons to new observations, and recalculations when updates to Habitable Zone models, stellar / temperatures, or parallax data become available. We expect to upgrade and expand CELESTA using data from the Gaia mission / as the data becomes available.

Entry Number: 111 UI

EVOLUTION OF PARTICLE ANGULARITY IN GRANULAR AND DEBRIS FLOWS

By: Molly McLaughlin

Geology

Faculty Advisor: Dr. Leonard Sklar

Abstract: Angularity can indicate proximity to sediment source, assuming abrasion leads to progressive smoothing of particle surfaces; however, particle fracture can create fresh angular surfaces, confounding estimates of travel distance. Experiments conducted using both a 4 m and 1.63 m diameter rotating drums, to recreate geophysical granular flows. Initially well-sorted, angular coarse particles evolved through wear in transport. Every 0.25 km of tangential travel distance, size is quantified with calipers for all particles above a minimum size. Methods include axis ratios and hand-placed equilibrium points. Angularity is determined with shape-measuring parameters including convexity, entropy, and isoperimetric ratios from 2-D binary images. The same methods are used along the 2 km relief of Inyo Creek in the eastern High Sierra, underlain by granodiorite and dominated by debris flows. Angularity of particles decreases without a change in axis dimensions with mass is lost at an accelerated rate. Rocks show evidence of smoothing that slows down after 1 km distance. Downstream evolution of angularity in the field is more variable, due to mixing of particles from multiple source areas. Results confirm that downstream changes in angularity contain information about proximity to sources and could constrain relations for particle size evolution in granular flows. /

Entry Number: 112 UI

THERMODYNAMIC MODELING OF FIVE ULTRAHIGH-PRESSURE TERRANES

By: Brandon Swanson

Geology

Faculty Advisor: Dr. Mary Leech

Abstract: Ultrahigh-pressure (UHP) metamorphism refers to the metamorphism of continental crustal rocks at pressures high enough to crystallize the index minerals coesite (a high-pressure polymorph of quartz requiring $P > 2.7$ GPa at $T > 600^\circ$ C) and diamond. Before the first discoveries of UHP minerals in crustal rocks, coesite and diamond were thought to only occur in meteorite-impact craters and mantle xenoliths. The discovery of crustal rocks metamorphosed at UHP conditions has changed our understanding of crustal-scale processes in continental collision zones. For this study, five ultrahigh-pressure terranes were compared using petrologic and geochemical analysis in combination with current thermodynamic data to model pseudo sections for each sample. Each model was then compared to minerals observed in thin section and to other samples in order to see if the current thermodynamic data could accurately plot the UHP mineral assemblages observed in thin section. The resulting models were able to accurately plot UHP minerals for the crustal rock samples and was able to show mineral assemblages observed in thin section.

Entry Number: 113 UL1

HEPN AND NT_KNTase_LIKE GENES TO RESIST A WIDE RANGE OF AMINOGLYCOSIDE ANTIBIOTICS IN THAUMARCHAEAOTA BS3 from Yellowstone National Park, Wyoming

By: Adam Carcamo

Microbiology

Faculty Advisor: Dr. José R. de la Torre

Abstract: Through advances in metagenomics we can study how organisms have adapted to survive, and in turn we can use this information to our benefit. A major problem that we as humans face are pathogenic bacteria with antibiotic resistance. We face an emerging world where less pharmaceuticals function as they are supposed too because of resistance. Through analysis of Thaumarchaeota BS3, one of the 4 unclassified archaea from Beowulf Springs in Yellowstone National Park, there is evidence of having received one of these antibiotic resistant genes from a bacterium to fight off a range of aminoglycosides. BS3 is an archaeon that lives in pH of around 3 and hot temperatures around 50-75 degrees Celsius. It uses these resistant genes to protect itself from pathogenic bacteria. By further understanding how microbial organisms, such as BS3, have been able to survive rough environments and pathogenic threats we can in turn create strategies of defense for ourselves. In a cells defense it can learn to detect and prevent the negative effects of a bactericidal or a drug. I have discovered how BS3 has altered a set of genes that would allow the archaea to shield itself from invading bacteria and their toxins. IMG and BLAST were used to deduce which genes were horizontally transferred, and what their function is across the vast majority. At some point in time, a sulfolobus species shared a short plasmid with BS3 that contained antibiotic resistant genes. The first gene belongs to a protein family of Higher Eukaryotes and Prokaryotes Nucleotide-binding domains, or HEPN domain-containing protein, and a DNA polymerase sigma, or Nucleotidyltransferase-like gene, called NT_KNTase_like gene on IMG. Evidence from IMG shows these genes to have a lower GC percentage than the genome in whole, and they are also found in the same neighborhood of the BS3 genome. This suggests that some sort of horizontal gene transfer from the sulfolobus to BS3 had occurred. I hypothesize that BS3 learned how to survive by the surrounding bacteria in its environment. Though many genes for resistance are to fend off invading material, BS3 is able to deactivate and further detect the presence of pathogenic strains. With further investigation into the genes that exist outside the standard deviation of the average GC content for BS3, we would understand what family of archaea thaumarchaeota BS3 derived from and any other potential gene transfers it may have had. /

Entry Number: 114 UL1

FUNCTIONAL ANALYSIS AND SIGNIFICANCE OF SUF COMPLEX IN CREATION OF FE-S CLUSTERS

By: Adam Josef

Microbiology

Faculty Advisor: Dr. José R. de la Torre

Abstract: The suf complex is the most ancient of three complexes composed of proteins responsible for making Iron-sulfur clusters. Iron-sulfur clusters have a variety of critical uses within cells of all three domains with functions ranging from electron transport to regulatory sensing. In archeal species the suf complex is usually composed of fewer proteins compared to that of bacterial species which usually contain a more intricate assembly of proteins for creation of Fe-S clusters. Thaumarchaeota archaeon BS3 is a specific strain of archaea found in the Beowulf springs of Yellowstone National park that is still highly unstudied. This organism thrives in the hot spring which is a highly acidic environment at a pH of 2.9 and reaching average temperatures of 67.6 C. This extreme environment is rich in compounds like Iron and Sulfur causing for increased oxidative stress in BS3 which is addressed partially through use of the suf complex. Using the IMG database the genes related to the suf complex were identified by searching for key genes as well as blasting the amino acid sequences of similar archeal species. As key genes related to the complex were identified, observation of the COG neighborhoods revealed other genes involved in the complex as the proteins which compose the suf complex are found on the same operon. The pfam database was then used to identify the detailed purposes of these proteins. Ultimately, the production of Iron-Sulfur cofactors is a key mechanism in BS3 beginning with transcription of the suf complex. Thaumarchaeota archaeon strain BS3 has a reduced suf complex structure composed of a core containing proteins sufB and sufC accompanied by a transport protein similar to the sufD component of other organisms which aids in transferring the sulfur stripped by a nearby cysteine desulfurase. The functional analysis

and significance of the suf complex in the creation of FE-S Clusters was conducted as a part of the research projects for Thaumarchaeota archaeon BS3 in Professor De la Torre's Microbial Genomics class. /

Entry Number: 115 UL1

ARCHAELLUM AND MOTILITY OF BS3

By: Andres Pineda

Microbiology

Faculty Advisor: Dr. José R. de la Torre

Abstract: Archaellum and Motility of BS3 / / Many members of the Archea domain are known to contain archaellum, which play an important role in locomotion and chemotaxis. Archaellum are known to resemble bacterial type IV pili, which are surface structures that can extend or retract to adhere or move on surfaces. Thaumarchaeota is a phylum of archaea that have been collected from soil, hot springs, and marine waters making it one of the most abundant archaea on Earth. These archaea have also been found to be highly adaptive as they can be found in extreme environments including acidic soils and hot springs. My hypothesis for this research study is that through exploration of recorded DNA protein functions and genetic make-up, I can discover possible indications for functions of motility, including signs of an archaellar structure. To further this hypothesis I will research nearby neighbors of the BS3 (Beowulf Spring 3) archaeota strain for indications of motility and its methods, also researching neighboring strains and current DNA libraries for indications of flagellum forming proteins. BS3 has a recorded archaellar hook-associated protein in Integrated Microbial Genomes (IMG), I will use this protein sequence to research similar species of BS3 to look for signs of common archaellar proteins and functions. I will be able to research these possibilities of genetic connections and relations by using genomic data bank programs such as: BLAST, IMG. At the end of this research I will hope to build enough information and evidence to conclude our hypothesis of BS3 having a form of flagellum that is involved in motility. Discovering more information about BS3 and its possible unknown structures can provide guidelines for how we learn and think about archaea. / / This project was part of the Bio446 Microbial Genomics course /

Entry Number: 116 UL1

CARBON MONOXIDE METABOLISM IN THAUMARCHAEOTA BS3

By: Anna Portelli

Microbiology

Faculty Advisor: Dr. José R. de la Torre

Abstract: Each year there are approximately 430 unintentional deaths caused by carbon monoxide poisoning in the U.S. Carbon monoxide (CO) is a clear, odorless gas that is highly toxic to animals with hemoglobin. CO is part of the global carbon cycle, and many microorganisms are able to use it in assimilatory and dissimilatory pathways. There are two types of CO metabolism: aerobic and anaerobic. Both are carried out by the enzyme carbon monoxide dehydrogenase (CODH). Respiratory carbon monoxide metabolism incorporates an external electron acceptor, whereas fermentative CO uses intermediate molecules generated as electron acceptors. The BS3 is a newly discovered, uncultivated archaeon in the phylum Thaumarchaeota. It was discovered at Beowulf Spring in Yellowstone National Park. It is a geothermal ecosystem that has a temperature range of 66° to 73°C and a pH of 3.2. Because BS3 cannot grow in lab, I will use its genome to predict its microphysiology. I hypothesize is that the BS3 is capable of utilizing CO as an energy source and as a source for inorganic carbon. The objective is to determine CO's role in carbon fixation and as an electron donor by doing comparative genomic studies with genetically similar species containing CODH genes. CODH genes were identified and assessed using IMG and Blast. Proteins were also questioned using Clusters of Orthologous Genes (COG) database to determine their function. Other bioinformatic databases and pathway modules were used. I discovered BS3 shares conserved regions and COGs with the following organisms: BS1, BS2, Candidatus caldiarchaeum subterraneum, Fervidicoccus fontis Kam940, Aigarchaeota archaeon JGI 0000106-J15, and Aeropyrum camini SY1. This implies that the BS3 uses aerobic CODH as an electron donor. CO redox reaction may be part of the electron transport system or the oxidation of CO using a Ni-Fe heme suggesting the fixation of carbon dioxide using the 3-hydroxypropionate/4-hydroxybutyrate pathway. / / This project was part of the BIOL 446 Microbial Genomics course.

Entry Number: 117 UL1

THAUMARCHAEOTA ARCHAEON STRAIN BS3 DEFENSE AGAINST THE DARK ARTS: VIRAL PHAGES AND INVADING DNA

By: Brittany Baker

Microbiology

Faculty Advisor: Dr. José R. de la Torre

Abstract: In order to effectively invade a host's cellular machinery, viral phages have evolved diverse mechanisms that pose a constant threat to all domains of life. When viruses were first identified in the 1970's, research focused solely on viruses specific to Bacteria and Eukarya. Archaeal viruses were too difficult to study by conventional lab techniques during that time, but ongoing advancements in genome sequencing and bioinformatics have finally led to a slightly better understanding of these viruses. Current research shows archaeal viruses could be an important key to better understand viral mechanisms across the three kingdoms; archaeal viruses exhibit greater evolutionary diversity when compared to Bacteria or Eukarya. Archaea live in extreme environments, and have not only adapted mechanisms to thrive in these extreme conditions, they have also adapted several defense mechanisms against the most morphologically diverse phages. The most recently discovered cellular defense mechanism against phages and more broadly, foreign DNA is known as the clustered, regularly, interspaced, short, palindromic, repeats (CRISPR)-CRISPR-associated (Cas) system. The individual steps of the CRISPR-Cas system are specific to Bacteria and Archaea, but the general concept is related to the adaptive immune system of Eukarya. Through shotgun genome sequencing, the genome of the thermophilic archaea, Thaumarchaeota archaeon strain BS3, was isolated from the geothermal hot spring, Beowulf Spring (BS) in Yellowstone National Park (YNP). Current literature classifies an organism's CRISPR-Cas system into three main types: I, II, or III, with further division of these types into subtypes; subtypes A-F of type I systems are most relevant to BS3. A preliminary gene search of BS3 for CRISPR-associated (Cas) genes on IMG resulted with four gene hits that indicated BS3 contained a Type I-D CRISPR-Cas system. The CRISPR-Cas system of any organism requires more than four genes to function in vitro, but due to a lack of uniformity in cas gene annotation, many core genes are incorrectly labeled (hypothetical proteins), or not associated with the CRISPR-Cas system. I hypothesize BS3 does contain a Type I-D CRISPR-Cas system due to the presence of the essential Type I cas gene, Cas3. Through phylogenetic comparison of the Cas3 gene of BS3, a strong correlation between Type I CRISPR-Cas systems and thermophilic archaea was found. This research is associated with the Microbial Genomics class Biol. 446 at San Francisco State.

Entry Number: 118 UL1

EXPLORING L-CYSTEINE BIOSYNTHESIS IN THAUMARCHAEOTA ARCHAEON STRAIN BS3

By: Bushra Mariam Bibi

Microbiology

Faculty Advisor: Dr. José R. de la Torre

Abstract: From the various sulfur-containing amino acids, cysteine is used for a variety of cellular functions. Cysteine biosynthesis is essential to maintain protein stability and catalytic role in all domains of life. In plants and bacteria, cysteine is synthesized from serine by incorporation of sulfide or thiosulfate. In animals, the transsulfuration pathway derives the sulfur group of cysteine from methionine. The key enzyme in transsulfuration pathway, cystathionine β -synthase (CBS), a pyridoxal phosphate-dependent (PLP) enzyme, converts homocysteine to cystathionine. Only CBS in mammals have evolved with a heme-binding domain, and the role of this heme domain is not clearly understood. It was believed that the transsulfuration pathway only occurs in eukaryotes, but recent studies show that some thermoacidophilic archaea are also able to convert methionine sulfur to cysteine. This provides an opportunity to use Thaumarchaeota archaeon BS3 from Beowulf Spring, Yellowstone National Park to understand the cysteine metabolic diversity in thermal habitats of the phylum Thaumarchaeota. The objective of this study is to use metagenomics sequencing to determine if Thaumarchaeota archaeon BS3 utilizes transsulfuration or another indirect route to cysteine biosynthesis and the likely evolutionary relationship of CBS across all domains. Phylogenetic and G+C content analysis will be used to unveil cysteine biosynthesis in Thaumarchaeota archaeon BS3. Whether the transsulfuration pathway or by a more indirect route utilized. In any case, a different biosynthetic pathway may also be present. It is important to note that this project is part of Microbial Genomics course at San Francisco State University.

Entry Number: 119 UL1

FE(III) REDUCTASE GENES IN THAUMARCHAEOTA ARCHAEON BS3: A COMPARATIVE STUDY BETWEEN BACTERIA AND ARCHAEA

By: Diane Custodio

Microbiology

Faculty Advisor: Dr. José R. de la Torre

Abstract: Iron is a fundamental element involved in numerous metabolic processes, playing an important role in many biogeochemical cycles as a cofactor for enzymes or as an electron acceptor. Even though Iron is one of the most abundant elements on Earth, it is generally viewed as a limiting nutrient because neutral pH accelerates the oxidation of ferrous iron [Fe(II)] into insoluble ferric iron [Fe(III)]. [Fe(II)] is used as an energy source by many microorganisms and is more stable, and therefore more abundant, in acidic environments with a low pH < 3. Many species of acidophilic Bacteria and Archaea have the ability to catalyze iron redox reactions. However, these pathways have only been well studied in bacteria and not in archaea. To better understand this process in Archaea, the genome of an archaeon collected from the acidic thermal waters of Beowulf Springs, *Thaumarchaeota archaeon BS3*, is analyzed to see if it possesses the same genes as Bacteria when undergoing oxidizing/ reducing iron. To find and identify which genes BS3 employ, known Fe(III) reductase genes from the gram positive thermophilic bacterium *Thermoanaerobacter indiensis BSB-33* are compared against BS3. The genes Dihydrolipoamide dehydrogenase and Redoxin reductase were identified in BS3 and the amino acid sequences were ran through the Basic Local Alignment Search Tool (BLAST). The first 10 with the highest percent identity were used to make a phylogenic tree via Phylogeny.fr. The archaeons *Thermoplasmatales archaeon I plasma* and *Sulfolobus tokodaii* were identified to be the closest relative based on BS3's amino acid sequences. Through analysis of the gene scaffolds, data suggested that the dihydrolipoamide dehydrogenase and Thioredoxin reductase genes were not conserved between all three organisms. This work is part of Biol 446 Microbial Genomics research project at SFSU.

