Sigma Xi
Student Research Poster Session

19-20 September 2014
Eldridge Commons, Swarthmore College
Poster locations for the 2011 Sigma Xi poster session

Cornell Library

To Sci 101
To Sci 102

Upstairs:

Coffee Shop

Color legend:
- pillars
- easels
- Windows/walls

Poster locations for the 2011 Sigma Xi poster session

1. Poster locations are marked with numbers from 1 to 10.
2. The poster session is located in the Cornell Library.
3. Poster locations are distributed on both floors:
   - Ground floor: 1 to 47
   - First floor: 48 to 93
4. Poster easels are available for display.
5. The Coffee Shop is located near the easels.
6. Elevators are available to access the upstairs location.
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The parameter geography of multisite protein post-translational modification

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This summer, I worked with Professor Cheever in the Engineering Department on development of a network phenomenon known as “The Internet of Things,” or IOT for short. An IOT network is a cloud-like network of low-power devices, which includes a gateway to the Internet. IOT networks allow low-power, low-level embedded devices (called microcontrollers) to be able to send data to and from the Internet, which is an extremely powerful concept. IOT networks are becoming more popular today in fields such as security and Smart Home development. Smart Home technology gives people the ability to monitor room temperatures, door positions, TV hours, pill consumption, etc. all on an interface connected to an IOT network sensor (see https://sen.se/store/mother/ for a commercial example of Smart Home technology).

This summer, Professor Cheever and I made a functional IOT network from scratch (unused microcontrollers and radios). To accomplish this, we first had to program a central device known as the coordinator. The coordinator is the most important part of an IOT network- it must be able to maintain a secure connection to the internet, communicate with a data collection web server (Xively.com, in our case), detect other microcontroller devices (called end devices), allow these end devices to join the network, send/receive data from end devices, and interpret commands given by end devices. In other words, the coordinator is the “brain” of the network. We decided to use a BeagleBone black as our coordinator: a high-level, low-power, 80 Pin device that allows for Ethernet connection, and is able to be programmed in a user-friendly language called Python. I started by experimenting with the BeagleBone/familiarizing myself with its features. Eventually, I was ready to write the program that allowed our BeagleBone to send data to a website called Xively. I, then, connected the BeagleBone to an XBee radio module, and programmed our BeagleBone to have the ability to send and receive data packets from this XBee radio module. After this, Professor Cheever and I made up a syntax for various coordinator commands (such as send data to Xively, pull data from Xively, send data to another device, etc.), and I implemented these commands in the BeagleBone Coordinator program. I, then, tested the coordinator’s functionality by sending manual commands to it using another XBee radio module plugged into a computer.

Once the coordinator was up and running, I was able to program end devices to talk to the coordinator/log onto our IOT network/send data to our
Xively Internet server (for a video of this, see http://bit.ly/1nZopT3). Once this was up and running, I was able to make more sophisticated end devices for our network such as diode-based light controllers, magnetometer readers, and light sensors (for a video of our light sensor, see http://bit.ly/1pC4kis). All of these end devices shown were programmed using Arduino boards and XBee radio modules. My final “project” with this network was building a bumper bot that was completely controlled by a homemade electrical controller connected to this network. This bumper bot was also able to talk to Xively, and send live updates if it was stuck (when it hit something on its left side, it sends a message “Left Bumper Hit!” to our Xively server, and when the collision is resolved, it sends a “Resolved” message to Xively). For a video demonstrating the robot functionality, visit http://bit.ly/1s1Prd9.

The core of this project is not that I built a robot; it’s that I built a network that gives Internet access to low-power, low-level devices such as Arduino boards. The applications of this network are limitless – there was even discussion of making a locker security system for Hicks using laser detectors hooked up to this network. IOT networks are revolutionizing home, service, and educational sectors all around the world, and being able to study/implement them with lower power devices, like the ones used in this project, is becoming increasingly more important. I would like to acknowledge all of the generous support for this project given by Swarthmore College, the Engineering Department, Professor Cheever, and donors to the Robin Shapiro Research Fellowship; this project has taught me so much, and has changed my entire vision of what I want to do with engineering in the future. If you have questions/ if you want more information on my project, do not hesitate to email me at gabraha1@swarthmore.edu.
Widespread coral bleaching as a result of human activity threatens coral-based aquatic ecosystems which serve as important sources of food and wellsprings of biodiversity. In healthy corals, a layer of gastrodermal cells contains photosynthetic symbionts of the genus *Symbiodinium*, providing their hosts with a significant source of nutrients in the form of reduced carbon. The breakdown of this metabolically important symbiosis results in “bleached” unhealthy aposymbiotic corals.

The symbiotic sea anemone *Aiptasia pallida* offers an accessible model system for studying the vital symbiotic relationship between *Symbiodinium* and their cnidarian hosts. If *Aiptasia pallida* is to be used as an effective model organism for such research, certain biological tools must be developed for laboratory use. This summer, Professor Elizabeth Vallen and I worked to begin development of a procedure for transfection of *Aiptasia* by electroporation.

Electroporation is a process by which an electrical current is used to stimulate the opening of pores in the cell membrane in order to allow for the uptake of large molecules, such as DNA or RNA. In our initial experiments, FITC-D (fluorescein isothiocyanate-dextran), a green fluorescent particle fused to a large chain of sugar monomers, was used as a proxy for nucleic acids due to its similar size and its detectability under a confocal microscope. Electroporation settings and FITC-D concentrations were based on the Fuchs procedure for electroporation of the cnidarian *Aurelia aurita* (Fuchs 2014).

Figure 1: Tentacles of *Aiptasia* electroporated with FITC-D reporter. Red shows the cells of *Symbiodinium* symbionts in the gastrodermal layer. Green fluorescence is attributable to FITC-D as well as background autofluorescence of the anemones. Anemones electroporated with FITC-D showed greater levels of fluorescence in the ectoderm (white arrow). Mock electroporated anemones and those electroporated with FITC-D show elevated green fluorescence in the gastroderm (blue arrow). Electroporated anemones unexposed to FITC-D show background levels of green fluorescence.

Initially, anemones electroporated with FITC-D appeared to show elevated levels of green fluorescence in the ectoderm. However, the anemones appeared to uptake FITC-D into the gastroderm...
naturally, without electroporation, and anemones never exposed to FITC-D still showed substantial background fluorescence (Fig.1). Because of these complications, we sought out the LacZ assay as a possible method for more clear-cut reporting of successful electroporation. In preliminary experiments, both symbiotic and aposymbiotic Aiptasia showed little to no LacZ expression after several hours of incubation with Xgal (data not shown).

We worked to clone a plasmid construct containing LacZ gene downstream of two putative Aiptasia promoter regions. Anemones electroporated with these constructs were assayed for LacZ. Clusters of cells were seen on multiple individuals which appeared to show blue staining indicative of Lac Z expression (Fig. 2).

