Entry Number 1 GL-A

THE ROLE OF ANTERIOR-POSTERIOR SIGNALING IN SOMITOGENESIS IN *XENOPUS LEAVIS*

By: Vanja Krneta
Cell and Molecular Biology
Faculty Advisor: Dr. Carmen Domingo

Abstract: Somites are segmental bocks of mesodermal tissue that give rise to the vertebral column and segmented musculature of the vertebrate adult. Somitogenesis consists of the periodic formation of somites that proceeds in an anterior to posterior progression. Disruption of somitogenesis is associated with congenital defects and spinal deformities. The cell behaviors and signals involved in somite formation along the anterior-posterior (AP) axis remain poorly understood. The current working model explaining the segmented nature of somite formation is the "clock and wavefront" model proposed by Cooke and Zeeman (1976). The " clock and wavefront" model suggest that cells in the pre-somitic mesoderm (PSM) must first become competent (wavefront) in order to respond to signals associated with the segmentation clock. The purpose of this study is to further investigate the nature of PSM cells in their competency to form somites along the AP axis. Preliminary results suggest that cells form the ventral mesodermal region of gastrulae, which are fated to give rise to posterior somites differ in their ability to respond to muscle forming cues in comparison to cells from the posterior paraxial mesoderm region of older tailbud-stage embryos. I show that cells from the ventral mesoderm are not able differentiate into elongated myotome fibers when transplanted to the anterior region of the paraxial mesoderm where mature somites are located. In contrast, cells from the posterior PSM of tailbud-stage embryos are able to form elongated myotome fibers when transplanted to the anterior region of the paraxial mesoderm where mature somites are located. These results reveal that although cells from the ventral region are fated to give rise to myotome fibers they require additional signals to undergo muscle differentiation in comparison to cells positioned in the PSM of tailbud-stage embryos. Results form this research will aid in our understanding of the process of somitogenesis and in particular how cells in the PSM region become competent to form somites that consist of aligned myotome fibers. Ultimately, this study may help in the development of innovative therapies for the prevention and treatment of vertebral patterning disorders.

Entry Number 2 GL-A

REGULATION OF SOMITOGENESIS BY Rho GTPase DURING *X. LAEVIS* DEVELOPMENT

By: Mary Greene
Cell and Molecular Biology
Faculty Advisor: Dr. Carmen Domingo

Abstract: The formation of somites during vertebrate development is a crucial step as these structures will give rise to the vertebrae, muscle, and dermis of the adult. In Xenopus laevis, somitogenesis involves the partitioning of the presomitic mesoderm (PSM) into somites, which undergo a 90-degree rotation to form myotome fibers that are aligned parallel to the notochord. Prior work from our lab showed that cell contact behavior is important for this process. These behaviors involve actin-based filopodial and lamelopodial protrusions that are highly dynamic. These structures appear to be regulated by the Rho family of GTP-binding proteins. We hypothesize that disruption of RhoA function will adversely impact somite morphogenesis. To test this hypothesis, mRNA that encodes for dominant negative RhoA was injected into Xenopus embryos at the one cell stage. Confocal images of mutant embryos reveal that the cells in the paraxial mesoderm do not undergo proper rotation. Although somites do form they consist of myotome fibers that are mis-aligned and disorganized. In addition, proper somite segmentation is adversely affected as confocal scans reveal incomplete and ectopic segmental boundaries within morphant RhoA embryos. These results provide evidence that the actin regulatory protein, RhoA is associated with the changes in cell behavior that lead to the normal development of somites. This study is significant because it will make an important contribution to our understanding of the regulatory molecules underlying the cell behaviors associated with vertebrate segmentation.

Entry Number 3 GL-A

OBSERVING ARGENTINE ANT BEHAVIORS AT THE MOLECULAR LEVEL

By: Jennifer Placek, Mike Wong, Jennifer M. Lee, Philip Burkhardt, Dr. Ilmi Yoon, and Dr. Christopher Smith
Cell and Molecular Biology
Faculty Advisor: Dr. Christopher D. Smith

Abstract: Linepithema humile (Argentine ant) is an invasive species that negatively affects other plants, animals, and whole ecosystems. It's success is due, in part, to its extreme aggression, cooperation, and its successful foraging. The foraging gene (for) has been identified in several insect species including the honeybee, harvester ant, fruit fly and wasps. While it is known that the honeybee foraging gene is up-regulated in individuals outside of the nest, it is down-regulated in foraging harvester ants, and the expression level of the foraging gene in other hymenopteran species remains unstudied. We have used bioinformatics to identify the foraging gene from Argentine ants and will use quantitative PCR to compare the expression levels of the gene between foraging and non-foraging ants. We will also expose foraging ants to various semiochemicals and use computer-assisted video monitoring to find chemicals that increase or decrease foraging and/or aggressive behaviors in Argentine ants. These studies will be helpful to understand the molecular basis of invasive behavior, identify more benign chemicals to assist control and eradication programs, and potentially allow reintroduction of native species to the environment.

Entry Number 4 GL-A

A COMPARATIVE ANNOTATION OF DROSOPHILID DICISTRONIC GENES

By: Lala Motlhabi
Cell and Molecular Biology and Computing for Life Sciences
Faculty Advisor: Dr. Christopher D. Smith

Abstract: Unlike viruses and bacteria, which can encode many proteins in a single messenger RNA (mRNA), most eukaryote genes express only one protein from each transcript. Due to the requirement for a modified 5'cap, the majority of eukaryote mRNAs have a single open reading frame (ORF) per transcript. In rare cases, eukaryotes have dicistronic genes with two non-overlapping open reading frames encoded in a single mRNA transcript. While the upstream gene is expressed through normal cap-dependent translation, it is unknown how the ribosome initiates translation of the downstream ORF. One mechanism used by viruses to internally recruit ribosome is a RNA structure called an internal ribosomal entry site (IRES). It is unclear to what extent eukaryotes dicistronic genes use IRES sequences, but whole genome sequence data and cDNA-verified gene annotations in the fruitfly, *Drosophila melanogaster*, reveal that dicistronic genes are much more prevalent than previously thought. The availability of 12 Drosophilid genomes allows for a comparative genomic annotation the ~50 well-supported *D. melanogaster* dicistronic genes and their orthologs. We hypothesize that conserved dicistronic genes will also share regions important for regulation of the downstream ORF, including putative IRES structures or cryptic promoters. We also predict that differences in the intron-exon structure of dicistronic genes between species will elucidate whether their regulation is conserved or the result of more recent gene structure changes. We have annotated several dicistronic genes in at least six Drosophilids (*D. simulans, D. sechellia*, *D. yakuba*, *D. erecta*, *D. pseudoobscura*, *D.virlis*). We used the FlyBase database along with Genscan, BLAST, Repeatmasker, and the MAKER annotation tool to identify the ORFs, matching cDNA sequences, align proteins, and find repeats present in syntenic dicistronic gene contigs. We also used CLUSTALX to align dicistronic annotations in six Drosophilid species and the Apollo annotation tool to refine these gene models. We found interesting trends in the gene structures of dicistronic genes across the species. For example, in some cases the Inter-Cistronic Region (ICR) region between the two ORFs reveals conservation across the species studied. We also observed decreases in ICR length with increasing evolutionary distance. To verify the presence and stability of monocistronic versus dicistronic transcripts *in vivo*, we are presently designing primers and will use quanitative PCR in several *Drosophilid* species. Future experiments will focus on employing RNA folding software (eg INFERNAL) to scan for potential IRES structures that can be tested *in vivo*. We conclude that comparative genomic annotation is a useful tool to dissect and elucidate the conserved regulatory and gene structure features of dicistronic genes.

Entry Number 5 GL-A

THE HISTONE H2A VARIANT HTAS-1 IS A SPERM-SPECIFIC FACTOR IMPORTANT

By: Colin Fitzpatrick
Cell and Molecular Biology
Faculty Advisor: Dr. Diana Chu

Abstract: Approximately half of all failed pregnancies are the result of male infertility. Those caused by sperm malfunction may stem from defects in the compaction of paternal DNA, which occurs uniquely during spermatogenesis. Our lab has identified a sperm-specific histone H2A variant, HTAS-1, which is 51% identical to canonical histone H2A in C. elegans. Because histones regulate DNA compaction and gene expression, we are characterizing how the HTAS-1 protein functions in these processes to affect male fertility.

HTAS-1 is a sperm-specific fertility factor. Immunolocalization of HTAS-1 revealed that HTAS-1 is localized proximally in gonads producing sperm, from pachytene through meiotic divisions to mature sperm. Our antibodies are specific for HTAS-1 as this pattern is absent in htas-1(tm1849) deletion mutants. Correspondingly, we find that HTAS-1 is important for fertility. Progeny counts comparing hermaphrodite htas-1(tm1849) and N2 worms found a reduction in brood size of the htas-1(tm1849) by approximately 25%. Comparison of progeny produced from htas-1(tm1849) and N2 males showed a 28.1% reduction, indicating that males are also sub-fertile.

To assess the basis of the infertility in htas-1(tm1849) we are assessing the consequence of loss of HTAS-1 on chromosome compaction and meiotic progression of male germ cells. To assess chromosome compaction, we compared germline nuclei of htas-1(tm1849) and wild type using DNA staining and fluorescence microscopy. Our initial results revealed no gross differences in overall chromosome compaction of mature sperm nuclei, suggesting the role of HTAS-1 is not solely to compact sperm DNA. We are currently trying to identify if there are more discrete areas of decondensation within nuclei of htas-1(tm1849) germlines.

Histones in other organisms can be post-translationally modified to function in progression of nuclei through sperm formation. Compared with canonical histone H2A, HTAS-1 has a longer N-terminal tail, which is rich in lysines and serines, implying potential regulation by post translational modifications (PTMs). We are using immunoprecipitation and mass spectrometric analysis to determine which residues of HTAS-1 are post translationally modified during spermatogenesis. In addition, we are assessing changes in PTMs that, occur throughout the male germline that, in combination with histone variants like HTAS-1, may be important for male fertility.

Entry Number 6 GL-A

SIMULATING DNA REPAIR MECHANISMS USING REACTION-DIFFUSION METHODS

By: Ari Akerstein, Ben Borgo, and Dr. Javier Arsuaga
Cell and Molecular Biology
Faculty Advisor: Dr. Javier Arsuaga

Abstract: The mechanisms by which DNA repair proteins are recruited to DNA double strand breaks (DSBs) remain mostly unknown. Recent Fluorescence Recovery After Photobleaching (FRAP) data has provided accurate measurements of a number of physical parameters related to the dynamics and the interactions between proteins of the RAD52 group homologous recombination proteins (Essers et al. 2002). Analysis of these data is not optimal and it frequently disregards the interactions of these proteins with the chromatin as well as mechanistic models that could account for these observations. Here we describe a new computational method that allows for the incorporation of chromatin structure as well as different mechanistic models of DNA recruitment and repair. Our method is based on a previously published extension of the Gillespie algorithm that includes reaction-diffusion in three-dimensional volumes (Bernstein 2005). Idealized nuclei are divided into microchambers where reaction-diffusion parameters are estimated locally.

Entry Number 7 GL-A

DETERMINING THE PHYSICAL INTERACTIONS BETWEEN FISSION YEAST Cdc24 AND FLAP ENDONUCLEASE Rad2

By: Garima Porwal
Cell and Molecular Biology
Faculty Advisor: Dr. Sally G. Pasion

Abstract: The novel fission yeast replication gene, cdc24 is essential for maintaining genomic stability in fission yeast cells. Cdc24 protein may play a role in lagging strand DNA synthesis based upon the reported genetic and physical interactions with other conserved DNA replication proteins. These conserved replication components have been reported to be associated with diseases in humans which occur due to genomic instability. Their is a genetic interaction between Rad2 and Cdc24. Rad2 is a multicopy supressor of Cdc24 temperature sensitivity. When combined with Cdc24 mutants Rad2 also exhibits synthetic growth defect. Moreover, physical interactions between Cdc24 and three multicopy supressors rfc1, pcn1 and dna2 have been reported in other systems. It is also absolutely established that rad2 directly interacts with pcn1. This led to my hypothesis that Rad2 directly interacts with Cdc24. If I find a physical interaction between Cdc24 and Rad2 then I can define the role played by Cdc24 in lagging strand synthesis.