Entry Number: 120 UL1

IRON CYCLING IN THAUMARCHAEOTA ARCHAEON STRAIN BS3

By: Huey Li

Biochemistry

Faculty Advisor: Dr. José R. de la Torre

Abstract: Yellowstone national park holds a large variety of archaea species, a large amount of microbes can't be cultivated in a lab, especially archaea which thrive in the harshest of areas. In this study, the specific archaea species that will be focused on known as Thaumarchaeota archaeon strain BS3, located in Beowulf spring, Yellowstone national park. By using BS3 to predict iron oxidation with known species of archaea can provide an additional insight to the electron pathway to generate energy for BS3 in the electron transport chain (ETC). The use of genomes of other known iron oxidizing archaeas, *Sulfolobus metallicus* and *Sulfolobus tokodaii* can be compared to BS3 through IMG and blast by matching protein structures coded by fox genes (ferrous oxidizing genes). The result will show that BS3 can oxidize ferrous iron as an additional way to generate energy in an inhospitable environment or a completely different pathway is used to generate energy in ETC.

Entry Number: 121 UL1

FIGHTING CRIME: HOW THAUMARCHAEATA ARCHAEON STRAIN BS3 DEFENDS AGAINST VIRUSES

By: Jenny Tapang

Cell & Molecular Biology

Faculty Advisor: Dr. José R. de la Torre

Abstract: There are ten times more viruses than microbes in any given environment. As a consequence, microbes have been found to contain two different adaptive defense mechanisms – CRISPR-Cas and restriction-modification – to prevent infection by viruses. These defense systems are important because they allow microbes to adapt to viruses in their environment. We are looking at which one of these mechanisms is present in Thaumarchaeota archaeon strain BS3, the third genome cultivated from Beowulf Springs. Organisms in Beowulf Springs can withstand its highly acidic pH and temperature at 70°C. We will also then compare the systems found in this genome to those found in other archaeal strains found in the same environment. / CRISPR-Cas can fight off rapidly-evolving viruses and also be used as a regulatory system by the host. The restriction-modification system contains a methyltransferase that modifies the self DNA and a restriction

endonuclease that cleaves non-methylated foreign genetic material. So far, we have identified genes belonging to the CRISPR-Cas system but no genes for the R-M systems have been identified using BLAST. Therefore, I hypothesize that BS3 solely uses the CRISPR-Cas system as its defense system against viruses. / First, genes in CRISPR-Cas Types I-III and R-M Types I-IV will be searched for via BLAST in BS3. Next, these genes will be searched for in Thaumarchaeota archaeon strains BS1, BS2, and BS4 to denote similarities or differences between the genomes. / We will present the data by providing a table of proteins in CRISPR-Cas Types I-III and R-M Types I-IV and the genomes that carry these proteins. We will also include images of the gene neighborhoods that are the most similar. This will show how drastically different or similar BS3 is from other archaeal strains assembled from Beowulf Springs. / / Disclaimer: / This project was part of the BIOL 446 Microbial Genomics course. /

Entry Number: 122 UL1

TYPE IV TOXIN-ANTITOXIN SYSTEM IN THAUMARCHAEAOTA ARCHAEON STRAIN BS3

By: Joseph Lau

Microbiology

Faculty Advisor: Dr. José R. de la Torre

Abstract: Toxin-antitoxin (TA) systems are one type of viral defense mechanisms that affects phage replication found across many bacterial and archaeal species. Currently, there are 3 known systems (Type I-III) and two recently proposed systems (Type IV-V). Although there is still much not known about Type IV, this system has been shown to be an abortive infection system (Abi), and specifically to be a bacteriostatic mechanism in *Escherichia coli*. A nucleotidyl transferase AbiEii toxin, Type IV Toxin-Antitoxin system was identified in Thaumarchaeota strain BS3. Thaumarchaeota strain BS3 is an archaeal organism found to live in a thermoacidic environment in Beowulf Springs within Yellowstone National Park, and was sequenced by metagenomics. The purpose of this project is to identify the AbiE/Type IV TA system and compare with related organisms living in neighboring hot springs. Due to the bicistronic operon characteristics that this system has, the antitoxin gene should be directly upstream of the toxin. Afterwards, conserved regions of the genes would be identified and be examined for mutations. A hypothetical protein was found directly upstream of the toxin gene, but when examined further, no motifs were found. Furthermore, four motifs were found in the toxin gene, but two had mutations after comparing to known sequences of the AbiEii toxin. Site-directed mutagenesis of the AbiEii toxin showed that mutation of important amino acids in the motifs resulted in elimination of toxicity. Therefore, these results show that the Type IV TA toxin found in BS3 lost its toxicity as a nucleotidyl transferase, due to mutations found in the gene and not having the antitoxin directly upstream. Another viral defense mechanism is likely to be found in BS3, such as another TA system that is not Type IV, or a CRISPR-Cas system. Furthermore, it is plausible that the hypothetical protein is an unidentified toxin gene, which resulted in the mutation of the AbiEii toxin. More research must be done to compare BS3 with other organisms that contain the nucleotidyl transferase and not the other component. / / This project was part of the Biol 446 Microbial Genomics course. /

Entry Number: 123 UL1

ACETOIN UTILIZATION IN THAUMARCHAEAOTA ARCHAEON BS3

By: Juliana Nzongo

Microbiology

Faculty Advisor: Dr. José R. de la Torre

Abstract: In order to minimize acidity, many organisms use intermediates and byproducts of metabolic processes as buffers for the external environment, one such intermediate is acetoin. Acetoin is neutral 2-oxoacid metabolite intermediate of alcohol fermentation that can be excreted from cells in response to increasing acidic environments during exponential growth. A hypothetical acetolactate synthase protein was annotated in Thaumarchaeota archaeon BS3, an organism that lives in a thermoacidic hot spring, whose harsh environment can be detrimental to cellular growth and protein function. This protein is responsible for converting pyruvate to acetolactate, an important precursor for metabolic processes. Mechanisms for acetoin metabolism occur through the 2-oxo-acid dehydrogenase Complex (OADHCs), which connects glycolysis to the citric acid cycle. OADHCs oxidatively decarboxylate 2-oxoacids into acyl-CoAs, and variations of this complex have been annotated and confirmed experimentally in archaeal species *Sulfolobus solfataricus* and *Haloferax volcanii*. OADHCs are well documented in bacterial species but enzymatic activity has been difficult to determine in

archaeal species. I hypothesize that OADHCs and other acetoin utilizing proteins are present in BS3. Online databases will be used to determine their presence. I searched for proteins involved in acetoin utilization, import and export from the cell, but results were inconclusive because the OADHC operon can use various 2-oxoacid substrates. Genomic analysis is not sufficient for determining substrate specificity as pyruvate and acetoin dehydrogenases are similar. Therefore, I propose that acetoin utilization cannot be determined without experimental confirmation, but it is equally likely that the scaffolds for OADHC are unorganized as the subunits are present in separate operons. / / This project is a part of Bio 446: Microbial Genomics. /

Entry Number: 124 UL1

THAUMARCHAEOTA BEOWULF SPRINGS 3 COBALAMIN BIOSYNTHESIS

By: Kimberly Mitchell

Microbiology

Faculty Advisor: Dr. José R. de la Torre

Abstract: Cobalamin, a precursor of vitamin B12, is a necessary cofactor that catalyzes many enzymatic reactions such as amino acid synthesis, return of carbon to carbon metabolism via the TCA cycle, and DNA synthesis. Cobalamin biosynthesis is limited to a small fraction of bacteria and archaea, whereas other organisms must rely on the archaea to secrete cobalamin into the environment. Thaumarchaeota are believed to be one of the largest cobalamin producers in marine ecosystems. Since cobalamin is a universal cofactor in all organisms, I will determine if Thaumarchaeota BS3 falls under the condition of a cobalamin producer in the hydrothermal environment of Beowulf Spring in Yellowstone National Park. The cobalamin biosynthesis pathways vary between different archaeal species leaving many gaps in complete biosynthesis pathways. There are three key genes throughout the pathway that are indicators of complete cobalamin biosynthesis: CbiA, CbiC and CobT. I hypothesize Thaumarchaeota BS3 will contain genes encoding for the three key genes, CbiA, CbiC and CobT, in the pathway resulting in a hypothetical cobalamin synthesis pathway. I have found the BS3 genome contains CysG, CbiA and BtuR. CysG is the enzyme that catalyzes the initial step in the biosynthesis pathway. CbiA is a key enzyme that leads to Cob(II)yrinic acid a,c-diamide which is reduced and enters the transport system via the BtuR enzyme. The KEGG pathway listed on IMG will provide the basis of the presence and absence of cobalamin genes. Missing genes will be compared against the BS3 genome using BLAST, conserved regions and significant residues will be analyzed using IMG and Pfam. This study will provide insight to the Thaumarchaeota mechanisms used for cobalamin biosynthesis and secretion, which has not previously been studied in hydrothermal environments. / This project was part of the Biology 446 Microbial Genomics course. /

Entry Number: 125 UL1

CELL DIVISION PROTEINS IN THAUMARCHAEOTA ARCHAEON STRAIN BS3

By: Lara Ramos

Microbiology

Faculty Advisor: Dr. José R. de la Torre

Abstract: Cell division is an important biological process used as a method of replenishing dead cells in multicellular organisms or as a method of reproduction in single cellular organisms. The different proteins that cause cells to divide are varied and diverse, but in the world of Archaea, these proteins generally fall under at least one of two protein systems: the FtsZ system or the CdvABC system. FtsZ is a gene generally found in Euryarchaeota while CdvABC, some forms of which are homologous to the ESCRT-III sorting complex seen in eukaryotes, is found in Crenarchaeota and Thaumarchaeota. ESCRT-III is a system responsible for forming long filaments that coil around membrane construction sites and cleave the two cells, causing them to divide. In contrast, FtsZ is a tubulin homolog whose role in cell division is similar to that of the actin-myosin ring in many eukaryotes. In order to examine the genetics of cell division, I planned to compare and contrast the cell division proteins in Thaumarchaeota archaeon strain BS3, an archaeal organism found in Beowulf Springs, Yellowstone National Park, with those of known cell division proteins in other closely related organisms. To do this, I used IMG and BLAST to search for and examine the proteins within BS3's genome. In my investigation, I have found that the BS3 genome carried the CdvB gene. Other organisms still need to be researched, but I have hypothesized that BS3 and phylogenetically related organisms should consist of closely similar, if not identical, forms of the cell division protein CdvABC. It should also be noted that this project was done as part of the BIOL 446 Microbial Genomics course of Spring 2016 under the supervision of Dr. José R. de la Torre.

Entry Number: 126 UL1

HEAT RESISTANCE PROTEINS IN THAUMARCHAEOTA ARHAEON BS3

By: Mifune Takahashi

Microbiology

Faculty Advisor: Dr. José R. de la Torre

Abstract: Yellowstone is famous for its geothermal activity that includes hot springs. Many types of microbes found in Yellowstone National Park hot springs are thermophilic archaea and bacteria. These organisms can tolerate or even thrive in temperatures that many organisms are not able to do. Thaumarchaeota archaeon strain BS3 was uncultivated archaea found in one of springs in the park, Beowulf Spring where an extremely acidic environment which average a pH of 2.9 and a temperature of 67.6°C. BS3 can thrive in this spring, which indicates the possibility that BS3 have ability of heat resistant with heat shock proteins. The objective of this study is searching of heat shock proteins in BS3 to determine how they are stay in extreme high temperature environment. / The first of the step of the method of this study is finding specific heat shock protein gene RacA, Hsp10, Hsp40, Hsp60, Hsp70, GrpE in BS3, also BS1, BS2, and BS4 by IMG. RacA, Hsp60, and GrpE were found in BS3, BS1, BS2, and BS4. Differences between BS 1 to 4, only BS3 has more RacA genes than others. / From the research, BS3 have these heat shock proteins, which help them to thrive in such a harsh environment. / For further research, using other database to search functions of proteins by Pfam. To narrow in the phylogenetic origin of the heat shock proteins by creating phylogenetic tree by phylogeny.fr. /

Entry Number: 127 UL1

VITAMIN PRODUCTION OF BS3 IN HYPER THERMAL ENVIRONMENTS

By: Mona Saadi

Microbiology

Faculty Advisor: Dr. José R. de la Torre

Abstract: Vitamins are key elements that are fundamental to the functioning of most enzymes, however most organisms such as humans are not able to synthesize them. Humans acquire all of their needed vitamins from nutrients or from the bacteria in our gut. Recently scientists studying Marine systems have found that in the ocean provide almost all of the B12 for the marine ecosystems. I was interested in determining whether that was also the case in a hyper thermal environment. I am investigating one of these uncultivated novel organisms found from a hyper thermal spring called Beowulf Springs in Yellowstone National Park, WY, USA by the name of Thaumarchaeota archaeon strain BS3. Beowulf Springs is known to be home to many extremophiles due to its high- temperature (65-72 c) and low pH (pH~3). It is a reasonably simple community of archaeons given that they live in extreme environments although they are not diverse but they are extreme thermodynamically. I hypothesize that the Thaumarchaeon BS3 acquire several pathways that enables them to make certain vitamins just like the Marine Thaumarchaeota do such as B12. I will be utilizing KEGG to identify certain pathways and genes of its relative organisms and looking for those genes in order to better understand which pathways I need to be looking for, and how different organisms make different vitamins. / / This project was a part of SFSU Bio 446 Microbial Genomics class /

Entry Number: 128 UL1

UNDERSTANDING THE EVOLUTION OF BS3 THROUGH ORTHOLOGY

By: Olivia Pham

Cell & Molecular Biology

Faculty Advisor: Dr. José R. de la Torre

Abstract: The ubiquitous ATP-binding cassette (ABC) transporters are one of the largest protein families in evolution that is conserved from archaea to humans yet classification of the archaeal lineage seems to be underrepresented or overlooked due to difficulties of being able to be cultivated in a lab. In humans, the ABC transporters move a variety of substrates into and out of the cell and are also involved in intracellular compartmental transport. Clinically, mutated ABC transporters have been related to different diseases in humans such as cystic fibrosis, drug-resistant tumors, and other inherited diseases. With some similarities, ABC transporters in Archaea play a crucial role in substrate uptake, export, and osmoregulation. Knowing this information, I will be doing a comparative analysis between ABC transporters of the uncultivated organism, Thaumarchaeota archaeon strain BS3 from the Beowulf hot springs in Yellowstone National Park, to human

ABC transporters. Comparing the ABC transporters in BS3 and humans will provide an evolutionary picture of how Archaea and Eukarya have adapted evolutionarily. / / *This project was a part of Biol 446 Microbial Genomics course.

Entry Number: 129 UL1

YOU ARE WHAT YOU EAT / CARBON DIOXIDE METABOLISM OF ARCHAEA FROM BEOWULF SPRINGS

By: Robin A. Herbert

Microbiology

Faculty Advisor: Dr. José R. de la Torre

Abstract: Humanity has increasingly impacted the global ecosystem as the world becomes more populated and productive, as illustrated by the influence of automobile emissions and other anthropogenic inputs of carbon dioxide. Buffering against these changing carbon climates are plants and microorganisms, which incorporate carbon into biomass through a variety of metabolic pathways. Of these carbon-fixing microorganisms, ubiquitous in both terrestrial and marine environments, Archaea represent a major influence in the global carbon cycle through their collective metabolism. Beowulf Springs of Yellowstone National Park is home to a variety of Archaeal species, particularly phylum Thaumarchaeota, members of which may metabolize carbon through photosynthetic or non-photosynthetic fixation of CO₂. In order to better understand how these microorganisms may influence their environment, I undertook an analysis of the genome of Thaumarchaeote BS3. Using bioinformatic resources such as the KEGG Pathway Database and ExPASy database for enzyme characterization I examined the BS3 genome from the Integrated Microbial Genome system for pathways involved in carbon metabolism. I have discovered genes encoding CO₂-assimilating enzymes involved in the reverse tri-carboxylic acid cycle in the BS3 genome. Through further analysis, I will characterize a potential homologue for the sole enzyme lacking in the complete rTCA pathway; fumarase, and through illustration of this carbon-fixing pathway classify BS3 as an autotroph. I will compare this metabolic capability to phylogenetically related microorganisms to illustrate the broad metabolic capability of the phylum for carbon fixation. This project is a part of the San Francisco State University Bio 446 Microbial Genomics course.

