University of Idaho
College of Science

14th Annual

Student Research Exposition

Thursday, October, 18 2018

2:30 – 4:30 P.M.

IRIC Atrium

Dean's Message

Welcome to this year's edition of the College of Science Student Research Exposition. This is the 14th year for this event, and we have a record number of participating students this year. I'm especially pleased to see the number of undergraduate expo participants continue to grow.

We're proud of what our students accomplish, and proud that our college presents such tremendous opportunities for students to engage in research. We believe that getting our students involved in research projects with world-class research faculty is one of the things that sets the University of Idaho apart, and the Student Research Exposition is a great place to see examples of the exciting work they do. I hope you'll take some time to look at the exhibits and talk to the participating students.

Part of the learning that students gain from the expo comes from putting their work before judges. At the conclusion of the program we'll present awards to several of the projects deemed to be exceptionally meritorious by our judging panel. Of course, congratulations are due to all of our participating undergraduate and graduate students. Congratulations and thanks are also due to the faculty who support, encourage, and mentor our students through these projects. Thank you to the Sigma Xi scientific research society for participating in this year's event. And finally, thanks to the judges who volunteer their time to give constructive feedback. We hope that all will enjoy the experience of this year's exposition.

- Dean Ginger E. Carney

Contents

Eligibility Requirements

Undergraduate Category: Any undergraduate with a declared major in the College of Science is eligible, regardless of the affiliation of the faculty member supervising the research. Also, undergraduates from majors outside the College of Science who work on research projects with College of Science faculty are encouraged to participate.

Graduate Category: Any University of Idaho graduate student participating in research supervised by a College of Science faculty member is eligible.

Procedures

- The exposition runs from 2:30 p.m. to 4:30 p.m. on Thursday, Oct. 18, 2018, with setup time between 2:00 and 2:30. Easels and display boards will be provided. Participants should be available at their displays to answer questions from 2:30 on.
- Judging will take place between 2:50 and 4:00. Each poster will be visited by two judges at separate times. The approximate times for the judge visits will be communicated to the participants in advance of the exposition. There may also be separate judging visits for the Sigma Xi prize.
- The judges will have roughly 8 minutes to spend at each poster. This should include a short 3-5 minute verbal presentation by the student, as well as a time for judges to ask questions.
- Each judge will have the option of having their judging sheets kept confidential or returned to the student.
- Participants will be judged on the methodology and results of the research (40%), the design and layout of the poster (30%), and the clarity of a short presentation given to judges as they tour the displayed posters (30%). See the sample judging sheet on the following page.
- At approximately 4:30 p.m. there will be a brief awards ceremony to recognize the winners. Two outstanding posters in each category will be recognized with $100 prizes. There is also an award made by the Sigma Xi Scientific Research Society consisting of $100 and a nomination for Sigma Xi membership. All participants will receive a College of Science T-shirt or mug.

2018 STUDENT RESEARCH EXPOSITION
SCORING SHEET

Student: _____

Poster Title: _____

Judge: _____

CRITERIA	DESCRIPTION	MAX SCORE	SCORE
Student presentation	How well does the student utilize the poster to explain the project and her or his role in the research?	15	
Research methodology and results	Of what quality is the research? Is the methodology appropriate, and are the findings significant?	20	
Poster design and layout	Do the design and layout of the poster make it easy to understand? Are graphics appropriately labeled and integrated with the text?	15	
TOTAL SCORE		**50**	

2018 Judges

Undergraduate Division:

- Ann Abbott, Instructor, Department of Statistical Science and Department of Mathematics
- Andrea Gonzalez, Postdoctoral Fellow, Department of Biological Sciences
- Jennifer Johnson-Leung, Associate Professor, Department of Mathematics
- Diana Mitchell, Assistant Professor, Department of Biological Sciences
- Jagdish Patel, Postdoctoral Fellow, Center for Modeling Complex Interactions
- John Phillips, Postdoctoral Fellow, Department of Biological Sciences
- Paul Rowley, Assistant Professor, Department of Biological Sciences
- Lihong Zhao, Postdoctoral Fellow, Center for Modeling Complex Interactions

Graduate Division:

- Katherine Hegewisch, Postdoctoral Fellow, Department of Geography
- Eric Mittelstaedt, Associate Professor, Department of Geological Sciences
- Christine Parent, Assistant Professor, Department of Biological Sciences
- Dharmeshkumar Patel, Postdoctoral Fellow, Center for Modeling Complex Interactions
- Bernhard Stumpf, Associate Professor, College of Science
- Michelle Wiest, Associate Professor, Department of Statistical Science
- Richard Williams, Professor, Department of Chemistry

Sigma Xi Award:

- Leslie Baker, Chair, Department of Geological Sciences, and Interim Chair, Department of Geography

2017 Winners

Undergraduate Division

Ubaldo Arana (Biology / Animal and Veterinary Science)
Investigating recovery pathways in attenuated viral genomes.
Faculty mentor: Holly Wichman

Emily Kizer (Biology)
Saccharomyces yeasts to combat fungal pathogens of humans.
Faculty mentor: Paul Rowley

Graduate Division

Marie Janneke Schwaner (Biology)
Muscle dynamics during vertical jumping by kangaroo rats (D. deserti).
Faculty mentor: Craig McGowan

Margot Vore (Geography)
Locating and monitoring subglacial conduits through seismology
Faculty mentor: Timothy Bartholomaus

Sigma Xi Scientific Research Society Award

Tom Jeute (Geology)
Characterizing nanophase materials on Mars: spectroscopic studies of allophane and imogolite.
Faculty mentor: Leslie Baker

2018 Participants

Undergraduate Division:

- **Madison Bergeman** (Biology), Viral dynamics in *Drosophila melanogaster* adult flies
- **Zach Blume** (Microbiology), Modulation of the retinal immune environment in a zebrafish system of rod photoreceptor-specific degeneration
- **Josephine Boyer** (Microbiology / Medical Sciences), Discovery of killer yeasts with diverse antifungal properties
- **Michael Camerino** (Molecular Biology / Biological Engineering), Density and spatial mapping of OFF-bipolar cell populations in the mouse retina
- **Alice Cassel** (Biology / Microbiology), Morphometic analysis of floral characteristics associated with shifts to wind pollination in meadow-rues (*Thalictrum,* Ranunculaceae): comparing herbarium specimens to fresh specimens
- **Tyler Clemens** (Computer Engineering), Past environmental change on rapa nui: elemental abundances and leaf waxes from two new lake sediment cores
- **Harrison Funk** (Microbiology), Mechanism of a kangaroo rodents tail affecting locomotion
- **Sarah Gibbs** (Microbiology), Creation and application of dual color reporters in Chlamydia *Trachomatis*
- **Tawny Gonzalez** (Chemistry / Biochemistry), Analysis of four software methods for estimation of protein-protein relative binding affinity
- **Kaylaa Gutman** (Chemistry), Substitution effects of redox-active arylazothioformamide ligands: synthesis, spectral properties, and binding association determination with Copper(I) salts
- **Samantha Heck** (Computer Science), Evolutionary tower defense: modeling evolution in video games using a metapopulation framework
- **Natasha Leigh Herbenson** (Microbiology), Identification of proteins that interact with down syndrome cell adhesion molecule
- **Daniel J. King** (Environmental Science), Connections between changing axial magma flux and oceanic core complex formation along the marathon fracture zone, mid-Atlantic ridge at ~12˚N
- **Sydney Kuther** (Microbiology), Bacterial membrane components damage gastrointestinal neurons through oxidative stress
- **Jared Lambert** (Biology), Live imaging to probe the role of microglia in developmental apoptosis in the zebrafish retina
- **Leah Lambert** (Biochemistry), Fatty acid analysis in *Euglena* strains
- **Garrett Larson** (Biology), Ionic and biomolecular movement through functionalized thin filmed polymers

- **Mark Lee** – see listing under Schlussler, Megan
- **Kyle Luchte** (Mathematics), a computational investigation of high-spin, square-planar Fe^{II} complexes
- **George May** (Miocrobiology), The effects of the gut microbiota on diabetic enteric neuropathy
- **Samuel Myers** (Physics / Mathematics), Using variable stars to constrain planetary formation theories
- **Jessica Nicholson** (Biology), Why your gut may be working against you: gut derived molecules cause dysmotility and neuropathy in high fat fed mice
- **Alexander Roseborough** (Chemistry), Investigating the metal-controlled cyclization of tris-hydroxyimino ligands and their coordinating properties
- **Megan Schlussler** (Medical Sciences) and **Mark Lee** (Molecular Biology and Biotechnology),Quantifying gene expression of DSCAML1 (down syndrome cell adhesion molecule-like 1) in the cerebellum to examine possible causes of autism
- **Tyler Siegford** (Biochemistry), A novel resin for chemical protein synthesis

Graduate Division:

- **Shiva Prasad Adhikari** (Chemistry), Detection of mixed-sequence dsDNA using bulged invader probes
- **Joseph A'Hearn** (Physics), Dynamics of multiple bodies in a corotation resonance
- **Tristan Amaral** (Geology), Predicting iceberg calving from the Greenland ice sheet
- **Sierra Beach** (Microbiology / Molecular Biology and Biochemistry), Modeling antibody escape mutations in respiratory syncytial virus
- **Mellisa Clemons** (Microbiology / Molecular Biology and Biochemistry), synaptic convergence for night vision in the mammalian rod visual circuit
- **Clinton Elg** (Bioinformatics and Computational Biology), Do human pathogens better retain novel multi-drug-resistant plasmids after coevolution with a single plasmid type?
- **Raymond Emehiser** (Chemistry), Utilizing invader probes for recognition of restriction enzyme sites
- **Ashley Farre** (Neuroscience), The effects of thyroid hormone on the expression of *rh2*-type cone opsin genes in zebrafish
- **Sarah Hendricks** (Bioinformatics and Computational Biology), Genetic isolation and a unique disease threatening the island fox
- **Emmanuel Ijezie** (Biology), Rhinovirus curtails disease severity in respiratory viral co-infections in mice

- **Lokendra Raj Khanal** (Physics), Magnetic property and nanostructural evolution of iron oxide nanoparticles heated up to 800˚C
- **Steven Kreyche** (Physics), The influence of orbital eccentricity on the obliquity stability of retrograde rotating planets
- **Kevin Lewallen** (Bioinformatics and Computational Biology) and **Amanda Stahlke** (Bioinformatics and Computational Biology), Comparative genomics, evolution, and transmissible cancers in Tasmanian devils (*sarcophilus harrisii*)
- **Shunji Li** (Microbiology / Molecular Biology and Biochemistry), Docing the virus: the interaction between HIV-1 and nucleoporin 153
- **Martyna Lukaszewicz** (Bioinformatics and Computational Biology), Approximate Bayesian computational statistical methods to estimate the strength of divergent selection in yeast
- **Robert Mackin** (Microbiology / Molecular Biology and Biochemistry), Endocrine regulation of multichromatic vision
- **Mahsa Moshari** (Chemistry), Theoretical and spectroscopic investigation of a series of Iron(II)-Selenide model complexes and of their Iron(II)-Sulfide analogues
- **Siavash Riazi** (Bioinformatics and Computational Biology), Phenotypic heterogeneity in tolerance permits rapid transition to growth with lethal levels of formaldehyde stress
- **Caroline Shepard** (Chemistry), Recognition of different chromosomal DNA sites using double-stranded invader probes
- **Amanda Stahlke** – see listing under Lewallen, Kevin
- **Anup Tuladhar** (Chemistry), Removal of Lead(II) from aqueous solution by amidoxime-based polyacrylic fibers
- **Derek Viall** (Biology), Topographic patterns of specific retinal neurons following retinal regeneration in the zebrafish

Abstracts

Undergraduate Division

(alphabetical by presenter)

Viral dynamics in *Drosophilia melanogaster* adult flies

Madison Bergeman (Biology)

Abstract:

Viruses are infectious particles that contain genetic material and invade living organisms to infect cells and cause several diseases including the common cold and smallpox. The goal of my research is to quantify the effects of viral co-infection (as compared to single infection) in adult *Drosophila melanogaster* fruit flies. More specifically, I will characterize the outcomes of two single viral infections and one viral co-infection by injecting *Drosophila melanogaster* with *Drosophila* X virus (DXV) or/and *Drosophila* C virus (DCV), and measuring the resulting changes in longevity of the hosts, as well as the changes in the abundance of the viruses post-infection in the hosts using qRT-PCR. Preliminary results suggest that death of singularly infected individuals was similar to death of the mock flies while mortality is twice as likely for co-infected individuals compared to singularly infected individuals. For the next step of this project I will use qRT-PCR to quantify the changes in the abundance of each virus in the hosts over time after initial infection. This project will generate key data to develop larger scale experiments with the aim of gaining a better understanding of the interactions between viruses within and with the host.

Faculty mentor: Christine Parent

Funding support from: College of Science Undergraduate Research Grant

Poster number: 1

Modulation of the retinal immune environment in zebrafish system of rod photoreceptor-specific degeneration

Zach Blume (Microbiology)

Abstract:

Activated and pro-inflammatory microglia, along with accompanying local inflammation, are associated with human retinal degenerative disease. However, it remains unclear if these aspects of the immune response are symptomatic or directly initiate and/or contribute to disease pathology, such as the death of additional retinal neurons. One hypothesis for continued loss of neurons in retinal degenerative disease is that microglia may engulf, or possibly initiate cell death of, otherwise healthy neurons. Our project attempts to test this hypothesis using a zebrafish system in which rod photoreceptors die due to a toxic transgene (XOPS:mCFP), but cone photoreceptors survive. We first characterized microglial characteristics in XOPS:mCFP retinas compared to wildtype and found that microglia localize to the photoreceptor layer and engulf dying rods, but total numbers of microglia are similar. Next, we successfully induced a pro-inflammatory retinal immune environment by intraocular injection of zymosan (a pro-inflammatory compound), as indicated by infiltration and division of immune cells in the retina and gene expression of selected transcripts. Our next goal is to determine if this induction of a pro-inflammatory retinal environment may result in subsequent cone death or disappearance in XOPS:mCFP retinas, thus directly probing contributions of a dysregulated immune environment to retinal degenerative disease.

Faculty mentor: Diana Mitchell

Funding support from: University of Idaho Summer Undergraduate Research Fellowship

Poster number: 2

Discovery of killer yeasts with diverse antifungal properties

Josephine Boyer (Microbiology / Medical Sciences)

Abstract:

Fungi are an important cause of human, animal and plant disease. Pathogens like *Candida glabrata*, which is one of the leading causes of nosocomial infections, are difficult to treat and often are resistant to many commercially available antifungal drugs. Many yeasts have the potential to produce antifungal compounds, called killer toxins. Our objective is to identify new killer toxins that could be used as novel therapeutics against important fungal pathogens. We have screened more than 400 yeast for the production of killer toxins, including a collection of 166 yeast isolated from coffee and cacao beans, and have identified more than 50 toxin producing yeast. Importantly, we have found a subset of killer toxins that are inhibitory to the pathogen *Candida glabrata*. We have extracted viral double-stranded RNA (dsRNA) from samples of the yeasts and have found an apparent relationship between the presence of this viral dsRNA and the ability of yeasts to produce killer toxins. Furthermore, we have observed heterogeneity in the molecular weight of dsRNAs in strains that produce killer toxins. In the future we plan to sequence toxins from the killer yeasts.

Faculty mentor: Paul Rowley

Funding support from: National Institute of General Medical Sciences of the National Institutes of Health

Poster number: 3

Density and spatial mapping of OFF-bipolar cell populations in the mouse retina

Michael Camerino (Molecular Biology / Biological Engineering)

Abstract:

In 2010, the National Institutes of Health (NIH) reported a combined 4.79 million cases of glaucoma and age-related macular degeneration (AMD) in the United States. Despite advancements in treatments for these conditions, the damage that they cause remains incurable. The primary focus of this study will be investigating OFF-bipolar cell (BPC) spatial arrangement and density mapping throughout the areas of the retina ex vivo with respect to the distance from the optic nerve using a mouse model. There is not currently any published research on cellular density mapping of BPCs, despite known differences in other cell populations when comparing different domains of the retina. This study's goal is to expand our understanding of connectivity in the retina and aims to provide a baseline reference for other transgenic neuro-morphological studies that compare phenotypic change in retinal tissue.

Faculty mentor: Peter Fuerst

Funding support from: NIH and Department of Biological Sciences, University of Idaho

Poster number: 4

Morphometric analysis of floral characteristics associated with shifts to wind pollination in meadow-rues (*Thalictrum,* Ranunculaceae): comparing herbarium specimens to fresh specimens

Alice Cassel (Biology and Microbiology)

Abstract:

The shift to wind-pollination is a significant transition in flowering plants that has evolved repeatedly in separate lineages. Wind-pollination is associated with a suite of morphological traits that allow for increased pollen dispersal and capture. Little is understood about how and why wind-pollination evolves, particularly whether wind-pollination arose via parallelism – independent evolution of the same traits via the same genetic pathways in different species. Few taxa exhibit both wind- and animal-pollination systems, so empirical studies of this transition have been limited. Within the genus *Thalictrum* (Ranunculaceae), or meadow-rues, both pollination syndromes are found, and wind-pollination has evolved from insect-pollination multiple times independently, making it an ideal study system. This project is part of a greater study investigating the phylogenetic, morphological, and genetic basis of the evolution of the complex suite of traits associated with shifts to wind-pollination. Because distinct floral morphologies are a key difference between insect- and wind-pollination, morphological measurements were taken for a suite of floral characteristics, here focusing on measurements from herbarium specimens, to characterize pollination syndrome across the clade. Preliminary morphological data had only been collected from a limited set of species where fresh material was available. By collecting trait data from a wider range of species using herbarium specimens, it may be possible to greatly expand our morphological dataset and better represent the diversity of *Thalictrum* species. Here we used multivariate statistical approaches to analyze morphological data collected from 213 herbarium floral samples representing 27 *Thalictrum* species. These data were compared to existing data from fresh material to determine whether morphometric patterns associated with pollination syndromes based on herbarium specimens are 1) similar to results from the smaller, preliminary dataset, and 2) if these data can be combined with the data collected from fresh material to better understand the traits associated with the wind-pollination syndrome.