Entry Number 8 GL-A

CONSTRUCTION OF Cdc24-GFP FUSION PROTEIN AND DETECTION OF ITS BIOLOGICAL ACTIVITY IN SCHIZOSACCHAROMYCES POMBE

By: Noel Cruz
Cell and Molecular Biology
Faculty Advisor: Dr. Sally G. Pasion

Abstract: Background: Cdc24 is an S-phase protein required for viability in the fission yeast *Schizosaccharomyces pombe*. The protein has no sequence homologs in other organisms, however it interacts physically and genetically with lagging strand replication proteins. It has been implicated in Okazaki fragment processing, but its precise role is still unclear. Cdc24 mutants - *cdc24-M38* and *cdc24-G1*- as well as the conserved replication proteins DNA ligase and Dna2 helicase undergo chromosome breakage in fission yeast cells. This failure in genome integrity can be indicative of a genetic interaction between Cdc24p and proteins involved in the checkpoint response pathway. Cds1 is a protein kinase that works in the in fission yeast checkpoint response pathway. The goal of this study is to demonstrate a physical interaction between and Cdc24 and Cds1 proteins. This research project will provide further evidence of Cdc24p involvement in the DNA replication process in fission yeast and will help define the role of Cdc24 in preserving genome integrity.

Method: A 1.5kb *cdc24*$^{+}$ cDNA fragment was ligated into a fission yeast vector containing a GFP (Green Fluorescent Protein) cassette with unique restriction enzyme sites to fuse the GFP gene to the C-terminus of the Cdc24 protein. The Cdc24 protein is essential for cell viability thus *S. pombe cdc24* mutants do not grow at 37^{o}C. Therefore, to test for the functionality of the Cdc24-GFP construct I transformed *cdc24-M38* temperature sensitive mutants with the plasmid carrying the construct and screened for the suppression of the temperature-sensitive phenotype.

Results: An analysis of a restriction digest in a gel electrophoresis demonstrated that the *cdc24*$^{+}$ cDNA fragment was correctly oriented in the GFP cassette to be tagged at its C-terminus with GFP. In addition, preliminary data shows transformed mutant cells growing at 37^{o}C, which is proof that Cdc24-GFP is functional. Visualization of the cells using fluorescence microscopy showed the expression of GFP, which was negative in a control containing an empty vector.

Conclusions: The *cdc24*$^{+}$ cDNA was successfully cloned into the pSGP572a plasmid and the tagged protein is functional. The recombinant plasmid, pNC1, will be sequenced to confirm the absence of mutations. Further experiments include the immunoblotting of Cdc24-GFP with anti-GFP antibodies, determining Cdc24 localization during the cell cycle, and the use of immunoassays to study the interaction between Cdc24-GFP and Cds1-HA tagged proteins.

Entry Number 9 GL-A

HOW DO HIGH SCHOOL STUDENTS AND BIOLOGY TEACHERS THINK WE LEARN? UNDERSTANDING NOVICES' VS. EXPERTS' CONCEPTIONS ABOUT THE BIOLOGICAL BASIS OF LEARNING

By: Rebecca Fulop and Dr. Kimberly D. Tanner
Cell and Molecular Biology
Faculty Advisor: Dr. Kimberly D. Tanner

Abstract: : Neuroscience is one of the most rapidly advancing fields in science. But how much knowledge does the general public have about these advances? This is one of the first studies attempting to understand how people conceptualize learning and the brain, even though teachers attempt to change students' minds every day! In this study we begin by investigating the conceptions of high school students (novices) – around the biological basis of learning and memory. Next we examine a likely origin of many student conceptions – those held by high school biology teachers. Finally, we compare students' and teachers' ideas with those of neuroscientists (experts).

Entry Number 10 GL-A

LOSS OF SPß IN A *sigY* MUTANT OF *BACILLUS SUBTILIS*

By: Alba A. Gutierrez
Cell and Molecular Biology
Faculty Advisor: Dr. Leticia Marquez-Magaña

Abstract: SigY is an alternate sigma factor in Bacillus subtilis that belongs to the extracytoplasmic function (ECF) family of sigmas responsible for monitoring external stress and controlling the expression of gene products required for adaptation to the stressor. We have demonstrated in our laboratory than when the sigY gene is disrupted the sunA and sunT within the Sp rophage are lost. These genes encode for an antibiotic called sublancin and its transporter (Paik et al., 1998). We predict that SigY normally controls sublancin production, and that loss of sigY leads to loss of these genes by an unknown mechanism. However, it is not known if other genes found on Sp re also lost, and if SigY plays a role in maintaining all or part of the phage genome within the B. subtilis chromosome. Therefore, we sought to determine if only certain genes are absent or if the whole Sp rophage is missing in a B. subtilis strain that bears a sigY null mutation (and where the sunA-T genes are known to be missing). Primers for the blyA, yomJ, yonD, yonK, mtbP and yopC genes that reside within Sp ere designed and polymerase chain reaction (PCR) was used to determine their presence or absence in the sigY null mutant.. Our results show that, in addition to sunA and sunT, the blyA, yomJ, yonK, mtbP and yopC genes are not present in this strain. In future work, we plan to determine if the Sp rophage is induced by loss of sigY resulting in the production of phage particles that contain the circularized Sp enome. To test for the presence of circularized phage DNA in the supernatant we have obtained PCR primers that detect the circular phage DNA. This work contributes to our overall goal of characterizing the SigY-dependent mechanism that governs Sp rophage maintenance in the B. subtilis genome as a function of external signals from the environment.

Entry Number 11 GL-A

A BAYESIAN STATISTICAL APPROACH TO MODELING GENE REGULATORY PATHWAYS IN MICROARRAY DATA

By: Elinor Velasquez
Cell and Molecular Biology
Faculty Advisor: Dr. Leticia Marquez-Magaña

Abstract: The goal of this study was to determine the gene regulatory pathways in the healthy human placenta. This study focussed on creating a Bayesian network to find the pathways and used a machine learning methodology. This study showed that it is possible to model via in-silico the gene regulatory pathways for 500 genes associated with the human placenta.

Entry Number 12 GL-A

IDENTIFYING POSITIVE AND NEGATIVE REGULATORS OF THE *sigY* OPERON IN *BACILLUS SUBTILIS* BY QUANTIFYING *sigY* EXPRESSION DURING NUTRIENT RICH AND NUTRIENT POOR CONDITIONS

By: Jasmin-Ann Reyes
Cell and Molecular Biology
Faculty Advisor: Dr. Leticia Marquez-Magaña

Abstract: Bacterial cannibalism ensures a starving bacterial population's survival during nutrient deprivation. Cells kill their neighbors, consuming them as nutrients in order to avoid sporulation, an energetically unfavorable process. They do so by producing a killing factor and its respective export pump. This genetically regulated phenomenon occurs in *Bacillus subtilis*. sigY is an extracytoplasmic (ECF) function sigma factor necessary for transcription initiation. It transcribes genes necessary for regulating a response to outside stress. A hallmark characteristic of ECF sigmas is that they too are also regulated – by repressor proteins encoded in their respective operons. The concrete physiological function of sigY is not yet known. We predict that sigY transcribes not only proteins that provide ECF regulation, but also proteins that encode the cannibalistic response during starvation. We hypothesize that in nutrient deprived conditions, putative repressors YxlD and YxlE release their inhibitory effect on SigY, thereby allowing transcription of proteins needed for the cannibalistic response. To look at sigY regulation, temporal sigY mRNA expression levels will be determined in a growing culture of gene deletion mutant strains of the sigY operon. This will be compared to the expression levels found in the wild type strain. RNA will be isolated at different time-points and QPCR will be used to quantify sigY expression. In the wild type strain, we expect low levels of sigY expression at when nutrients are rich, and high levels of sigY expression when nutrients are limiting. For mutant strains that have the putative repressor genes (yxlD and yxlE) knocked out, we expect a slight opposite. Instead there will be high levels of sigY expression when nutrients are limiting. Data generated from this project will provide the missing link between a physiological response against starvation and genetic ECF regulation. This study will uncover the molecular mechanism of a SigY regulated cannibalistic response. Being novel on two accords, this study will provide evidence of a bifunctional role for the sigY operon – a duality that is atypical of ECF operons. It will also provide evidence for bacterial cannibalism – a recent concept that supports the new perception of bacterial populations as multicellular organisms rather than simple masses of clonal cells.

Entry Number 13 GL-A

microRNA EXPRESSION PROFILING IN 40 BREAST CANCER CELL LINES

By: Molly Klein-McDowell, Graeme Hodgson (UCSF),
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Cell and Molecular Biology
Faculty Advisor: Dr. Leticia Marquez-Magaña

Abstract: The aims of this research were to determine if microRNA (miRNA) expression correlates with specific breast cancer subtypes, and to investigate possible roles of miRNAs in the development and progression of breast cancer. miRNAs are small, natural, genetic regulatory elements that control several cellular functions including development, cell fate, cell death, and proliferation. We profiled the expression of ~500 miRNAs in 40 breast cancer cell lines using microarray and qRT-PCR technology. We have determined that miRNA expression correlates with distinct subtypes of breast cancer, Luminal, Basal A, and Basal B. Furthermore, we have identified several miRNAs that serve as genetic markers for these breast cancer subtypes. Thus, miRNA expression profiling in breast cancer may yield novel methods, oncogenes, and/or tumor suppressor genes that can be exploited for more successful diagnosis and treatment of breast cancer.

Entry Number 14 GL-A

TRANSCRIPTIONAL REPRESSOR ATF3 BINDS TO THE IFN-b PROMOTER IN MACROPHAGES

By: Roberto M. Barrozo
Cell and Molecular Biology
Faculty Advisor: Dr. Steve Weinstein

Abstract: Transcriptional Repressor ATF3 Binds to the IFN-β Promoter in Macrophages

The cytokine Interferon-beta (IFN-β) promotes beneficial immune responses to infection and exacerbates or prevents adverse immune responses that contribute to autoimmunity and allergy. Macrophages are a major source of IFN-β production. Under stress-free conditions, macrophages secrete low to undetectable levels of IFN-β. However, following exposure to stimuli associated with microbial infection, macrophages rapidly increase transcription of this cytokine. Recently our lab found that macrophages deficient in the transcriptional regulatory protein, Activating Transcription Factor 3 (ATF3), produce significantly higher amounts of IFN-β mRNA than wild type macrophages, suggesting that ATF3 is a transcriptional repressor of the IFN-β gene. To determine whether ATF3-mediated repression of IFN-β occurs via direct interaction between ATF3 and the IFN-β promoter, chromatin immunoprecipitation (ChIP) assays were performed. ChIP results indicate that ATF3 is not bound to the IFN-β promoter in unstimulated macrophages, but it is bound in macrophages stimulated with the bacterial membrane component lipopolysaccharide (LPS). Preliminary kinetic experiments indicate that ATF3 is recruited to the IFN-β promoter within 2-3 hours of LPS exposure. These data are the first indication that ATF3 binds to the IFN-β promoter in macrophages in an inducible manner and they are fully consistent with the model that ATF3 mediates negative feedback regulation of IFN-ß transcription. Presumably, this mechanism would function to limit IFN-β production, thereby preventing host pathology associated with prolonged or excessive levels of this cytokine.

Entry Number 15 GL-A

ANTIMICROBIAL RESISTANCE AND PULSED-FIELD GEL ELECTROPHORESIS OF OUTBREAK-ASSOCIATED SALMONELLA BRANDENBURG AND SAINTPAUL ISOLATES

By: Ashley Ungermann, Kit-Man Yeung, Dr. Woutrina Miller (UCD), Dr. Sally Pasion, and Dr. Lily Chen
Biomedical Laboratory Science
Faculty Advisor: Dr. Lily Chen

Abstract: Non-typhoidal *Salmonellae* species are among the most common microorganisms implicated in food borne gastroenteritis in the United States. An outbreak of rare *Salmonella* serotypes Brandenburg and Saintpaul occurred concurrently in June 2005 within Monterey County, CA. The aim of this project is to perform biochemical and molecular characterizations on isolates involved in the two outbreaks in order to observe and analyze outbreak strains, antimicrobial resistance phenotypes, and indicate the possible presence of a specific antimicrobial resistance island among the different isolates involved.