![Figure 2: Bodies of two individual anemones electroporated with a plasmid containing the LacZ gene upstream of a putative Aiptasia actin promoter and assayed for lacZ expression. Possible groups of blue cells are indicative of lac Z expression (black arrow)](image)

More work remains to be done in refining the electroporation procedure for *Aiptasia*. However, preliminary results suggest a possible procedure for electroporation which allows not only the entry but the expression of DNA, a feat which has never been accomplished before in this model system. Furthermore, preliminary evidence suggests that the putative Actin promoter sequence isolated may be an effective constitutive promoter for use in further research. Future work in this aim will involve fine-tuning electroporation settings for maximum electroporation efficiency and attempts to isolate *Aiptasia* embryos for electroporation in order to create whole transgenic organisms.

**Notes on Materials and methods:** All LacZ staining procedures were based on the Swarthmore College developmental biology lab protocol for staining of *Ciona intestinalis*. Plasmids containing the LacZ gene were provided by the Swarthmore College developmental biology lab. Putative Aiptasia promoters were isolated by T. Bieri and their collaborators at Stanford University.

**Acknowledgements:** Many thanks to Professor Elizabeth Vallen for her advice and guidance, as well as Christina Cota for her invaluable aid throughout electroporation, cloning, and interpreting results. Thanks in addition for the guidance of Anna Cha in the cloning process, and Iris Chan for help in anemone care.

**Works Cited:**
Crystallization of two catalytically inactive mutants of the AI-2 processing protein, LsrF

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Abstract

Several species of bacteria produce and respond to small signal molecules termed autoinducers. In this process called quorum sensing, bacteria can coordinate gene expression within a population. Behaviors regulated by autoinducers include biofilm formation, production of virulence factors, and more (Federle et al. 2003). One kind of autoinducer, autoinducer-2 (AI-2), is unique because multiple species of bacteria produce, recognize, and respond to it (Xavier et al. 2005).

My research focuses on LsrF, a protein in the LuxS regulated AI-2 processing pathway of Escherichia coli. Previous research in the lab has shown that LsrF catalyzes the final step in processing AI-2; it converts P-HPD (an isomer of AI-2) into the metabolites acetyl-CoA and dihydroxyacetone phosphate (DHAP). The crystal structure of a catalytically inactive mutant (K203A) in complex with the substrate has been determined, but the resolution was not sufficient to provide mechanistic details of the reaction. My work focused on crystallizing two different catalytically impaired mutants, D251A and D57A, in complex with AI-2 to provide atomic-level details and insight into the enzymatic mechanism.

Literature Cited


Planar Chiral Approach to Diastereoselective Bis-Spiroketal Synthesis

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Abstract

Bis-Spiroketalts are part of a cyclic class of molecules consisting of oxygen and carbon atoms, which are generated from an acyclic precursor. This research project uses sulfinyl iron(0) diene complexes as chiral auxiliary groups in the hopes of synthesizing a more enantiopure product. To generate precursor 1 shown below, an alkynyl iodide reacted with an amide to form a ketone. However, efforts to form the iron complex with the diene afterwards had very low yields. In an alternative approach complexation occurred before adding the alkynyl iodide to synthesize 2. All attempts to alkylate the aldehyde in 2 failed, but allyltributylstannane successfully converted the aldehyde to a homoallylic alcohol. In the future we plan to use olefin metathesis to combine the homoallylic alcohol with an enone to form precursor 3, which would then cyclize to form bis-spiroketal 4 under acidic conditions.

Figure 1: Four structures at various steps in the synthesis of a bis-spiroketal using sulfinyl iron(0) diene complexes. S* = (R)-p-tolyl sulfoxide and THP, TES, TBS and TIPS are alcohol protecting groups.
**Biomarkers to assess therapy related nephrotoxicity in children and adolescents with cancer**

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Wilms’ tumor is the most common primary malignant renal tumor of childhood. Osteosarcoma is the most common primary malignant bone tumor in children and young adults. Treatment for each of these cancers involves a multimodality approach including surgery to remove the primary tumor in kidney or bone, intensive chemotherapy, and radiation for some children with Wilms’ tumor. The most effective known treatment regimens for these diseases involve the use of nephrotoxic drugs. Renal injury including decreased glomerular filtration rate (GFR) or damage to renal tubules can result from anticancer therapy and may be acute or lead to chronic, irreversible renal insufficiency. We sought to examine the new biomarkers cystatin C (cysC), Kidney Injury Molecule-1 (KIM-1), and Neutrophil Gelatinase-Associated Lipocalin (NGAL) in two separate cohorts of children and adolescents receiving anticancer therapy to assess the impact of anticancer therapy on renal function (GFR and renal tubular function). The main objective is to determine if these novel biomarkers can detect changes in GFR and renal tubular function that occur as a result of anticancer therapy. Our data indicates that new biomarkers detect changes in GFR and renal tubular function that are not seen when using standard measures of these functions. The results suggest that there is a need for new biomarkers of renal function and renal tubular function in children and adolescents with cancer in order to accurately detect treatment-induced nephrotoxicity before significant, irreversible renal injury occurs.
Elucidating the *Chlamydomonas* carbon concentrating mechanism

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**Abstract**

Many photosynthetic organisms concentrate CO$_2$ around Rubisco, the main carbon fixation enzyme. This allows more efficient carbon fixation by avoiding photorespiration, an energetically costly consequence of Rubisco’s low CO$_2$ selectivity (Moroney et al., 2013). However, little is known about the CCM in the model eukaryotic algae *Chlamydomonas reinhardtii*. We therefore took a two-pronged approach to better understanding the molecular mechanism of the *C. reinhardtii* CCM by developing genetically encodable pH sensors and attempting to short-circuit the CCM.

Carbonate chemistry is highly dependent on pH, and the pH of many subcellular compartments has never been directly measured (Miesenböck et al., 1998). We therefore developed and have been constructing genetically encodable pH sensors targeted to specific intracellular compartments. These sensors and imaging techniques will allow us to determine the pH of compartments important to the CCM, providing insight into where carbon concentration occurs.

To more directly access where carbon is concentrated, we are targeting carbonic anhydrase, which catalyzes the interconversion of HCO$_3^-$ and CO$_2$, to intracellular compartments where inorganic carbon may be concentrated out of equilibrium (Price and Badger, 1989). We predict that if bicarbonate is accumulated in a compartment, introducing carbonic anhydrase will impair CCM function, identifying that compartment as required for carbon concentration.

Using these approaches to increase knowledge of the *Chlamydomonas* CCM could eventually allow us to engineer it into crop plants. Since CCMs enhance carbon fixation efficiency, this could increase yield, which will be important as the world’s population grows and climate change continues.

**Literature Cited**


Morphological and Molecular Classification of the Genus *Lobophora*

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Abstract

*Lobophora* is a brown algal genus that is represented by erect, blade-forming species, although a few species form crusts. *Lobophora* is found in tropical and subtropical areas worldwide. Currently, there are twelve known species of *Lobophora*. However, in the Atlantic the genus is currently represented by a single species, *L. variegata*. Since the original description of *L. variegata* was very broad, the species has come to represent a variety of phenotypes in different locales in the western Atlantic (Schultz et al, 2014).