Faculty mentor: David Tank

Poster number: 5

Past environmental change on rapa nui: elemental abundances and leaf waxes from two new lake sediment cores

Tyler Clemens (Computer Engineering)

Abstract:

There is reason to believe that large changes have occurred in the hydrology of Easter Island over time. Previous studies on lake sediments from the island suggest there were major changes in the water depths of the island's crater lakes. Lakes and wetlands trap organic material from plants and minerals from bedrock erosion, while lake sediment cores contain a record of changing environmental conditions. In this study we evaluate the potential to use new analyses on three of the island's major crater lakes: Rano Aroi, Rano Raraku, and Rano Kau. These analyses involve the use of XRF-scanning (x-ray fluorescence) and lipid biomarkers to examine the changing hydrologic conditions on Easter Island. Flash chromatography and gas chromatography-mass spectrometry will be used to take a first look at isolated plant-based alkane lipids in the cores. Records of how precipitation patterns have changed in the past can help us understand how climate has naturally varied and can put current and future climate changes into perspective. The goals of this study focus on determining how moisture on the island has varied through the paleoclimate, developing a geologic time record using new analyses and comparisons to previous work, and establishing a precise time as to when island's inhabitants first settled there.

Faculty mentor: Billy D'Andrea (Lamont Earth Observatory)

Funding support from: National Science Foundation (REU) and Columbia University/Lamont-Doherty Earth Observatory

Poster number: 6

Mechanism of a kangaroo rodents tail affecting locomotion

Harrison Funk (Microbiology)

Abstract:

The goal of the study was to understand the tail of the kangaroo rat and determine if it plays a role in balance during flight, we tracked the movements using a device that imitates a snake attack to get them to jump. The device released out causing the rodent to jump into the air and following the motion of the tail. A video analysis showed the action of the tail moving rapidly in a circular motion. Adjustment of the tail allows the body of the rodent to land in a direction and away from the predator. The importance for understanding the rodent's tail will allow understanding of predator versus prey interaction between the rat and the snake. In the future this allows further understanding of angular momentum and the transfer across multiple axis.

Faculty mentor: Craig McGowan and Jannete Schwaner

Poster number: 7

Creation and application of dual color reporters in Chlamydia *Trachomatis*

Sarah Gibbs (Microbiology)

Abstract:

Chlamydia trachomatis is an obligate intracellular, gram-negative pathogen. There are an array of studies that describe developmental cycle of *C. trachomatis,* but many unknowns lie within the biological driving forces between each step. As *C. trachomatis* moves through its developmental cycle it differentiates between two main cell types, the Reticulate Bodies (RB), the growing/dividing cells, and the Elementary Bodies (EB), the infectious cell form of the pathogen. Previously to test those driving forces, two separate plasmids have been used and their experimental results compered at the end of each trial. In efforts to have a deeper understanding of the genes controlling this cell differentiation, we have made a plasmid with Fusion Red expressing the infectious EB developmental gene and Clover expressing with the Reticulate body gene expression. This dual color plasmid will allow us to follow the two cell types sequentially as Clover turns off and Fusion Red turns on all within the same cell.

Faculty mentor: Scott Grieshaber and Nicole Grieshaber

Funding support from: National Institutes of Health

Poster number: 8

Analysis of four software methods for estimation of protein-protein relative binding affinity

Tawny Gonzalez (Chemistry / Biochemistry)

Abstract:

Biophysical descriptions of protein-protein interactions provide insight into how and why proteins behave in specific ways. These behaviors can be efficiently investigated by combining various descriptors into modeling software capable of analyzing a wide variety of protein complexes. Biophysical modeling is a useful tool to understand how amino acid mutations modify protein-protein binding affinity, a topic with significant clinical applications.
Binding affinity prediction software vary in the complexity of information used to create predictions. Our hypothesis is that software methods relying on a variety of information will provide more accurate binding affinity predictions than those relying on a single descriptive energy function. Here, we discuss a comparison between FoldX, an empirical energy scoring program, and BindProfX, a program based on structural interface profiling and pharmacophore mutation counts, and two additional submethods, FoldX using molecular dynamics (MD) snapshots and BindProfX with FoldX calculations added into final score. We used ten protein complex test systems for initial data generation and then grouped the systems based on size for analysis of program performance. We determined the correlation to experimental binding affinity data and the percentage of binding affinity sign matches between calculated and experimental data in three binding affinity categories based on the effect of single-point mutations to amino acids along complex binding interface.

Faculty mentor: F. Marty Ytreberg

Funding support from: National Institute of General Medical Sciences of the National Institutes of Health

Poster number: 9

Substitution effects of redox-active arylazothioformamide ligands: synthesis, spectral properties, and binding association determination with Copper(I) salts

Kaylaa Gutman (Chemistry)

Abstract:

Redox-active N,N-diethylphenylaziothioformamide (ATF) ligands possess the unique ability to behave in an innocent or non-innocent fashion in their chelation patterns with specific transition metals. A recent investigation has confirmed this redox-activity through the coordination of Copper(I) salts with various counteranions. From this study, a variety of ATF ligands featuring electron donating and electron withdrawing properties on the aromatic ring have been successfully synthesized. When coordination complexes were formed with Copper(I) halides with an electron donating ATF ligand, surprisingly, a different complexation pattern was seen in the X-ray crystal structure.. This finding suggests that the nature of metal-ligand interactions is largely dependent upon the substituents on the ATF ligand. Computational modeling of both complexes suggests the newly synthesized ATF analogue complex is appreciably higher in energy than the previously observed ATF complex. The effects of other electron-donating and electron-withdrawing substituents on complexation patterns and binding energies are currently under investigation.

Faculty mentor: Kristopher Waynant

Poster number: 10

Evolutionary tower defense: modeling evolution in video games using a metapopulation framework

Samantha Heck (Computer Science)

Abstract:

Project Hastur is an evolutionary tower defense video game in which the player defends their base from the aggressive alien species called *Vermis apostata. V. apostata* are modeled as a biological population with digital genomes of additive quantitative trait loci. On each game map, the player builds towers to defend their base. The enemies that get closest to the player base or that do the most damage to player structures have the highest fitness and are more likely to contribute offspring to the next generation. We are currently testing "Metapopulation Mode," in which each of the game maps are linked by migration.

Faculty mentor: Barrie Robison

Funding support from: Idaho Global Entrepreneurial Mission, and IBEST

Poster number: 11

Identification of proteins that interact with down syndrome cell adhesion molecule

Natasha Leigh Herbenson (Microbiology)

Abstract:

A genome-wide association study of more than 16,000 individuals on the autism spectrum disorder underwent a meta-analysis which resulted in a positive association between the gene mutation and the Down Syndrome Cell Adhesion Molecule (DSCAM) (SFARI, 2018). DSCAM functions to promote or prevent cells in dendrite arborization as well as axon pathfinding. The purpose of this experiment is to identify which proteins interact with the c-terminus of the DSCAM protein. The DupLEX-A Yeast Two-Hybrid System is used to determine protein-protein interactions. This technique was used to detect which variety of screened brain proteins interact with DSCAM followed by PCR and DNA sequencing. Further researching the interactions between the proteins will assist in finding potential therapy strategies that could reverse the effects of autism.

Faculty mentor: Peter Fuerst

Poster number: 12

Connections between changing axial magma flux and oceanic core complex formation along the marathon fracture zone, mid-Atlantic ridge at ~12˚N

Daniel J. King (Environmental Science)

Abstract:

Oceanic core complexes (OCCs) are the surface expression of long-lived, low-angle faults (i.e. detachment faults) along mid-ocean ridges (MORs), where the tectonic plates spread apart. Previous work suggests that magma flux along MORs may be a primary control on detachment fault formation; detachments are likely initiated during periods of low magma flux and may cease slipping after a magma pulse. However, observational constraints on the correlation between magma flux variations and OCC lifecycles are sparse. We present new data derived from shipboard bathymetric and gravimetric measurements collected by the R/V *Atlantis* (cruise AT33-03) along a ~700 km long track parallel to the Marathon Fracture Zone near ~12°N, west of the Mid-Atlantic Ridge. Combining seafloor ages with our bathymetry data, we separate the region into five morphological domains that alternate between periods of normal mid-ocean ridge faulting, 0-11, 23-31.5, and 34-45 million years ago (Ma), and OCC formation, 11-23 and 31.5-34 Ma. Digitization of faults along our track reveals a ~11° rotation in the strike of seafloor fabric from 16° at 23 Ma to 5° at 11 Ma, potentially coinciding with initiation of the most recent OCC domain. Gravity data is reduced to a Residual Mantle Bouguer Anomaly (RMBA) by removing the effects of the ocean-sediment, sediment-crust, and crust-mantle interfaces assuming a 6 km thick crust, as well as the effects of lithospheric cooling. The resulting RMBA has relative highs over the OCC domains and relative lows over regions of normal abyssal hills, implying differences in crustal thickness. We link the coincident changes in spreading rate and direction, as well as relative differences in gravity-derived crustal thickness values to examine the conditions for OCC formation. The new data supports the hypothesis that oceanic core complex formation is strongly correlated with axial magmatic flux at MORs.