Pulsed field gel electrophoresis will be used on outbreak isolates to characterize the strains and indicate whether one or more strains were involved. Antimicrobial resistance testing will also be performed on these isolates for the purpose of identifying resistance profiles for further comparison with PFGE profiles. A single *Salmonella* strain is expected to be the cause of each outbreak. Additionally, a single antimicrobial resistance profile is expected to be associated with each strain. Information about these strains will prove useful in case of future outbreaks, particularly for supervisory groups such as FoodNet, PulseNet, and the Monterey County health department, which monitor fluctuations of food borne pathogenic bacterial strains over time using epidemiological and molecular characterization methods.

Prevalence of *Salmonella* strains exhibiting antimicrobial resistance is continually rising; one strain of particular interest is the multi-drug resistant Defintive Type 104 (DT104). Often found associated with Typhimurium serotype, this isolatessusceptibility profile is characterized by resistance to five major groups of antibiotics: ampicillin, chloramphenicol, streptomycin, sulfonamides, and tetracyclines. Although evidence indicates close association with DT104 integration and the Typhimurium serotype, serotypes such as Agona or Albany have been found, though somewhat less frequently, to contain DT104 integrations. This is cause for concern, particularly in cases where *Salmonella* infection spreads beyond the gastrointestinal tract and becomes systemic.

Polymerase chain amplification will be used on isolates which exhibit characteristic resistance pattern stated previously. Integrated DT104 DNA will be detected with custom primers (Invitrogen) specific for the integrated 5 and 3 ends of the integron. PCR amplification will also be used to confirm the presence the multi-drug resistant region within the integron itself.

Entry Number 16 GL-A

IDENTIFICATION AND FUNCTIONAL ANALYSIS OF PROTEINS THAT INTERACT WITH RUS1-MEDIATED SIGNALING PATHWAY

By: Benjamin Onyeagucha
Cell and Molecular Biology
Faculty Advisor: Dr. Zheng Hui-He

Abstract:

Entry Number 17 GL-A

THE HUNT FOR RUS SUPPRESSORS

By: Amy M. Shelton
Cell and Molecular Biology
Faculty Advisor: Dr. Zheng-Hui He

Abstract: The light environment is a key factor that affects the biochemical pathways initiated during photomorphogenesis. An *Arabidopsis thaliana* mutant that is hypersensitive to UV-B light, named *rus*, exhibits a retarded growth phenotype when exposed to very low fluence (VLF) UV-B light during early seedling development. A suppressor screening identified a total of 75 plants with secondary mutations that suppress the *rus* phenotye. Subsequent gene mapping revealed that mutation of specific aspartate and alaninine aminotransferases individually will rescue *rus*-mutated plants, resulting in normal development that simulates the wild-type phenotype. From this finding we propose a model that attributes the onset of photomorphogenesis to the nitrogen/carbon balance in the plants.

Entry Number 18 GL-A

EXAMINING THE REGULATION OF PLANT MINERAL RESPONSES USING COMPUTATIONAL AND MOLECULAR METHODS

By: Tobias Sayre
Cell and Molecular Biology
Faculty Advisor: Dr. Zheng-Hui He

Abstract: Understanding how plants respond to their environment is an important part of biology. In the model organism *Arabidopsis thaliana*, the gene wakl4 is believed to play a role in maintaining mineral levels, and this research will identify and characterize the sequence motifs that are responsible for regulating this gene. Additionally, further understanding of regulatory sequence motifs in plants such as rice and other food crops would be useful. Applications for this research could include designing lines of plants with high tolerance to toxic levels of minerals for bioremediation of industrial waste areas. It could also enable the creation of cereal crops with enriched levels of minerals, to be grown in parts of the world where mineral-deficiency is a health problem.

Entry Number 19 GL-A

SPHINGOMYELIN LIPID ABUNDANT IN ECTODERM, ENDODERM AND ENDOTHELIAL CELL LAYERS RESULT IN A LOSS OF MYOTOMAL FIBERS IN SOMITE WITH ECTODERM SPHINGOMYELINASE TREATMENT IN THE 2.5 DAY-OLD CHICKEN EMBRYO

By: Christina Staubus
Cell and Molecular Biology
Faculty Advisor: Dr. Wilfred Denetclaw

Abstract: Sphingomyelin (SM) is a major lipid that makes up approximately 20% of the lipid species present in the plasma membrane, is a precursor for several lipid second messenger molecules and functions as a physical barrier in epithelial cells. In the chicken embryo, membrane rafts are abundant in the epithelial cell layers of ectoderm and somite dermomyotome and they are membrane platforms, enriched with sphingomyelin and cholesterol that have numerous functional roles in the cell including signal transduction. Therefore, we hypothesize that alterations in sphingomyelin abundance will affect embryo development. To investigate, we treated the ectoderm of 2.5 day-old chicken embryos with acidic sphingomyelinase (SMase) for 6 hours followed by a wash and 15 hours of recovery. Lysenin sphingomyelin probe was use to determine sphingomyelin presence in embryo and somite tissues. Our results show sphingomyelin is highly abundant in the ectoderm and endoderm layers and in the developing dorsal aorta. However, the neural tube and somites (dermomyotome, sclerotome) show low amounts of sphingomyelin. Ectoderm treatments with SMase also caused both partial loss and complete loss of myotome formation in somites. Furthermore, no abnormalities in somite formation or growth were found to indicate a non-specific action by SMase treatment. In conclusion, ectoderm signaling via sphingomyelin in membrane rafts or through its signaling lipid derivatives regulates early embryonic myogenesis.

Entry Number 20 GL-A

FORCED DIFFERENTIATION OF SKELETAL MUSCLE CELL CULTURES WITH DISRUPTED MEMBRANE RAFTS SHOW MYOSIN HEAVY CHAIN EXPRESSION AND MYOTUBE FORMATION

By: Jung Lim and Philipp Walczak
Pre-Med and Chemistry
Faculty Advisor: Dr. Wilfred Denetclaw

Abstract: Skeletal muscle development in culture is characterized by myoblast proliferation, migration, alignment and cell fusion for myotube formation all under genetic differentiation control. Our previous studies show that membrane rafts in the plasma membrane are regulators of muscle differentiation, but it is not understood how they regulate myoblast differentiation and cell fusion. To investigate membrane rafts for their role in muscle differentiation, we used primary breast muscle cell cultures, prepared from 11 day-old chicken embryos and treated with MBC, a membrane raft disrupting reagent. MBC cultures were then treated with reagents affecting the MAPK or nitric oxide signalling pathways to assess their effects on inducing muscle differentiation as shown by immunofluorescence, myotube formation, and western blotting for myosin heavy chain expression. MBC cultures show very low expression of MHC and almost no myotube formation over a 72 hour period of diffentiation. In contrast, normal culture (without MBC) show progressive and extensive myotube development and increasing MHC expression. MBC cultures treated with U0126 (a MAPK signalling inhibitor) showed almost normal myotube formation and MHC expression. In contrasts, MBC cultures with DETA-NO (nitric oxide donor) show extensive cell death by 24 hours after treatment and total loss of cells by 48 hours. Muscle cultures in L-NAME (a nitric oxide synthase inhibitor) showed only MHC expression but reduced myotube formation. We conclude that membrane raft disruption does not block the ability of myoblast to fuse in spite of its inhibitory effect on muscle protein differentiation. Therefore, it may be possible to investigate separable events on cell fusion regulated by nitric oxide and muscle differentiation regulated by MAPK signalling.

Entry Number 21 GL-A

THE EFFECTS OF DISRUPTION OF ECTODERM LIPID RAFT SIGNALING ON MYOGENIC STEM CELL BEHAVIOR

By: Matthew Smith
Cell and Molecular Biology
Faculty Advisor: Dr. Wilfred Denetclaw

Abstract:

Entry Number 22 GL-A

PHENOTYPE MICROARRAY OF SINORHIZOBIUM MELILOTI

By: Maisha Haywood-Smith, Janett Ortiz,
and Dr. Joseph C. Chen
Microbiology
Faculty Advisor: Dr. Joseph C. Chen

Abstract: Caulobacter crescentus is a Gram-negative bacterium that serves as an excellent model organism for investigating bacterial physiology. Studies of this microbe have revealed that it has the ability to metabolize lactose as a carbon source, although it is highly unusual to find lactose in the fresh water environments that Caulobacter cells inhabit. Mutant screens and subsequent analysis have led to the identification of the gene responsible for lactose metabolism. Characterization of strains with null mutations in the lac gene suggests that the gene is required for the utilization of several other carbon sources in addition to lactose. The significance of this research is that it can eventually help identify the metabolic pathways involving this gene. Ultimately, cell metabolism affects where the bacteria are able to grow and replicate.

Sinorhizobium meliloti is another model organism that is closely related to Caulobacter. Although it is a soil microorganism, it also has the ability to metabolize lactose. A homolog of the Caulobacter lac gene was identified in S. meliloti by examining the genome and sequence alignment. Understanding of the lac genes function can be improved by looking at the homolog. My current project is investigating whether the homolog of the lac gene, SMc-04392, plays a similar role in S. meliloti. Our research in Caulobacter suggests that this homolog may have a significant role in the metabolism of other nutrient sources, since we found that disruption of the SMc-04392 gene in S. meliloti does not affect utilization of lactose. To determine this, a mutant strain of S. rhizobium with a disruption in the SMc-04392 gene will be compared to the wild-type.

An effective method of identifying metabolic differences in bacteria is through the use of Biologs phenotype microarray plates. Biolog, Inc., developed microarray plates that allow for efficient testing of phenotypic differences by looking at hundreds of nutrient sources simultaneously 1. Each phenotype microarray (PM) plate contains 95 different nutrient sources, with each plate specialized for a category of nutrients. For this study, five different phenotype microarray plates per strain will be inoculated. PM1 and PM2 have carbon sources, PM3 has nitrogen sources, PM4 has phosphorous and sulfur sources, PM5 has a carbon source with nutrient supplements such as various amino acids. Following PM inoculations, plate readings will be taken using a 96-well plate reader to assess growth. The results will help determine differences in utilization of these nutrients between the mutant and wild-type strains. Finally, metabolic differences identified will be confirmed by constructing a strain with a complete deletion of the SMc-04392 gene and testing its growth on individual carbon sources.

Entry Number 23 GL-A

THE IMPACT OF BIOFILM FORMATION ON ANTIMICROBIAL RESISTANCE OF PSEUDOMONAS AERUGINOSA ISOLATED FROM AIRWAYS OF NEWLY VENTILATED AND CYSTIC FIBROSIS PATIENTS

By: Juliana Lima
Microbiology
Faculty Advisor: Dr. Susan Lynch (UCSF) and Dr. Frank Bayliss

Abstract:

Entry Number 24 GL-B

USING SPIDERS AS BIOINDICATORS TO ASSESS SUCCESS OF RESTORATION PROJECTS

By: Pedro Morgado, Theresa Shelton, and Misha Leong
Conservation Biology
Faculty Advisor: Dr. John Hafernik

Abstract: Land management and restoration project success is often assessed solely through analysis of vegetation growth. While vegetation characterization alone is informative, it does not fully assess the ecological success and sustainability of a site. Incorporation of faunal patterns improves evaluation of the success of land management and restoration projects. Spiders are important predators whose species richness and abundance are tied to a variety of biotic factors. They are widespread and have diverse life histories making spider sampling feasible for a broad range of habitats. In this study, we investigate how restoration efforts and habitat characteristics affect and shape spider community composition and diversity. We sampled spiders in 13 sites within the Presidio National Park, San Francisco, encompassing various habitats found in the park. Habitats sampled included, riparian oak woodlands, coastal scrub, serpentine grasslands and sand dunes. We sampled bimonthly from February 2007 through April 2008 using pitfall traps, sweeping, beating and hand collecting techniques. Each site was characterized in terms of plant species richness, percent cover and frequency. Additional habitat features measured were shrub canopy cover, sub-shrub canopy cover, ground cover height, and percent cover of debris and litter. Spider distributions and species richness patterns were compared to restoration history and habitat vegetation to determine what features enhance spider diversity and richness. Such information should prove useful to future restoration plans or land management strategies designed to promote diverse animal and plant communities.