An assessment of the species diversity of *Lobophora* in the Carribean, specifically in Bermuda, the Florida Keys, and Guadeloupe, was conducted. Five species of *Lobophora* were found to be present in the western Atlantic, *L. variegata* and four novel species. COI-5P and Cox3 DNA sequences were used to determine the phylogenetic relationships of the species. Taxonomic observations, including cell layering, cortex morphology, and blade number, serve to distinguish between the species. The discovery of the four novel *Lobophora* species indicates a much larger species diversity than originally thought in the western Atlantic.

Literature cited

Abstract

This project concentrated on mHealth, or mobile health, which is the use of mobile devices to improve an individual’s health and well-being. The practice of mHealth has become increasingly popular with the growing availability of smartphones and tablets as a way to monitor patients, their illnesses, and their treatments. This is especially prominent in developing countries, where a smartphone might be the only source of computing power and internet. mHealth can be useful for the monitoring of chronic conditions, which can be managed but not cured, and thus often require lifestyle changes of the patient. They also account for 75% of health care costs (CDC). Our goal was to make self-management of chronic illness easier by providing patients with a simple app on their smartphones. While the technology exists to solve this problem, the infrastructure does not.

We built a framework for creating mobile applications that manage chronic illnesses. Rather than write separate apps for diabetes, asthma, and so on, we wanted to develop one common structure, and then implement that structure for each specific app. We decided that this structure should allow for the integration of sensor data and web services data within the app, and our main design choice was the decision to store all the data in a local, secure database on the phone. This aligned with our goal to provide users with complete control over their (often sensitive) information, which is a more private option compared to most health applications on the market that store user data on the internet. Furthermore, this common application framework could eventually help other developers easily produce new smartphone applications tailored to specific chronic conditions. With a complete and available base structure, future developers would not need to be computer scientists.

During the rest of the summer, we developed two proof-of-concept applications that successfully implemented this architecture. Both gather data regularly, store it on the phone, and present it to the user. The first test application, WeightTracker, fetches the user’s weight from a WiFi-enabled scale every day. The second, ActivityTracker, fetches data from the phone’s built-in sensors every 20 seconds to determine what activity the user is currently performing, and it logs their time spent exercising. Finally, we ran tests that confirmed the low overhead and minimal battery drain of our applications, meaning that they would be a suitable and feasible aid to those suffering from chronic illness.

Literature Cited
http://www.cdc.gov/chronicdisease/
Isolation of soil bacteria capable of metabolizing the triazole fungicide myclobutanil

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Abstract

Triazole fungicides are a common class of xenobiotic compounds used in both agricultural and horticultural environments, and are persistent in the soil. While these fungicides are intended to target fungal cell wall synthesis, in high concentrations they have been shown to have negative health consequences in other biota, including humans. Prior research observed bioremediation of the triazole fungicides propiconazole, tebuconazole, and myclobutanil by environmental microbial communities with a prior history of exposure to these fungicides.

This research focuses on the isolation of bacteria capable of metabolizing the triazole fungicide, myclobutanil. Bacteria consortia were isolated from soil regularly exposed to triazole fungicides; samples DCC001-DCC005 were taken from the Newark, DE Country Club, while SC001 was taken from the Rose Garden at Swarthmore College, PA. Bacteria were plated on Pseudomonas minimal media (PMM) containing myclobutanil (100ppm) as the sole carbon source, as well as PMM and myclobutanil (100ppm) with glycerol (0.01%) as a supplemental carbon source. Degradation of fungicide is quantified through high-pressure liquid chromatography (HPLC) analysis, measuring changes in myclobutanil concentration in the agar.

Initial tests showed neither growth on fungicide-only plates, nor degradation of myclobutanil in any of the media. Current approaches involve further manipulation of PMM media to limit both carbon- and nitrogen-containing compounds, creating a stringent growth environment. In doing so, myclobutanil serves as the only source of these vital nutrients. Additional time trials were conducted on Nutrient Agar and 1/10th Nutrient Broth media types; these trials indicated that strain DCC005 demonstrated significant degradation of the fungicide after 4 and 7 days. Further studies will offer the bacteria richer, more permissive media, with the strategy that they degrade the triazole compound through co-metabolism. Furthermore, we will employ a “stepping down” method that limits nutrients in the media to create selective pressure for those bacteria capable of degrading the fungicide.

We gratefully acknowledge support of this work by a grant from the Research Corporation, that funds a collaboration between the Vollmer lab in Biology and the Holliday lab in Chemistry.
Abstract

In the animal kingdom, monogamy is one of the least common mating systems. Often, monogamy serves as an exception to the rule of polygyny due to trade-offs concerning biparental care. However, there are some species of animal that do not engage in biparental care but still perpetuate monogamous mating systems. In the monogamous snapping shrimp *Alpheus angulosus*, there are a number of theories that aim to explain why monogamy is maintained in the absence of biparental care. Suggestions include an exaggeration of mate-guarding behavior, benefits from dual burrow defense, optimizing of foraging strategies, and female enforced spacing through aggression. Within these hypotheses underlies an idea about the risk of reinvesting because of predator-prey interactions or because of conspecific territoriality.

Understanding the trade-offs involved in moving through a risky environment, we aimed to determine whether or not the habitat arrangement of an environment could influence a shrimp's site fidelity, with the assumption that low site fidelity may correlate to low pair fidelity.

We collected wild snapping shrimp from two locations, Grice and MPD Park. With those shrimp, we evenly divided them by sex, size, and location into bins of two experimental habitat types—Clumped and Dispersed. Individuals were placed in 12.5 inch by 8.6 inch bins with four burrows made of open ended Falcon Tubes. Wild caught paired shrimp were placed together in bins of roughly twice the size of an individual's container with twice the amount of burrows. Of the eight trials run, half were run in the presence of a predator. Trials lasted three days with the primary data being the presence or absence of burrow switching after each night.

Results trend towards site fidelity differences between collection locations, less site fidelity in Clumped habitats, more site fidelity in the presence of predators, and less site fidelity from paired females compared to paired males in the absence of predators. While the data are still inconclusive, current information points to the exciting prospect of using habitat to not only predict the rates of monogamy *between* populations but *within* them as well because of the variability of habitat in even one population. Even more, this kind of data will lead to understanding differences between how each sex influences the output of the mating system based on habitat conditions.
Windowmancy: Modifying the Receive Window to Control Transfer Rate

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Abstract

The increasing popularity of the Internet has expanded the scope of devices present in modern home networks. While technological capabilities have become more advanced, the home routing architecture used has remained largely unchanged over the past decade. The goal of windowmancy is to use the resources present in modern home routers to provide greater control over local network traffic than current practices give.

Windowmancy is built atop two preexisting and ubiquitous protocols. These are the Transmission Control Protocol (TCP) and Network Address Translation (NAT). TCP provides reliability by a client sending acknowledgments (ACKs) to a server as confirmation that the server’s data was received. In the ACK is a field called the receive window which prevents the server from sending the client more data than the client can handle. NAT connects a local home network to the Internet under the guise of being a singular device. This device is typically the router.