Faculty mentor: Eric Mittelstaedt

Funding support from: National Science Foundation

Poster number: 13

Bacterial membrane components damage gastrointestinal neurons through oxidative stress

Sydney Kuther (Microbiology)

Abstract:

Type 2 Diabetes (T2D) is a debilitating disease that affects nearly 10% of Americans. Approximately 75% of diabetics experience symptoms of gastrointestinal (GI) dysfunction--mainly dysmotility and abdominal pain which are thought to be linked to damaged inhibitory motor neurons in the enteric nervous system (ENS). Recent studies suggest that dietary factors (glucose/palmitate), bacterial component lipopolysaccharide (LPS), and supernatants from ileocecal contents of mice with high fat diet- (HFD) induced diabetes damage to inhibitory motor neurons as observed in diabetic humans. However, it is unknown whether other bacterial factors such as lipoteichoic acid (LTA) damage ENS neurons. Furthermore, the mechanism by which LTA and GI supernatants damage neurons is not known. We hypothesized that LTA and supernatants from diabetic mice damage ENS neurons through oxidative stress. To test our hypothesis, preparations consisting of small intestine muscle layer (muscularis) were obtained from seven, healthy male mice. Tissues were cultured in LPS, LTA and ileocecal supernatants from either HFD or standard chow (SCD) mice for 24 hours. Tissues were stained by immunohistochemistry (IHC) for neuronal nitric oxide synthase (nNOS), which is expressed in inhibitory motor neurons and markers for oxidative stress: dihydroethidium (DHE) and anti-glutathione (GH). Our results revealed that LTA causes damage to inhibitory neurons more significantly than LPS and HFD supernatant. LTA and LPS increased DHE intensity. LTA increased anti-GH intensity. These results suggest that LTA and LPS damage inhibitory motor neurons through oxidative stress. HFD supernatant does not damage inhibitory motor neurons via oxidative stress.

Faculty mentor: Onesmo Balemba

Funding support from: INBRE, IDeA Network of Biomedical Research Excellence

Poster number: 14

Live imaging to probe the role of microglia in developmental apoptosis in the zebrafish retina

Jared Lambert (Biology)

Abstract:

During mammalian retinal development, programmed cell death (apoptosis) occurs in large waves in a spatio-temporal fashion to generate functional retinas. In zebrafish comparably smaller waves have been observed and are thought to represent fine-tuning of developing retinal tissue (Biehlmaier 2001). It is appreciated that tissue resident macrophages clear apoptotic cells (Hochreiter-Hufford 2013), however, specific roles for microglia in cell survival/death and clearance during retinal development in zebrafish have not been documented. We used an inducible system to specifically deplete macrophages/microglia during retinal development (Petrie 2015) and found an increased number of apoptotic cells in the retina compared to controls. This finding suggests that microglia clear larger numbers of apoptotic cells than is currently appreciated, or alternatively, that microglia provide survival signals to developing retinal cells. To address clearance of apoptotic cells during zebrafish retinal development in real-time, we live imaged fluorescently labeled retinal microglia together with apoptotic cells using acridine orange (AO). We observed that microglia sense and engulf cells prior to AO incorporation, and that engulfed apoptotic cells undergo dynamic movements as microglia continue active migration. This suggests that apoptotic cells visualized in fixed tissues using AO may not represent true levels of apoptosis and their retinal locations may differ from where apoptosis was initiated.

Faculty mentor: Diana Mitchell

Funding support from: Idaho State Board of Education

Poster number: 15

Fatty acid analysis in *Euglena* strains

Leah Lambert (Biochemistry)

Abstract:

Polyunsaturated fatty acids are essential in the human diet and help to promote cardiovascular health, brain function, visual development, and help to reduce inflammation. Dietary supplements containing these essential fatty acids can be produced commercially from various methods ranging from algae to fish. *Euglena* are photosynthetic protozoa that are adept at producing polyunsaturated fatty acids including the essential lipids DHA and EPA. We compared four strains of *Euglena* under different growth conditions in order to maximize the production of specific fatty acids. Isolated from different environments, the strains were grown in minimal acidic media (pH 3.5) with supplements that included sodium pyruvate or isoleucine. Nitrogen-deficiency was also tested for increased fatty acid production. The total fatty acid content was determined using a GC-MS while the relative abundance of each type of fatty acid was determined commercially through Microbial ID (Newark, Delaware). Among the results that will be discussed are the conditions that promoted a 300% increase in odd chain fatty acid production.

Faculty mentor: Doug Cole

Funding support from: INBRE, IDeA Network of Biomedical Research Excellence

Poster number: 16

Ionic and biomolecular movement through functionalized thin filmed polymers

Garrett Larson (Biology)

Abstract:

Ions and biomolecules are essential for many functions of the human body such as bone strength and development, muscle contractions, and cell functions like membrane transport and membrane potentials. This experiment will use post-polymerization functionalization to bind to Calcium ions (Ca^{2+}), using ion selective electrode polymers; this binding could be a way of monitoring calcium levels in the body. The polymer scaffolding will be made from Poly-(3-sulfopropyl methacrylate). This sulfonic acid polymer will capture Ca^{2+} through negatively charged terminal ends, in acidic environments, that can ionically bond to the Ca^{2+}. These polymers will be grown on carbon nanotubes. We will characterize these polymers with transmission electron microscopy (TEM) and RAMAN spectroscopy. The transport of Ca^{2+} through the polymer surfaces will be monitored by measuring the voltage change on the polymer electrode as a Calcium solution is passed over it. A device was designed to hold the polymer in a closed system to allow the solution to pass over it and out, which allows us to monitor the concentration of the calcium solution after polymer interaction.

Faculty mentor: Kristopher Waynant

Funding support from: Summer Undergraduate Research Fellowship

Poster number: 17

A computational investigation of high-spin, square-planar Fe^{II} complexes

Kyle Luchte (Mathematics)

Abstract:

In this project we explore the factors that contribute to the stabilization of high-spin, square-planar Fe(II) and tetrahedral Zn(II) complexes supported by fluorinated pinacolate ligands (pin^F). High- spin, square-planar Fe(II) compounds are not only extremely rare, fewer than ten examples have been characterized, but also the factors responsible for their stabilization are not understood. Here we used Density Functional Theory (DFT) calculations performed using the Gaussian 09 and multiconfigurational CASSCF calculations completed using the ORCA 4.0 computational chemistry software packages to explore the electronic structures of these compounds. These tools allowed us to make detailed inquiries regarding their electromagnetic properties through theoretical computations and modeling. Our theoretical analysis suggests that the high electronegativities of the twelve fluorine atoms of the individual pin^F ligands lead to large negative charges localized on the periphery of these complexes. These charges lead to a strong electrostatic repulsion between the two pin^F ligands which favors a square-planar geometry. However, the change from a tetrahedral geometry observed for the $[Zn^{II}(pin^F)_2]^{2-}$ complex anion to a square-planar geometry observed for $[Fe^{II}(pin^F)_2]^{2-}$ can only be explained by considering an additional Crystal Field Stabilization Energy (CFSE) contribution only present for the Fe(II) ion. Thus, my research provides evidence that the high-spin square-planar structure is a result of a "tug-o-war" between CFSE and the electrostatic repulsion between the ligands.

Faculty mentor: Sebastian Stoian

Poster number: 18

The effects of the gut microbiota on diabetic enteric neuropathy

George May (Microbiology)

Abstract:

Diabetes is increasing at an alarming rate. The direct cost of treating this disease in the US is $176 billion annually. Diabetic patients suffer from gastrointestinal (GI) motility disorders, which include gastroparesis, diarrhea and constipation. GI nerve cell death (neuropathy) is thought to be the underlying cause of these disorders. Consumption of a high fat diet causes type two diabetes (T2D) and enteric neuropathy in mice, which correlates with dysmotility Research suggests the interactions between diet, gut microbiota and the host play a role in the development of diabetes. These interactions result in the production of metabolites and compounds including short chain fatty acids. However, the link between these interactions, resultant metabolites and diabetic enteric neuropathy is not fully known. The first goal of this study was to test the hypothesis that intestinal microbiota has a role in the development of diabetic enteric neuropathy. The second goal was to determine whether byproducts of gut microbiota activity, specifically short chain fatty acids (SCFA), cause enteric neuropathy. Two groups of mice, germ free (GF) and conventionally raised, were fed a standard chow diet (SC) or a high fat diet (HF) for 8 weeks. Intestinal muscularis samples from SC fed conventional mice were also cultured with SCFAs for 24 hours. The samples were then analyzed for neuropathy.The final conclusion is that a HF cause diabetic neuropathy in conventional mice, but not in germ free mice. It was also noted lipoteichoic acid (LTA) and lipopolysaccharides (LPS) may play a role in nNOS neuropathy, but SCFA do not significantly contribute to diabetic neuropathy.