Entry Number 25 GL-B

AN ASSESSMENT OF WATERSHED HEALTH IN
THE PRESIDIO OF SAN FRANCISCO USING AQUATIC MACROINVERTEBRATE COMMUNITIES

By: Theresa Shelton
Conservation Biology
Faculty Advisor: Dr. John Hafernik

Abstract: Freshwater streams support a diversity of aquatic and terrestrial plants and animals. They are a habitat for numerous organisms as well as a transportation route between wetland areas for water, chemicals, minerals and propagules. Conservation and protection of freshwater stream habitats is critical not only for natural habitats, but because of the many services they provide, including washing out pollutants from the ground, recreation, and both agricultural and drinking water. My study provides an assessment of habitat health at four streams sites within the Presidio of San Francisco, a national park in San Francisco, California, through an analysis of the communities of benthic macroinvertebrates collected during summer 2007, autumn 2007 and spring 2008. Diversity among the sites was compared with measurements of richness, evenness, abundance, % EPT taxa, % of functional groups and the Family Biotic index. The results of two sites are compared with data collected nine years ago to uncover differences in invertebrate community composition after various types of site management. My research also evaluates the success of the restoration in 2005 of one of the four sites through a comparison among invertebrate assemblages at the restored site, a site of the same watershed further upstream, and a site with minimal degradation. The results of this study provide guidance to ecologists and wildlife managers within the Presidio to maintain and improve aquatic habitats and can be applied to management of other small urban watersheds.

Entry Number 26 GL-B

URBAN IMPACT ON SPIDER COMMUNITIES IN
THE SAN FRANCISCO PRESIDIO

By: Misha Leong, Pedro Morgado, and Theresa Shelton
Ecology and Systematic Biology
Faculty Advisor: Dr. John Hafernik

Abstract: Research on arthropods in urban environments (outside of pest control) is still in its early stages, and thus is mainly concerned with predicting abundances and distributions along rural to urban gradients. Spiders have the potential to be good indicator species due to their abundance and diversity. For this study, we examine how different urbanization factors affect spider communities on a micro-scale, specifically in ways that can be reasonably altered. Spiders were sampled at 13 sites within the Presidio of San Francisco representing the diversity of habitats and urban impact. Collecting was done bimonthly from February-December 2007 using pitfall trapping, tree beating, brush sweeping, and hand collecting. Habitats of the San Francisco Presidio include serpentine landscapes, coastal sand dunes, and oak woodlands. There is also variability in a number of urban variables (roads, buildings, created edges and isolation, human foot-traffic, proximity to the urban matrix, surface cover, land use history, etc) amongst the 13 sites. We compare effects of these variables to more natural variables such as habitat complexity, moisture, and lithology to analyze how these variables influence distribution of different spider groups such as natives vs. non-natives, large vs. small-bodied, location guilds, hunting-strategy guilds, and taxonomic families. We also show how sites are differentially affected over the course of a year. This project not only further contributes to what is known about urban ecology and spider ecology in general, but it generates practical information for park and city managers to promote arthropod conservation.

Entry Number 27 GL-B

EXPLORING UNDERGRADUATE STUDENT CONCEPTIONS OF ENVIRONMENTAL PROCESSES

By: Briana McCarthy and Dr. Kimberly D. Tanner
Ecology and Systematic Biology
Faculty Advisor: Dr. Kimberly D. Tanner

Abstract: We investigated the assumption in the science education research literature that biology and environmental studies majors graduate as experts in their fields. Through written assessments and videotaped interviews, we probed students' conceptions of environmental processes in order to identify potentially universal misconceptions and further investigate their origins. At the COSE showcase, we will share written and video data from responses to the challenge statements, "The greenhouse effect can be made smaller by planting trees" and "Holes in the ozone layer are made worse by the greenhouse effect."

Entry Number 28 GL-B

MATING SYSTEM CHARACTERIZATION OF
TWO POPULATIONS (ANNUAL AND PERENNIAL) OF
ZOSTERA MARINA IN SAN FRANCISCO BAY

By: Esa Crumb
Ecology and Systematic Biology
Faculty Advisor: Dr. Sarah Cohen

Abstract:

Entry Number 29 GL-B

INVESTIGATING BAY AREA FILIPINO'S KNOWLEDGE OF AND ATTITUDE TOWARD
ENVIRONMENTAL
CONSERVATION IN A MUSEUM SETTING AT
THE CALIFORNIA ACADEMY OF SCIENCES

By: Courtney L. Scott and Dr. Kimberly D. Tanner
Marine Biology
Faculty Advisors: Dr. Meg Burke (California Academy of Sciences) and Dr. Kimberly D. Tanner

Abstract: The public's knowledge and attitudes towards environmental conservation is not well understood. In addition, there are very few published studies that investigate the environmental attitudes and knowledge held by Filipino-Americans. My research will investigate how experiencing the new CAS Philippine Coral Reef Exhibit influences Bay Area Filipinos knowledge of and attitude toward environmental conservation. As a biology education research graduate student, I am working in collaboration with the SFSU SEPAL: The Science Education Partnership and Assessment Laboratory and the California Academy of Sciences (CAS). To conduct, this research, I will collect pre- and post-assessment responses from Bay Area Filipinos' before and immediately following their viewing of the exhibit. In addition, a subset of these subjects will be interviewed 3 months following their viewing experience to gauge their enduring impressions. This research has the potential to provide insight into the Bay Are Filipinos' understanding of environmental conservation and the impact of visiting the CAS Philippine Coral Reef Exhibit on these views. In addition, it will be one of a handful of studies that examines the impact of a museum exhibit on a population of Americans that are underrepresented in the sciences.

Entry Number 30 GL-B

AN INTRODUCED COPEPOD IN SF ESTUARY: GENETIC DIVERSITY IN A RECENT INVASION

By: Allegra Briggs, Dr. Sarah Cohen, and Dr. Wim Kimmerer
Marine Biology
Faculty Advisor: Dr. Wim Kimmerer

Abstract: The first recorded occurrence of the copepod *Tortanus dextrilobatus* in San Francisco Estuary was in 1993 and within a year the population had become abundant. It is thought that the copepod was introduced via the ballast water of cargo ships from South China and in this study we investigate whether there is genetic evidence for this hypothesis.

Besides the native region of southern China, *T. dextrilobatus* has been reported occurring in two other locations: San Francisco (SF) Estuary and Somjin River in South Korea. We collected samples from three estuaries: Somjin River, SF Estuary, and Jiulong River Estuary in southern China. A weakness of this study is that we were only able to get samples from one estuary in China.

We have sequenced 41, 14, and 16 individuals from the SF Estuary, South Korea, and China, respectively. We are currently preparing more DNA sequences from Asian samples. We used these sequences to construct maximum parsimony and neighbor-joining phylogenetic trees.

There are no shared haplotypes between the three populations. The average genetic distance between the SF population and China population is 4.2% whereas their within-population genetic distance is about 1.5%. The average distance between the SF population and Korea population is 4%. The two Asian populations cluster together with a bootstrap value of 92% and greater.

The SF population is characterized by little phylogenetic structure and a unimodal frequency distribution of pairwise genetic distance, i.e., mismatch distribution. This is consistent with a history of introduction followed by rapid expansion. The haplotype diversity and nucleotide diversity of the SF population are similar to the Chinese population, suggesting either multiple introductions or an introduction of many individuals from a single source population.

Entry Number 31 GL-B

FOODWEB SUPPORT FOR THE THREATENED DELTA SMELT: PHYTOPLANKTON PRODUCTION IN THE LOW SALINITY ZONE OF THE NORTHERN SAN FRANCISCO ESTUARY

By: Ulrika Lidstrom
Marine Biology
Faculty Advisor: Dr. Edward Carpenter

Abstract: The goal of this research wa to further understand an important foodweb component (primary production), in order to elucidate the causes of the decline of the threatened delta smelt and other organisms in norther San Francisco Estuary. Primary production, biomass and species composition of phytoplankton in the low salinity zone were studied during March-August 2006 and 2007.

Entry Number 34 GL-B

TEMPERATURE DETERMINES PLASTICITY IN GROWTH OF THE REEF-BUILDING CORAL, *PORITES LOBATA*

By: Tyler P. Waterson, Dr. Jonathon Stillman,
and Daniel Barshis (University of Hawai'i/HIMB)
Cell and Molecular Biology
Faculty Advisor: Dr. Jonathon Stillman

Abstract: In the back reef lagoons of Ofu, American Samoa, corals thrive in temperatures (up to 36^0C) higher than most corals can tolerate, and daily temperatures fluctuate 3-4^0C. A reciprocal transplant study showed that corals from both forereef (constant temperature) and back reef environments grow more quickly in the back reef lagoon, although native back reef corals grow more quickly in all environments relative to conspecifics from the forereef. Here we examined whether these growth differences were due to temperature or other environmental factors. We collected samples of *Porites lobata* from forereef and back reef sites, with n=5 colonies per site and 25-30 replicates per colony. We transported the corals to our laboratory in Tiburon, California at the Romberg Tiburon Center and split them between two tanks imitating either the forereef (29^0C) or back reef (fluctuating 27-32^0C). After one month, new vertical tissue extension was measured. Both back reef and forereef corals had significantly higher tissue extension rates in the fluctuating tank than the constant-temperature tank. In both tanks, back reef corals had significantly higher vertical extension rates than forereef corals. Our laboratory experiments yielded similar results to prior field experiments, suggesting that the major environmental factor influencing plasticity of growth rate is temperature. In future experiments, calcification and other growth factors should be considered to better characterize the physiological patterns observed. Supported by USGS BRD GCC program.

Entry Number 35 GL-B

HOW DOES CORBULA INFLUENCE THE NITROGEN REGIME OF SUISUN BAY?

By: Amy Kleckner and Dr. Frances Wilkerson
Marine Biology
Faculty Advisor: Dr. Frances Wilkerson

Abstract: There is an ongoing threat to the ecology of the San Francisco Estuary brought on by invasive species. One particular invasive species that has major impact on the estuary is the Asian clam *Corbula amurensis*. It was first discovered in <?xml:namespace prefix = st1 ns = "urn:schemas-microsoft-com:office:smarttags" />Suisun Bay in 1986 and has been generally accepted as the cause of a significant decline in phytoplankton biomass and related fish abundances. Invasive species are thought to impact ecosystems because of their effects on biological diversity, through competition with native species of similar ecological roles for resources and space; yet much less in known about the changes that they may cause to ecosystem nutrient dynamics. In parts of northern San Francisco Estuary, observed high densities of *Corbula* may influence the nutrient regime as a result of ammonium excretion. We have been exploring the role of *Corbula* in the remineralization of nitrogen through ammonium excretion. This novel impact of an invasive clam on the nutrient ecosystem may have management implications.

Entry Number 36 GL-B

ANOMALOUSLY LOW pCO2 MEASURED IN THE SAN FRANCISCO ESTUARY

By: Jim Fuller, Dr. Frances Wilkerson, Dr. Alex Parker, Dr. Richard Dugdale, and Al Marchi
Marine Biology
Faculty Advisor: Dr. Frances Wilkerson

Abstract: Increased atmospheric CO2 levels from anthropogenic emissions are expected to interact with the photosynthetic processes of phytoplankton. That is, algae living under enhanced CO2 levels will have reduced need for energy-demanding carbon concentrating mechanisms (presently used to provide saturation levels of CO2 in the chloroplast) and will devote more energy to growth and reproduction. The carbon chemistry of the southern embayment of the San Francisco Estuary (SFE) provides a population of algae that have adapted to a high pCO2 environment. Measured and calculated levels of pCO2 between 1976-1980 and more recently (2006-8) were found consistently between 600 and 1000 ppm. These levels are comparable to the IPCC (Intergovernmental Panel on Climate Change) projection for the year 2100 (750 ppm). Measurements of pCO2 in other estuaries show much more variation and significantly higher concentrations (>5000 ppm). It is believed that the stability of southern SFE is due to a regular and dominating input of high pCO2 treated waste-water and a consistently high natural alkalinity. The phytoplankton population offers a unique opportunity for evaluating the physiological effects of year 2100 levels of pCO2.