In windowmancy, we modify this window value to be even lower to thus represent not the most the client can handle, but rather the most the user wants the client to receive at once. At the router, windowmancy modifies the receive window value for different connections depending on what the user’s desired rates are. Thus, the user can control the network traffic rates.

The windowmancy system was implemented on a TP-LINK N750, a typical home router that is widely available and a good representation of the standard hardware that can be found in modern commercial routers. OpenWRT, an open source embedded operating system for routers, was loaded onto the router so the code for windowmancy could be run. To test windowmancy, a simulated home network was set up. On one end was a client connected to the router. On the other end was a server connected to another machine connected to the router capable of simulating network delay. At the router, windowmancy read information regarding the transfer rates of all network connections. To make these rates closer to target rates, windowmancy modified the receive windows the client gives in its ACKs to the server to influence the rate of data transfer.

Though its development is still ongoing, results so far have been extremely positive. Windowmancy is able to read and modify traffic at the router with good efficiency and high reliability. Most importantly, it does not change the frameworks of the NAT or TCP protocols themselves. Rather, windowmancy uses them in slightly different than intended ways. Thus, this system of controlling network traffic could be easily adapted by most home networks.
Filamin contributes to polarized induction of heart progenitor cells in *Ciona intestinalis*

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Abstract

Matrix adhesion is intimately linked to developmental signaling and fate induction. Precise cellular mechanisms impacting inductive signaling downstream of adhesion, such as the contribution of cytoskeletal activity, remain unclear. The cellular and genetic simplicity of our model organism, *Ciona intestinalis*, allows us to study in vivo cellular processes driving early heart specification events. We have shown that heart progenitor induction requires Fibroblast Growth Factor (FGF) signaling and involves polarized distribution of FGF receptors (FGFR). Polarized receptor distribution is aided by adhesion and membrane-stabilizing Caveolin-rich domains. We have also demonstrated that cytoskeletal protrusive activity coordinates a differential response to uniform FGF. However, the precise mechanism underlying localized retention of FGFRs in the heart progenitor cells remains poorly understood. Here we investigate the potential contribution of a cytoskeletal protein, Filamin (FLN). FLN modulates Caveolin trafficking downstream of matrix adhesion and may thereby stabilize FGFR. To test this hypothesis, we expressed a dominant-negative form of FLN in the heart lineage. Targeted disruption of FLN function caused increased induction, indicating that FLN destabilizes FGFR by promoting internalization and membrane turnover. We are therefore investigating the effect of FLN disruption on receptor distribution. Future studies disrupting specific binding domains of FLN may elucidate the functional interaction responsible for increased induction. Our work has the potential to unravel the role of cytoskeleton in coordinating a localized response to uniform inductive signals.

Literature cited

The role of copper accumulation on collagen assembly in the mesoglea of the sea anemone, *Aiptasia pallida*

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Abstract

Coral reef ecosystems are essential as a source of biodiversity. They have been declining globally due to environmental stresses which cause coral bleaching, a process that results in the expulsion of algal symbionts from the host cnidarian. Studying the interactions of the symbiotic relationship between the model host cnidarian *Aiptasia* (sea anemone) and photosynthetic dinoflagellate *Symbiodinium* (algae) will provide a further understanding of the mechanisms behind the onset, maintenance and breakdown of this symbiosis.

Previous studies have suggested there are differences in the protein components of the mesoglea (extracellular matrix) when the anemone, *Zoanthus robustus*, is exposed to copper, a common marine pollutant (Grant et al. 2010). We investigated whether there are changes to the mesoglea structure when *Aiptasia pallida* is exposed to accumulation of water-borne copper.

*Aiptasia* were exposed to various copper concentrations and compared to untreated anemones. Final copper concentrations ranged from 105-210 microg/L, which mimics the range of copper present in some marine environments. Morphologically, anemone bodies appeared scrunched, and tentacles retracted at even the lowest copper treatment. However, histological examination of the copper-treated and untreated anemone cross-sections revealed that copper caused no differences in collagen thickness, in contrast to the 5x increase in collagen thickness found in copper-treated zoanthids (Grant et al. 2010).

Literature cited

Spectroscopic and computational studies of vinylanisole isomers

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Abstract

There are many scent and flavor molecules with a minor structural difference that vary widely in their fragrance and odor. Vinylanisole is an example: its three structural isomers differ by the placement of vinyl and methoxy group around a benzene ring but its scents range from floral to leafy to rubber. Spectroscopic and computational methods were used to study and characterize the different structures and motions of these isomers. The calculations were run on Gaussian 09, a computational chemistry program, through the supercomputing system Trestles under XSEDE. The experimental spectra of these samples were recorded using jet-cooled fluorescence spectroscopy, using a nitrogen-pumped dye laser to induce fluorescence in isolated sample in the UV wavelength region.

As expected, the proximity of the vinyl and methoxy group in vinylanisole increased the energy of the molecule: 4-vinylanisole (4VA) trans conformer with the least steric hinderance was most stable while 2-vinylanisole (2VA) conformers with the most amount of steric hinderance were the least stable. A publication quality laser-induced fluorescence (LIF) spectrum of 3-vinylanisole (3VA) has been acquired but its individual transitions have not been assigned yet. Compared to the 4VA literature spectra, the 3VA origin bands were more “red” (higher wavelengths). The energy difference between the two potential 3VA origins was almost twice as large as the difference between 4VA origins. 2VA was also recorded partially, but the fluorescence spectroscopy experiment could not be continued due to equipment failure.

In total, the minimum energy conformations, transition state and excited state structures and potential energy surface (PES) scans of all isomers of vinylanisole were found. The PES scans show the energy of the path a molecule takes as its substituent group’s dihedral angle is twisted 360 degrees. The calculated minimum energy and transition state structures were observed along the PES path. This data will help assign and analyze the recorded 3VA LIF spectrum as well as spectra of other isomers that will be taken in the future.

Literature cited

Intersexual and Intergroup Social Differences of Two Captive Chimpanzees (*Pan troglodytes*) Groups with Varying Hierarchical Stability

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Abstract

Intrasexual relationships tend to fit a model of sex-biased dispersal in which the philopatric sex is social and the dispersing sex is relatively asocial. Chimpanzees (*Pan troglodytes*), a species with female-biased dispersals, are considered to fit this model. Recent findings, however, have suggested that there is more intergroup variation with regards to female sociality than previously thought (Lehmann and Boesch 2008). In addition, male social bonds, though observed to occur more frequently than females social bonds, have been found to be less stable, fluctuating largely with hierarchical instabilities. This study explored these intersexual and intergroup variations by scan sampling two captive chimpanzee groups (N_Ed=14, M=6, F=18; N_Kasey=14, M=5, F=9), one with male hierarchical instability. The study found significant differences between the groups with regards to female sociality. One group’s females exhibited more female-female bonds than the other, and these bonds were more clustered than those of the other group. Among both groups, male-male bonds occurred more frequently than those of female-male and female-female bonds. There was no difference observed between the sexes in occurrences of social behavior nor between the two groups with regards to male sociality. These results provide some support to increased sociability of males and support recent findings of female social variation between groups.