Entry Number: 130 UL1

CRISPR-CAS SYSTEM IN THAUMARCHAEOTA ARCHAEON STRAIN BS3 THROUGH COMPARATIVE GENOMIC STUDIES AGAINST RELATED THERMOPHILIC ARCHAEA

By: Roxanne Tadina

Microbiology

Faculty Advisor: Dr. José R. de la Torre

Abstract: The arms race between viruses and their hosts has ultimately led to discovering antiviral defense systems that have progressed over time in free-living archaea and bacteria. Therefore, it has led me to an interest about the developed regulatory defense mechanisms organisms use to survive virus attacks and numerous environmental stressors. The specific arsenal I intend to analyze, the CRISPR-Cas system, is an RNA-based adaptive immune system that control invasions of viruses, plasmids and various mobile genetic elements. The organism of interest is Thaumarchaeota archaeon strain BS3, an aquatic thermal microorganism originated from Beowulf Spring, Yellowstone National Park, WY, USA. Not much is known about BS3, especially in terms of its defense mechanisms against prevailing phages. The objective of this study was to examine these questions: What are the characteristics of the CRISPR-Cas system and what are the vital genes that would code for this immune system in BS3? After performing a comparative genomic studies of genomes with organisms similar to BS3 that are known to have the CRISPR-Cas system, what similarities or differences would we find within the genes to show the relationships between each organism. In order to determine whether or not BS3 has the CRISPR-Cas, I first utilized phylogenetic databases such as JGI-IMG pipelines to find the genes within BS3, and at the same time compared it to the genomes of 5 similar organisms (Thaumarchaeota archaeon BS1, BS2, BS4, DS1, and SAT1) that I anticipated would have the CRISPR-Cas. From this search, I discovered that BS3 does contain three associated genes to code for the system. Additionally, out of the comparisons of the genomes with BS3, Thaumarchaeota archaeon BS2 and BS4 showed orthologous genes of one of the protein CRISPR-associated helicase Cas3, subtype CYANO. Further analysis through BLAST revealed conserved domains surrounding the gene, including Helicase_C within the C-terminal domain using Pfam database; and Cas3_cyano, a CRISPR-associated (Cas) family strictly associated with the Cyano subtype

of CRISPR/Cas locus using TIGRfam database. This discovery suggests that the CRISPR-Cas is one of the major proteins used for defense within BS3. This knowledge has also led to a deeper understanding between the relationships of Thaumarchaeota archaeon strain BS3 and organisms BS2 and BS4. Further studies will focus more on analyzing the other vital genes coded for the CRISPR-Cas. / / THIS PROJECT WAS A PART OF SFSU BIOL 446 MICROBIAL GENOMICS COURSE

Entry Number: 131 UL1

CELL DIVISION MECHANISM OF THAUMARCHAEOTA ARCHAEON STRAIN BS3

By: Zhainib Adel Amir

Microbiology

Faculty Advisor: Dr. José R. de la Torre

Abstract: Cell division, the process by which cells divide, is necessary for survival of all living things. Cell division is not very well understood in the archaeal phylum Thaumarchaeota. Thaumarchaeota are closely related to eukaryotes, and learning more about cell division in thaumarchaeota will therefore give us better insight into the evolution of cell division in eukaryotes. Most archaea use one of two cell division systems: FtsZ and Cdv. The FtsZ mediated division mechanism is specific to bacteria and Eukarya, Crenarchaea use the Cdv system, and thaumarchaeota divide with both the FtsZ and Cdv mechanisms. Homologies have been found between CdvB and CdvC of the Cdv system and ESCRT-III system, thereby, suggesting the possibility these systems may have been involved in earlier cell division of Archaea and Eukarya. I am interested in determining the mechanisms Thaumarchaeota archaeon strain BS3 of Beowulf Spring uses for cell division. I searched for homologs of the important proteins involved in cell division of the thaumarchaeota genome sequence of the BS3 against other phyla in order to determine what proteins are involved in the cell division mechanism of BS3. I have found that BS3 uses both the FtsZ and Cdv mediated cell division mechanisms. This work is part of the Bio 446 genomics research.

Entry Number: 132 UL1 DISPLAY ONLY

THAUMARCHAEOTA BS3 MAY SHOW A SENSE OF DEQUORUM

By: Christian Mariano

Biology

Faculty Advisor: Dr. José R. de la Torre

Abstract: Quorum sensing is the unique system that regulates gene expression in response to fluctuations in cell-population density. In Bacteria, quorum sensing is an established mechanism for cell-to-cell communication. In Archaea, quorum sensing is a mechanism that has received very little investigation and no concrete conclusions have been drawn yet. Only relatively recently have studies shown the possibility of quorum sensing as a mechanism for archaea to communicate. Thaumarchaeota are amongst the most abundant archaea on Earth, many of which are found in the hot springs of Yellowstone National Park. Thaumarchaeota archaeon strain BS3 was discovered in Beowulf Springs of Yellowstone National Park, an extremely harsh environment home to vast amount of microbes. Because quorum sensing is important for regulating the gene expression in a large number of bacteria, it may also be true for archaea. For this reason, studying quorum sensing in Thaumarchaeota archaeon BS3 could provide additional insight into various population controlled behaviors, including this archaeon's defense mechanisms, and its ability to inhabit extreme environments. After selecting known proteins involved in bacterial quorum sensing, I utilized NCBI's, BLAST software and various comparative genomic techniques to locate possible quorum sensing genes in BS3's genome. Some of the proteins of interest were the LuxS protein in *Vibrio fischeri* and the ComA protein in *Streptococcus pneumoniae*. The LuxS protein regulates the synthesis of auto-inducers in gram-positive bacteria. The ComA protein is responsible for activating competence in gram-negative bacteria. My initial experimentation has linked these proteins to possible protein matches in the BS3 genome. Although not concrete evidence, these findings may provide further insight in BS3's communication mechanisms. Further experimentation will analyze the phylogenetics of these proteins, as well as compare proteins in *Methanosaeta harundinacea* and *Natronococcus occultus* to BS3. Recently, evidence has been published to support that these archaeon may utilize a unique system of quorum sensing. / / This project is associated with SFSU BIOL 446 Microbial Genomics /

Entry Number: 133 UL1 DISPLAY ONLY

CENTRAL, ENERGY, AND CARBON METABOLISM IN BS3

By: Haig Sadakian

Biology

Faculty Advisor: Dr. José R. de la Torre

Abstract: Thaumarchaeota strain BS3 is a largely unstudied archaeon found in the Beowulf hot spring in Yellowstone National Park. Very little is known about its metabolism or diet, and its carbon and energy sources are unknown. This knowledge is key because further research done on the organism will likely build on this, and findings from this project can reveal interesting pathways used by other extremophilic bacteria. Since this organism cannot be grown in the lab, the only way to determine its central metabolism and energy production pathways is to examine the gene content of the genome. The Beowulf hot spring is known to have an average temperature of 70°C, with an average pH of 3.2. This project aims to consider what we know about Beowulf spring and BS3, then determine the central metabolism, carbon metabolism, and energy metabolism of BS3. The research for this project was done using online pipelines and databases such as IMG, KEGG, and BLAST. KEGG was the main pipeline used, as it is useful in showing which pathways and associated enzymes are found inside the organism. Other research will have to be done to determine the key enzymes of other, more unique pathways, such as iron and sulfur oxidation, as these pathways are not well detailed on KEGG. Preliminary results show that BS3 performs gluconeogenesis and the tricarboxylic acid cycle. Key enzymes for glycolysis and the pentose phosphate pathway were not found in this organism. I hypothesize that BS3 performs iron oxidation for energy metabolism and that it uses carbon monoxide as a carbon source. A potential issue with this project is that the genome data for BS3 is incomplete and divided into a number of unarranged contigs. This project was part of the BIOL 446 Microbial Genomics course. /

Entry Number: 134 UL1 DISPLAY ONLY

A SECRET OF ACID LOVING ARCHAEA

By: Mari Grange

Microbiology

Faculty Advisor: Dr. José R. de la Torre

Abstract: Thaumarchaeota are proposed in 2008. The main distributions are in ocean, soil and hot spring. Nitrogen cycle and carbon cycle of Thaumarchaeota likely to play important role in biochemical cycles, and it might be chemolithoautotrophic ammonia-oxidizers. Thaumarchaeota are distributed fairly mild environment when compared to other archaea group. However, Thaumarchaeota BS3 lives in acidic environment (pH2-3) in Beowulf spring in Yellow Stone National Park. Protein has optimal pH, so it denatures at out of range. Bacteria which live in acid environment have two response systems. Acid tolerance response (ATR) for mild acid stress such as actively expelling protons out of the cell via the F1F0-ATPase, deiminase and deaminase system, urea break down, mechanisms of repair or damage prevention of proteins, and modification of the cell membrane. The second one is Amino acid-dependent extreme acid resistance (XAR) for extreme acid stress such as amino acid-dependent decarboxylase/antiporter systems. It is reasonable to support that BS3 might have significant acid resistant like bacteria have from other stains. Searching about ATR and XAR is done using JGI if BS3 have a particular and significant different proteins compared to other strains BS1, BS2 and BS4. Pfam shows functions of the proteins and KEGG is helpful to understand in which part the proteins involve in the metabolism. Only BS3 has glutamate decarboxylase (GAD, EC4.1.15), and it involves amino acid metabolism. In anaerobic conditions, GAD switches alpha-carboxyl group to proton to produce gamma-Aminobutyric acid (γ -GABA). GABA in the cell was exchanged with glutamate from outside of the cell to maintain acidity of intracellular environment. From the data, it is inferred that Glutamate-dependent system would be particular acid resistance for Thaumarchaeota BS3.

Entry Number: 135 UL1 DISPLAY ONLY

PUTATIVE GENES OF THAUMARCHAEOTA ARCHAEON STRAIN BS3 INVOLVED IN THE NITROGEN CYCLE

By: Olayemi Akintunde

Pre-Health

Faculty Advisor: Dr. José R. de la Torre

Abstract: Nitrogen is a crucial element that is essential to all forms of life, but nitrogen is not freely available. Atmospheric nitrogen is converted to ammonia and used to synthesize basic building blocks such as amino

acids for proteins and nucleotides for DNA and RNA. The phylum Thaumarchaeota consist of archaea that use various assimilatory pathways for nitrogen metabolism. The extreme environments of Thaumarchaeota has prevented the cultivation of the organism. Instead, metagenomic analysis has been used to make predictions about physiology. Until recently, it was believed that the dissimilatory pathway that relies on the oxidation of ammonia was limited to ammonia-oxidizing bacteria. Despite the fact that Thaumarchaeota archaeon strain BS3 lives in the acidic (pH ~3) high temperature (65-72°C) Beowulf Springs in Yellowstone National Park, it does not have an ammonia monooxygenase gene. The objective of this research project is to investigate how BS3 assimilates nitrogen from the environment and identify which genes are involved in the process. The genomes of archaea that do not undergo ammonia oxidation, such as Thaumarchaeota archaeon strains BS1 and BS2, will be compared against BS3 using BLAST and IMG. The genome of BS3 will also be compared against the genome of ammonia-oxidizing archaea and a non ammonia-oxidizing archaeal phylum. If nitrogen metabolism genes are not found, BS3 might be using a novel pathway. This project was part of the BIOL 446 Microbial Genomics course. /

Entry Number: 136 UL1 DISPLAY ONLY
DOES BS3 USES SULFATE AS ENERGY METABOLISM?

By: Rizafaye Pada

Biology

Faculty Advisor: Dr. José R. de la Torre

Abstract: Thaumarchaeota embodies a unique phylum within the domain Archaea. They live under autotrophic conditions and fix CO₂, while some rely on the presence of other bacteria or organic material. Thaumarchaeota lives in extreme environments such as the hot springs in Yellowstone National Park preferably the Beowulf Springs and Dragon Springs. Thermophilic archaea and bacteria are various microbes that are found in this region. Microbes that can thrive in this highly acidic environment are acidophiles. There is a diverse collection of bacteria thriving in these hot springs. In this study, I will focus on how energy metabolism is related to environment in the Beowulf Springs and Dragon Springs. The two organisms that I will be focusing on are Aquifex and Hydrogenobaculum. I will be using genomics techniques such as BLAST, KEGG, phylogenetics to find information not these organisms and their metabolic features. These organisms will need a variety source of nutrients such as elemental sulfur and hydrogen as electron donor and oxygen as electron acceptor. From sampling these two sites, they found that Fe(III) oxide mats within Beowulf and elemental sulfur in Dragon Springs.

Entry Number: 137 UL2 DISPLAY ONLY
PLASMID DESIGN TO HELP CHARACTERIZE THE HAX ENZYME

By: Robin A. Herbert

Microbiology

Faculty Advisor: Dr. José R. de la Torre

Abstract: Nitrification represents a major part of the global nitrogen cycle, impacting plant nutrition as well as aquatic and atmospheric pollution. Ammonia-oxidizing Archaea, or AOA, have recently been characterized as rivaling ammonia-oxidizing bacteria (AOBs) in their contribution to nitrification. Both AOA and AOBs share analogous enzymes catalyzing the first reaction of this process, oxidation of ammonia to hydroxylamine; however the archaeal enzyme used in the subsequent oxidation of hydroxylamine to nitrite, HAX, is yet uncharacterized. In order to better-understand the archaeal HAX enzyme, it must be produced in some scale and purified. Because Archaea typically take longer to grow than industrially useful microorganisms like E. coli and often do not reach similar cell-densities, in order to produce the quantity of HAX necessary for its characterization the encoding gene must be cloned into a microorganism which is more easily culturable. To this end I cloned a "Rosetta" plasmid complete with genes for archaeal tRNAs and the hydroxylamine oxidoreductase gene from AOB Nitrosomonas europaea into E. coli genotype DE3. As a positive control, production and purification of HAO from N. europaea will illustrate how the archaeal HAX gene can be produced in scale for its subsequent characterization.

Entry Number: 138 UL2
COLORECTAL ADENOCARCINOMA: A COMPARATIVE STUDY
By: Summer Reames and Jenna Bottorff

Biology

Faculty Advisor: Gloria Nusse

Abstract: The prevalence of adenocarcinoma in the US is approximately 5%. Around 1 in 20 Americans will be diagnosed with cancer of the colon or rectum in their lifetime. As of January 1, 2012, there were almost 1.2 million Americans alive with a history of colorectal cancer. Some of these people were cancer-free, while others still had evidence of cancer and may have been undergoing treatment. Some risk factors of adenocarcinoma include diet, family history and prior intestinal conditions. It is most often found in people over the age of 50. Our study compared the morphology of a cancerous and healthy colon through dissection. The cadaver that was dissected was an older man who had hypertension, diabetes, and was obese which was believed to have contributed to the adenocarcinoma. As a result, the adenocarcinoma progressed to the colon walls producing small nodules. The dissection of the descending and sigmoid colon was applicable to the study demonstrating the differences between a cancerous and noncancerous colon. Colon adenocarcinoma is an understudied cancer and conducting this comparative study provided a better understanding of what can cause this cancer to progress, who it affects, its morphology, and how to treat it. /

Entry Number: 139 UL2

THE PROTEIN JAGUNAL IS REQUIRED FOR PROPER EYE DEVELOPMENT IN DROSOPHILA

By: Jose Ortega Jr.

Cell & Molecular Biology

Faculty Advisor: Dr. Blake Riggs

Abstract: The Endoplasmic Reticulum (ER) has multiple functions in eukaryotic cells. The ER is known to regulate calcium ion concentration, aid in lipid biosynthesis, and it is involved in protein secretion. Also, the ER is the only organelle to be found in all regions of the cell, however little is known of the ER's role in the generation of cell diversity. Preliminary data in the Drosophila embryo shows that the ER partitions asymmetrically during cell division, just prior to the generation of multi-potent stem cells called neuroblast. Furthermore, we have demonstrated that this asymmetrical division relies on the evolutionary conserved ER trans-membrane protein Jagunal (Jagn). Currently the genes involved in the Jagn signaling pathway remain unknown. In order to identify Jagn interactors, we ectopically expressed Jagn double stranded RNA (Jagn RNAi) in the Drosophila compound eye. We observed a disruption in eye topology, generating a rough eye phenotype. We found a 56.65 percent (n= 298 flies) of flies to express the Jagunal rough eye phenotype, while our controls expressed 100 percent wild type eye phenotype. In conclusion, Jagn is a key protein in guiding asymmetric ER division. Future Drosophila genome studies will help identify genes involved in the Jagn pathway through enhancer/suppressor of the rough eye phenotype. Results will provide insight on how the ER is asymmetrically dividing, which will then help us understand how ER asymmetry leads to cell diversity in the Drosophila embryo.