Entry Number 37 GL-B

AMMONIUM SURGE UPTAKE AND INHIBITION OF NITRATE UPTAKE BY SMALL AND LARGE CELL-SIZED PSEUDO-NITZSCHIA SPECIES FROM THE PACIFIC NORTHWEST

By: Regina L. Radan, Maureen E. Auro, and Dr. William P. Cochlan
Marine Biology
Faculty Advisor: Dr. William P. Cochlan

Abstract: Despite the importance of nitrogen in maintaining blooms of toxigenic diatoms and their production of the neurotoxic amino acid, domoic acid, the nitrogenous nutrition of Pseudo-nitzschia species is still poorly known, and is primarily limited to the larger cell-sized species. Quantification of the physiological capacity for nitrogen uptake by Pseudo-nitzschia species under both N-replete and N-deplete conditions is a necessary prerequisite for an understanding of the success of Pseudo-nitzschia relative to other phytoplankton in coastal systems, and may help to identify the proximate causes of toxin production by these diatoms. The nitrogen uptake capabilities of three Pseudo-nitzschia species, isolated from the Pacific Northwest and maintained in unialgal cultures, are presented here: the transient elevated 'surge' uptake rates of ammonium by P. cf. delicatissima and P. multiseries, the ammonium inhibition of nitrate uptake by P. cf. cuspidate, and the ammonium and urea inhibition of nitrate uptake by P. multiseries. Elevated ammonium uptake rates were determined in duplicate, N-starved cultures of the two species (cultures depleted of external nitrate for ~ 2 generations) by following the disappearance of ammonium from the medium at varying intervals (5-30 min) over a six-hour period. Both the large and small cell-sized species demonstrated a capacity for transient 'surge' uptake in the first minutes following ammonium enrichment, but P. cf. cuspidata exhibited faster initial rates than P. multiseries. However within 0.5-1.0 h, ammonium specific uptake rates decreased and stabilized to values sufficient to support the pre-conditioned growth rates observed for both species prior to N starvation. During multi-day experiments, duplicate nitrogen-replete cultures of P. cf. cuspidata demonstrated complete inhibition (suppression) of nitrate uptake by elevated ammonium concentrations. Similarly, duplicate nitrogen-replete cultures of P. multiseries revealed inhibition of nitrate uptake by elevated ammonium and urea concentrations. Only after the ammonium concentrations were decreased by the cells to below the 'threshold' concentration (< ~4-5 μM) did these diatoms begin their utilization of nitrate. These laboratory results will be discussed with respect to the relative surface area per unit cell volume of the large and small cell-sized species, and the possible ecological consequences of simultaneous uptake of nitrate and ammonium at the ambient N concentrations normally found in the coastal waters of the Pacific Northwest.

Entry Number 38 GL-B

BEHAVIOR OF THE SAN NICOLAS ISLAND FOX

By: Robyn Powers
Physiology and Behavior Biology
Faculty Advisors: Dr. Jan Randall and Dr. Chris Moffatt

Abstract: Home ranges and activity patterns of 18 San Nicolas Island foxes (*Urocyon littoralis dickeyi*) were examined in relation to the annual reproductive cycle. Home range sizes varied with reproductive status across reproductive phases (mating, post-mating, pupping, non-reproductive) and were largest during mating. Home range overlap varied by reproductive status and reproductive phase with the home ranges of mated pairs overlapping the most. Fox activity varied among daily periods with highest activity at night and lowest at sunrise. Space use and activity patterns of island foxes are consistent with a socially monogamous mating system.

Entry Number 39 GL-B

INHIBITION OF THE INFLAMMATORY CASCADE IN MICROGLIA PROTECTS NEURONS FROM CELL DEATH FOLLOWING IN VITRO STROKE MODEL TREATMENT

By: Carla M. Webster, Hualong Ma (UCSF-SFVAMC),
Rona G. Giffard (Stanford University),
and Midori A. Yenari (UCSF-SFVAMC)
Physiology and Behavior Biology
Faculty Advisor: Dr. Megumi Fuse

Abstract: Stroke is the 3rd leading cause of death in the United States, claiming 143,000 deaths per year (CDC, 2008). The acute inflammatory cascade in brain cells following stroke is thought to be a major contributor to its mortality and morbidity. It is hypothesized that the brain's resident macrophages, microglia, are detrimental to neighboring neurons once activated by the inflammatory stroke insult, thereby causing neuron cell death, decreased performance on behavioral tests, and possibly death to the patient. This research aims to identify whether microglia are protective or toxic to neurons *in vitro* following model stroke treatment, oxygen-glucose deprivation (OGD). We also aim to evaluate whether the addition of astrocytes, cells that provide structural and metabolic support to brain cells, enhances neuron cytotoxicity. To address the question of the role of inflammation in microglia on neuroprotection or cytotoxicity, we used "gene silencing" to knock down a nuclear transcription factor, nuclear factor kappa B (NF□B), in microglial cells (BV2s) and co-cultured these cells with either neurons, or neurons plus astrocytes. This nuclear transcription factor is activated by inflammatory insults, such as stroke, and results in increased transcription of numerous inflammatory cytokines and proteins as well as oxygen radicals, such as nitric oxide.

We found 1) astrocytes are required for neuron cell death following OGD and enhance neurotoxicity by microglia; microglia co-cultured with neurons alone are not sufficient to induce neuron cell death via our model. 2) When neurons plus astrocytes are co-cultured with the microglial cells lacking NF□B subunits (either p50 or p65), and exposed to OGD, the neurons are protected from cell death relative to control groups ($p<.05$, $n = 6$). Finally, we found 3) when neurons are co-cultured with microglial cells that have been treated with negative control scrambled short-interfering RNA (siRNA), they form clusters; however, when they are co-cultered with microglial cells treated with siRNA targeting NF□B to knock this protein down, they do not form these clusters, indicating a role for a neuron attractive chemokine or cell surface marker in the inflammatory cascade of microglia.

Entry Number 40 GL-B

MODELING OF INSECT ECDYSIS MOTOR PATTERNS: ANALYSIS OF A COMPLEX BEHAVIOR VIA VIDEO-TRACKING AND ELECTROPHYSIOLOGICAL RECORDING

By: Ian Kimball

Physiology and Behavior Biology

Faculty Advisor: Dr. Megumi Fuse

Abstract: Insect ecdysis has long been used as a model of complex behavior due to its highly stereotyped motor patterns and underlying neuroendocrine activation. The relatively large nervous system of the hawkmoth, *Manduca sexta* has made its larvae (commonly known as the tobacco hornworm) particularly useful in the study of neurosecretory cell networks implicit in the generation and regulation of the ecdysis behavior. Several peptides can be injected to induce precocious ecdysis to aid this study. Recent work in the field has called some previous assertions into question and added further complexity to the model of peptide roles and hierarchies in ecdysis induction. With the development of robust video-tracking software for biological studies, it is now possible to analyze motor patterns of the ecdysis behavior during the naturally occurring behavior and the behaviors induced precociously via injection of exogenous neuropeptides. Early comparisons have shown that *in vitro* motor neuron burst frequencies occur approximately half as often as *in vivo* muscle contractions. The current study aims to further explore this relationship and develop a working model of the underlying neural network controlling contractions. We have assessed the contraction patterns of various ecdysing animals over the entire period of the behavior, using *in vivo* video-tracking and compared these to the motor neuron burst frequencies.

Entry Number 41 GL-B

DEVELOPMENT OF FLUORESCENT PEPTIDOMIMETIC INHIBITORS AS POTENTIAL IMAGING AGENTS FOR PROSTATE-SPECIFIC MEMBRANE ANTIGEN

By: Steven Ho and Marat Kazak

Biochemistry

Faculty Advisors: Dr. Clifford Berkman and Dr. Marc O. Anderson

Abstract: The objective of the project is to development fluorescent peptidomimetic inhibitors and evaluate their affinity potencies and biochemical applications as potential imaging agents for prostate-specific membrane antigen. Two fluorescent peptidomimetic inhibitors has been synthesized and screened for their inhibitory
potencies. A study of cell-surface labeling via fluorescent microscopy is currently in progress.

Entry Number 42 GL-B

SYNTHESIS OF NDGA ANALOGUES FOR INHIBITION STUDIES AGAINST TUMOR GROWTH

By: Johnny Pham and Yumi Watanabe

Chemistry

Faculty Advisor: Dr. Marc O. Anderson

Abstract: Nordihydroguaiaretic acid (NDGA) has been shown to exhibit anticancer properties in beast cancer cell lines. Thus, it is imperative to synthesize various analogues for potential use as therapeutic agents against tumor growth. This study aims to create a faster approach to developing a large library of NDGA derivatives by utilizing compounds as building blocks bound to a dichlorotrityl resin in a solid-state method.

Entry Number 43 GL-B

IDENTIFYING CELL SURFACE GLYCOPROTEINS USING HYDRAZIDE CHEMISTRY IN COMBINATION WITH 2D-LC/ESI-MS/MS

By: Claudia Alejandra McDonald and Jane Yang
Biochemistry
Faculty Advisors: Dr. Bruce A. Macher and Dr. Ten-Yang Robert Yen

Abstract: Introduction Cell surface proteins are important therapeutic targets and have been exploited for targeted treatment in several diseases including cancer. Thus, identification of cell surface proteins as therapeutic targets has been a prime area of interest in the proteomics field. However, technical difficulties have hampered efforts to effectively isolate and identify cell surface proteins. Many cell surface proteins are known to be glycosylated. Therefore, a strategy integrating periodate oxidation and hydrazide resin coupling into a proteomics approach for the identification of cell surface proteins would seem to have merit. In this study, we oxidized the carbohydrates on cell surface membrane glycoproteins with periodate, and enriched them via coupling to hydrazide resin, followed by identification of trypsin-released peptides and PNGaseF released, N-linked glycopeptides using 2D-LC/ESI-MS/MS (MudPIT).

Methods HeLa cells were grown in culture, oxidized with periodate, lysed using a Tris buffered saline lysis solution containing a non-ionic detergent and protease inhibitors. The cells were scraped from the plates using a rubber policeman. The lysate was applied to the hydrazide column to isolate glycoproteins, and a series of washes were used to eliminate non-specifically bound proteins. Proteins retained on the hydrazide column were digested with trypsin and the tryptic peptides collected. The glycopeptides bound to the hydrazide column were released using PNGaseF and this fraction was collected. Fractions contained tryptic peptides and PNGaseF released glycopeptides were analyzed by MudPIT. The proteins were identified by Sequest and MASCOT programs.

Preliminary Results In the development of this methodology, we observed that identification of both the tryptic digestion products and the PNGaseF released glycoproteins increased the number of glycoproteins detected by MS analysis. Our initial results demonstrate that the periodate/hydrazide column protocol efficiently enriches cell surface membrane proteins from cultured cells. The composition of the peptides released from the hydrazide column by trypsin demonstrated that the column washing steps effectively separated cell surface membrane glycoproteins from other cellular proteins present in the total cell lysate. Information on the sites of N-linked glycosylation was obtained from the peptides released from the hydrazide column by PNGaseF. Protein database searching programs incorporated into the proteomics approach provide information on cellular location of the identified proteins. The incorporation of a multidimensional liquid chromatography further improved the sensitivity and selectivity of the method. The application of the optimized protocol will be presented. In addition, the results obtained from the periodate/hydrazide column protocol will be compared to those obtained using lectin chromatography.

Entry Number 44 GL-B

INVESTIGATING THE BINDING MECHANISM OF OXIDIZED FAD TO SMOA

By: Michelle Beaton

Biochemistry

Faculty Advisor: Dr. George Gassner

Abstract: Styrene is an organic compound that can undergo polymerization to form polystyrene, which then is used in rubber, plastic, insulation, fiberglass, pipes, automobile parts, and food containers. Although polystyrene has many beneficial commercial uses, its monomer styrene has been classified as a possible human carcinogen. Several microorganisms are capable of initiating styrene degradation.This research focuses on the first reaction in the styrene-degradation pathway of Pseudomonas putida S-12 which is catalyzed by styrene monooxygenase (SMO). SMO is a flavoenzyme that contains two components: SMOB, a NADH-specific flavin reductase, and SMOA, a FAD-specific styrene epoxidase. SMOA receives its reduced FAD from SMOB via a complex that forms during the catalysis of the enzyme. The goal of this research is to further understand the mechanism by which oxidized FAD binds N-SMOA through the use of fluorescence spectrosopy.