Faculty mentor: Onesmo Balemba

Funding support from: INBRE grant #P20GM1034

Poster number: 19

Using variable stars to constrain planetary formation theories

Samuel Myers (Physics / Mathematics)

Abstract:

Observations of exoplanets over the past twenty years have revealed a diverse arrangement of planetary systems. This diverse arrangement, consisting of planets orbiting their host stars in all manner of orbital configurations, poses problems for traditionally accepted models of planetary formation and evolution. Such models predict that planets should orbit their host stars in roughly the same plane as the star's equator, however this is not the case for all observed planetary systems. Different models have been proposed to explain this discrepancy. We set out to constrain these models by measuring the spin-orbit misalignment of planets with orbital periods between 10 and 100 days orbiting high-mass stars. Planets in this range likely have orbital configurations preserved from initial formation due to weaker stellar tidal forces farther from the host star. Measurements of spin-orbit misalignments of these planets can thus help to constrain theories of planetary formation and evolution by providing a glimpse into the early history of different planetary systems. Stars in this mass range, however, are often variable stars: stars that have inherent variance in their brightness that can be problematic for efforts to constrain the orbital parameters of planets orbiting them. This requires additional work to properly analyze these systems. We examine *Kepler* Object of Interest 972, a planetary candidate orbiting such a star, and demonstrate our technique for removing stellar photometric variability from lightcurves to constrain spin-orbit misalignment. We then briefly discuss our work with other systems and the implications of our results on theories of planetary formation and evolution.

Faculty mentor: Jason Barnes

Funding support from: NASA and University of Idaho Honors Program

Poster number: 20

Why your gut may be working against you: gut derived molecules cause dysmotility and neuropathy in high fat fed mice

Jessica Nicholson (Biology)

Abstract:

Type 2 diabetes (T2D) is a prevalent disease in the United States, affecting 21.9 million people. Patients often suffer from gastrointestinal (GI) issues like stomach cramps and constipation. This is caused by a reduction in inhibitory motor neurons in the intestinal tract. Recent studies have shown the development of gastrointestinal dysmotility and neuropathy before the onset of T2D, and ileocecal supernatants from high fat (HF) fed mice caused dysmotility and neuropathy ex vivo. However, the specific cause of dysmotility and neuropathy are still not known. We hypothesized that fractions from HF ileocecal supernatants would cause dysmotility and neuropathy. High Performance Liquid Chromatography (HPLC) was used to separate supernatants into aqueous (water) and methanolic fractions which were tested on mice intestinal muscularis tissue. Contractions of the tissue samples were counted, and immunohistochemistry and imaging used to determine if these fractions caused neuropathy. Water fractions from HF mice caused a significant decrease in muscularis contractions after 24 hours; water fractions of standard chow fed (SC) mice and methanolic fractions of HF and SC mice did not significantly induce dysmotility. It was also found that HF water fractions caused a reduction in neuronal nitric oxide synthase (nNOS) staining, indicating that the inhibitory motor neurons were damaged. These results suggest a molecule(s) in the HF water fractions are causing dysmotility and neuropathy. Sub-fractionation and chemical analysis of these fractions will narrow down on gut derived molecules that may be causing these symptoms; and lead to treatment options before the start of T2D.

Faculty mentor: Onesmo Balemba

Funding support from: University of Idaho Summer Undergraduate Research Fellowship

Poster number: 21

Investigating the metal-controlled cyclization of tris-hydroxyimino ligands and their coordinating properties

Alexander Roseborough (Chemistry)

Abstract:

Tris (2-hydroxyiminopropyl) amine was synthesized from the reaction of hydroxylamine with chloroacetone. This molecule is expected to undergo a metal-controlled cyclization, to yield adamantane-like cages incorporating multiple NO groups. Both the tris (2-hydroxyiminopropyl) amine and the adamantane-like species can function as ligands and are able to coordinate metal ions that have multiple oxidation states, i.e., a varying number of electrons. We will investigate the reactions of the two ligand forms with iron, cobalt, and copper ions. These electronic structures of the metal-containing complexes will be investigated using ^{57}Fe Mössbauer spectroscopy (for Iron compounds) and EPR spectroscopy.

Faculty mentor: Sebastian Stoian

Poster number: 22

Quantifying gene expression of DSCAML1 (down syndrome cell adhesion molecule-like 1) in the cerebellum to examine possible causes of autism

Megan Schlussler (Medical Sciences)
Mark Lee (Molecular Biology and Biotechnology)

Abstract:

Autism Spectrum Disorder (ASD) affects 1 in 59 children in the United States and is thought to be caused by a combination of environmental and genetic factors. Among the many genes implicated in the etiology of ASD are Down Syndrome Cell Adhesion Molecule (*Dscam)* and a closely related gene found on chromosome 11, *Dscaml1.* We examine *Dscaml1* in mouse models to examine its role in ASD. As a first step in this exploration, we explore methods of quantifying gene expression in the mouse brain. Our lab has developed mouse models in which a beta-galactosidase gene is linked to *Dscaml-1.* This allows for assessment of DSCAML-1 expression using X-Gal staining. Secondly, we stain tissues with Hematoxylin and Eosin, to assess structural changes and cell density. Post-mortem studies of people with ASD have revealed changes in the cerebellum, but the genetic factors behind these changes are unknown. In addition, the cerebellum provides a well-differentiated structure in which to define measurements in wild type and loss of function mutants.

Faculty mentor: Peter Fuerst

Poster number: 23

A novel resin for chemical protein synthesis

Tyler Siegford (Biochemistry)

Abstract:

Therapeutic proteins have successfully treated a range of diseases and offer potential to treat many more. Using chemical synthesis, proteins can be fabricated uniformly with precise control over chemical structure. High purity synthesis of proteins larger than 50 amino acids relies on the use of ligation strategies to link smaller peptides. The most notable of these ligation strategies, Native Chemical Ligation, requires peptides with C-terminal thioesters. We have produced a novel resin for solid phase peptide synthesis by coupling 1,2-phenylenediamine directly to trityl chloride resin, which when cleaved, leaves a C-terminal *o*-aminoanilide. Using the chemistries reported by Weidmann et al. this *o*-aminoanilide can be activated and substituted with a variety of thiols giving a peptidyl C-terminal thioester primed for ligation.

Faculty mentor: Darren Thompson and Kristopher Waynant

Funding support from: INBRE, Institutional Development Award from National Institute of General Medical Sciences of the Nation Institutes of Health under grant #P20GM103408

Poster number: 24

Abstracts

Graduate Division

(alphabetical by presenter)

Detection of mixed-sequence dsDNA using bulged invader probes

Shiva Prasad Adhikari (Chemistry)

Abstract:

Oligonucleotide-based probes capable of sequence-specific recognition of double-stranded (ds) DNA have tremendous potential as tools in diagnostics, gene editing, and molecular therapy. Double-stranded probes binding to dsDNA via invasion modes offer the promise of favorable binding thermodynamics, high binding specificity, and straightforward design. Our laboratory has introduced so-called Invader probes, which rely on large stability differences between probe duplexes and recognition complexes to drive recognition of mixed-sequence dsDNA targets. The arrangement of 2'-intercalator-functionalized RNA monomers in +1 interstrand zipper motifs is the central design feature that activates Invader probes for dsDNA recognition. Here, we present improved mixed-sequence dsDNA recognition using Invader probes that are additionally modified with non-nucleotidic bulges. Invader probes with appropriately selected and positioned bulges display more efficient, specific, and faster recognition of mixed-sequence dsDNA targets than conventional Invader probes.

Faculty mentor: Patrick Hrdlicka

Poster number: 25

Dynamics of multiple bodies in a corotation resonance

Joseph A'Hearn (Physics)

Abstract:

Saturn's moons Aegaeon, Anthe, and Methone and their surrounding ring arcs are in corotation resonances with Saturn's moon Mimas that cause their semi-major axes to oscillate stably every few years. These resonances also longitudinally confine debris launched from these moons into arcs. How these moons became trapped in these resonances is still not well understood. Also, it is unclear why Aegaeon is the closest to exact resonance. We simulate orbits of multiple massive bodies in a corotation resonance in order to better understand these systems. In these simulations, the bodies exchange angular momentum and energy during close encounters, altering their orbits. Nevertheless, since a typical encounter occurs on a timescale that is short compared to the synodic period of Mimas, the relationships between the energy transferred by the encounter and the locations of the objects relative to the sites of exact corotation is more complex than one might expect. More massive bodies are more likely to remain in the corotation resonance, while less massive bodies are more likely to exit it. This can explain why Aegaeon has remained in the corotation resonance with Mimas, but does not explain why it is so close to exact resonance. Further investigation of these interactions may be relevant to understand denser systems like the arcs in Neptune's Adams ring and how they can be maintained in the face of frequent inelastic collisions.

Faculty mentor: Matthew Hedman

Funding support from: NASA

Poster number: 26

Predicting iceberg calving from the Greenland ice sheet

Tristan Amaral (Geology)

Abstract:

The process of iceberg calving drives glacier mass loss via direct ice removal and through its control on glacier front position. Accurate representation of iceberg calving in ice sheet models is therefore critical for reliable sea level rise projections, yet there is a lack of consensus on how to best parameterize iceberg calving at glacier or ice-sheet scales. At present, more than ten iceberg calving models exist that employ glaciological properties to predict either the position of the calving front or a calving rate. However, calving model generation has far outpaced thorough validation of existing calving models and thus the relative accuracies of these calving models are largely unknown. Here, we validate and inter-compare six iceberg calving models, including those considering height above buoyancy, crevasse penetration, and a von Mises criterion, against a large and varied selection of 100 Greenland marine-terminating outlet glaciers using remotely sensed data and model outputs. We determine the single best value for each calving model tuning parameter and quantify associated calving model uncertainties in terms of the misfit between modelled glacier terminus position and observed terminus position. Based on our evaluation of calving model performances, we recommend iceberg calving criteria for use in ice sheet models. Preliminary results from Greenland find that, in the height above buoyancy calving model, a threshold height of 34 m minimizes error in the predicted terminus location, with a standard deviation in terminus misfit of 610 m. These results inform the Ice Sheet Model Inter-comparison Project for CMIP6 (ISMIP6) and offer a path for improved simulation of dynamic glacier change in Greenland.