Literature Cited

Ontology Learning: Structured Terms for Automatic Concept Mapping

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Abstract

Domain ontologies, network structures representing important concepts and the relationships between them within a particular field, have important applications in science including identifying gaps in knowledge and literature, standardizing terminology, and increasing the relevance of search results. Though semi-automatic ontology generation tools exist, they are highly interactive, requiring significant time and effort on the part of the user. We examine the possibility of using consistently structured terminology to represent concepts in automatically-generated ontologies. This system converts natural-language phrases such as electron cyclotron current drive into human-readable but syntactically unambiguous structures such as electron-cyclotron-current_drive in which hyphens separate phrasal heads from their qualifiers and in which underscores combine two constituent stems into a single unit. In this example, current_drive is taken as a unit and is modified by electron-cyclotron. Semantically, the phrasal head represents the most generic category and is made more specific by modifiers; electron-cyclotron-current_drive represents a more specific type of current_drive.

After discussing the methods by which these terms are selected and constructed, we discuss how they can be used to represent ontologies. Because of the semantic interpretation of the structured terms, some relationships are inherent in our concept representation; specifically, terms represent hierarchical relationships with their phrasal heads (represented as the rightmost stems in the structured terms). This allows us to quickly generate a very important set of relationships in our automatically generated ontology.

We then discuss how to construct relationships aside from the ‘is-a’ relationship described above. We identify relationships using a document comparison analysis that compares the relative co-occurrence frequency of various terms. This allows our technique to identify concepts that commonly co-occur and which are likely to have some relationship with one another. These can be used to recommend additional links in the output concept map. Up to this point, the ontology generation can be made fully automatic using our methods; however, to label these additional relationships we use human computation and machine learning to identify similar relationships in the future.

In this way, our new method for generating domain ontologies is almost completely automatic, with some optional human computation. It combines several well-established natural language processing algorithms to create a new system that is capable of performing this complex task efficiently and accurately.
Burying efficiency and sediment preferences reveal complexities in habitat choice for Dungeness (Metacarcinus magister) and red rock (Cancer productus) crabs

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Abstract

Particle size distribution is a key physical factor in determining where organisms live in sedimentary marine habitats because it strongly influences the mechanical properties of the medium and thus the energy required to move through it. We examined burying efficiency in and preference among five natural sediments for Dungeness (habitat specialists) and red rock (habitat generalists) crabs. Crab burial speeds and sediment stiffnesses were measured at five field sites. Dungeness crabs buried equally well in less stiff, well-sorted sands and more stiff, poorly-sorted mud/cobble mixtures. At all sites they buried more quickly than red rock crabs whose performance decreased with increasing heterogeneity of the sediment. These results are contrary to expectations based on reported habitat specificity of the two species. Burial speed decreased with increasing carapace size especially for red rock crabs. The burial success and speed of Dungeness crabs is associated with the relatively larger surface area of their propoduses and the sharper angle formed by the posterior border of the carapace and abdomen. In replicate mesocosms, crabs explored five substrates and then buried in one. Dungeness crabs tended to select well-sorted sediments similar to where we found them in the field. In contrast, red rock crabs were least likely to bury in the mud/cobble sediment in which they had the most difficulty burying although this sediment was typical of the field site where they were most common. The discrepancies among burial performance, sediment preference, and natural distribution reveal the complexity of habitat use between these co-occurring species and are in contrast to the pattern shown by burying fish and some other crab species.
An Analysis of Residential Demand Response Design Potential from Consumer Survey Data

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Abstract—Residential demand response programs offer incentives to households for reducing or shifting their electric load, thereby increasing grid stability and economic benefits. Segmenting residential consumers by demographics and willingness to participate will allow for more effective program implementation. A consumer survey was conducted by CURENT in May 2014, and customers were asked to quantify the incentive they would need in 12 response programs. Customers were clustered into incentive levels and divided into demographic groups. The representation of demographic groups across incentive levels was observed, and statistical tests were used to determine significant demographic preferences. Several significant trends were determined, such as the preference of young customers for low incentives and the preference of older customers for high incentives. Demographic patterns can be expanded upon and applied to future customer segmentation.
Iron Import by TbpA in *Neisseria gonorrhoeae*

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Abstract

*Neisseria gonorrhoeae* causes gonorrhea, an STI which is rapidly developing antibiotic resistance. As a result, increasing emphasis has been placed on developing a vaccine to eliminate the need for antibiotic therapy. The TbpA/TbpB iron import pathway is a promising target for vaccine development because it is highly conserved and displays neither phase nor antigenic variation (Cornelissen, 2008). The recently solved crystal structure of TbpA suggests that the Loop 3 (L3) helix finger is particularly important for human transferrin (hTf) binding and iron release (Noinaj et al., 2012). To assess the functional role of this region, strains lacking TbpB were created with point mutations affecting amino acids K351-Q360 of TbpA L3 through site-directed mutagenesis. Their ability to bind hTf was assessed with whole-cell ELISAs using HRP-labeled transferrin. All mutations were found to result in a statistically significant drop in hTf binding, but none completely eliminated it.

Literature Cited


Investigation of the Effects of Porphyrin Side Chain Charge and length on Quadruplex Binding and Stabilizing Abilities

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Abstract

The enzyme telomerase is over-expressed in 90% of malignant tumors. Its expression propagates uncontrolled growth by extending the telomeres, thus preventing induction of cellular senescence normally signaled by shortened telomere length. Inhibition of telomerase has high potential as a selective cancer treatment due to its overexpression in cancer cells in contrast to the very low expression in somatic cells. This study focuses on the steric inhibition of telomerase through the stabilization of non-canonical G-quadruplex DNA structures on telomeres. In particular, a group of porphyrin derivatives of the well-characterized TMPyP4 ligand are studied, each having a modified side chain with varying charge and length. A combination of FRET melting studies, Circular Dichroism studies, and UV-Vis titrations were performed to determine the ability of the ligands to selectively stabilize G-quadruplex structures and characterize their binding. Results indicate that as charge increases (becomes more positive), stabilization of quadruplex DNA increases, but selectivity for quadruplex over duplex DNA decreases. In addition, an increased length of one side chain provides increased stabilization as well as increased selectivity. Refinement of such properties to increase the selective stabilization abilities of the ligand may lead to an improved cancer drug.

Literature cited

Target Genes In The Notch Pathway Of Drosophila Neuroblasts

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Abstract

A mini-screen to determine whether mutation of Klu, Cyclin E, Castor, Nup 93.1, CG9650, Smr or Nejire genes affect the Notch pathway in Drosophila responsible for tumor genes in cancers and leukemia. Notch is a trans-membrane protein receptor in Drosophila with human homologues, which determines the cell fate of asymmetrically dividing progenitor cells during embryonic development. A screen of genes affected by overexpression of Notch revealed possible candidates for target genes in the Notch pathway. A selection of genes (Klumpfuss, Cyclin E and Castor), indicated by the mini-screen were investigated to determine any change in protein expression in response to inhibited Notch expression within the neuroblasts. Other genes (Nup 93.1, CG9650, Smr and Nejire) were mutated and tested for phenotypes within the neuroblast and changes in Notch target gene expression. Castor showed a decrease in expression within the brain in response to a mutation in Notch, while Cyclin E, CG9650 and Smr showed inconclusive results. The results from the manipulation of Nejire and Nup 93.1 suggest that these genes may be affecting the Notch pathway and would be worthwhile for further research.