Entry Number: 140 UL2

THE ROLES OF CLASSICAL MHC I ON NEUROGENESIS

By: Alan Gutierrez

Cell & Molecular Biology

Faculty Advisor: Dr. Saul Villeda

Abstract: Major histocompatibility complex class I (MHC I) molecules are well recognized for their vital role in the adaptive immune system. Contrary to the outmoded dogma that the brain is "immune-privileged", MHC I molecules have / been found in neurons¹, and shown to negatively regulate synaptic dynamics and plasticity in development and adulthood²⁻⁴. However, the role of these molecules in neurogenesis, another form of plasticity important in regeneration, / remains to be explored. Preliminary data generated in the Villeda lab showed that absence of classical MHC I molecules (H2-Kb and H2-Db) in a genetic mouse model exhibited an increase in proliferation of neural stem cells in vivo.

Entry Number: 141 UL2

EXAMINING THE BIOPHYSICAL STRUCTURE OF H2A-H2B DIMER AND VARIANTS

By: Austin Murchison and Troy Lowe

Cell & Molecular Biology

Faculty Advisor: Dr. Raymond Esquerra

Abstract: "Histones are DNA binding proteins that pack and arrange DNA into ordered structure called chromatin. The higher ordered structure of chromatin and DNA accessibility are dependent on histone structure. Histones can promote or repress DNA accessibility through histone modification. There are four canonical histone types H2A, H2B, H3, and H4. Variants are utilized during different phases of the cell cycle and affect chromatin structure. We will examine the thermodynamic stability of H2A variants HTZ and HTAS and how they compare to the canonical H2A in H2A-H2B dimer structure. The purpose of these studies will be comparing the canonical dimer to the dimer composed of variants in order to understand how changes in sequence impact stability. The stability of the histones composing chromatin is important when considering how DNA is expressed and repressed, these studies will contribute to our understanding of DNA accessibility. We will use circular dichroism to monitor the unfolding of the histone dimer under denaturing conditions such as ionic strength and thermal denaturation."

Entry Number: 142 UL2

CHARACTERIZATION OF VIBRIO CHOLERAЕ SpeG SPERMIDINE/SPERMINE N-ACETYLTRANSFERASE MUTANTS AND THEIR IMPORTANCE FOR ENZYMATIC ACTIVITY

By: Danielle Asaro and Elison Jung

Cell & Molecular Biology

Faculty Advisor: Dr. Misty L. Kuhn

Abstract: Biofilm formation is important for the survivability and virulence of the organisms, such as *Vibrio cholerae*, that form them. The formation of biofilms on medical instrument, such as catheters, have led to secondary infections in hospital patients. Studies have shown that polyamines in part have a role in the formation of biofilms under stressed conditions. Spermidine/spermine N-acetyltransferase, encoded by the gene *speG*, is the initial catalytic step in the degradation of polyamines in *V. cholerae*. This bacterium causes the potentially life-threatening disease Cholera and is a globally important pathogen. *SpeG* is an allosteric enzyme that uses polyamines in both its allosteric and active sites, however the specific amino acid residues important for its regulation and activity are not known. To test the importance of various residues, we created point mutations in the active site, allosteric site, and sites of inter-subunit interactions and compared their kinetic parameters with the wild-type protein. Our results show that certain residues play a greater role than others in the activity of the enzyme. A deeper understanding of the structure/function relationship of this enzyme will provide critical information that will be important for drug development.

Entry Number: 143 UL2

MYOGENESIS IN SOMITES IN TISSUE CULTURE INITIATED THROUGH NO SIGNALING IN EARLY STAGES OF DEVELOPING CHICKEN EMBRYOS

By: Jipsa Panchal, Monica Reynoso-Prieto, and Gretchen Hazel Ford

Cell & Molecular Biology

Faculty Advisor: Dr. Wilfred Denetclaw

Abstract: Nitric oxide (NO) is a messenger gas signaling molecule that has important roles in the physiology of the body including immune defense mechanisms and regeneration of tissues. The regeneration of skeletal muscle fibers require NO to activate muscle stem cells called satellite cells to begin proliferation and subsequently to undergo muscle differentiation. However, NO signaling in embryo development and in embryonic myogenesis is largely unknown. Previously we have demonstrated that NO is dynamically produced in the ectoderm layer of chick embryos and signals into the subjacent dorsal epithelial layer of somites, called the dermomyotome that produces muscle. Our goal was to determine the role of NO signaling in somitic muscle formation using in vitro somite cultures stimulated by signal pathway regulators for NO and compared to untreated sister-paired somites. Our results show that cultured somites taken from embryos as young as 5 somites in age can form muscle and for the first time shows that NO has regulatory control through its canonical signaling pathway over myogenic mechanisms promoting skeletal muscle development in chicken embryos.

Entry Number: 144 UL2

LYMPHATIC DRAINAGE OF THE BRAIN

By: Maiya Akhmetzhanova and Gerardo Amador

Cell & Molecular Biology

Faculty Advisors: Gloria Nusse and Charles Barbieri

Abstract: It has been long believed by the scientific community that the brain is an organ without / lymphatic vessels. However, part of CSF drains into cervical lymph nodes. A recent study by / Kari Alitalo at University of Helsinki finds lymphatic vessels in the dura mater of a mouse brain. / Dural lymphatic vessels absorb CSF and brain interstitial fluid via the glymphatic system. We / are going to try to locate those vessels in a human cadaver brain. / The purpose of lymphatics is to clear the leftovers of proteins, solutes etc. that are not absorbed / by blood capillaries and to maintain pressure balance. It has recently been discovered that a / lymphatic--like vessel exists in the eye, which was previously believed to be another / immune--privileged organ. That leads us to questioning whether the brain really is / immune--privileged (aka lacking lymphatics). / According to the study “A dural lymphatic vascular system that drains brain interstitial fluid and / macromolecules” published in the Journal of Experimental Medicine, June 2015, the reason why / lymphatics vessels haven’t been commonly observed is because they found them to be / collapsed structures between the meninges that cannot be found unless one knows how they / look. / The subject of lymphatic vessels in the brain has a lot of potential for research, and we are / hoping to trace the lymphatic vessels in the brain by using various dyes and other mechanisms / in the course of this study.

Entry Number: 145 UL2

CHARACTERIZATION OF JAGUNAL KNOCKDOWN IN THE DROSOPHILA COMPOUND EYE

By: Ulises Diaz

Cell & Molecular Biology

Faculty Advisor: Dr. Blake Riggs

Abstract: Asymmetric cell divisions are a fundamental mechanism for establishing cell fate by producing two different cells during mitosis. This unequal partitioning of information during mitosis to the newly formed daughter cells is highly conserved and a key mechanism during development for the generation of cell diversity. However, a complete understanding of the mechanism of asymmetric divisions is poorly understood. An excellent model for examining these divisions is the establishment of neuroblasts in the fruit fly, *Drosophila melanogaster*. Neuroblasts are formed and maintained through asymmetric partitioning of cell fate determinants in proneuronal cells. Preliminary data has shown an unequal partitioning of the Endoplasmic Reticulum (ER), prior to an asymmetric division and selection of cell fate. This unequal ER partitioning occurs in cells destined to become the posterior lobe of the brain in the adult fly. RNA inhibition (RNAi) of the highly conserved ER transmembrane protein Jagunal (Jagn) disrupts this ER asymmetry during mitosis. In order to identify genes involved in Jagn function, we expressed Jagn RNAi in the *Drosophila* compound eye, which displayed a rough eye phenotype. I show this rough eye phenotype can be rescued by overexpression of Jagn. Specifically, the Jagn RNAi rough eye appears to cause defects in the axis of symmetry found in the compound eye. These results of Jagn involvement in the compound eye are the basis for a modifier screen of the *Drosophila* genome for genes in the same pathway.

Entry Number: 146 UL2

ACETYLATED POLYMYXIN ANTIBIOTICS: CLUES TOWARD SUBSTRATE SPECIFICITY OF PA3944 GCN5-RELATED N-ACETYLTRANSFERASE OF UNKNOWN FUNCTION

By: Brian Zhang and Layton Joe

Microbiology

Faculty Advisor: Dr. Misty L. Kuhn

Abstract: Acetylated Polymyxin Antibiotics: Clues Toward Substrate Specificity of PA3944 Gcn5-related N-acetyltransferase of Unknown Function / / Brian Zhang¹, Layton A. Joe¹, Brian J. Amsler¹, Karolina A. Majorek², Robert Yen¹, Weiming Wu¹, George Gassner¹, Teaster Baird¹, Wladek Minor², and Misty L. Kuhn¹ / / ¹Department of Chemistry and Biochemistry, San Francisco State University, San Francisco, CA, 94132 / / ²Department of Molecular Physiology and Biological Physics, University of Virginia, Charlottesville, VA, 22908 / / Gcn5-related N-acetyltransferases (GNATs) have been studied for decades, but because / / the GNAT superfamily is so vast the majority of the proteins that belong to this family / / have no known function. GNATs catalyze the transfer of an acetyl group from acetyl / / coenzyme A to an amino group on a variety of substrates. To improve our understanding / / of GNAT functions in bacteria, our laboratory studies the structure/function relationship / / of uncharacterized GNATs from *Pseudomonas aeruginosa*. This bacterium is found in / / diverse environments, is a known human pathogen, and is notorious for its resistance to / / antibiotics. Since the rate of discovering novel antibiotics to treat bacterial infections lags / / considerably

behind the rise in antibiotic drug resistance, it is important to understand // how resistance to these antibiotics occurs and how to maintain the effectiveness of the // current drugs in the clinic. In this work we present the kinetic characterization of a P. // aeruginosa GNAT that is capable of acetylating polymyxin antibiotics (PA3944). These // antibiotics are cyclized antimicrobial peptides that disrupt the cell membrane and // currently have little resistance reported compared to other antibiotics. To our knowledge // this is the first enzyme that has been shown to modify polymyxin antibiotics and offers a // new space in which to study potential adaptive drug resistance mechanisms toward this // important class of antibiotics.

Entry Number: 147 UL2

EXPLORING BACTERIAL DIVERSITY ON BAY AREA RAPID TRANSIT (BART) DUE TO A MAJOR PUBLIC EVENT

By: Jennifer MacFarlane, Allen Caden, Jacky Lo, and Kimberly Tsui

Microbiology

Faculty Advisors: Dr. Lily Chen, Darleen Franklin, and Dr. Brinda Govindan

Abstract: Infectious disease can easily spread through public transportation, especially in urban locations such as the San Francisco Bay Area. Past studies show microbes found in transit systems can be potentially pathogenic and can lead to serious health risks, such as food borne illness, respiratory tract and skin infections. Our study focuses on the Bay Area Rapid Transit (BART) system and determining bacterial diversity when there is an influx of passenger traffic during the National Football League's Super Bowl 50 that was held in the Bay Area on February 7, 2016. Swabbed samples from the hand straps and seat handles (located on the back of the seats) were collected from BART trains over a period of two weeks. Samples were analyzed using standard microbial culturing techniques, staining methods and biochemical analysis. Preliminary results indicate more diverse bacterial populations are found in the evening samples than the morning samples, and Gram-positive cocci bacteria are most abundant in the overall BART sampling collection.

Entry Number: 148 UL2

DOES SCHIZOSACCHAROMYCES OCTOSPORUS CDC24+ RESCUE SCHIZOSACCHAROMYCES POMBE CDC24 MUTANT?

By: Justine Ramos

Microbiology

Faculty Advisor: Dr. Sally Pasion

Abstract: Schizosaccharomyces pombe is a fission yeast species that is used as a model organism to study the cellular processes of higher eukaryotes. It includes genes that interact with certain proteins, such as DNA ligase, that are conserved in these eukaryotes. One of S. pombe's genes, cdc24+, is one that interacts with conserved proteins. It is a significant actor in DNA replication and genomic integrity. Mutations in the cdc24+ gene cause cell non-viability due to (deficient) DNA. To test whether the S. pombe cdc24- gene can be rescued, I am studying a related fission yeast species called Schizosaccharomyces octosporus. S. pombe and S. octosporus have a 65.5% amino acid identity and a 54.8% cdc24+ genomic sequence similarity. Therefore, I hypothesize that S. octosporus can rescue the S. pombe cdc24- gene.

Entry Number: 149 UL2

A CHALLENGE TO ACCESS THE SECONDARY METABOLITES OF AN UNTAPPED MICROBIAL RESOURCE

By: Nichole Legaspi

Microbiology

Faculty Advisor: Dr. Taro Amagata

Abstract: Archaea comprise the most unique groups of organisms within the three domains of life. Archaea are unique in that they possess special characteristics that allow these organisms to thrive what would be considered in very harsh conditions. However, their secondary metabolites are poorly studied since it is extremely difficult to grow them in laboratory conditions. The De La Torre labs were able to develop a culture condition that allowed for the isolation of an ammonia-oxidizing Archaeum Nitrosocardus Yellowstownii HL-72. In collaboration, the Amagata and De La Torre labs have been investigating the secondary metabolites produced by the HL-72 strain. Through a scale-up culture (100L), we were able to isolate several pure compounds. One which was identified as 1,3,5-triphenylpentan-1-one based on the 1D and 2D NMR data. Interestingly, this

compound was originally isolated from a marine sponge. Using various detailed cultivation techniques, the various chemical and structural elucidations of 1,3,5-triphenylpentan-1-one were examined.

Entry Number: 150 UL2

CHARACTERIZING THE BIODIVERSITY OF BOTRYLLID AND DIDEMNID ASCIDIANS IN THE PHILIPPINES THROUGH CO1 BARCODING

By: Ryan Fergusson and Darragh Clancy

Ecology, Evolution & Conservation Biology

Faculty Advisor: Dr. C. Sarah Cohen

Abstract: As basal chordates, ascidians are frequently studied for their remarkable abilities in molecular self/non-self recognition, and for their regenerative capabilities. These traits show intriguing patterns of variation across clades and species. Yet, it is difficult to discover the evolutionary patterns related to these abilities with our current limited knowledge of species distributions and phylogenetic relationships. Basic aspects of biogeographic patterns of distribution and speciation are understudied. We are limited by a lack of ability to identify species and thus elucidate distribution and abundance patterns among species. For ascidians, species identification and discovery of cryptic species using barcoding has frequently focused on the discovery of invasive species distributions, often in populations growing on artificial substrata. Here, we take advantage of substantial new collections of ascidians from the Verde Island Passage of the Philippines, named the center of the center of marine biodiversity in the Coral Triangle based on studies of other invertebrates and fish. Recent expeditions led by the California Academy of Sciences, with the Natural History Museum of the Philippines are providing a new look at ascidian biodiversity. This project is aimed at comparison of barcode distributions around the Verde Island Passage as a first step towards characterizing biodiversity and leading towards linking molecular data with historic species descriptions based on morphological features. Our first preliminary barcode data revealed a high diversity of cryptic botryllid species, none of which match existing barcodes including known globally invasive species already characterized at the molecular level. The likelihood that more new species will be identified is very high. The knowledge gained from expanding and clarifying ascidian phylogeny will contribute towards conservation efforts of model organisms, and of a very important ecosystem.

/

Entry Number: 151 UL2

POST-FUSION CHIMERISM IN THE COLONIAL TUNICATE DIDEMNUM VEXILLUM

By: Rachel Weinberg

Marine Biology & Limnology

Faculty Advisor: Dr. C. Sarah Cohen

Abstract: *Didemnum vexillum* is an invasive species of colonial tunicate found throughout the Pacific Northwest region of the United States. Like many other colonial tunicate species, colonies of *D. vexillum* are capable of fusing after coming into contact with one another, forming what appears to be a single colony with a shared tunic. This project seeks to identify chimerism in fused *D. vexillum* colonies to determine if alleles can be shared between fused colonies by genotyping samples collected from colonies before and after fusion using 11 neutral micro satellite markers. Alleles present in only one colony prior to fusion were detected in the fused colony at distances up to 6 centimeters from the fusion line, indicating chimeric growth in fused colonies of *D. vexillum*.

Entry Number: 152 UL2

ASSESSING THE ANTINOCICEPTIVE EFFECT OF NEUROPEPTIDE, LEUCOPYROKININ (LPK) ON THE DEFENSIVE STRIKE OF THE HORNWORM, *MANDUCA SEXTA*

By: Alicia Rice

Physiology

Faculty Advisor: Dr. Megumi Fuse

Abstract: Neuropeptides are responsible for the function of many physiological processes. An example consists of the opioid family that serves as endogenous analgesics in most vertebrates. Pyrokinins are a class of peptides with a common N-terminal found to affect many physiological functions of insects such as pheromone biosynthesis and muscle contraction. Leucopyrokinin (LPK) member of the pyrokinin family and found native in the cockroach, *Leucophaea maderae*. LPK was discovered to have an antinociceptive effect when injected

into mice, putatively through binding to opioid receptors (Plech et al., 2004; OTHER REF). The hornworm, *Manduca sexta*, is becoming a model for studying nociception through quantification of its defensive strike response (McMackin et al., 2015). It was therefore hypothesized that when LPK was injected into *M. sexta* it would also have an antinociceptive effect. Each hornworm was tested for their strike threshold by poking them with a series of von Frey filaments that produced specific forces, until a defensive strike was elicited. *M. sexta* were tested with filaments before and after being injected with 1 μ L of 10-12 M LPK and compared to control animals injected with 1 μ L of vehicle (*Manduca* saline). Animals were tested for their basic nociceptive response to a touch, as well as their sensitization response after a pinch. Our results showed that after *Manduca* were injected with LPK, the force required to elicit a strike was higher than controls, whether animals were touched or pinched first. These data suggest that LPK has an antinociceptive effect in *M. sexta*, and may also reduce sensitization to a noxious stimulus such as a pinch. These data further validate the use of *M. sexta* as a model for studying pain and mechanisms of analgesia in animals.