Entry Number 45 GL-B

THE CONFORMATIONAL CHANGES IN THE ACTIVATION OF SOLUBLE GUANYLATE CYCLASE

By: Jasmin Kristianto, Kensuke Yamamoto, and Thieu Bleu

Biochemistry

Faculty Advisor: Dr. Nancy Gerber

Abstract: Soluble Guanylate Cyclase (sGC) is the principal receptor of Nitric Oxide (NO) in which its activity increases up to 400 fold upon NO binding. Although the structure of sGC has not been elucidated, it is known to be a heme containing heterodimer with alpha and beta subunits. Its primary function is to catalyze the formation of cGMP, a second messenger responsible in regulating cGMP dependent protein kinases, ion-gated channels, and phosphodiasterases, from GTP. sGC also holds many important physiological functions including vasodilation, smooth muscle relaxation, and platelet aggregation. Hence, sGC becomes an excellent therapeutic agent for cardiovascular diseases and vasodilations. Carbon monoxide has also been implicated as a signaling molecule acting through sGC, although it appears to require the presence of an allosteric effector to achieve full activation. Our experimental objective is to probe the different conformational complexes of sGC upon activation with NO versus CO/YC1 via fluorescence spectroscopy. Recent studies have shown that sGC/NO and sGC/CO complexes form a 5-coordinate and 6- coordinate structure respectively. However, the lack of understanding of the binding regions may pose an issue in determining the allosteric regulation in sGC mechanism. Therefore, the different mutants of sGC were generated to elucidate the local environment of the binding site and the conformational changes that occur upon binding. Single mutants of the four known Trp were made to observe possible movement of the protein domains upon activator binding using fluorescence spectroscopy. Using these mutants we were able to localize the regions of the protein that change conformation upon NO binding and determine their movement relative to the heme and GTP groups. We plan to use these mutants to study the binding of CO and YC-1 to determine how activation by those effectors differs from that of NO.

Entry Number 46 GL-B

S-NITROSYLATION OF SOLUBLE GUANYLYL CYCLASE

By: Kensuke Yamamoto
Biochemistry
Faculty Advisor: Dr. Nancy Gerber

Abstract:

Entry Number 47 GL-B

CHARACTERIZATION OF A PHYTOPATHOGENIC BACTERIAL P450 SYSTEM CONTAINING AN IRON-SULFUR AND TRANSKETOLASE-LIKE PROTEIN

By: Mayra Pastore
Biochemistry
Faculty Advisor: Dr. Nancy Gerber

Abstract: Background: Rhodoccocus Fascians is phytopathogenic bacteria able to induce leafy galls through the expression of the virulent promoting Fas Operon. The operon, located within the Fi plasmid, codes for, among other proteins, Cytochrome P450fas, and its ferredoxin-and-transketolase-like partner, FasRedoxin (FasRdx). Both proteins are essential for plant fasciation. The proposed mechanism for infection puts P450fas and FasRdx at the last step of zeatin biosynthesis. (Crespi, M., et.al. J. of Bacteriology. 176, 2492-2501, 1994).

Methods: In order to study the proposed mechanism, we have cloned the genes coding for polyhistidine-tagged P450fas and FasRdx into the pCWori vector and expressed the proteins in *E. coli*. The protein expression levels were confirmed using SDS-PAGE, Western blotting, and Ultra Violet-Visible spectrometer while protein purification was achieved using Nickel ion-exchange column.

Results: We have obtained positive evidence of P450fas expression and successfully purified the protein. FasRdx was expressed using ArticExpress ™ RP Competent cells and we are in the process of refining purification conditions for protein assay.

Conclusions: previous work have shown that P450fas is able to bind to cytokinin precursors such, isopentenyladenine, while this current project allowed the investigation of protein-protein interaction between P450fas and FasRdx and to test for the proposed transketolase-like activity in the latter protein.

Entry Number 48 GL-B

CHANGES INDUCED BY COFACTOR BINDING MODULATES ACTIVE SITE REACTIVITY IN nNOS

By: Russ Jensen and Mike Minton
Biochemistry
Faculty Advisor: Dr. Raymond Esquerra

Abstract: Nitric oxide is a physiological signaling molecule that is important in normal mammalian physiology. Abnormal levels of nitric oxide have been implicated in cardiovascular pathologies, including atherosclerosis and hypertension. Therefore it is important to understand how nitric oxide is produced and regulated. Nitric oxide production is activated in the cell by the binding of a ubiquitous regulatory complex, calcium(II)/calmodulin (CaM), to nitric oxide synthase (NOS). The molecular mechanism of NOS regulation by CaM is not understood. Time resolved absorption spectroscopy following carbon monoxide photolysis of neuronal NOS (nNOS) was performed in order to probe the nNOS active site environment. It was found that the addition of CaM to nNOS increases the active site availability, which is consistent with the notion that CaM allows enzymatic activity. This is the first work to show that CaM binding to nNOS directly affects the active site, and may contribute to an accurate model of nNOS regulatory mechanisms.

Entry Number 49 GL-B

EXPLORING HOW S1' SUB-SITE MUTATIONS AFFECT TRYPSIN'S ENZYMATIC ACTIVITY

By: Candace Wong
Biochemistry
Faculty Advisor: Dr. Teaster Baird, Jr.

Abstract: Using site-directed mutagenesis, we have explored how the amino acid make up the S1? subsite of the serine protease trypsin may introduce extended substrate selectivity into this normally digestive enzyme. The C42-C58 disulfide bridge was removed by replacing the cysteines with Val-42 and Ala-58 to create C42V/C58A-trypsin (VA-Tn). A triple variant, F41A/C42V/C58A-Tn (AVA-Tn), was also generated to determine if F41 contributes to catalytic activity and selectivity. The hydrolytic activity of the trypsin variant was determined using the commercially available substrate Z-Gly-Pro-Arg-p-nitroanilide (Z-GPR-pNA). VA-Tn exhibited a 2-fold decrease in kcat/ KM compared to wild type (68 uM-1*min-1vs uM-1*36 min-1) primarily due to the greater than 5-fold decrease in kcat (431 min-1 vs 2408 min-1). This may be attributed to increased mobility of His57, affecting its ability to remove a hydrogen from Ser195. In addition, a 3-fold decrease in KM for VA-Tn (35 uM vs. 12 uM) may be accounted for by the increased hydrophobic interaction between the phenyl moiety of the pNA leaving group and hydrophobic residues in the modified S1? subsite. Replacing the phenylalanine with an alanine in addition to the truncation of the disulfide bridge (AVA-Tn) likely introduces greater flexibility in the S1 subsite and weakens affinity between the enzyme and substrate. This is shown in the 36-fold decrease in kcat/ KM compared to VA-Tn (1 uM-1*min-1 vs 36 uM-1*min-1), which is primarily due to the 12-fold decrease in kcat (432 min-1 vs 36 min-1). This relaxed binding is reflected in the increase in KM, which has tripled compared to VA-Tn (29 uM vs 12 uM).

Entry Number 50 GL-B

SELENATE AND SELENITE REDUCTION BY NANOMETER-SCALE ZEROVALENT IRON PARTICLES

By: Jovilynn Olegario
Chemistry
Faculty Advisor: Dr. Bruce A. Manning

Abstract: Selenium oxyanions can be present in agricultural drainage waters, coal mining effluent, and as fission products in radioactive wastes. The objective of this work was to evaluate the effectiveness of both nanometer scale zerovalent iron (nano-Fe) and 100 mesh Fe filings for reduction and immobilization of aqueous selenate Se(VI) and selenite Se(IV). The uptake of Se(VI) and Se(IV) using batch equilibrium, kinetics, and X-ray absorption spectroscopic (XAS) techniques was investigated. In addition, a thorough investigation of the solid phase corrosion products by X-ray diffraction was conducted. The crystalline corrosion product was similar to magnetite, though some distinct differences in the XRD results were noted between Se(IV)- and Se(VI)-treated samples. Application of quantitative X-ray absorption near edge spectroscopy (XANES) revealed that both Se(VI) and Se(IV) were reduced to a mixture of elemental Se(0) plus iron(II) selenide (Se(-II)). The Se local atomic structure in Se(VI)- and Se(IV)-treated nano-Fe was determined using extended x-ray absorption fine structure spectroscopy (EXAFS) and a Se-Se interatomic distance of 2.44 angstroms was revealed. This work suggests that nano-Fe is an efficient material for removing dissolved Se(VI) and Se(IV) from waste waters by formation of an insoluble, reduced FeSe product.

Entry Number 51 GP

AN ISOMORPHISM THEOREM FOR COTRANSVERSAL MATROIDS

By: Amanda Ruiz
Mathematics
Faculty Advisor: Dr. Federico Ardila

Abstract: Given two graphs, it is of interest to know whether the cotransversal matroids they generate are isomorphic. We define local moves on a graph which preserve the matroid, and prove that any two graphs which give rise to the same cotransversal matroid can be obtained from each other by these local moves.

Entry Number 52 GP

COMMUTATOR FORMAL AUTOMORPHISMS IN CHARACTERISTIC 2 AND 3

By: Maree Afaga
Mathematics
Faculty Advisor: Dr. Joseph Gubeladze

Abstract: This project investigates the commutator subgroup of truncated rings whose coefficients have prime characteristic 2 and prime characteristic 3. This investigation will be approached through a mix of theoretical and computational methods. Motivation for this project stems from a paper cowritten by Joseph Gubeladze and Zaza Mushkudiani in which they characterize commutator formal automorphisms in prime characteristic greater than 3 as well as for rings containing the rational numbers.

Entry Number 53 GP

HIGH-RESOLUTION FROM LOW-RESOLUTION

By: Reuben Brasher
Mathematics
Faculty Advisor: Dr. Shidong Li

Abstract: Use a digital camera take picture of a scene. The quality of that picture is limited by the resolution of the camera, which is the size of the pixels produced by the camera. Move the camera slightly, so that it will take a second picture offset from the first picture by half a pixel. Together these two images contain more information than either one alone. Take another two pictures, this time offset first by half a pixel down from the first picture and next by half a pixel to the left and half a pixel down. Now there are four images of the same scene. Together these four images should contain all of the information of a single image with twice the resolution. If the camera that takes the image if perfect and the scene has not changed between pictures, then constructing high-resolution image from the low-resolution images is just a linear algebra problem. Unfortunately, the problem is ill-conditioned, so that if the camera produces noisy images, the reconstruction magnifies the noise. I present some new ideas for improving the reconstruction using frame theory and functional analysis (hard math to solve an easy problem).

Entry Number 54 GP

ENUMERATING TENSIONS IN GRAPHS

By: Aaron Dall
Mathematics
Faculty Advisor: Dr. Matthias Beck

Abstract: Given a graph G=(V,E), a tension is an edge labelling (i.e. a function from the set of edges to some group) that respects certain linear constraints. In this project we will use inside-out polytope theory to show that the counting function #{integral tensions on G with labels not exceeding k in absolute value} is, in fact, a polynomial in k. We then give an interpretation for this polynomial at negative integers.

Entry Number 55 GP

A GEOMETRIC APPROACH TO BERNOULLI-DEDEKIND SUMS

By: Anastasia Chavez
Mathematics
Faculty Advisor: Dr. Matthias Beck

Abstract: In the 1880's, Richard Dedekind derived a finite arithmetic sum that today is called the *Dedekind sum*. Since then the Dedekind sum has appeared in many areas of mathematics such as topology, geometry, and combinatorics. Apostel, Carlitz , and others have introduced Dedekind-like sums involving *Bernoulli polynomials*. Bernoulli polynomials are defined by a generating function and give rise to the *Bernoulli numbers* when a polynomial is evaluated at 0, which has also appeared in various mathematical areas. In recent work by Beck, Haase and Matthews (2008) a polynomial analogue of Dedekind sums, the *Carlitz polynomial,* was used to prove results using discrete geometry. I present the formulas for *Dedekind sums, Carlitz polynomials*, *Bernoulli polynomials* and *numbers*, and give motivation for my thesis work to reprove known theorems and hopefully discover new results of Dedekind sums involving Bernoulli polynomials.