Faculty mentor: Timothy Bartholomaus

Funding support from: NASA and National Science Foundation

Poster number: 27

Modeling antibody escape mutations in respiratory syncytial virus

Sierra Beach (Microbiology / Molecular Biology and Biochemistry)

Abstract:

Human respiratory syncytial virus (RSV) is the second leading cause of infant mortality in the world and is responsible for over 100,000 deaths each year. There is currently no licensed vaccine and the only treatment is palivizumab, a prophylactic monoclonal antibody, that targets the viral fusion glycoprotein (F protein). Given the lack of therapeutic options, mutations in the F protein that allow the virus to escape antibody neutralization are of high concern. We seek to establish a molecular model to predict antibody escape mutants in the F protein. Molecular dynamic simulations of the F gene were performed at the binding site of motavizumab, a palivizumab derivative. The predicted antibody escape mutations were engineered into an infectious clone for testing viability, fitness, and neutralization. In a parallel study, the wild type infectious clone was subjected to selective passages *in vitro* in the presence of motavizumab or the antibody AM14, to compare predictions to the variants isolated under selective pressure. Following selective passaging, samples that required higher antibody concentration for neutralization were sequenced and compared to predicted mutations. One predicted and one unpredicted F gene mutation were found in the AM14 samples and one predicted mutation was found in the motavizumab samples. While the results are promising, further experiments are needed to test the limits of the model. This study seeks to capture the powerful predictive capability of molecular modeling and transform it into clinically relevant watchlist and potential new therapeutics, setting the foundation for predicting mutations in other important viruses.

Faculty mentor: Tanya Miura

Funding support from: National Science Foundation EPSCoR Research Infrastructure Improvement Program: Track-2

Poster number: 28

Synaptic convergence for night vision in the mammalian rod visual circuit

Mellisa Clemons (Microbiology / Molecular Biology and Biochemistry)

Abstract:

Age-related macular degeneration is the leading cause of vision loss among older adults in the US (Ying, G., et al., 2008). Disease progression leads to visual impairment in night vision due to the death of rod photoreceptors. The spatial connectivity of retinal cells, from rod photoreceptors to ganglion cells, is currently unknown. Various genes play important roles in determining the healthy arrangement of cells in the retina. Dscaml1 (Down Syndrome Cell Adhesion Molecule-like 1) plays a role in dendrite self-avoidance among retinal cells. The Bax gene (B-cell-lymphoma-2Associated X Protein) plays a major role in neuronal apoptosis. We compare the cellular requirements between these loss of function genotypes in the development of this pathway. Using electron micrographs we are able to visualize the cellular organization of the rod to bipolar cell pathway in the mouse model. Our results suggest that rod pathways are less spatially separated than cone pathways responsible for color vision. These findings provide a basis for understanding information flow through a neural circuit.

Faculty mentor: Peter Fuerst

Funding support from: INBRE and National Institute of General Medical Sciences Grant #P20 GM103408

Poster number: 29

Do human pathogens better retain novel multi-drug-resistant plasmids after coevolution with a single plasmid type?

Clinton Elg (Bioinformatics and Computational Biology)

Abstract:

Human health is increasingly threatened by antibiotic resistance, which at current rates will cause more deaths than cancer by 2050. Horizontal gene transfer facilitated by broad-host-range (BHR) plasmids is a key underlying factor in the emerging post-antibiotic era. BHR plasmids carrying multi-drug resistant (MDR) plasmids often impose fitness costs on their bacterial hosts. Continuous antibiotic selective pressure is rare in most environments, so how these MDR plasmids are otherwise maintained in bacterial populations is not well understood. Our goal is to determine if chromosomal mutations selected for during coevolution of a bacterial host with an MDR plasmid in the presence of antibiotics results in an evolved host with generally improved persistence of novel plasmid types in the absence of known selective pressure. We selected three human opportunistic pathogens belonging to the γ-proteobacteria from previous evolutionary studies in which compensatory chromosomal mutations increased the persistence of their co-evolved plasmid. Four novel BHR MDR plasmids, each representing a different Inc-group, were then respectively transformed into cured segregants of the ancestral and evolved bacteria from theses previous studies. To assess the persistence of these novel plasmids, these bacterial hosts were passaged daily for ten days at ~10 generations/day in the absence of antibiotics. The populations were scored daily for the fraction of plasmid-bearing cells by replica-plating onto plasmid-selective and non-selective media. Initial results demonstrate that after coevolution with a particular plasmid, bacterial pathogens better retain one or more types of other MDR plasmids. This is important, as rare antibiotic presenting environments that drive bacterial evolution towards increased generalized plasmid persistence could help explain why costly MDR plasmids are maintained without known selective pressure in bacterial populations.

Faculty mentor: Eva Top

Funding support from: National Institute of Health R01 AI084918, U.S. Department of Defense, Grant #DM110149, and University of Idaho Bioinformatics and Computational Biology Fellowship

Poster number: 30

Utilizing invader probes for recognition of restriction enzyme sites

Raymond Emehiser (Chemistry)

Abstract:

Current methods for treating protein associated diseases are to modulate activity or levels of the toxic protein through two different strategies; using small molecules, which bind to the protein resulting in reduced protein activity; or by reducing the protein levels through mRNA degradation using miRNA or siRNA techniques. While these two methods have resulted in many useful drugs, the development of new drugs is very challenging and expensive and often result in unpleasant side effects.

Targeting DNA can potentially affect more protein and RNA targets than current methods, with fewer side effects. DNA is a very stable molecule because of hydrogen bonding and pi-stacking, making it a challenging target. To this end Invaders have been designed with pyrene moieties attached in the correct orientation as to clash sterically when positioned opposite each other, thus resulting in an easily denatured Invader probe. The clashing is alleviated when a single-strand Invader probe is bound to complementary DNA because there is only one pyrene present which can participate in pi stacking increasing the stability of an Invader:cDNA duplex. This strategy has resulted in the design of Invader probe which can recognize double-stranded DNA under non-denaturing conditions, potentially allowing for its use as a DNA targeting drug. While much work has been done in optimizing Invaders and testing them in a model system there has been little work in evaluating their ability to target plasmids or block DNA protein interactions.

In the present work, we have evaluated Invaders ability to recognize 3 specific restriction enzyme cut sites on a 4000 base-pair plasmid. Invaders are tested for their ability to bind to the plasmid as well as block the restriction enzyme from interacting with the DNA.

Faculty mentor: Patrick Hrdlicka

Poster number: 31

The effects of thyroid hormone of the expression of *rh2*-type cone opsin genes in zebrafish

Ashley Farre (Neuroscience)

Abstract:

Color vision is possible because different cone opsins with distinct peak spectral sensitivities are expressed in separate cone populations, providing differential input to downstream neurons. In humans, the genes for red and green-sensing cone opsins (*LWS/MWS*) are arrayed in tandem and share a single locus control region. These genes evolved through tandem duplication and sequence divergence. Independently, a similar evolutionary process occurred in zebrafish with both the long wavelength-sensitive array (*lws*; red-sensing cone opsins) and the *rh2* array (blue/green-sensing cone opsins). Our published studies demonstrate that retinoic acid affects the ratio of LWS cones, decreasing LWS2 and increasing LWS1. Unpublished research from our laboratory indicates that thyroid hormone similarly affects the ratio of LWS cones, and that thyroid hormone downregulates expression of *rh2-1* and upregulates that of *rh2-2*. The goals the current project were: to determine whether transgenic reporter lines for the *rh2* genes also report the effects of thyroid hormone; and to determine whether thyroid hormone regulates the expression of *rh2-3* and *rh2-4*. To do this, we treated *rh2-2*:GFP and *rh2-3*:GFP;*rh2-4*:RFP transgenic embryos with thyroid hormone, imaged whole eyes and cryosections, and quantified reporter-expressing cones. Our results suggest that the transgenic reporter for *rh2-2* does not show the same response to thyroid hormone as the native locus. The *rh2-2*:GFP reporter transcript may be upregulated but not present in additional cones, or the reporter construct may respond to thyroid hormone differently than the native locus. Our results also suggest that *rh2-3*, but not *rh2-4*, is upregulated by thyroid hormone.

Faculty mentor: Deborah Stenkamp

Funding support from: Nation Science Foundation and National Institutes of Health

Poster number: 32

Genetic isolation and a unique disease threatening the island fox

Sarah Hendricks (Bioinformatics and Computational Biology)

Abstract:

Severe loss of genetic diversity due to founder effect, historical bottlenecks, limited carrying capacity, and anthropogenic threats may contribute to a high incidence of ceruminous gland carcinoma in the Santa Catalina (SCA) island fox (*Urocyon littorialis catalinae*). These cancers form in the ear canals of approximately half of adult SCA foxes, and are associated with chronic inflammation caused by ear mite infection. We test the hypothesis that the remarkably high incidence of carcinoma in SCA foxes is the result of genetic variants for cancer susceptibility. We apply genomic tools including RAD-seq and whole-genome sequencing to identify specific candidate genes. Preliminary results indicate that a point mutation near a tumor suppressor gene may be involved in tumor development. Ultimately, we aim to develop a susceptibility panel to genetically assess an individual's probability of developing cancer, which could be used for population management in this threatened subspecies.