Entry Number: 153 UL2

EFFECT OF DIFFERENT ALGAL DIETS ON REPRODUCTION RATE OF *BRACHIONUS PLICATILIS*

By: Christina Lardie and Lauren Lopes

Physiology

Faculty Advisor: Dr. Robyn Crook

Abstract: Rotifers are microscopic multicellular organisms that are widely used in raising marine animals. Rotifers are highly desired due to their high tolerance for marine environments, excellent nutritional profile when fed algae, and appropriate size for many marine hatchlings. In our lab, the rotifer species *Brachionus plicatilis* is part of the food chain used to culture *Euprymna scolopes*, commonly known as the Hawaiian Bobtail Squid. // In the present study, we investigate the effect of algal diet variation on the reproduction rate of *B. plicatilis*. To test this, we created four treatment groups: (1) *Nannochloropsis* (2) *Isocrysis* (3) mixed diet of *nannochloropsis*, *isochrysis*, and *tetraselmis* (4) control (no algae). Although results are preliminary and experiments are continuing, our data suggest that rotifers 1. Show a steady decline in population over 5 days in starved conditions, suggesting even relatively short periods of undernourishment can dramatically damage population growth rates, and 2. reproduce at similar, steady rates in all three algae diet conditions.

Entry Number: 154 UL2

EFFECT OF VARYING ALGAE DIETS ON *TISBE BIMINIENSIS* & *TIGRIOPUS CALIFORNICUS* REPRODUCTION

By: Joshua Hernandez and Sara Tom

Physiology

Faculty Advisor: Dr. Robyn Crook

Abstract: Copepods are a diverse group of small aquatic crustaceans that serve as a food source for many species of fish, as well as other crustaceans. For this reason, Copepods are extremely important in maintaining marine ecosystems. Two species of Copepod, *Tisbe biminiensis* & *Tigriopus californicus*, are utilized in our lab. They are an important member of the food chain used to sustain *Euprymna scolopes*, also known as the Hawaiian Bobtail squid. // In our study, we examine the effect of various algae blends on the reproduction and sustainability of copepods. In order to determine the optimal diet for culturing our copepods, we formed four treatment groups: *Nannochloropsis*, *Isocrysis*, control of no algae, and a mix of *Nannochloropsis*, *Isocrysis*, and *Tetraselmis*. Analysis of initial trials showed an increase in adult copepod population for *Nannochloropsis* and mixed algae treatment groups, while the control group showed a decline in adult population. Although results are preliminary and experiments are continuing, our data suggest that Copepods: 1. show a continuous decline in population under nutrient-deprived conditions, suggesting even relatively short periods of malnourishment can dramatically reduce population growth rates, and 2. reproduce at similar, steady rates in all three algae diet conditions. /

Entry Number: 155 UL2

EXAMINING DIFFERENCES IN NON-CONTENT INSTRUCTOR TALK ACROSS VARYING INSTRUCTOR DEMOGRAPHICS

By: Kristen Liang, Katie Lam, and Alycia Escobedo

Physiology

Faculty Advisors: Dr. Kimberly Tanner and Dr. Colin Harrison

Abstract: What instructors say in class can have a large effect on student motivation, self-efficacy, identity and learning. As such language can have a direct impact on phenomena such as Instructor Immediacy, Student Resistance, and Stereotype Threat. We have previously characterized Instructor Talk (IT) - non-content language said by instructors that helps establish the learning environment – as a framework for identifying what language is being used in the classroom (Seidel 2015). In this study we wanted to analyze how different demographic characteristics of instructors could influence the amount and types of IT used in biology classrooms. We found that there is a significantly more IT used by Non-Majors instructors compared to Majors instructors and no significant difference in the amount of IT used between Males and Females or for New and Experienced instructors. While we begin to see differences in the amount and types of IT used when comparing different instructor demographics, ultimately the IT framework will allow us to test whether these patterns of IT use in different demographics correlates with Instructor Immediacy, Student Resistance, and Stereotype Threat.

Entry Number: 156 UL2

REPRODUCTION RATE OF ROTIFERS UNDER DIFFERENT LIGHT CONDITIONS

By: Kristen Liang, Lemo Dayekh, Stephanie Yin, Stephanie Skidmore, and Paul Perez

Physiology

Faculty Advisor: Dr. Robyn Crook

Abstract: The rotifer *Brachionus plicatilis* is a microscopic zooplankton that is commonly used in aquaculture. They contain eyespots, or photo-sensors, that are sensitive to various lengths and intensities of light. The reproduction rate of *Brachionus plicatilis* can be altered with different light conditions (Kim et al., 2013). *Brachionus plicatilis* females have a lifespan ranging from 6-45 days, while males only live for a day or so because their only purpose is to fertilize eggs (Bailey, 2012). The effects of varying levels of pH, temperature, and salinity on *Brachionus plicatilis* have been studied, but the effects of varying levels of light on *Brachionus plicatilis* lifespan have not been carefully looked at in previous studies. / Here we show that the rotifer *Brachionus plicatilis* has different reproduction rates with exposure to different conditions of light (ambient light, 24h light, 24h dark). We found that they reproduce best in dark conditions and most poorly in the control conditions (regular room light). To our surprise, rotifers reproduced faster when exposed to continuous direct light compared to regular room light exposure. / Our results demonstrate that not only pH, temperature, and salinity are factors that affect the reproduction rates of rotifera *Brachionus plicatilis*, but also different light conditions are a factor that affects their reproduction rates. / Our work applies to a larger group of scientists attempting to rear their own populations of rotifers for either experimentation, or in the husbandry of other marine species. Our results suggest that rotifers grow best under minimal light. This information could be useful for future researchers that are trying to produce their own colonies in a controlled lab setting, which can be used for experimentation. /

Entry Number: 157 UL2

LYMPHEDEMA

By: Mayrane Gonzalez

Physiology

Faculty Advisor: Gloria Nusse

Abstract: This case study involved the investigations of genital enlargement on a 93 year-old woman. She had a hysterectomy in 1992 when she was 70 years old. A possible side effect of a hysterectomy is lymphedema. This can happen during the performance of the hysterectomy surgery when the lymph nodes near the area can become damaged causing the vulva to enlarge. A visual comparison can be seen between a regular vulva and the enlarged vulva. Measurements were done between the two genitals in order to reveal the size difference. An illustration of the lymph nodes involved and microscopic views of the connective tissue can be seen. /

Entry Number: 158 UL2

HOW I MADE SLIDES THE OLD SCHOOL WAY

By: Minerva Orellana

Physiology

Faculty Advisor: Gloria Nusse

Abstract: The initial concept of my experiment was to do a comparative analysis of the female and male genitalia by looking at connective tissue. To do this analysis, I needed to prepare microscope slides. This experiment then took a different turn with me learning instead how to make slides the old school way with the use of a Spencer 820 Rotary Microtome from the 1950's and the internet to help me prepare the tissues. The entire process will be described along with some slides I made.

Entry Number: 159 UL2

INTERACTIVE EFFECTS OF TEMPERATURE AND SALINITY ON SKELETONEMA MARINOI AND SAN FRANCISCO BAY PHYTOPLANKTON COMMUNITY ASSEMBLAGES

By: Nina Ciara B. Reyes, Kate Barretto, Morgan Meyers, and Andrew Kalmbach

Physiology

Faculty Advisor: Dr. Edward Carpenter

Abstract: With ocean temperatures rising due to climate change and the fluctuating salinity levels of estuarine systems such as the San Francisco Bay, it is crucial to understand the potential effects of temperature and salinity on phytoplankton. *Skeletonema marinoi* is a ubiquitous species of phytoplankton and an important player in many marine and estuarine food webs. Previous in situ studies of SF Bay phytoplankton have shown that regardless of initial communities, *S. marinoi* dominates assemblages over time (A. Costanza, unpublished data). To study the interactive effects of salinity and temperature on *S. marinoi*, we grew monocultures under four fully crossed temperature (20°C and 24°C) and salinity (18 and 34) treatments. Cells counts were conducted to generate a growth curve for each of the four treatments, and chlorophyll a and c were measured fluorometrically at the end of each growth curve cycle. To further understand the field relevance of our in vitro data, we studied naturally occurring phytoplankton community assemblages at three sampling sites in the San Francisco Bay. Species composition was determined microscopically and abiotic factors were determined by measuring pH, salinity, temperature, and dissolved oxygen of each sampling site. We found that *S. marinoi* cells in mixed temperature and salinity regimes reached death phase later than cells in High Salinity – High Temperature or Low Salinity – Low Temperature compositions. We also found that temperature (P-Value < 0.0005), and to a lesser extent salinity (P-Value < 0.05), had a significant effect on chlorophyll a production, but that there were no interactive effects between the two. Our site data indicated that the Romberg Tiburon Center Finger Pier and Golden Gate sites clustered together multivariately and taxonomically, and were significantly different than the much more dynamic and estuarine Point Isabel. The data generated from this experiment will strengthen our understanding of how phytoplankton communities and critical species will respond to anthropogenic climate change and changing surface water patterns.

Entry Number: 160 UL2

THE EFFECTS OF DEMENTIA ON THE HUMAN BRAIN

By: Samuel Boikaner

Physiology

Faculty Advisor: Gloria Nusse

Abstract: The human body is very unique in the way in which it is able to adapt to different life-styles and health problems. In order to adapt, and continue physiological function despite alterations in natural function, the human body uses compensatory mechanisms. In this study, I analyzed a brain of a human cadaver that was diagnosed with dementia, and tried to understand which compensatory mechanism was used by the brain in order to compensate for the short-term memory loss and other symptoms that are common among dementia patients.

Entry Number: 161 UL2

EXPLORATION OF NAPYADIOMYCIN DERIVATIVES PRODUCED BY THE MARINE SEDIMENT-DERIVED STREPTOMYCETES SP. CP55-76

By: Scott Campit

Physiology

Faculty Advisor: Dr. Taro Amagata

Abstract: Cancer is a global medical problem and chemotherapy is commonly used as a treatment regiment for many types of cancers. However, new chemotherapeutics are needed to address problems with current pharmaceuticals such as associated deleterious side effects and their inability to treat some cancer types. As part

of our program to discover novel anticancer leads with excellent solid tumor selectivity from marine-derived actinomycetes, we have screened an extract library of our actinomycete collection against two different in vitro anticancer screenings including disk diffusion assay (DDA) using seven solid tumor cell lines and cytological profiling (CP) using HeLa cells. One of the tested strains, *Streptomyces* sp. CP55-76, showed significant prostate cancer (LNCaP) selective activity as well as potent cytotoxicity against HeLa cell (90% cytotoxicity at 60ug/mL of the extract). In fact, we have isolated a series of cytotoxic napyradiomycin derivatives from a scale-up culture. In the presentation, the principles of the two cancer screenings, isolation and spectroscopic analysis for the isolated compounds will be discussed. /

Entry Number: 162 UL2 DISPLAY ONLY

RELATIONSHIP BETWEEN KIDNEY TRANSPLANT AND BONE DENSITY

By: Veronica Gernhardt and Ashley Del Dosso

Physiology

Faculty Advisor: Gloria Nusse

Abstract: The question our team wished to address was how a kidney transplant affects the body post-surgery, specifically how it can result in bone loss. According to research, the highest loss of bone density was found in the lumbar of the spine. Of one cadaver who had a kidney transplant, both transplant and atrophied kidney were dissected and compared to not only each other but the kidney of a cadaver who had no history of kidney disease. L5 of the spine was dissected out and compared to a healthy spine section found from an external source to visually determine

Entry Number: 163 UL2 DISPLAY ONLY

SPATIAL LEARNING IN ANATOMY

By: Lena Alazzeh

Kinesiology

Faculty Advisor: Gloria Nusse

Abstract: / Spatial organization is essential in the study of gross anatomy. Spatial organization is important because it plays a central role in understanding the different regions of the body and their anatomical organization differences. It also is important to understand because it differentiates the relationships of different body parts from each other. However, students consistently struggle with this concept and their difficulties in understanding this presents itself in poor performance on spatial organizing conceptual problems. The focus of this study was to understand where the root of the misconceptions originate from and what topics they were misunderstanding. Also to see whether intervention strategies could be used to target these misconceptions. This was accomplished by having higher-level multiple-choice questions regarding spatial organization given to anatomy students that multiple semesters of classes have consistently gotten wrong. To understand the student's logic in approaching spatial questions we gave them a scientific reasoning paper and told them to respond to each option and explain why it would be scientifically correct or incorrect. The results showed the main misconceptions to be how they think of planes, mixing up the planes, and how body cavities are divided. These results give some insight into the concepts of spatial organization that students consistently struggle with and can thus help instructors better target the sources of confusion and figure out ways to better teach the material effectively. /

Entry Number: 164 UL3

TMEM16A INHIBITORS: SYNTHESIS OF SMALL NOVEL COMPOUNDS

By: Alannah Moises

Biochemistry

Faculty Advisor: Dr. Marc Anderson

Abstract: The goal of this research project is to develop small novel molecules that are inhibitors to the calcium-activated chloride channels (CaCCs) of the membrane protein TMEM16A. The overexpression of this protein is found in several types of cancers. Creating inhibitors to TMEM16A could help develop therapeutic treatment for diseases such as head and neck squamous cell carcinoma, pancreatic cancer, and cystic fibrosis.

Entry Number: 165 UL3

EXPLORING HOW H3 AND H3.3 VARIANTS AFFECT THE STABILITY OF THE HISTONE TETRAMER

By: Amaryllis Aguilar, Dagim Legesse, Austin Murchison, and Troy Lowe

Biochemistry

Faculty Advisor: Dr. Raymond Esquerra

Abstract: Histones are the support structure of chromatin. Chromatin is composed of DNA wrapped around histone proteins. There are four major histone proteins H2A, H2B, H3, and H4. Histone proteins group into two H2A-H2B dimers and a (H3-H4)₂ tetramer to form a protein complex, called the histone octamer.

Approximately 147 bp of DNA will wrap around this octamer to form a Nucleosome Core Particle (NCP). The stability of the nucleosome affects gene expression, cell differentiation, DNA development, and DNA repair. In addition to the canonical histone proteins, histones have several variants. / / Specifically the histone variant H3.3 which differs from the canonical histone by only five amino acids has been linked to active transcription, nucleosome positioning, and chromatin remodeling upon fertilization. In addition, the histone H3.3 variant is needed to assure a proper embryonic development; however, not much is known about how the H3.3 variant affects the stability of the histone tetramer. This study compares the structural stability of the canonical histone tetramer to the histone variant H3.3 tetramer as function of ionic strength and thermal denaturation. We hypothesize that the (H3.3-H4)₂ tetramer will be less stable than the conical tetramer. This work will help our understanding of the molecular mechanism of how histone variants direct the course of cellular development. /

Entry Number: 166 UL3

ENGINEERING TRYPSIN TO WEAKEN INHIBITOR INTERACTION

By: Anthony Nzessi

Biochemistry

Faculty Advisor: Dr. Teaster Baird Jr.

Abstract: Serine proteases may potentially be administered as drugs in order to help with many health maladies, but their activity is limited by natural regulatory inhibitors which serve to regulate the action of proteolytic enzymes. Trypsin variant Y39L was made in order to weaken interaction with macromolecular inhibitors. Y39L showed to have comparable activity to that of wild type trypsin, and demonstrated activity on protein substrates due to its ability to auto-activate. Interaction with benzamidine demonstrated that the active site was not compromised by this substitution. These studies will be instrumental in the development of trypsin-fold serine proteases that may potentially be used as therapeutic agents. /

Entry Number: 167 UL3

ROLE OF RNAI SUPPRESSOR IN VIRAL PATHOGENESIS

By: Brianna Rivera

Biochemistry

Faculty Advisors: Dr. Teaster Baird Jr. and Dr. Arabinda Nayak

Abstract: RNA interference (RNAi) is a natural antiviral defense mechanism in insects. In the RNAi pathway, Argonaute2(Ago2) plays a critical role in defending cells against virus infection. To counter this host antiviral mechanism, viruses express factors that suppress RNAi. Cricket Paralysis Virus (CrPV), an insect RNA virus, expresses the RNAi-suppressor protein CrPV-1A, which interacts Ago2 and inhibits its anti-viral function in insect cells. We now show that, besides inhibiting Ago2 function, CrPV-1A interacts with cellular Nup88 nucleoporin protein and induces cell death and pathogenesis in insect cells and adult flies. Using X-ray crystallography, we determined the structure of CrPV-1A to 2.6 angstroms resolution and mapped these two functions to distinct interfaces of the protein. In summary, the CrPV-1A RNAi suppressor is a multifunctional viral protein that serves important pathogenic functions in CrPV life cycle.