Literature cited


Sleep plasticity due to sexual experience in *Drosophila melanogaster*

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Abstract

Sleep behavior is essentially universal across taxa and is widely agreed to be biologically important, but the regulatory mechanisms underlying it remain mysterious. Interestingly, *Drosophila* sleep behavior is plastic, and a growing body of literature suggests that this behavioral plasticity can be induced by the flies’ social conditions. This research specifically examined the way sexual interactions can affect *Drosophila* sleep behavior, at the level of individual mating events and general cohabitation, or socio-sexual interactions (SSI) between males and females.

It was recently demonstrated that female flies experience a post-copulatory reduction in daytime sleep that is mediated by Sex Peptide (SP), a molecule transferred from the male to the female during mating via seminal fluid. In our first set of experiments, using electronic activity monitors to measure the sleep of individual flies, we successfully replicated both of these findings. Next, we further explored this phenomenon, and discovered that the daytime sleep reduction lasted 6 days post-mating and had no apparent critical period with regard to female age or previous mating experience. Furthermore, we established that *Drosophila* mating status, despite reducing overall female sleep, had no bearing on circadian rhythmicity. This line of research provides evidence that sexual experience can temporarily modify an organism’s sleep behavior and raises interesting questions regarding the mechanism by which SP reduces female daytime sleep.

Social enrichment through increased population density causes flies to consolidate their sleep into a small number of long-duration episodes - an architectural pattern thought to be beneficial for memory formation. Analogously, we subjected flies to different durations of socio-sexual interaction, hypothesizing that a longer history of SSI would promote more consolidated sleep due to the presumably greater memory demands that accompany a cohabitating as opposed to gender-separated social climate. Though the relationship was non-significant, engagement in SSI did cause a trend towards increased sleep consolidation for both male and female flies. Preliminary evidence suggests that SSI-induced sleep plasticity may extend to the next generation. In another non-significant trend, parental socio-sexual experience appears to promote less consolidated sleep in both male and female offspring. Clearly further experimentation is required to substantiate these preliminary findings, but they offer the intriguing possibility that social effects on sleep plasticity may involve epigenetic mechanisms.

These results expand our understanding of the connection between an organism’s sexual experience and its subsequent sleep behavior. Due to the neurochemical similarities shared between *Drosophila* and mammalian sleep, a biochemical understanding of the molecular mechanisms underlying these forms of plasticity in *Drosophila* sleep may inform us about the mechanisms underlying social control of our own sleep patterns.


The scale of social interaction in *Silene vulgaris*

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Abstract

Most organisms live among other individuals in their species, and the fitness of an individual will often depend not only on its phenotypes but also on the phenotypes of its social partners (Wolf *et al.* 1999, Formica *et al.* 2011, Smith 1964). In sessile organisms, the spatial distribution of conspecifics around the organism may better describe the relevant social partners for that organism. Sometimes, heterospecific organisms can interact with sessile organisms and create patterns of social interactions that might extend farther than just proximity, through the heterospecifics’ behaviors. For example, angiosperms are sessile plants whose mating system is regulated by pollinators. Because the social partners of an angiosperm may be explained by patterns in pollinator travel movement, we were interested in (1) what the effect of different spatial scales are on fitness and (2) how far pollinators generally travel in order to help explain why particular spatial scales can have a greater effect on a plant’s fitness. We used artificial populations of *Silene vulgaris* to determine the effect of pollen availability at different scales on the fitness of an individual plant, and we also observed pollinator behavior by analyzing pollinator travel distances. We found that for female plants, pollen availability on the population scale and at the 2.7-3.6 m scale had effects on the fitness of the focal plant, if the focal plant was female. However, pollinator visits were mostly observed within less than 0.9 m meters from the plant. This suggests that pollinators may be carrying pollen through multiple flower visits. Overall, it indicates the social partners that make up the social environment of sessile organisms are not necessarily those that are in close spatial proximity, and that group phenotypes do affect an individual’s fitness.

Literature Cited


Testing the Assumptions Underlying the use of Absorbance to Quantify Concentration of Methicillin-resistant *Staphylococcus aureus*

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Abstract

As use of antibiotics becomes increasingly common in the medical and veterinary fields, bacteria are developing resistance to traditional antibiotic treatments at an alarming rate. Pharmaceutical companies struggle to stay ahead of this public health threat by developing new antibiotics in response to each resistant strain that emerges. Methicillin-resistant *Staphylococcus aureus* (MRSA) is one of the most common causes of resistant bacterial infection worldwide. MRSA responds quickly to novel antibiotics, evolving and propagating resistance to new drugs within as little as two years. Studies are underway that aim to develop strategies for combating bacterial infection that skirt the antibacterial arms race. Many of these studies rely on in vitro models of bacterial infection. In order to assess the efficacy of a potential treatment being tested in the lab, one must measure bacterial viability over time and compare it to that of a control. In vitro, bacteria are grown until they reach a critical population size based on their available resources. Aliquots of bacteria are drawn from this prepared stock for subsequent plating and experiments. This procedure requires an accurate measurement of the starting concentration of the bacteria being used. However, the concentration of this stable population size is unknown. One commonly-used method of estimating bacterial concentration is measuring the optical density (OD) of the aliquot at 600nm. Observations illustrate that this method of estimating starting concentration frequently yields inaccurate predictions of the number of bacterial colonies that will emerge from smaller volumes of the stock, leading to wasted time and resources, and to uncountable plates. This investigation invalidates the hypotheses underlying the previously-accepted, OD method and presents a novel empirical method for estimating stock concentration of wild type MRSA. This new method operates independently of absorbance and outperforms the OD method in preliminary tests.
A Model for the Self-Synchronization of Actin Oscillators
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2014 University of California San Francisco Summer Research Training Program
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One can observe spatially regulated flashes, waves and oscillatory foci in the actin cytoskeleton of a motile cell during polarization and chemotaxis. The motile cells possess excitable structures which translate small changes in inputs to large changes in cytoskeletal organization. While intracellular inputs to actin polymerization are understood, the mechanism the actin oscillators employ in order to be tuned high enough to perform chemotaxis but low enough to resist spontaneous self entrainment is unknown. We can induce a pathological state in which normally independent actin oscillators are synchronized by inactivating the heterotrimeric G protein subunit Gβ. The synchronization of actin oscillators interferes with the establishment of cell polarity and motility. We have observed that Gβ limits coupling and allows the cell to regulate an appropriate level of actin excitability, which supports cell polarity. We further developed a model to approximate and predict the effects of a self-synchronous system of oscillators when exposed to an input that couples to a fraction of the oscillators.
Assessing the Presence of Halo Predators at Sub-Tropical Reefs