Faculty mentor: Paul Hohenlohe

Funding support from: National Science Foundation, IBEST, and National Institutes of Health

Poster number: 33

Rhinovirus curtails disease severity in respiratory viral co-infections in mice

Emmanuel Ijezie (Biology)

Abstract:

Patients suffering from viral respiratory disease are often infected with multiple unrelated viruses, known as co-infection; however, it is unclear how viral co-infections influence disease pathogenesis. Our lab previously established a mouse model of respiratory viral co-infection to answer this question. Mice were inoculated with a mild respiratory virus (rhinovirus, RV1B) two days before a virus that causes severe disease (influenza A virus, PR8). Co-infection with RV1B reduced the severity of PR8 infection, as determined by mortality, weight loss, and clinical signs of disease. Mouse lungs were collected on days 4, 7, and 10 post-infection for pathological analyses. Lung tissues were paraffin-embedded for staining and further analysis. Histology slides were stained with Masson's trichrome stain and hematoxylin and eosin (H&E) stain to evaluate inflammation and tissue damage, and immunohistochemistry was used to show localization of virus and immune cells. These analyses showed that RV1B mediates an early immune response that is characterized by neutrophil recruitment, followed by viral clearance and tissue repair. Host-pathogen interactions during viral co-infection are still poorly researched and these results will likely have an important role in elucidating mechanisms necessary for reducing the severity of influenza infection during respiratory viral co-infection.

Faculty mentor: Tanya Miura

Funding support from: National Institutes of Health P20GM104420, National Science Foundation 1460696, and Center for Modelling Complex Interaction

Poster number: 34

Magnetic property and nanostructural evolution of iron oxide nanoparticles heated up to 800˚C

Lokendra Raj Khanal (Physics)

Abstract:

For nuclear energy, safety performance is very important but there are few options for *in-situ* radiation detectors due to the high-temperature up to 500 ˚C in the core of nuclear reactors. Recently, studies on the iron-based magnetic nanoparticles have shown their applications as radiation sensor materials. Magnetite nanoparticles (NPs) have become ferromagnetic under irradiation at room temperature due to the particles size growth and microstructural evolution. Our work aims to study the high-temperature effect on the magnetite NPs for the possible application as a radiation sensor material in the high-temperature core of nuclear reactor. Magnetite NPs synthesized by nanocluster deposition system were heated up to 800 ˚C in three different environments: argon, oxygen and vacuum. The NPs are characterized by magnetometer, SEM and XRD in order to understand the magnetic property-structure relationships and nanostructural evolution at the elevated temperature. The results have shown enhanced magnetization of the NPs due to the sintering of the NPs and over all particles size growth by the agglomeration of the particles at high-temperature in vacuum. The phase and morphology almost remain unchanged up to 800 ˚C. However, in argon and oxygen at high-temperature antiferromagnetic hematite appeared, which results in the reduced magnetization and size of the particle changes abruptly above 500 ˚C. Since the core of the nuclear reactor is vacuum, the stable nanostructure in vacuum with the enhanced magnetization at the elevated temperature strengthen the possibility of the magnetite NPs as in-situ radiation sensor material for the next generation nuclear reactor, and as the advanced data storage nanomaterials in the harsh environments.

Faculty mentor: You Qiang

Poster number: 35

The influence of orbital eccentricity on the obliquity stability of retrograde rotating planets

Steven Kreyche (Physics)

Abstract:

Understanding how a terrestrial planet's obliquity, or axial tilt, varies over time is essential when judging its potential habitability, as it largely governs changes in the planet's climate. Previous studies suggest that planets with retrograde obliquities (rotating backwards with respect to their orbital motion), may generally experience less severe obliquity variations than those with prograde obliquities (rotating in the same direction with respect to their orbital motion). Opposing this claim, we find that for specific initial conditions, the orbital eccentricity of a planet can influence the obliquity stability of planets with retrograde obliquities by creating a spin-orbit resonance that occurs when the planetary system's orbital frequencies overlap with the planet's own rotational precession frequency. This overlap can lead to a commensurability, where the obliquity variations of the planet can be important in the consideration of habitable conditions.

Faculty mentor: Jason Barnes

Funding support from: NASA program Astrobiology: Exobiology and Evolutionary Biology

Poster number: 36

Comparative genomics, evolution, and transmissible cancers in Tasmanian devils (*sarcophilus harrisii*)

Kevin Lewallen (Bioinformatics and Computational Biology) and
Amanda Stahlke (Bioinformatics and Computational Biology

Abstract:

Devil facial tumor disease (DFTD) afflicts the Tasmanian devil and has spread rapidly through the species since its emergence in 1996. Previous research has revealed genomic signatures of a rapid evolutionary response in devils to the strong selection imposed by DFTD. We expanded this work to include a much broader range of populations, individuals, loci, and timepoints, and found concordant signatures of selection in 186 SNPs within 100 kb of 136 annotated genes functionally enriched for immune pathways. We then used orthologous regions in three other marsupial species as a genomic background to test the devil for evidence of historical selection. We found a significant difference between the distribution of sites under positive selection in the devil and the marsupial background. Additionally, we performed gene term enrichment analysis and found immune function pathways common to both our contemporary and historical selection results. Finally, we are whole genome sequencing two species of quoll from the devil sister clade, *Dasyurus.* We intend to compare these and the recently published thylacine genome with the devil genome to assess whether the Tasmanian devil and perhaps other dasyurid marsupials are uniquely susceptible to developing transmissible cancers.

Faculty mentor: Paul Hohenlohe

Funding support from: IBEST, National Science Foundation, and National Institute of Health

Poster number: 37

Docking the virus: The interaction between HIV-1 and nucleoporin 153

Shunji Li (Microbiology / Molecular Biology and Biochemistry)

Abstract:

Efficient HIV-1 nuclear trafficking is dependent upon the interaction with nucleoporins (Nups) that constitute the nuclear pore complex and allow HIV-1 to infect non-dividing cells. Nup153 is required for HIV-1 nuclear entry and directly interacts with the HIV-1 capsid with a small motif within a Phenylalanine-Glycine (FG) enriched domain. Little is known regarding what governs the specificity of the HIV-1 capsid for this binding site within Nup153. Using molecular modeling techniques, we have investigated the importance of the amino acids in this motif for HIV-1 capsid binding and derived a consensus sequence for this interaction motif (PxxVFxFG). To test our *in silico* models, we created mutations in Nup153 that are predicted to disrupt or improve this interaction. Using Nup153 fused to the Rhesus TRIM5α effector domain, we screened a diversity of Nup153 mutants in cell culture for their effect on HIV-1 capsid interaction. Surprisingly, we found that certain Nup153 mutants were able to improve the interaction, whereas most others had no effect. This study provides insight into which amino acids are important to determine the specificity of the Nup153-capsid interaction. Specifically, why the interaction between capsid and the simple PxxVFxFG motif is preferred over other similar FG sequences in Nup153 and other FG-rich nucleoporins that are abundant within the nuclear pore complex.

Faculty mentor: Paul Rowley

Funding support from: National Science Foundation EPSCoR Track-2

Poster number: 38

Approximate Bayesian computational statistical methods to estimate the strength of divergent selection in yeast

Martyna Lukaszewicz (Bioinformatics and Computational Biology)

Abstract:

Genomic data provides the possibility to learn how the environmental conditions structure genetic make-up of organisms. However, analytical tools have not kept up with the wealth of genomic data, so that we are still limited in our ability to make detailed inferences about how natural selection and other evolutionary processes affect genomic variation. Markers with elevated genetic differentiation between populations have traditionally been used to detect loci under divergent selection. But the regions with most differences in genome sequence may expand over large, physically linked regions on chromosomes, a phenomenon known as *genomic islands of divergent selection*. Genomic islands are not simply predictable result of divergent selection but rather the region size of genomic islands depends on strength of selection on genes, migration between populations and recombination rate of parental genomes, making it difficult to identify by comparative genomics alone. We aim to test on *Saccharomyces cerevisiae* whether under low selection and migration the genomic islands of divergent selection lead to frequency of alleles being different than if the loci were independent, and if weaker selection and higher migration and recombination rates breakdown linkage disequilibrium around new mutations. The recombination and migration rates are controlled in laboratory environment and experimental data are used to develop and test analytical tools of inferences about the evolutionary process. We develop a simulator to simulate genomic data under different parameter values for divergent selection. We determine which population genetics statistics are the most informative under the model of divergent selection with migration and recombination. The simulator is used to develop Approximate Bayesian Computation methods to make inferences on population genetic parameters such as strength of divergent selection, rate of recombination and migration.