Entry Number: 168 UL3

REPURPOSING THE STYRENE CATABOLIC PATHWAY FOR THE SYNTHESIS OF THIOESTERS: DEVELOPING A KINETIC ASSAY FOR STYRENE MONOOXYGENASE REDUCTASE BASED ON THE DISCONTINUOUS MONITORING OF HYDROGEN PEROXIDE

By: Coby Varela, Tania Martinez, Kitty Michel, Nancy Her, and Samantha Donaldson

Biochemistry

Faculty Advisor: Dr. George Gassner

Abstract: Phenylacetaldehyde dehydrogenase, the last enzyme in the styrene catabolic and detoxification pathway catalyzes the oxidation of phenylacetaldehyde to phenylacetic acid. When provided mono or dithiols, NPADH catalyzes the biotechnologically relevant reaction of thioester synthesis. This reaction occurs with the net reduction of NAD⁺ to NADH which binds as a product-inhibitor of NPADH. This inhibition can be offset by coupling activity of NPADH with that of styrene monooxygenase reductase, which reacts rapidly with NADH and oxygen to yield hydrogen peroxide in the presence of flavins. In this work we develop a discontinuous assay for hydrogen peroxide and use it to compare the kinetics of SMOB reacting with riboflavin, FMN, and FAD. NSMOB was found to react with all three flavins with no significant difference in specificity based on continuous monitoring of the absorbance at 340 nm. FAD worked well as a coenzyme but both riboflavin and FMN were found to interfere with the discontinuous hydrogen peroxide detection. This study provides a reliable means of discontinuously monitoring the enzymatic synthesis of hydrogen peroxide by using FAD as a coenzyme and opens the possibility of monitoring the progress of coupled reactions of SMOB and NPADH.

Entry Number: 169 UL3

CHARACTERIZATION OF THE TRANSTHIOESTERIFICATION REACTION OF NPADH FOR THE SYNTHESIS OF NATURAL PRODUCTS USING MONO AND DITHIOL SUBSTRATES

By: Donovan Ruiz, Lucia Hau, and Cystal Perez

Biochemistry

Faculty Advisor: Dr. George Gassner

Abstract: Project Description: NPADH is an N-terminally histidine-tagged phenylacetaldehyde dehydrogenase, which catalyzes NAD⁺-dependent oxidation of phenylacetaldehyde via a covalent cysteine thioester intermediate. In the normal reaction mechanism of NPADH, the thioester intermediate is hydrolyzed to by water, to yield phenylacetic acid, but in the presence of thiols, NPADH catalyzes an alternate reaction, thioesterification. It was previously shown that NPADH can react the p-nitrophenolester of phenylacetic acid in an esterase reaction to yield the cysteine thioester intermediate of the enzyme and chromogenic p-nitrophenolate anion. We used this reaction under steady-state conditions to generate and study the reactivity of the cysteine thioester intermediate with mono and dithiol acceptors. Thiol uptake was established by assaying with Ellman's before and after reactions thiol acceptors. We find the NPADH reacts with both monothiols and dithiols as substrates and the mechanism of the reaction changes depending on the substrate. Pyridine nucleotides were found to affect both the esterase and thioesterification kinetics of NPADH accelerating the reactions at low pyridine nucleotide concentration and inhibiting them at higher concentrations. The activating effect of pyridine nucleotides is thought to related to the homotropic allosteric activation of NPADH observed under normal steady-state reaction conditions with NAD and phenylacetaldehyde as substrates. The inhibitory effect is more severe when p-nitrophenylphenylacetate is used as an esterase substrate that when the less bulky p-nitrophenyl and o-nitrophenylacetates are used. The data obtained suggests the primary mode of inhibition of the esterase and thioester synthesis reactions is competitive binding of the pyridine nucleotide effector and esterase substrate. The study indicates that NPADH is capable synthesizing a range of phenylacetylthioesters and establishes the role of pyridine nucleotides in the esterase and transthiesterification reactions. The thioester of Coenzyme A, Phenylacetyl-CoA, is a known N-acyltransferase substrate. In our future work, we will engineer a pathway joining the transthoesterification activity of PADH and targeted acyl transferases for the synthesis of natural products such as phenylacetylglutamine and phenylacetyl glycine.

Entry Number: 170 UL3

MECHANISTIC INVESTIGATION OF SPEG SPERMIDINE/SPERMINE N-ACETYLTRANSFERASES FROM ESCHERICHIA COLI AND VIBRIO CHOLERAE

By: Ellison Jung and David Tran

Biochemistry

Faculty Advisor: Dr. Misty L. Kuhn

Abstract: Bacterial SpeG enzymes belong to the Gcn5-related N-acetyltransferase (GNAT) superfamily and catalyze the acetylation of polyamines spermine and spermidine. These enzymes are important for regulating cellular polyamine concentrations under stress conditions, which is critical for bacterial biofilm formation. Understanding the mechanism of polyamine acetylation by SpeG enzymes will provide important insight for designing drugs that target SpeG to prevent or reduce biofilm formation. GNATs use a variety of kinetic

mechanisms to acetylate their substrates, but it is not known if there is a common core set of residues that dictate which mechanism will be used by the enzyme. Typically GNATs acetylate their substrate either directly (direct transfer mechanism) or form an acetylated enzyme intermediate prior to substrate acetylation (ping-pong mechanism). We previously characterized the *Vibrio cholerae* SpeG enzyme (VcSpeG) and found that it uses a bireactant random steady-state (direct transfer) mechanism, which is contrary to what we observed during kinetic characterization of the *Escherichia coli* SpeG enzyme (EcSpeG). The EcSpeG enzyme uses a ping-pong mechanism. Since VcSpeG and EcSpeG are structurally similar and have largely conserved active site residues, it is puzzling as to why both enzymes use different kinetic mechanisms to accomplish the same task. Nevertheless, this difference in mechanism may provide an avenue for designing selective SpeG inhibitors that specifically target certain bacterial species.

Entry Number: 171 UL3

INVESTIGATION OF CYTOTOXIC SECONDARY METABOLITES PRODUCED BY MARINE SEDIMENT-DERIVED STREPTOMYCES SP. CP47-79

By: Eric Yip

Biochemistry

Faculty Advisor: Dr. Taro Amagata

Abstract: The focus on discovering novel cytotoxic compounds with excellent solid tumor selectivity has led our research group to marine sediment-derived actinomycetes. From our chemical library containing organic extracts obtained from strains of actinomycetes, several extracts showed significant selective activity against cancer cell disk diffusion assay (DDA) using nine different cell lines at Josephine Ford Cancer Center. One of these strains, *Streptomyces* sp. CP47-79, showed selective activity against the prostate cancer cell line (LNCaP) and was selected for further investigation. Several media conditions were used to increase the productivity of the strain CP47-79. We have isolated two cytotoxic compounds based on bioassay-guided fraction using the results of DDA assay. These two compounds were identified as oligomycin D (1) and rutamycin B (2) based on analysis with NMR and HRMS. In the poster, the principle of anticancer screening, the results of media study, structure determination, and cytotoxic effects of the isolated compounds will be presented. / /

/

Entry Number: 172 UL3

PROMOTING CELLULAR DIFFERENTIATION

By: Jasmine Sims

Biochemistry

Faculty Advisor: Dr. Teaster Baird Jr.

Abstract: In this project, we were interested in modeling how yeast cells are able to act in unison to perform functions. More specifically, we wanted to tailor yeast responses to make them more specialized. We tested this by adjusting parameters such as cell-cell proximity, receptor recruitment, and varying levels of mating factor. We hope that these studies can influence the realm of immunology to include T and B cell differentiation or hemopoietic stem cells in general. This information has the implication of helping people with diseases that range from allergies to autoimmune disease, and more.

Entry Number: 173 UL3

TO OPTIMIZE OR NOT TO OPTIMIZE-THAT IS THE QUESTION: MODIFYING PURIFICATION METHODS FOR GCN5-RELATED N-ACETYLTRANSFERASE ENZYMES

By: Kristen Jew, Alina Revilla, and Melissa Law

Biochemistry

Faculty Advisor: Dr. Misty L. Kuhn

Abstract: Purifying enzymes that belong to the Gcn5-related N-acetyltransferase (GNAT) superfamily is a crucial step for many of the structural and functional experiments in our research group. It is important to have a robust purification procedure that yields large quantities of highly pure protein. As a result, our laboratory over-expresses proteins with a polyhistidine tag and purifies them using Ni-affinity chromatography. Unfortunately, we have found that the tag negatively affects the kinetic activity of all enzymes we have tested in the laboratory and must be removed. We use TEV protease to cleave the tag, which adds an additional step to the purification procedure, exposes the protein to more contaminants, and lowers the protein yield. Therefore, our goal is to

develop a streamlined and efficient purification method that can be applied to all GNATs. We hypothesize that producing proteins without a tag and purifying them using classical purification methods will reduce the length of the purification process and increase protein yield compared to our current methodology. To achieve our goal, we have cloned four GNAT genes into a pCR-Blunt II-TOPO cloning vector without a tag and are assessing expression. We will compare our methods to define an optimal expression and purification strategy for GNAT proteins.

Entry Number: 174 UL3

REPURPOSING THE STYRENE CATABOLIC PATHWAY FOR THE SYNTHESIS OF THIOESTERS: COUPLING THE ACTIVITIES OF NSMOB AND NPADH IN THE TRANSFORMATION OF ALDEHYDES TO ORGANIC ACIDS OR THIOESTERS.

By: Nancy Her, Samantha Donaldson, Tania Martinez, Kitty Michel, and Coby Varela

Biochemistry

Faculty Advisor: Dr. George Gassner

Abstract: The first and last steps of the styrene catabolic pathway are linked through their respective roles in the recycling or reduced and oxidized pyridine nucleotides. In the present work we take advantage of this pyridine nucleotide recycling reaction as means of optimizing conditions for the sustained synthesis of thioesters by NPADH. Joining the activities of NSMOB and NPADH in thioester synthesis prevents the net consumption of NAD⁺ and accumulation of product inhibitor, NADH. We first established the optimum ratio of NPADH and NSMOB needed to maintain a near zero steady-state concentration of NADH. Under these conditions the rate of NADH oxidation in the hydrogen peroxide-generating reaction of NSMOB is limited by rate NADH synthesis in the aldehyde oxidation reaction of NPADH. This allows us to make indirect initial rate measurements of the reaction of NPADH with aldehydes by discontinuously monitoring the rate of hydrogen peroxide production by NSMOB. Comparison of the kinetics of aldehyde oxidation in the presence or absence NSMOB indicates that the pyridine substrate inhibition of NPADH by NADH is effectively eliminated when NSMOB is included as a pyridine nucleotide regenerating system. This work supports the inclusion of NSMOB as a component part of any engineered pathway for the synthesis of thioesters from aldehydes by NPADH.

Entry Number: 175 UL3

MODIFYING TRYPSIN AS A MODEL FOR SERINE PROTEASE INHIBITOR RESISTANCE

By: Parris Diaz

Biochemistry

Faculty Advisor: Dr. Teaster Baird Jr.

Abstract: In trypsin, we substituted amino acids in S1' pocket and examined if these variants would be resistant to inhibitors, while also retaining catalyzing efficiency and capabilities. The S1' pocket contains residues Tyr-39, Phe-41, and Lys-60 and has been chosen as a target site due to this being the location at which macromolecular inhibitors typically bind to trypsin. We made amino acid substitutions at Phe-41 because the large phenyl group locks the backbone carbonyl into a conformation / that causes it to directly hydrogen bond with amide groups on inhibitors. In our experiments, we have seen that F41L has a high binding affinity to the substrate Z-GPR- pNA ($K_m = 7.55 \pm 4.2 \mu\text{M}$) along with sufficient catalyzing capability ($K_{cat} = 4.76 \times 10^3$). In addition, the variant F41L has not affected the binding capability of the inhibitor benzamidine to the active site ($K_i = 5.82 \mu\text{M}$) when compared to WT ($K_i = 6 \mu\text{M}$). These results tell us that the active site is still intact and can still interact with substrates such as Z-GPR-pNA as well as competitive inhibitors such as benzamidine or para-aminobenzamidine.

Entry Number: 176 UL3

EVALUATING THE ALDEHYDE SUBSTRATE SPECIFICITY OF PHENYLACETALDEHYDE DEHYDROGENASE FROM THE STYRENE CATABOLIC AND DETOXIFICATION PATHWAY

By: Sima Rantisi, Karina Ky, and Andrew Hong

Biochemistry

Faculty Advisor: Dr. George Gassner

Abstract: Phenylacetaldehyde dehydrogenase (PADH) catalyzes the NADH-dependent oxidation of Phenylacetaldehyde to phenylacetic acid in the styrene catabolic pathway of *Pseudomonas putida* (S12). This Class-1 Mg²⁺-dependent tetrameric enzyme proceeds through an ordered reaction mechanism with NAD⁺

serving as the leading substrate and homotropic activator. // In catalysis, an active site cysteine-nucleophile attacks bound phenylacetaldehyde (PAL) to generate a thiohemiacetal. Hydride-transfer from this intermediate to bound NAD⁺ results in a thioester intermediate with NADH-product bound. Under normal reaction conditions, an active site general base catalyzes the hydrolysis of the thioester to release phenylacetate (PAA) as the first product and NADH dissociates in the last step of the reaction. Following the dissociation of PAA product, the enzyme is subject to inhibition through the formation of a “dead-end” complex of PAL (substrate) and NADH (product). // We have found that as an alternative to the penultimate ester hydrolysis step of the dehydrogenase reaction mechanism, the cysteine-thioester intermediate can react with mono- and di-thiols in transthioesterification reaction. This reaction extends the utility of the NPADH as a catalyst for the synthesis of thioester products of biotechnological value. // In the present work we use stopped-flow kinetic studies to establish the intrinsic specificity of NPADH for a series of target aldehyde substrates ranging from acetaldehyde to 4-OH,3,5-dimethoxycinnamaldehyde differing in polarity and steric-bulk. In our studies, the extent of substrate inhibition varied depending on the aldehyde. Smaller, more polar aldehydes were found to be less potent as substrate inhibitors. We find that NPADH has broad aldehyde substrate range that should allow for the synthesis of a diverse set of thioesters. The findings of this work suggest that in reactions involving sterically bulky aldehyde substrates, the catalytic efficiency of NPADH may be significantly improved by coupling it with the flavin reductase component of styrene monooxygenase, which uses NADH as a substrate.

Entry Number: 177 UL3

LITHIUM IONIUM CHLORIDE AS SOLID-ELECTROLYTE: COMPUTATIONAL EXPERIMENTS ON DRIVERS OF LI⁺ DIFFUSION

By: Thomaz Alves

Biochemistry

Faculty Advisor: Dr. Nicole Adelstein

Abstract: The search for solid electrolytes with fast Li⁺ diffusion is essential to the development of safer and higher energy-density all-solid state batteries. The presented simulations aim to understand the effect of the dynamic electronic structure on Li⁺ diffusion by not only identifying the atomic scale Li⁺ diffusion process, but also the effect of anion substitution on the interaction of the Li⁺ and the surrounding lattice. In this report, the diffusion processes of Li⁺ in Li₃InCl₆ is probed using molecular dynamics simulation.

Entry Number: 178 UL3

METAL INHIBITION OF A SPERMIDINE/SPERMINE N1-ACETYLTRANSFERASE (SPEG) IN VIBRIO CHOLERAE

By: Winnie Hong and Joseph Dang

Biochemistry

Faculty Advisor: Dr. Misty L. Kuhn

Abstract: Biofilms are communities of bacteria that are found in a variety of environments, including the intestinal mucosa of humans and on medical devices. These biofilms protect bacteria from antibiotics and other adverse environmental stresses. Polyamines are polycationic small molecules that are involved in biofilm formation. When polyamines are acetylated, biofilm formation increases. SpeG is important for regulating polyamine levels and responding to bacterial stress conditions. We previously determined the structure of the SpeG enzyme from *Vibrio cholerae*, and found that it can acetylate spermidine and spermine using the activated donor acetyl coenzyme A. Recent 3D structures show that metals bind to both active and allosteric sites on the enzyme, prompting us to further investigate the role metals play on the enzyme. We kinetically characterized SpeG in the presence of a range of divalent metals (Ca²⁺, Co²⁺, Cu²⁺, Mg²⁺, Mn²⁺, Ni²⁺, Zn²⁺) and found that they inhibit enzyme activity. To confirm inhibition, further kinetic experiments are being performed to verify whether metals are competing with polyamine binding. These results will lead to the rational design of inhibitors that inactivate this enzyme in pathogenic bacteria.