Entry Number 56 GP

LONG MEMORY PARAMETER ESTIMATIONS WITH AN APPLICATION TO EEG DATA

By: Stacey Hubbard
Mathematics
Faculty Advisor: Dr. Alexandra Piryatinska

Abstract: Long memory process is used to model data with a highly self-similar structure. Self-similarity can be expressed using a long memory parameter, also known as the Hurst parameter, denoted H. If $1/2<H<1$, the data exhibits long range dependence. In the literature, there are many methods proposed to estimate this parameter. We use the periodogram method, the local Whittle method and the aggregated variance method. In order to validate the above existing methods, we simulate time series from fractional Gaussian noise and fARIMA processes with known long memory parameter H. We study EEG sleep data of neonates. Sleep can be separated into two stages: active and quiet. We suspect that during the active sleep stage the signal can be modeled as a long memory process. The quiet sleep stage cannot be considered as a long memory process. To check our hypothesis, we estimate the long memory parameter for the active and quiet sleep stages.

Entry Number 57 GP

VISUALIZATION OF SURFACE-BASED MOLECULAR CHARACTERISTICS USING DEFORMABLE MODELS

By: Nicolay Postarnakevich
Mathematics
Faculty Advisor: Dr. Rahul Singh

Abstract: The structure of a molecule can have direct influence on how the molecule behaves biologically. Also, structurally similar molecules often have similar biological behavior. Computer visualization techniques have an important role in reasoning about molecular structures. A molecule can be represented in different ways: as a character string such as 'H2O', as a two dimensional graph, ball and stick model, or in terms of its surfaces. All these representations have their own advantages and drawbacks. One particular method for visualizing a molecule is to consider its three dimensional surface representation. This approach has many advantages since it closely mimics the actual physics of the molecule. The main challenge in this context is to visualize and visually compare the complex features on the molecular surface such as clefts, cavities, and surface regions having salient geometries. Additionally, visualization of the distribution of physicochemical properties also is of crucial importance. In this project we propose a new method, based on deformable surfaces to map arbitrary molecular surfaces to a standard spherical coordinate system. The use of deformable surfaces results in an injective map from the molecular surface to the sphere. Moreover, for non genus-zero molecular surfaces, the holes are also mapped onto the sphere. Any value of a molecular property that can be measured or assigned at a surface can then be transferred to the sphere. A molecule can then be represented and visualized by its spherical map. Two molecules can also be compared by viewing their representative sphere mappings.

Entry Number 58 GP

EXPLORING DNA UNKNOTTING BY
TYPE II TOPOISOMERASES: A STUDY OF WRITHE

By: Juliet Portillo, Trevor Blackstone, Reuben Brasher,
and Dr. Mariel Vazquez
Mathematics and Computing for Life Sciences
Faculty Advisor: Dr. Mariel Vazquez

Abstract: Our group studies DNA using topology, knot theory and various computational methods. In particular we are interested in the function of Type II Topoisomerases as a DNA unknotting mechanism. Type II topoisomerases perform strand passage to unknot DNA. It is known that this process is non-random. Our goal is to find a model for the enzymatic action that reproduces the experimental data. We model DNA as polygons in three dimensional space, and using different algorithms we sample the space of knotted conformations and organize these knots by knot type. We perform random strand passage using Dowker Thistlethwaite (DT) Codes to show that repeated strand passage results in unknotting. We here present a study of the average writhe of these knotted conformations. The writhe is a geometrical invariant of knots that measures their entanglement complexity and may contribute to the function of type II topoisomerases. We propose that that the sign of the average writhe is topological invariant of knots.

Entry Number 59 GP

MODELING DNA AND
ITS THERMAL FLUCTUATION IN SOLUTION

By: Zoe Talbot, Xia Hua (MIT), Juliet Portillo, and Rob Scharein
Mathematics
Faculty Advisor: Dr. Mariel Vazquez

Abstract: Understanding the conformation of DNA and its thermal uctuations in solution is a important step in understanding biological processes that have great impact on the life of a cell. We are interested in studying closed circular DNA which is primarily found in bacteria. Circular DNA may be knotted and super- coiled in the cellular medium. In order to gain an understanding of the behavior in solution of such DNA forms, we model closed circular DNA as polygons in the simple cubic lattic, Z3. We use the BFACF algorithm which is a dynamic Monte Carlo method to generate a sample space of polygons for each _xed length and knot type. However, polygons in Z3 are not good models for DNA due to their rigidity and bending properties. Furthermore, lattice chains manipulated by the BFACF do not take into account parameters such as such as the solution's ionic strength, which can alter the DNA conformations. We propose to make the polygonal chains generated by the BFACF into a better model for DNA by incorporating a potential energy function used by Tesi et. al. (1994) that takes into account ionic conditions. The energy is dependent on the short range force between non-bonded monomers (edges) and a Coulomb potential which can be reduced to making adjustment on only one parameter, _, which is proportional to ionic concentration. We here present our preliminary results.

Entry Number 60 GP

TANGLESOLVE AND XER SITE-SPECIFIC RECOMBINATION

By: Jennifer S. Lopez, Yuki Saka, Wenjing Zheng, and Dr. Mariel Vazquez
Mathematics
Faculty Advisor: Dr. Mariel Vazquez

Abstract: TangleSolve (http://bio.math.berkeley.edu/TangleSolve/) is a java applet/application that implements the tangle method for site-specific recombination. The tangle method is a mathematical method based on knot theory, which is used to compute the topological mechanism of certain enzymes called site-specific recombinases. Site-specific recombinases catalyze the exchange of genetic material between specific sites on a DNA molecule. In general substrates and products of recombination belong to a well characterized family of knots and links called 4-plats. Each site-specific recombination reaction gives rise to a system of tangle equations which can be solved using the tangle method. TangleSolve offers an interactive tool to compute solutions to such systems of tangle equations.

We here present the TangleSolve tutorial, which we have updated to be more user-friendly. We will illustrate the tangle method using the Xer recombination example. Xer recombination is catalyzed by a pair of tyrosine recombinases XerC and XerD, which display topological selectivity and specificity. Under certain biological and mathematical assumption the tangle method finds 3 solutions to the Xer equations.

Entry Number 61 GP

PREDICTING CANCER PATIENT PROGNOSIS FROM CGH PROFILES USING ALGEBRAIC HOMOLOGY

By: Daniel DeWoskin
Mathematics and Computing for Life Sciences
Faculty Advisor: Dr. Javier Arsuaga

Abstract: The Array Comparative Genomic Hybridization (CGH) method generates a full picture of an individual's genome. The multidimensional nature of this data, however, has not been fully explored. Current methods for CGH analysis focus on specific markers, but deeper understanding can be gained by examining overall genomic instability in entire chromosomes. We propose a novel method for characterizing CGH profiles mathematically using algebraic homology, specifically looking at the betti numbers of a surface generated from breast cancer patient CGH profiles. This model is able to distinguish between frequency of cancer recurrence in chemotherapy and non-treated patient populations.

Entry Number 62 GP

AN AUTOMATED APPROACH FOR CHROMOSOME LABEL DETECTION AND CHROMOSOME SIMULATION

By: Rocco Varela
Computing for Life Sciences
Faculty Advisor: Dr. Javier Arsuaga

Abstract: My research involves developing a computational model for chromosome territories during the Interphase portion of the cell cycle. I am taking two different approaches to this problem. First, I am analyzing experimental data in an attempt to identify trends of fluorescently-labeled chromosome regions in healthy human cells. I am developing an automated method to analyze labeled chromosomes in attempt to reconstruct the geometry and position of chromosomes within a replicating cell. My second approach requires implementing a Monte Carlo simulation of chromosome arrangements during the G0/G1 phase of the cell cycle. My simulation automatically generates ensembles of DNA configurations that allows us to compare both experimental and simulated data and formulate justified conclusions about the relative positions of chromosomes during the G0/G1 phases of the cell cycle. Analysis of chromosome arrangements and developing a biologically sound computational model will enhance our understanding and investigation techniques of the formation of chromosome territories during the early stages of the cell cycle.

Entry Number 63 GP

CLASSIFICATION OF LARGE PERIAPICAL LESIONS

By: Arturo Flores and Steve Rysavy
Computing for Life Sciences
Faculty Advisors: Dr. Kazumori Okada and Dr. Reyes Enciso (USC)

Abstract: This poster proposes a novel application of computer-aided diagnosis to a clinically significant dental problem: non-invasive differential diagnosis of periapical lesions using cone-beam computed tomography (CBCT). The proposed semi-automatic solution combines graph-theoretic random walks segmentation (presented in a separate poster) and machine learning-based LDA and AdaBoost classifiers. We propose a novel robust algorithm to unify AdaBoost and LDA by introducing sample weights to the LDA formulation. Our quantitative experiments show the effectiveness of the proposed Adaboost and Weighted LDA method by demonstrating higher classification accuracy when compared to other Adaboost combinations on multiple data sets, as well as requiring less iterations to reach a low training/test error. Furthermore, the proposed Dental CAD system achieves a 94.1\% correct classification rate, which demonstrates the validity of this approach.

Entry Number 64 GP

SEGMENTATION OF LARGE PERIAPICAL LESIONS TOWARD DENTAL COMPUTER-AIDED DIAGNOSIS IN CONE-BEAM CT SCANS

By: Steve Rysavy and Arturo Flores
Computing for Life Sciences
Faculty Advisors: Dr. Kazumori Okada and Dr. Reyes Enciso (USC)

Abstract: This poster presents an experimental study for assessing the applicability of general-purpose 3D segmentation algorithms for analyzing dental periapical lesions in cone-beam computed tomography (CBCT) scans. In the field of Endodontics, clinical studies have been unable to determine if a periapical granuloma can heal with non-surgical methods. Addressing this issue, Simon et al. recently proposed a diagnostic technique which non-invasively classifies target lesions using CBCT. Manual segmentation exploited in their study, however, is too time consuming and unreliable for real world adoption. On the other hand, many technically advanced algorithms have been proposed to address segmentation problems in various biomedical and non-biomedical contexts, but they have not yet been applied to the field of dentistry. Presented here is a novel application of such segmentation algorithms to the clinically-significant dental problem. This study evaluates three state-of-the-art graph-based algorithms: a normalized cut algorithm based on a generalized eigen-value problem, a graph cut algorithm implementing energy minimization techniques, and a random walks algorithm derived from discrete electrical potential theory. We extend the original 2D formulation of the above algorithms to segment 3D images directly and apply the resulting algorithms to the dental CBCT images. We experimentally evaluate quality of the segmentation results for 3D CBCT images, as well as their 2D cross sections. The benefits and pitfalls of each algorithm are highlighted.

Entry Number 65 GP

COMPUTATIONAL CANCER BIOMARKER DISCOVERY

By: Emmanuel R. Yera
Computing for Life Sciences
Faculty Advisors: Dr. Kazumori Okada, Dr. Colin Collins (UCSF Cancer Center) and Dr. Pamela Paris (UCSF Cancer Center)

Abstract: This research entails performing computational methods on array comparative genomic hybridization (aCGH) data to find subsets of probes which can accurately perform cancer classification from progressed to non-progressed cancers. The discovered subsets can then be biologically analyzed to see if they can be potential biomarkers. This research is especially important to prostate cancer research, since, according to some estimates, up to half of all patients who undergo radical prostatectomy in the US do not need surgery.

Entry Number 66 GP

A LEAKY BUCKET POLICING AGENT FOR SITEWIDE CONGESTION CONTROL

By: Teresa L. Johnson
Computer Science
Faculty Advisor: Dr. Marguerite Murphy

Abstract: This project involves the creation of a policying agent that polices both TCP and UDP traffic, smoothing burstiness so that traffic patterns are more uniform. It also involves the development of heuristics to dynamically vary the egress traffic rate based on incoming connections.

Entry Number 67 GP

TANGIBLE MELODY: USING THE METAPHOR OF GRAPHICS MANIPULATION TO COMPOSE MELODY

By: Marc Sosnick, Xinhang Shao, Joshua Melcon, Rushan Cheng, and Sadia Anwar
Computer Science
Faculty Advisor: Dr. William Hsu

Abstract: The Tangible Melody Project is an HCI project designed to investigate the use of the metaphor of graphical manipulation--i.e. stretching, turning, etc.--to manipulate notes to aid in melodic composition. The software for this project is designed to be used by novice and advanced musicians and computer users. The final platform for this software is a touch surface.