Faculty mentor: Erkan Buzbas and Paul Hohenlohe

Funding support from: National Science Foundation

Poster number: 39

Endocrine regulation of multichromatic vision

Robert Mackin (Molecular Biology and Biochemistry)

Abstract:

Cone photoreceptors mediate high acuity and color vision, the consequence of selective expression of an opsin protein with a specific spectral sensitivity. Zebrafish are multichromatic, with cone opsins sensitive to UV (*sws1*), blue (*sws2*), blue-green (*rh2*), and red (*lws*). The *lws* and *rh2* genes are tandemly-duplicated and quadruplicated, respectively. *lws2* and *rh2-1* encode a more blue-sensitive opsin compared to the other member(s) of the respective array (*lws1*, *rh2-2/3/4*). Gain-(GOF) and loss-of-function-(LOF) approaches were used, together with qPCR, in situ hybridization, and confocal microscopy of transgenic fluorescent reporters, to test roles for thyroid hormone (TH) in regulating differential expression from these tandem arrays. GOF consisted of treatment with 100nM triiodothyronine (larvae) or 386nM thyroxine (juveniles). LOF involved the transgenic *Tg(tg:nVenus-2a-nfnB)*$^{wp.rt8}$, which allows thyroid-selective ablation by 10mM metronidazole-mediated conversion of thyroid-expressed nitroreductase. TH-GOF in larvae and juveniles upregulated *lws1,* and downregulated *lws2* and *rh2-1*, with evidence of an *lws2* to *lws1* switch in individual cones. *rh2-2* was upregulated by TH in larvae and downregulated in juveniles. TH-LOF downregulated *lws1* and *rh2-2*, and upregulated *lws2*. Exogenous TH therefore promotes expression of opsins sensitive to higher wavelengths, even within individual cones, and endogenous TH signaling regulates a shift to higher wavelength-sensitivity as zebrafish grow.

Faculty mentor: Deborah Stenkamp

Funding support from: National Institutes of Health RO1 EY012146, National Science Foundation-REU site 146096

Poster number: 40

Theoretical and spectroscopic investigation of a series of Iron(II)-Selenide model complexes and of their Iron(II)-Sulfide analogues

Mahsa Moshari (Chemistry)

Abstract:

Iron-sulfur proteins are prevalent throughout biology. In most cases, the observed iron-sulfur sites are pseudo-tetrahedral and are supported by four sulfide ligands. In this project we investigate the electronic structure of a series of iron-selenide complexes and compare it with that of their iron-sulfide analogues. Selenium is a potent antioxidant and a significant micronutrient that plays an important role in human health. Therefore, in the last decade the research of Se-containing proteins has attracted increased interest. Iron-containing selenoproteins are involved in the defense against oxidative stress induced by excess reactive nitrogen species (NOS) and reactive oxygen species (ROS).

In this work, we investigate the structural and electronic properties of a series of pseudo-tetrahedral iron (II) complexes with a Se and S first coordination sphere, namely, $[Fe^{II}[(\boldsymbol{E}P^{i}Pr_2)_2N]_2]$, $[Fe^{II}[(\boldsymbol{E}PMe_2)_2N]_2$ and $[Fe^{II}[(\boldsymbol{E}PH)_2N]_2$ where E = S, Se. These compounds are structural model-complexes of mononuclear Iron-Sulphur and iron-selenium proteins. Some of these compounds have been structurally characterized through X-ray crystallography and their electronic structure was investigated using field-dependent ^{57}Fe Mössbauer spectroscopy and high-field EPR. In this poster we present the theoretical investigation of these compounds. Thus, the predicted geometries were obtained using Density Functional Theory (DFT) performed at the BP86/6-311G and B3LYP/6-311G level of theory. Furthermore, the zero-field splitting (ZFS) of the quintet, S = 2 ground state was explored using multiconfigurational methods such as CASSCF/NEVPT2. Together, these calculations allowed us to assess the magnitude of the pseudo Jahn-Teller effect anticipated for this class of compounds.

Faculty mentor: Sebastian Stoian

Poster number: 41

Phenotypic heterogeneity in tolerance permits rapid transition to growth with lethal levels of formaldehyde stress

Siavash Riazi (Bioinformatics and Computational Biology)

Abstract:

Despite the ability of methylotrophs to grow on C_1 compounds while producing formaldehyde as an intracellular intermediate, they remain sensitive to fairly modest levels of extracellular formaldehyde. As part of fairly routine testing of sensitivity of *Methylobacterium extorquens* PA1 to formaldehyde, we noted a surprisingly rapid transition from exponential death to exponential growth in our cultures. With multiple approaches we were able to demonstrate that this was due to phenotypic heterogeneity in the ability to grow in the presence of formaldehyde. This heterogeneity is a continuous trait – unlike the discrete survival phenotype of non-growing persister cells – and we find that this distribution changes rapidly in response to selective or non-selective environments. We developed a quantitative phenomenological model that allowed us to test hypotheses regarding the manner of formaldehyde killing as a function of tolerance level, and to learn what form and rate of movement in phenotypic space occurs under different environments. Given the tremendous variation observed between *Methylobacterium* strains for this trait, this tolerance may play a critical role during the daily pulses of methanol generated by leaves.

Faculty mentor: Christopher Marx, Christopher Remien, and Benjamin Ridenhour

Funding support from: BCB-IBEST fellowship

Poster number: 42

Recognition of different chromosomal DNA sites using double-stranded invader probes

Caroline Shepard (Chemistry)

Abstract:

Future advancements in chemical biology will necessitate probes capable of targeting specific sites of chromosomal DNA. Established approaches such as triplex-forming oligonucleotides, peptide nucleic acids (PNAs), and minor groove binding polyamides only allow detection under limiting experimental conditions (homopurine targets; denaturing steps; low ionic strengths; short target sites), whereas more recent CRISPR-based approaches require transfection of plasmids and in cell synthesis of the detection platform. To address this need, our laboratory has developed designer DNA probes termed Invader probes, which are energetically activated for sequence-unrestricted DNA recognition by positioning 2'-O-(pyren-1-yl)methyl RNA monomers in +1 interstrand zipper arrangements. Herein, we evaluated ten Invader probes designed against different targets within the *DYZ-1* satellite region (~$6x10^4$ tandem repeats) of the bovine (*Bos Taurus*) Y chromosome. Fluorescence in situ hybridization (FISH) assays conducted under non-denaturing conditions revealed specific binding of several of the Invader probes, resulting in high signal intensity. Continual improvement of the Invader probe design will lead to the development of efficient probes for applications in molecular biology, nucleic acid diagnostics, and biotechnology.

Faculty mentor: Patrick Hrdlicka

Poster number: 43

Removal of Lead(II) from aqueous solution by amidoxime-based polyacrylic fibers

Anup Tuladhar (Chemistry)

Abstract:

A new amidoxime-based polyacrylic fiber is synthesized from the acrylic yarn – cheap and commercially available raw material – by reacting with hydroxylamine followed by alkaline hydrolysis to prepare amidoxime [$C(NH_2)$ = NOH] and carboxylate (COO^-) groups on the polymer strands. Characterization of the fiber is done by FTIR which shows the characteristics vibrational bands at 1647.9, 1563.7 and 908.1 cm^{-1} for C=N, COO^- and N-O groups, respectively. The adsorption capacities for lead (II) by the fibers was evaluated by the batch equilibration method at different temperatures at pH 5.44. It shows that the removal of lead by the fiber is positively dependent on the increase in the temperature and the fitting of the curve shows one site to one ion model. The adsorption capacity of lead (II) at room temperature is about 169.9 mg per gram of the fiber. FTIR study of the lead-adsorbed fiber after the batch equilibration experiment shows the red shift in the COO^- peak in comparison to the free adsorbent. This infers that the sorption of the lead (II) ion is dominated by the surface complexation. The spectroscopy observation suggests that the COO^- group on the fiber is possibly involved in binding with the metal ion. The rate of adsorption of heavy metal ions in aqueous solution by the fiber adsorbent is rapid, and kinetic sorption can be described by a pseudo-second-order model very well. The results indicate a significant potential of the fibers as the adsorbent for lead (II) ion removal.

Faculty mentor: Chien Wai

Poster number: 44

Topographic patterns of specific retinal neurons following retinal regeneration in the zebrafish

Derek Viall (Biology)

Abstract:

The retina is the light-sensitive part of the eye. Different regions of the retina have distinct arrangements of neurons that have important visual functions. Following retinal damage and neuronal death, zebrafish will regenerate retinal tissue. However, it is unknown whether patterns of specific neuron types return normally. This study aimed to examine whether global topographic patterns of retinal neurons are altered following regeneration of the retina in zebrafish. Adult zebrafish from two different transgenic lines were given an extensive retinal lesion via a neurotoxin. The zebrafish were then left to recover for 21 or 63 days to allow for regeneration, then euthanized and their retinas were removed, mounted on slides, and imaged. Analysis of global patterns was performed by identifying regions and distribution of specific types of neurons, while local patterns were analyzed by nearest neighbor pattern analysis. Results show that some features of global and general patterns of some retinal neurons were altered while other features were retained following regeneration. This suggests that patterning mechanisms operating during regeneration may be somewhat distinct from those operating during development and growth.

Faculty mentor: Deborah Stenkamp and Diana Mitchell

Funding support from: National Institute of Health, and National Institute of Health Idaho INBRE

Poster number: 45