Entry Number: 179 UP1

CONNECTABLE: MODULAR SYNTHESIZER INTERFACE

By: Michael Castanieto

Computer Science

Faculty Advisor: Dr. Bill Hsu

Abstract: ConneCTable is an interactive modular synthesizer designed for use on an Android tablet. This instrument uses movable components that act as sound sources, sound triggers, or sound filters. A user can move these components close together to connect them in various ways, producing different sounds.

Entry Number: 180 UP1

FOOD ROULETTE

By: Samuel Gluss, Hari Manivannan, Nikolay Pavlov, and Afshin Binesh

Computer Science

Faculty Advisor: Marc Sosnick

Abstract: A location aware Android application with dynamic graphics which helps users find popular nearby food establishments with Yelp and Google APIs.

Entry Number: 181 UP1 DISPLAY ONLY

BOMBERMAN

By: Su Khai Koh, Suhan Koh, Steven Nguyen, and Raymond Thai

Computer Science

Faculty Advisor: John Roberts

Abstract: Bomberman is a multiplayer real time gaming website programmed in Ruby on Rails.

Entry Number: 182 UP1 DISPLAY ONLY

SLEEP APNEA DETECTION

By: Stephanie Benavidez, Jordan Butler, and Kelvin Lee

Computer Engineering

Faculty Advisor: Dr. Thomas Holton

Abstract: The detection and analysis of sleep apnea serves as a platform for our senior project. Loud snoring and short pauses are associated with sleep apnea. When breathing is halted, passage of the airway is obstructed. Sleep apnea can be life threatening if not detected earlier. The risks include heart attack, stroke, impotence, irregular heartbeat, high blood pressure, heart disease and daytime sleepiness. By analyzing sound waves of snores, we can detect areas that reflect signs of sleep apnea. In order to conduct this type of analysis, our team is required to demonstrate skills of digital signal processing, basic mathematics and basic programming. We were provided code in MatLab as the underlying layer which would read the snoring sound wave in and establish where a person is in danger of sleep apnea. We convert the code to Java in the Android Studio environment to interface via phone app in which the mic records the snore. The application processes the signal and sends a vibration notification to the Nabu X, which is a programmable wrist watch, to alert the sleeper to breathe (as the brain lacks oxygen from the sleep apnea to remind send a signal throughout the body for the sleeper to continue breathing) without interrupting the sleep.

Entry Number: 183 UP1 DISPLAY ONLY

MYINTERN MOBILE APP

By: Timothy Friesen and Thai Nguyen

Computer Engineering

Faculty Advisor: Dr. Thomas Holton

Abstract: The goal of our project is to create a system to increase efficiency and clarity within the // application, review, interviewing and hiring of interns within large multi-dimensional organizations, through a mobile // application. The mobile application will require the applicant to create a login identification. The // applicant can then use the app to fill out all relevant information, such as name, address, school, major, // etc. This information can be modified to the organizations preferences. The mobile application can also // be used to upload relevant documents, review and edit information and finally submit the application // for hiring managers to review. During the reviewing process the mobile app will keep the applicant // informed on any potential interviews and selections, hopefully limiting confusion on the side of the // applicant.

Entry Number: 184 UP1

RESTAURANT WAITLIST MANAGEMENT SYSTEM

By: Agajan Jumakuliyev and Pedrum Aghamir

Computer Engineering

Faculty Advisor: Dr. Thomas Holton

Abstract: San Francisco is known for its diverse selection of restaurants. The restaurant scene in the city continues to churn at a furious pace. Not all the restaurants in the city prefer to take reservations. Instead of taking reservations, some of the busy restaurants prefer first come first serve system. Currently most of these restaurants use a simple waitlist system with pen and paper or buzzers. / / The purpose of our final project was to design an automatic wait list management system on Android platform. Using our app customers can browse restaurants in their area and find wait times that fit their schedule before leaving their house. In addition, restaurant staff will be able to easily manage their waitlist using our Android application.

Entry Number: 185 UP1

DESIGN OPTIMIZATION OF WRITE CIRCUIT FOR SPIN TRANSFER TORQUE MAGNETIC LATCHES AND LOOK-UP-TABLES IN 32/28NM CMOS PROCESS

By: Andrew Miller and Tyler Sheaves

Computer Engineering

Faculty Advisor: Dr. Hamid Mahmoodi

Abstract: Spintronics is an emerging discipline of electronics concerned with manipulating the spin of electrons to exploit various effects. We see this technology already commercialized in Hard Disk Drives (HDDs) where the Quantum Tunneling effect of electrons is exploited to great effect. Modern research of these applications include a basic storage device called the Magnetic Tunnel Junction (MTJ), where the resistance across the device store a single bit of information, and switching occurs due to Spin-Transfer-Torque (STT) among other phenomena (GRM, TMR.. etc). Many latch designs have been proposed to read these cells but writing to the cells remains a challenge as scaling increases due to the amount of current required to flip the magnetic axes. In this research we investigate one such process node, 32nm, and quantify the sizing requirements of these write circuits against representative process constraints provided by a Synopsys Educational Design Kit.

Entry Number: 186 UP1

ANDROID GAME: TANK ENGINEER

By: Arvin Lau

Computer Engineering

Faculty Advisor: Dr. Thomas Holton

Abstract: This project is a mobile game developed for Android using the Unity engine. It is a two-dimensional turn-based artillery game which also includes the customization of a players own vehicle. Players design their own vehicles by positioning and rotating armor and modules, e.g., engines, fuel tanks, and gearbox in a strategic fashion. Players use these customized vehicles to compete against computer controlled vehicles in a turn-based, shot for shot, battle.

Entry Number: 187 UP1

SMART SHOWER SYSTEM AND DRINK DISPENSER

By: Charles Shaw, Rodolfo Alejandro Ayala Palacios, and Rosemarie Martin Dehesa

Computer Engineering

Faculty Advisor: Dr. Thomas Holton

Abstract: We are designing a water saving device that recirculates the cold water in the pipes back into the hot water heater so that the water is at the designated temperatures at all times. This will eliminate the need to let the shower run for a few minutes before getting in. We also wanted to demonstrate the future ability to add to this by also including a drink dispenser that runs off the same microprocessor as the shower.

Entry Number: 188 UP1

MINIATURE DATA LOGGER FOR WEIGHING LYSIMETER

By: Ian Santos and Kevin Valenzuela

Computer Engineering

Faculty Advisors: Dr. Hao Jiang and Dr. Andrew Oliphant

Abstract: Data loggers that record precise measurements can be relatively large and expensive. For measuring weight changes of a plant, a small data recorder helps minimize its effect on the controlled environment, while

storing accurate information. As an alternative to advanced data loggers, our Tiva-C microcontroller-based platform is configured to meet the necessary functions in a cheap and affordable manner.

Entry Number: 189 UP1

DATA SCIENCE CONSOLE

By: Kevin Valenzuela, Yong Wen Wu, and Benjamin Lopez

Computer Engineering

Faculty Advisor: Dr. Thomas Holton

Abstract: Our project, the Data Science Console, is an accessible and affordable machine that empowers students to mine data, store data, and analyze data from various internet sources. Data science normally has a very high barrier to entry and this machine makes it much more accessible to the general public and/or school children. Our console makes exciting data science concepts accessible such as web scraping, parallel processing, and hadoop.

Entry Number: 190 UP1

NFC ON LOCK

By: Lance Narbaitz, Consuelo Jimenez, and Mikael Miller

Computer Engineering

Faculty Advisor: Dr. Thomas Holton

Abstract: Utilizing Near Field Communication (NFC) technology, our project attempts to eliminate the need for keys in door locks. Our project integrates NFC logic through an Arduino micro-controller to control the electric locking mechanism of a deadbolt. This allows us to prototype the workings of future NFC-based projects and we hope to continue expanding this project further to integrate advanced technology, more users, and increased security in the system.

Entry Number: 191 UP1

HEART SYNC

By: Roseanne Damasco, McKenzie Campagna, and Adrian Solorio

Computer Engineering

Faculty Advisor: Dr. Thomas Holton

Abstract: We know that finding motivation to work out and to stay healthy is a difficult task sometimes, and that even when you do get the energy to get up and work out, sometimes the workouts can be very time consuming and not the most effective. Heart Sync is an Android fitness app that connects to an external heart rate monitor via Bluetooth and it will provide an effective work out based on your target heart rate and the readings from your heart rate monitor. Our application keeps track of user progress and provides feedback to help keep them motivated and excited to exercise and be healthy.

Entry Number: 192 UP1

A LOW INPUT WIRELESS POWER TRANSFER FOR BIOMEDICAL IMPLANTS

By: Alejandra Franco

Electrical Engineering

Faculty Advisor: Dr. Hao Jiang

Abstract:

Entry Number: 193 UP1

PROGRAMMABLE RESISTIVE CROSSBAR ARRAY

By: Alex Chen, Sravanth Bolla, and Taylor Chesnut

Electrical Engineering

Faculty Advisor: Dr. Thomas Holton

Abstract: We have seen many technological advances in computer system in the past few decades. As computers get faster and denser, the platform that it is based on will eventually plateau. Our goal is to develop a new platform to assist today's technology and break through the glass ceiling that our current model for computation can't past. We are attempting to mimic the process that an organic brain uses to process

information. By combining the computation and storage elements into a single component, we can improve certain inherent traits in today's technology such as long processing time and power consumption.

Entry Number: 194 UP1

SELF TUNING GUITAR

By: Brett Rinehart and Fidel Quezada Guzmán

Electrical Engineering

Faculty Advisor: Dr. Thomas Holton

Abstract: Construction of a guitar which can be set to a specific tuning and will automatically turn the guitar pegs until the desired tuning is reached.

Entry Number: 195 UP1

MOTORCYCLE HELMET HUD

By: Cameron Nauman and Brian Rondolo

Electrical Engineering

Faculty Advisor: Dr. Thomas Holton

Abstract: The project is a motorcycle helmet with a 1.8" screen that displays GPS information. It utilizes an Android app to set destination and current location.

Entry Number: 196 UP1

DUAL AXIS SOLAR TRACKER

By: Carlos Martinez, Abdulrahman Alshaikhi, and Zenas Waa Saepfan

Electrical Engineering

Faculty Advisor: Dr. Thomas Holton

Abstract: The main objective is to design a dual axis solar tracker that tracks and follows the movement of the sun throughout the day. / / The device could be applied to optimizing the efficiency of solar panels by mechanically moving the solar panels according to the position of the sun. The device would track the sun by detecting maximum average intensity indicated by four photoresistors. The output from the photoresistors would then be sent to an arduino microcontroller where a program would decide on the necessary adjustments needed to move two servo motors that would readjust the solar panels to a position where the panels would achieve maximum intensity from the sun

Entry Number: 197 UP1

AUTONOMOUS OBSTACLE AVOIDANCE VEHICLE AND OBJECT FINDER

By: Hector Estrella, Sonam T. Lama, and Justin Quitariano

Electrical Engineering

Faculty Advisor: Dr. Thomas Holton

Abstract: It's main objective is to find and approach our target object. We will use a Pixy CMUcam5 camera to find that specific object. Our vehicle will also have infrared sensors to detect obstacles along it's path. When there is an obstacle, it will avoid them by turning left or right, clearing the obstacle and turning around to find our object. We use dc brush motors to power the tank wheels. The motors will be programmed to start by turning the vehicle left, but it will also be able to turn right or go straight when it has found our object. Our microcontroller is the Arduino Uno with the Arduino Motor Shield. We will use the Pixy and intrared sensors as inputs and the dc brush motors as outputs on the Arduino Uno.

Entry Number: 198 UP1

EZ AQUARIUM

By: Karla V. Vega, Anish Kumaramangalam, and Philip Hu

Electrical Engineering

Faculty Advisor: Dr. Thomas Holton

Abstract: Novice aquarium enthusiasts frequently do not have the necessary time, energy or knowledge to keep fish alive and thriving. Our goal is to provide a user-friendly system, which would contain the necessary information, to help maintain the aquarium with little time and effort. / / Appropriate maintenance requires turning on and off lights at constant times during the day, keeping a constant water temperature, and most

importantly the correct pH level for the type of fish living in the tank. We designed a system that will automate all three of these aspects of owning happy fish without all the headaches of constant supervision, and cut out the research needed to keep different species happy.

Entry Number: 199 UP1 DISPLAY ONLY

DEFECT-INDUCED EXCITONIC PROPERTIES OF THE EDGES AND GRAIN BOUNDARIES IN SYNTHESIZED MONOLAYER MOLYBDENUM DISULFIDE

By: Alexander Yore

Electrical Engineering

Faculty Advisor: Dr. AKM Newaz

Abstract: Micro-photoluminescence (μ PL) spectroscopy has become an attractive and standard tool to probe the exciton properties of atomically thin transition metal dichalcogenides (TMDCs). Here, we present our experimental work on spatial PL scanning of monolayer MoS₂, grown by chemical vapor deposition (CVD), using a diffraction limited blue laser beam spot (wavelength 405 nm) with beam diameter as small as \sim 200 nm. We found several important features: (i) there exists a sub-micron width strip (\sim 500 nm) along the edges that fluoresces \sim 400% brighter than the region far inside; (ii) there is another brighter wide region consisting of parallel fluorescing lines ending at the corners of the zig-zag outer edges; (iii) there is a giant blue shifted A-excitonic peak, as large as \sim 120 meV, in the PL spectra moving from flake edges to center. Using density functional theory calculation, we attribute this giant blue shift to the adsorption of oxygen dimers at the edges which reduces the excitonic binding energy. Our results not only shed light on defect-induced excitonic properties, but also offer an attractive route to tailor optical properties at the TMDC edges through defect engineering.

Entry Number: 200 UP2

ARM - AUTONOMOUS ROBOTIC MOVEMENTS

By: Andrew Roby and Jonas Ruthfuss

Mechanical Engineering

Faculty Advisor: Dr. Mojtaba Azadi

Abstract: Robotic arm that locates objects, grasps onto the objects, and relocates the objects into a specified area. / This robot is supposed to be able to simulate the movements of larger, industrial robots that are utilized in manufacturing and warehouse applications.

Entry Number: 201 UP2

E ARM

By: Ethan Tseng, Richard Pham, Tsun Ming Kwan, and Alejandro Ortiz

Mechanical engineering

Faculty Advisor: Dr. Kwok-Siong Teh

Abstract: An assistive arm that helps the user lift heavy objects. The prototype is based upon an an exo-skeleton that goes outside the users body.

Entry Number: 202 UP2

ACCESSIBLE WHEELCHAIR

By: Henry Yu, Xi Zhao, and Ruiming Liu

Mechanical Engineering

Faculty Advisor: Dr. Kwok-Siong Teh

Abstract: We are redesigning the wheelchair to have an easy access entrance and exit. Elders and Paraplegics often have difficulty getting on and off a wheelchair and we want to make it easier for them to get on and off. The wheelchair will have our new designs such as a sliding seat and a collapsible back-rest. Our main focus is to incorporate a back-rest and a sliding seat function to allow entrance and exit. First the seat height is adjusted so that the back-rest can fold down flat onto the platform. The seat then slides on top of the back-rest, using the back-rest as a support system. Now, the person can load on or off using the sliding seat function.

Entry Number: 203 UP2

MANUAL CAR HAND CONTROLS

By: Igor Abramson, Calvin Tran, and Ariel Smith

Mechanical Engineering

Faculty Advisor: Dr. Kwok-Siong Teh

Abstract: Our goal is to help paraplegics gain their independence and provide them with a convenient ability to drive cars with manual transmissions if so they choose or due to necessity. We propose to build a device that operates in conjunction with an already existing hand controls type of device used to drive automatic cars. It would operate the clutch pedal through a steering wheel mounted lever a user controls with their hand. This device would be compatible with a wide range of manual cars, require no permanent modifications to the car, and be easily installed and removed.

Entry Number: 204 UP2

SENIOR DESIGN PROJECT - TAKE COVER

By: Joshua Kessner, Michael Hill, and Michael Cornish

Mechanical Engineering

Faculty Advisor: Dr. Kwok-Siong Teh

Abstract: Using telescoping poles, a scissor-like mechanism with aluminum assemblies, and a single lead screw actuator, we created an automatic expanding canopy for all outdoor activities. This allows for a hassle free setup and closing of the canopy at the push of a button. The bottom of the legs are attached to wheels to allow for smooth expansion and collapsing.