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Abstract

Piscivores at sub-tropical reefs directly influence prey populations via consumption as well as through indirect behavioral effects. For example, midwater predators facilitate predation by demersal predators by driving prey downward, producing ephemeral feeding opportunities at the sea floor. At Gray’s Reef National Marine Sanctuary off Georgia, diving surveys have sought to quantify the changing web of behavioral interactions between reef predators and their prey inside and outside an area closed to fishing. While diving surveys are effective for surveys of demersal predators and prey highly associated with reefs, they may not capture the presence of reef-associated predators beyond the range of visibility. Due to this possible discrepancy, we tested a novel method to assess the presence of “halo” predators at reefs, at ecologically relevant spatial scales, using towed underwater video. A commercially available Trollpro video housing was used with a GoPro hi-def video camera, attached to the center of a spreader with hookless spoons and fish mimics, and towed at 2-3kts over reefs approximately 3-5m off the seafloor. The success of the approach was based on comparison of video with diving surveys at the same stations. The towed video was found to be a successful halo predator survey method, with more predators encountered in the halo zone above reefs than those enumerated during dives. A total of 12 piscivore species were observed, with greater amberjack, great barracuda, and black sea bass (following and attacking artificial baits in the water column) being the most common. Noteworthy is that some species were observed by towed video and not divers at some sites, while the reverse occurred at other sites. We conclude that both approaches are needed to best characterize the mid-water piscivore guilds.
The creation of a toolkit for the production of phosphorylated recombinant protein

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Abstract

Post-translational modifications are critical to cell signaling networks and result in changes in protein activity. Phosphorylation of a tyrosine residue can alter protein structure and function thereby facilitating signal transduction. A difficulty in this area of research arises because researchers are generally unable to phosphorylate a desired substrate. In this project we are creating a system for efficient phosphorylation of recombinant protein by increasing the affinity of the kinase for the substrate. We do this by engineering a pair of proteins in a bacterial system. One protein includes a kinase catalytic domain and an SH3 targeting domain which binds polyproline regions. The second protein, the substrate protein, contains a polyproline region with an affinity for the SH3 domain.

We have designed kinase and substrate plasmids and are in the process of cloning sequences into the plasmids and then purifying the expressed proteins. We have created a model to find the optimal linker length between the SH3 and kinase domains as well as the optimal SH3-polyproline affinity. We used Matlab to model a series of kinetic equilibria based on a number of ordinary differential equations (ODEs) to fine-tune the engineered plasmids. We will then do in-vivo and in-vitro tests using the phosphorylation mechanism and adjust our model as necessary. Once this system is optimized, we can quickly gain a better understanding of the impact of phosphorylation events on key protein domains involved in cellular networks.
Exploring TAM Mediated Immune Escape in Cancer

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Abstract

This study is interested in exploring the relationship between the activation of TAM receptors and the expression of proteins with known immunological roles in the context of immune escape in cancer. The hypothesized mechanism of immune escape is that the upregulation of TAM receptor Mer leads to the upregulation of A2A, A2B, CD39, CD73, PD-L1, and PD-L2 which suppresses the immune response to tumorigenic cells. Receptor tyrosine kinases (RTKs) are transmembrane proteins with roles in cell proliferation, malignant tumor transformation, and differentiation, making them a subject of oncological study. TAM receptors are RTKs that specialize in efferocytosis, the clearance of apoptotic cells. FC-TAMs are soluble TAM receptors that are constitutively active. ATP and adenosine receptors are involved in pro- and anti-inflammatory immune responses respectively. A2A and A2B are adenosine receptors while CD39 and CD73 are cell surface enzymes that convert ATP to adenosine. PD-L1 and PD-L2 are ligands for PD-1 which is believed to have anti-inflammatory roles.

Lipopolysaccharide (LPS) induction at concentrations of .1 and 1 ng/μL at 2, 4, and 8 hour time points was used as a positive control for the overexpression of A2A, A2B, CD39, and CD73 in RAW 264.7 mouse macrophage cells in pro-inflammatory conditions. Mer ligand gas6 induction was conducted at unknown concentration at 4, 6, and 24 hour time points to determine whether A2A, A2B, CD39, and CD73 are overexpressed following Mer upregulation in RAW 264.7 cells. FC-TAMs were transiently transfected into MCF7 human epithelial cells for 48 hours. Their incorporation into the target cells was verified via western blotting. mRNA was isolated from all cells and was analyzed using two step semi-quantitative RT-PCR followed by agarose gel electrophoresis.

The results of this study were mixed. The LPS induction of A2A, A2B, CD39, and CD73 in RAW 264.7 cells was successful. It was also verified that A2A, A2B, CD39, and CD73 are expressed in MCF7 cells, which was a matter of some debate in the literature. However, the main Mer induction and FC-TAM experiments were not successful, producing inconclusive, poor quality results.

Literature cited

A Superpixel Pipeline for Neurodiagnosis

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Abstract

We developed a pipeline to diagnose neurological disorders in humans using multiple supervised machine learning approaches. Neurological disorders severely affect quality of life, with Alzheimer’s disease currently ranked the third most likely cause of death in the United States (Bahrampour, 2014). Current diagnosis techniques are subjective and most diseases can only be identified after the onset of symptoms; the only time the brain structure comes into play is at autopsy (Mayo Clinic Staff, 2013). While attempts have been made to diagnose based on magnetic resonance images (MRI), these depend on a technique called atlassing which warp images for the purpose of labeling, often obscuring large structural abnormalities (Magnano et al, 2014). We constructed an alternative pipeline where our images, taken from the Alzheimer’s Disease Neuroimaging Initiative (ADNI) database, were segmented into the three brain tissue types by a technique developed by Magnano et al. (2014) using a conditional random field (CRF). These images were then further segmented into superpixels, or conglomerations of voxels in similar areas and of similar colors (Achanta et al, 2010). Once these segments were created, we generated features based on their properties including size, tissue segmentation, location, etc. These features were then analyzed with multiple different techniques, including but not limited to support vector machines, spectral clustering, and adaboost (Natarajan et al, 2012). Research is still ongoing. Current results have three-way prediction accuracy ranging from 35 to 43 percent depending on diagnosis, which are too poor for diagnosis but does imply that our features have sufficient information on our diagnosis to beat chance.

Literature cited

Chris S. Magnano, Ameet Soni, Sriraam Natarajan, Gautam Kunapuli, “A Graphical Model Approach to ATLAS-free Mining of MRI Images.”, SDM 2014
Characterizing the Assemblies of Pinacyanol Acetate

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Abstract

Liquid crystals are a fascinating class of compounds that are characterized by having a unique state of matter in between that of a solid and a liquid. In this state, liquid crystals possess both the orientational order of a solid and the ability to flow like a liquid, giving rise to a number of useful properties that have popularized their use in LCDs (liquid crystal displays) and various other applications. [1]

Our research focused on lyotropic chromonic liquid crystals, which are compounds that can enter the liquid crystal phase when dissolved in water. Pinacyanol acetate (PA), the first such substance we studied, enters the liquid crystal phase at a very low concentration in water (about one percent by weight) and forms elaborate assemblies right below this concentration. The nature of these assemblies is not well understood and was one focus of our research. We attempted to characterize these assemblies primarily using UV-Vis spectroscopy, thereby acquiring a number of interesting absorption spectra.