Entry Number 68 GP

COMPARISON OF IBC 2006 AND PERFORMANCE BASED DESIGN OF REINFORCED CONCRETE SPECIAL MOMENT RESISTING FRAME

By: Rob Mau
Civil Engineering
Faculty Advisor: Dr. Wenshen Pong

Abstract: This project focuses on comparison of Performance-Based Engineering Design (PBED) with the International Building Code 2006 (IBC 2006). This is done through comparative seismic designs of reinforced concrete Special Moment Resisting Frame (SMRF). Structure designed according to International Building Code 2006 is based on force capacity design parameter. Structures designed according to these provisions will sustain deformations in the event of a design-level earthquake. Taking deformation into consideration as a design parameter, PBED utilize structural deformations when assessing the seismic performance or design of seismic resistant system. To examine the performance and advantages of PBED design method, an analytical design comparison of a reinforced concrete SMRF based on PBED and IBC 2006 will be presented.

Entry Number 69 GP

EFFECT OF MOBILTY PATTERNS ON SAFETY MESSAGES IN VEHICULAR NETWORKS

By: Anna Pereira
Computer Engineering
Faculty Advisor: Dr. Hamid Shahnasser

Abstract: The main objective of Vehicular Networks (VANETs) is reliable delivery of emergency warning messages so that drivers can make well-timed decisions and prevent any mishaps. Broadcasting such messages using current routing protocols does not prove to be feasible because of the inability to adapt to the constantly changing vehicular environment. The objective of this study is to compare the existing 802.11 broadcasting protocol, and 802.11e based mechanism for priority access, as well as a priority access mechanism with an adaptive congestion window. The performance of these protocols will be observed keeping in mind their sensitivity towards modeling of the vehicular environment. The results will indicate the amendments necessary to the retransmission mechanisms, that will help build an efficient, robust and reliable broadcasting protocol, suitable for vehicular networks.

Entry Number 70 GP

THE DESIGN AND IMPACT OF PLANETARIUM INSTRUCTION BASED ON A 5E CONCEPTUAL CHANGE APPROACH TO ASTRONOMY EDUCATION

By: Michelle Krok
Physics
Faculty Advisors: Dr. Adrienne Cool and
Dr. Kimberly D. Tanner

Abstract: : Employing the research-based curricular planning approach called the 5E Model (Engage, Explore, Explain, Elaborate, Evaluate), five labs for non-science majors are being developed to address three overarching content learning objectives: students will leave the instruction 1) with the ability to find and describe the location of celestial objects using compass direction, altitude, magnitude, and angles between stars, 2) knowing that the motions of celestial objects are predictable, and 3) with the ability to tie changes in view of these celestial objects to different locations on Earth. Using two-tiered assessment, the effectiveness of the curriculums ability to foster conceptual change will be evaluated over a semester of students. Student confidence and interest will also be assessed.

Entry Number 71 GP

NONLINEAR DYNAMICS IN PERIODIC OPTICAL LATTICES

By: Laura Daniel
Physics
Faculty Advisor: Dr. Zhigang Chen

Abstract: When coherent light propagates through a special material called a photorefractive crystal, it is focused as though passing through a lens. When this focusing effect balances light's natural tendency to spread out, the light forms a nonlinear localized state called a soliton. Solitons interact within periodic optical lattices inside photorefractive crystals by transfer of energy, linear momentum and angular momentum. I show experimentally that a dipole soliton will rotate about its center as it passes through a periodic optical lattice, and that this phenomenon is amplified when the lattice is anisotropic.

Entry Number 72 GP

CS-DOPED NANOPOROUS FILMS: FUNDAMENTAL PHYSICAL

By: Georgi Diankov
Chemistry
Faculty Advisor: Dr. Andrew Ichimura

Abstract: Thin films of zeolites (nanoporous crystalline materials with the SiO2 framework) have been synthesized in-situ on silanized gold, quartz and silicon. On doping zeolites with alkali metals, a broad NIR absorption band attributable to free electrons in the zeolite channels is observed. Cs-doped zeolite films are shown to be electrically conducting, with semiconductor-like resistivity, as measured in temperature-dependent, 4-probe DC Conductivity. Various instrumentation techniques - X-Ray Diffraction, Scanning Electron Microscopy, Atomic Force Microscopy and optical spectroscopy - are used in the investigation. Procedures to determine the hybrid films' band structure and incorporate the materials in optoelectronic devices are outlined.

Entry Number 73 GP

MINING SOIL SURVEY DATABASES TO EXPLORE LITHOLOGIC AND CLIMATIC CONTROLS ON HILLSLOPE PRODUCTION OF BEDLOAD-SIZE ROCK FRAGMENTS

By: Jill Marshall
Applied Geosciences
Faculty Advisor: Dr. Leonard Sklar

Abstract: The grain size distribution of sediments supplied by hillslopes to channel networks may strongly influence landscape dynamics at both the long time scale of landscape evolution and the short time scale of channel response to changes in land use. Little is known, however, about how lithology, climate, and the processes and rates of sediment production and transport on hillslopes, control the grain size distribution supplied to channels. A wealth of soil size distribution measurements have been collected and archived by state and local agencies, which to my knowledge have not been systematically examined to uncover patterns in the mass fraction and size distribution of rock fragments large enough to move as bedload in rivers. Here I report on results obtained from data mining soil survey archives in the western United States. The data provides new insights into soil production and climatic influences on the grain size distributions supplied to rivers

Entry Number 74 GP

PREDICTING ROAD-FILL FAILURE USING VIRTUAL FIELDWORK AND DIGITAL TOPOGRAPHY

By: Bob Sas
Geology
Faculty Advisor: Dr. Leonard Sklar

Abstract: The task of managing aging roadways in mountainous topography becomes increasingly difficult as budgets to management agencies decline. Such budgetary concerns can be addressed by developing new low-cost methods that use resources already available to management agencies. A method that minimizes time in-the-field and that uses readily available data was developed to address one of the most common and catastrophic issues in mountainous roads, road-fill failures. I developed a method that uses virtual fieldwork and slope distributions within a calibrated distance of the Blue Ridge Parkway, North Carolina to detect potential, road-fill failures. Locations of previous failures and arc-shaped pavement cracks were located using virtual fieldwork, and the slopes surrounding failed-or-cracked sites were extracted from a digital elevation model and compared to uncracked portions of road. Using these slope distributions, I determined that there is a statistical difference in slope between failed-or-cracked sites and uncracked sites. The final product of this work is a probabilistic, hazard-assessment model that uses the median slope of these distributions to zone road-fill failure hazards via a geographic information system.

Entry Number 75 GP

RIVER EROSION ON TITAN:
HOW ICE STRENGTH VARIES WITH TEMPERATURE

By: Beth Zygielbaum
Geosciences
Faculty Advisor: Dr. Leonard Sklar

Abstract:

Entry Number 76 GP

TESTING A NEW METHOD FOR MEASURING MICRO-MORPHOLOGICAL CHANGE USING EMBEDDED MAGNETS IN A TRAVERTINE DEPOSITIONAL ENVIRONMENT, FOSSIL CREEK, ARIZONA.

By: Brian Fuller
Geosciences
Faculty Advisor: Dr. Leonard Sklar

Abstract: Measuring micro-morphological change of bed topography in a fluvial setting is often done by installing erosion pins or drilling holes that serve as fixed reference points. A shortcoming to these methods is that protruding pins and open holes can influence the local processes that alter the channel bed. Here we report on the development of a new method for documenting micro-topographic change, using magnets embedded within actively forming travertine along Fossil Creek, Arizona. These natural travertine structures occur as channel-spanning dams that create a step-pool morphology that provides important aquatic habitat. Biotic processes in turn, such as microbial and algal growth and the trapping of floating leaves and branches, can catalyze travertine deposition and vertical growth in travertine dams. The goal of this overarching study is to document travertine growth rates, downstream of a recently decommissioned diversion dam, to determine the relative influence of various biotic and abiotic processes.

The method consists of gluing individual magnets (1cm in diameter and thickness; 1gauss magnetic intensity) onto the end of 10cm lengths of PVC pipe with the magnetic poles parallel to the pipe. We then drill a vertical hole in either bedrock or travertine, place the magnet-pipe assembly into the hole, and back-fill the hole with crushed travertine, to approximate the pre-existing surface as best as possible. Prior to installing the magnets we measure the background magnetic field, using a Schonstedt GA-72CD magnetic locator, to ensure there are no nearby magnetic anomalies. Because the strength of the magnetic field decreases geometrically with distance, we created a calibration curve specific to these magnets, which is valid over a range of up to 40cm. We use repeat measurements of magnetic field intensity to document vertical travertine growth over time. We use repeat surveys with a total station as an independent check on the change in dam elevations, at and adjacent to the magnet locations.

Although the basic method is simple, a number of challenges have arisen. There are differences in magnetic permeability of travertine, bedrock and air or water, which we are addressing with calibration curves for specific materials and dam geometries. Although we commonly installed magnets at local topographic high points along dam crests, non-uniform travertine growth can shift the location of dam crests, complicating efforts to re-occupy the exact magnet location for later measurements. We address this problem by searching for the highest intensity location in a horizontal plane above the dam crest, and by careful photo-documentation of the evolving travertine structures. So far, the method provides individual measurements of micro-topographic vertical position with a precision of about 1mm, and elevation differences due to travertine growth are precise to within 1 to 2cm, depending on the distance to the embedded magnet and the material composition of the new increment of dam growth.

Entry Number 77 GP

HARNESSING NATURAL C ISOTOPES TO UNDERSTAND ORGANIC MATTER TRANSFORMATIONS IN MARINE SEDIMENTS

By: Jonathon Polly
Geosciences
Faculty Advisor: Dr. Toby Garfield

Abstract: Coastal and continental margin sediments supply dissolved organic carbon (DOC) to the overlying water at rates comparable to the riverine flux of DOC into the ocean. The DOC in sediment porewater originates from the solubilization of particulate organic carbon (POC), the majority of which is rapidly respired to dissolved inorganic carbon (DIC). Part of the DOC pool resists degradation and accumulates in the porewater and is available to efflux from the sediments. The biogeochemical role that this benthic DOC flux plays in the marine cycle is unclear, given that the majority of the DOC pool is uncharacterized at the molecular level. As a first step to better understanding the role this benthic DOC flux plays, we incubated intertidal sediment for 130 days, monitored the concentrations of POC, DOC, DIC and isotopic signatures ($d^{13}C$ and $D^{14}C$) of our samples, and examined bulk C transformations using mass balance. We hypothesized that isotopic fractionation results as the more labile fraction of POC is selectively solubilized to DOC and the more labile fraction of DOC is selectively oxidized to DIC, with the premise that the natural-abundance $^{14}C/^{12}C$ ratios can be used to distinguish between the labile and resistant organic carbon. Results indicate the $D^{14}C$-signature of the POC oxidized to DIC was ^{14}C-enriched relative to bulk POC by approximately 170. The $d^{13}C$ signature of DIC was ^{13}C-enriched relative to bulk POC by approximately 10, and appears to overlap with the $d^{13}C$ signature of cordgrass, which is found in the area where our sediment was collected.

Entry Number 78 GP

AN ANALYSIS OF SURFACE CURRENTS IN THE GULF OF THE FARALLONES USING HF-RADAR

By: Matt Gough
Oceanography
Faculty Advisor: Dr. Toby Garfield

Abstract: Three high frequency radar (CODAR) instruments began monitoring sea surface currents in the Gulf of the Farallones off the Coast of San Francisco, California in May 2006 as part of the State Coastal Conservancy funded Coastal Ocean Currents Monitoring Program (COCMP). This has provided an unprecedented spatial and temporal view of sea surface currents in this region. There are three aims to this project: 1) Describe the seasonal trends in surface circulation, 2) Develop and test a process in which harmonic tidal analyses using T_tide (Pawlowicz, 2002), a MATLAB toolbox, are performed on measured HF radar sea surface currents to separate out calculated tidal currents from measured currents, and 3) Analyze correlations between wind data and HF radar measured surface currents. The results of this study can be applied towards oil spill and pollution response, Coast Guard search and rescue techniques, and transport of plankton and nutrients.