Entry Number: 205 UP2

KASPRBOT

By: Lawrence Chiu, Lucas Marsh, and Gerryl Esperacion

Mechanical engineering

Faculty Advisor: Dr. Kwok Siong Teh

Abstract: Our project is a device that is a mobile robot strong enough to carry several hundred pounds and be remote controlled by a smart phone app.

Entry Number: 206 UP2

Adaptive Green: Vertical Indoor Gardening

By: Michael Barriger, Michael Calder, Diana Chang, Victor Lin

Mechanical Engineering

Faculty Advisor: Dr. Kwok Siong Teh

Abstract: Food is an basic commodity that should be accessible to all in any given geographical, spatial or economical state. Adaptive Green seeks to create an Automated System for Indoor Gardening to allow our target market to grow in any urban setting. Our controls team has taken into consideration multiple designs based off our design requirements and chosen controllers, sensors and materials to fit our automation design. In addition to managing basic requirements for plant growth such as water and temperature, this system can relocate and store plants at different heights to provide utility for the commonly unused vertical space in homes. We have implemented a vertical design with stacking environment units in which planter boxes and environment control elements are stored. Planter boxes may be ejected from the environment units for harvesting and replanting.

Entry Number: 207 UP2

DENSITY FUNCTIONAL THEORY MOLECULAR DYNAMICS SIMULATIONS OF LI⁺ IONS IN BETA-LI₃PS₄ AND AMORPHOUS SOLID-ELECTROLYTES

By: Nima Leclerc

Mechanical Engineering

Faculty Advisor: Dr. Nicole Adelstein

Abstract: INTRODUCTION / / Using first principle Density Functional Theory (DFT) simulations of both the crystalline and amorphous phases of β -Li₃PS₄, the cause of high conductivity of Li⁺ ions in the amorphous phase is explored. β -Li₃PS₄ and other lithium thiosulphates are promising electrolytes for all solid-state batteries, even in their amorphous phases. However, the high conductivity in the amorphous phase is not understood. This research aims to predict conductivity in amorphous electrolytes by comparing diffusion in the

crystalline and amorphous phases of a known conductor. // METHODOLOGY // This project uses first principle DFT simulations to simulate diffusion paths in the β -Li₃PS₄ solid electrolyte and its amorphous analog. These simulations are done using the planewave DFT in the Quantum ESPRESSO package, with a 128 atom supercell for the crystalline phase and a 640 atom amorphous electrolyte. By varying different factors such as, cell volume and temperature and lattice disorder, we were able to compare and understand the diffusion of Li⁺. // RESULTS and DISCUSSION // In this research, we aim to improve conductivity in amorphous and crystalline electrolytes by simulating the lithium ion diffusion pathways in lithium thiophosphates. The data is analyzed to identify the following effects on lithium ion diffusion: / 1.Covalent-type bonding between Li⁺ and the anion sub-lattice / 2.The disorder within the cell, from local disorder to the full amorphous phase / 3.Lithium ion motion correlations // The results presented will be molecular dynamics of both amorphous and crystalline structures of β -Li₃PS₄. Comparison of local structure and diffusion pathways in the amorphous and crystalline phase, in particular the effect of covalent bonding and correlated Li⁺ motion. /

Entry Number: 208 UP2

VEHICLE HUD SYSTEM

By: Robert Phung and Alex Mak

Mechanical Engineering

Faculty Advisor: Dr. Kwok-Siong Teh

Abstract: Driver distractions have been proven to divert attention from checking one's blind-spot when changing lanes, turning or parking. We developed and tested a new display system, which will minimize the 'blind-spot' and side-view mirrors with cameras that will project what they would see onto the windshield. Our design utilizes emissive film that glows under light from a specific wavelength and still remains transparent; the cameras will project what they see onto the film so that drivers can avoid taking their eyes off the road.

Entry Number: 209 UP2

CLEAN-TOW

By: Spencer Klaiber-Short, Cristina Van Epps, and Jose 'Polo' Chavez

Mechanical Engineering

Faculty Advisor: Dr. Kwok-Siong Teh

Abstract: Often times in areas where freshwater is most needed, there isn't enough power or time to use traditional desalination methods. For our Senior Design project, we built a human powered desalination unit that will remove the salt from salt water and is portable.

Entry Number: 210 UP2

SPOT - AN AID FOR THE VISUALLY IMPAIRED

By: Tim Mitchell, Yassine Ouassif, and Sanjeev Gupta

Mechanical Engineering

Faculty Advisor: Dr. Kwok-Siong Teh

Abstract: According to the National Federation of the Blind(NFB), there are more than 7 million people in the United States who are visually disabled or blind. Being blind obviously presents monumental challenges to otherwise ordinary tasks such as going to the market or visiting friends. By coupling distance sensing technology and clever algorithms, our team was able to conceive a device whose capabilities supersede products currently available on the market. Our device employs a standard white cane commonly in use today. The user interface of the device is similar in that the cane is held by the user in one hand. However, at the end of the cane, at floor level, our device rolls in front of the user providing feedback in the form of optimum path determination and execution. The user simply follows the path taken by the device without worries. With the incorporation of a 9 degree of freedom sensor, the user of our device can be sure that upon avoiding obstacles, they will be returned to their original path. As a society it is our responsibility to take care of each other and this instrument is our method of addressing that responsibility.

Entry Number: 211 UP2

ANTI-CLUMPING ELECTRIC DRYER

By: Trevor McArthur, Norman Robles, and Faisal Shaji

Mechanical Engineering

Faculty Advisor: Dr. Kwok-Siong Teh

Abstract: The design is for a multi sectioned electric dryer. The two sections are open creating a single load space for the drying load. Using a simple gear assembly to change the direction of rotation of the motor these two sections are spun in opposite directions. The desired effect is to allow the dryer to better handle pillows without the material in the pillow clumping up and ruining the pillow. By alternating the direction of rotation the pillow won't fall in the same direction repeatedly preventing the material from being shifted to one side of the pillow and the pillow will tumble between the dryer baffles more often pummeling the pillows. This pummeling should work to break up any clumps that do start to form.

Entry Number: 212 UP2

INTERACTIVE REMOTE SHAKE TABLE LABORATORY FOR INSTRUCTION IN EARTHQUAKE ENGINEERING

By: Alec Maxwell

Civil Engineering

Faculty Advisor: Dr. Zhaoshuo Jiang

Abstract: Bench-scale shake table is an engaging tool to conduct hands-on experiments for educating students about the importance of earthquake engineering by demonstrating how structures respond to earthquake ground motions. Through these hands-on experiments, students may easily build or modify scaled structural models to test theories and implement their own innovations to examine how these structures behave. A collaborative effort was initiated in 1998 to establish the University of Consortium of Instruction Shake Table (UCIST) which endeavored to enhance the education of students through the procurement of instructional bench-scale shake tables, the development of curricula, and the dissemination of these tools to other institutions. Partnered with a former NSF-sponsored premier cyberenvironment project, the George E. Brown Network for Earthquake Engineering Simulation (NEES), UCIST developed a shake table laboratory, which allows the remote control and participation of the shake table for hands-on experiments. In this study, a modified version of the remote shake table laboratory which adopted the more widely used Transmission Control Protocol/Internet Protocol (TCP/IP) as the communication protocol is developed. The modification allows a much more user-friendly set up process and opens up opportunities to connect the shake tables with modern mobile devices such as smartphones, tablets and wearable devices for potential control and participation of the shake table experiments. Thanks to the versatility of the TCP/IP, a mobile remote shake table laboratory is further proposed to meet the learning style of the new generation. In this project, the developed interactive remote shake table laboratories will be discussed in detail and a corresponding teaching module for the proposed mobile shake table laboratory is demonstrated.

Entry Number: 213 UP2

COMPUTING SEISMIC FRAGILITY CURVES

By: Chaoyu Qiu and Yifeng Xu

Civil Engineering

Faculty Advisor: Dr. Cheng Chen

Abstract: Fragility curves are commonly used in civil engineering to evaluate building's weakness to earthquake. The probability of failure is estimate as it's maximal inter-storey drift is greater than a prescribed inter-storey limit. We used to compute the fragility curves by using a large number of ground motion (measured ground motion or artificial ground motion, and in this research artificial ground motion are used to computing fragility curves) to do dynamic analyses of a OpenSees modeled 3-Story frame, and in this research we will use sparse polynomial chaos expansions as a way to reduce the analyses time we needed. This research is divided into two part, seismic generation and OpenSees modeling.

Entry Number: 214 UP2

TIMBER BRIDGE - HATEA BRIDGE

By: Edmund Ng, Casey Alado, Jean Sanchez, Sarah Sojo, Mike Owyang, Andre Espinoza, Usama Tuqan, Johnny Luu, Jason Yu, and Erin Aguilin

Civil Engineering

Faculty Advisor: Dr. Timothy Dorazio

Abstract: To create a resilient timber bridge, we applied our understanding of various bridge designs and structural integrity of wood. Per standards, the bridge must be able to withstand a loading test of 20kN at four given load points on the deck for a duration of 60 minutes. Considering several designs of bridges for inspiration, the Hatea Bridge, located in Whangarei, New Zealand, was chosen due to its modern and sleek appearance, yet innovative architecture. Angled towers with suspension cables restraining the deck of the bridge provided inspiration for our design. In order to achieve a deflection well within the limit dictated by deck span, our bridge was modified with steel bars under the deck for additional reinforcement. Steel cables were added to ensure support maximization at the center of the deck of where the test loading would occur. /

Entry Number: 215 UP2

EFFECT OF INTEGRATION ALGORITHM ON UNCERTAINTY ANALYSIS OF STRUCTURAL RESPONSE UNDER EARTHQUAKE EXCITATION

By: Kawai Law

Civil Engineering

Faculty Advisor: Dr. Cheng Chen

Abstract: In earthquake engineering, uncertainty quantification is a fundamental role to design a structure at confident level. The structure's response can be variance due to the limited knowledge and the mutative parameters. The application of uncertainty quantification can lead to a more optimization design on a structure; in other word, the cost of the design can be reduced. Newmark method (Newmark, 1959) is commonly used in calculating a structure's response, but a different method called CR integration algorithm is developed in 2008 by Cheng Chen and James M. Ricles. Therefore, this research will study on the effect of integration algorithm on uncertainty analysis of structural response under earthquake excitation. / The approach of this study will use Matlab (Mathworks, 2015) to simulate the response of a Single-Degree-of-Freedom structure. The main object of this study are divided into two parts: the effect of parameters such as ground motion, damping ratio, natural frequency and varies uncertainties on a structure's response and what is the response difference between Newmark's method and the CR integration algorithm. / The result shows that both integration algorithms will lead to a same result under given damping ratio and ground motion data. Different uncertainties will create a small difference between two integration algorithms, and the difference between both integration algorithms become slightly bigger when the number of uncertainties increases. The difference between both methods becomes significant when the natural frequency of the structure increase. This study shows that both Newmark's method and CR integration algorithm can lead to a very close result; however, the natural frequency of a structure play the most important role between them. The higher natural frequency will lead to a large difference between both methods. / /

Entry Number: 216 UP2

SFSU STEEL BRIDGE

By: Manuel Uribe, Jesus Gutierrez, Alvaro Arias, Yazeed, Mikdam, Omar, Mohamad, Mohanad, Karim, and Hayder

Civil Engineering

Faculty Advisor: Dr. Timothy Dorazio

Abstract: This year we have worked on a steel bridge. It is about 21 feet long and weighs roughly 300 pounds. It was made to withstand at least 2500lbs. Painted the color of the Golden Gate Bridge it is quite a sight to see.

Entry Number: 217 UP2

EARTHQUAKE ENGINEERING RESEARCH INSTITUTE 2016 SEISMIC DESIGN COMPETITION

By: Stephen Schork, Jamie Brownell, Lungyuen Lau, Marisa Araujo, Kathleen Ocampo, Ryan Schofield, and Omar Plata

Civil Engineering

Faculty Advisor: Dr. Timothy D'Orazio, Dr. Zhaoshuo Jiang, and Dr. Cheng Chen

Abstract: On the week of April the 4th, San Francisco State University (SFSU) participated in the 2016 Earthquake Engineering Research Institute (EERI)'s annual Seismic Design Competition. This competition challenges students to design and construct a scaled balsa wood model of a skyscraper with high seismic risks. The models, weighing less than 3 pounds each, are loaded with over 20 pounds of weights and are subjected to three different devastating earthquakes on an earthquake simulator (shake table). The team whose structure has

the best design, architecture, and seismic performance is deemed the winner. / / Seven students from the School of Engineering at SFSU formed this year's seismic design team as part of the Civil Engineering capstone design project. The team, Marisa Araujo, Jamie Brownell, Lungyuen Lau, Kathleen Ocampo, and Ryan Schofield, led by the project manager Stephen Pereira Schork and the faculty advisor Prof. Zhaoshuo Jiang, began working on their design at the end of the spring 2015 semester. In the 10 months that followed, the team compared dozens of different designs, performed extensive testing on the materials, and constructed two full size models. The first prototype model was tested to failure on the shake table in the Intelligent Structural Hazards Mitigation Laboratory at SFSU to investigate the realistic structure performance, which allowed the team to refine their numerical models and verify their predictions from the computer analyses. With the knowledge gained from the testing of the first model, the team constructed an improved model to bring to the competition. / / This year, 45 teams from around the world signed up for the competition, among which 33, including SFSU, were invited after the first round screen process. With the innovative design incorporating the findings from structural topology optimization and spectrum analysis, SFSU received very encouraging results in this international seismic competition. To be more specific, SFSU scored the 3rd in design proposal, the 6th in seismic performance, and the 9th in the overall final ranking. Of all the U.S. participants, SFSU ranked the 5th; and among the six participating California State Universities, SFSU ranked the 1st. More details can be found on the official website: <http://slc.eeri.org/SDC2016.htm> (Opens in New Window). This year's team is proud of how well their structure performed and is pleased to have elevated the SFSU and the School of Engineering with their outstanding performance.

Entry Number: 218 UP2

TIMBUK BRIDGE

By: Tomas Trojacek, Justin Esquivel, Marcus Peppers, Azalia Madrigal, Emewodish Tadesse, Suyesh Shrestha, Yong Feng, David Lei, Matthew Carter, and Shawn Graf

Civil Engineering

Faculty Advisor: Dr. Timothy D'Orazio

Abstract: / When faced with the challenge of designing and constructing a timber bridge, our first task was to determine what type of bridge we wanted to build. From our research we found three different types of bridges that interested us the most, the truss bridge, the arch bridge and the cable stayed bridge. All were interesting choices, but we could only build one. We made some calculation to see how each design would fare on deflection and cost. With those calculation kept in mind we decided to build the cable stayed bridge. / / / With the basic design selected, we needed to find the appropriate size of columns to support our bridge. The columns had to resist both forces in compression and bending. From our calculations we found that the 6x6 was able to fare well in both compression and bending, and was therefore chosen for our column size. For an additional safety factor we decided to reinforce the columns with a 2x8 in the direction of the cables to resist bending. We then had to decide what type of spacing between our bolts on the column would be the best. In order to properly connect the eye-bolts to the column we could not go below 3 in. and therefore did calculation for 3, 4 and 5 in spacing. From those we selected 3 in. spacing as cable tension was the lowest. / / The next item on our agenda was the deck design. We needed to determine what type of deck we would use. We decided to go with the simply supported symmetrical deck design as it is common and most practical. Due to the span of the bridge being longer than 4 m and the rules of the competition stating that no wood member could exceed 3.2 m, a cut had to be made somewhere. From a symmetrical stand we decided to make the cut in the middle of our bridge. This became a weak point in our structure which we reinforced with a splint. For our bridge we decided not to save money on connections and to properly make sure that everything was connected well. As for the cables we decided to go for galvanized 3/8 in. thick cables. This was decided since this size was sufficient enough to resist the amount of force calculated and not go beyond its inelastic range while including a factor of safety. Due to the nature of our bridge design, we had to add two cables linking columns longitudinally below the deck together. This was done in order to prevent the columns from bending inward. /

Entry Number: 219 UP2

SEISMIC STRUCTURAL BUILDING MODEL DESIGN - SP16-FA16

By: William Lee, Farah Alshuaib, Wen Li Tang, Tooraj Yegan, and Wei Jie Liu

Civil Engineering

Faculty Advisor: Dr. Cheng Chen

Abstract: We will design an earthquake prone building between 15 and 28 levels using the 2013 rules and guidelines of the Earthquake Engineering Research Institution (EERI). The building must be within rule set dimensions and follow rule set standards. Following our design, we will be constructing a building model that resists earthquakes and will use a shake table to mimic the frequencies of earthquakes.