Literature Cited

An Agent-Based Model of Group-Level Sexual Selection

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Abstract

Traditional evolutionary models treat natural selection as a force that acts only on individual organisms. However, evolutionary theorists have for several decades pointed to the possibility of selection on other levels of biological organization (Okasha 2009). Most prominently, researchers have focused on group-level selection in which selection acts on population-level traits, rewarding some populations at the expense of others. Group-level selection is of particular interest because it offers one explanation for the evolution of altruistic traits (Wilson 1975).

This project investigates possible modes of group selection in forked fungus beetles (Bolitotherus cornutus). Forked fungus beetles live in spatially isolated populations on fungus brackets growing on dead trees. A single dead tree or fallen log provides the habitat for a single population. The beetles in a single population interact socially by touching, courting, and fighting. Because the beetles live in distinct populations and interact extensively within their own populations, forked fungus beetles are appropriate study organisms for group selection (Formica et. al. 2011).

However, two factors make it difficult to study between-population selection in this organism. First, it is difficult to study enough populations with enough resolution to make between-population comparisons. Second, population-level traits can emerge unpredictably from the traits of the individuals within a population. In order to investigate how population-selected traits might emerge from individual behavior without the constraint of studying physical populations in the wild, I designed an agent-based model that simulates forked fungus beetle sexual selection and keeps track of population-level characters and fitness. Further exploration of this model, in conjunction with ongoing work in the field, will shed light on how multi-level selection works in the context of sexual selection.

Literature Cited

Abstract:

The influenza protein M2 is 97 residue integral protein involved in viral budding and proton conductance. While crystal and NMR structures exist of truncated constructs of the protein, there is significant disagreement between models, and very little data exists for the full length protein. Here, the structure of an amphipathic cytoplasmic helix is investigated in the full length construct using SDSL-EPR structural studies on residues 50-60. Continuous wave and power saturation data, when compared to the truncated construct, confirm that the cytoplasmic helical region lies on the membrane, as previously hypothesized. The depth of integration into the membrane appears similar between the two constructs.
The 1.43 Å X-ray crystal structure of the Aggregatibacter actinomycetemcomitans Ribose Binding Protein (RbsB)

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Abstract
Many species of bacteria coordinate gene expression within a population through a phenomenon called quorum sensing, in which bacteria produce organic signaling molecules called autoinducers. These signals ultimately mediate synchronous gene expression in the population. Autoinducer-2 (AI-2) is recognized by numerous different species of bacteria via one of two known receptor proteins, LsrB or LuxP, and triggers responses such as bioluminescence, biofilm formation and virulence (Pereira et al. 2009).

However, recent studies (James et al. 2006, Shao et al. 2007) have suggested that Aggregatibacter actinomycetemcomitans, which expresses a ribose binding protein (RbsB) and lack the two known AI-2 receptors, appears to respond to AI-2. rbsB-mutants showed a decline in response to AI-2, similar to lsrB mutants in species known to utilize LsrB as an AI-2 receptor. RbsB has also been shown to bind AI-2 competitively with LuxP in Vibrio harveyi.

RbsB from A. actinomycetemcomitans was cloned and purified, and crystallizing conditions were determined. X-ray diffraction data was obtained for RbsB crystals prepared with a direct freeze as well as frozen following a soak in AI-2, at resolutions of 1.43 Å and 1.63 Å, respectively. Examination of the active site revealed an electron density identified as the pyranose form of ribose in both structures. That ribose was found in the active site after soaking in a concentrated solution of AI-2 suggests that RbsB does not bind AI-2 with high affinity, instead binding ribose even without the addition of exogenous ribose.

Literature Cited


Abstract

The influenza-virus M2 protein is a 97-residue membrane homotetrameric protein embedded on the viral coat of the Influenza A virus. M2 has been implicated in several stages of the viral replication cycle, including serving as a proton channel that acidifies the internal pH of the virion as well as an agent to control the shape of viral particles that bud from membrane rafts. Due to the difficulty associated with expression and purification of the full-length protein, there is limited information regarding the structure of the full-length protein. In the present study, we utilize site directed spin labeling (SDSL) – electron paramagnetic resonance (EPR) structural studies to probe sites 50-60 in the full-length protein. Using continuous wavelength spectra of protein reconstituted into vesicles and power saturation data, we confirm the existence of the amphipathic helix predicted based on previously conducted structural studies on a truncated construct of the protein (M2TMC 23-60). Furthermore, oxygen accessibility suggests that the amphipathic is tilted towards to the transmembrane domain. CW line shapes of the full-length and truncated protein and power saturation profiles suggest the two regions have similar dynamic properties and similar topology with respect to the membrane.

Literature cited

Calculating and manipulating velocities of plasma plumes traversing an MHD wind tunnel

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Abstract

Research done at the Swarthmore Spheromak Experiment (SSX) focuses on turbulence in magnetohydrodynamic (MHD) plasma. Experiments involve the use of a MHD plasma wind tunnel, a long conductive tunnel through which plumes of plasma are launched. For summer 2014, the plasma wind tunnel was extended and modified so that it opened into a chamber with a top mounted camera positioned so that pictures of the emerging plasma could be taken. The main focus of the work detailed here was the creation of a program to calculate the velocity of the plasma. To do this, the program used data from four soft x-ray detectors placed along the tunnel. The purpose of creating this program was to use these calculated velocities to create an estimate for when the plasma would arrive within view of the camera.

To calculate velocities for one run, a moving average was applied to the soft x-ray data (or signal) from each detector, then the data from each detector was normalized by dividing each signal’s intensity by that signal’s maximum intensity. A location on each detector’s peak was then chosen to indicate the plasma’s time of arrival at the detector. The plasma’s velocity was calculated from the plasma’s travel time and distance. Two locations on each detector’s peak were used separately to indicate the plasma’s time of arrival at the detector; one location was the peak’s maximum and the other was the first point to reach half of the signal’s maximum. The results from the two were compared. Another method used was to create a distance vs. time scatterplot of the plasma’s travel through the wind tunnel using the plasma’s travel times from multiple shots. Fitting a curve to this scatterplot would yield estimates of the plasma’s velocity and acceleration.

Once this was done, the stuffing flux and voltage used in launching the plasma were varied to determine their effects on the plasma’s velocity. Here the maximums method was used to calculate velocities. Our results suggested that increasing the voltage had the most effect on increasing the speed of the plasma. The plasma’s maximum velocity, about 83.2 km/s, occurred at 4.5 kV and 0.75 mWb stuffing flux.

Literature Cited

Schaffner, D. A., Swarthmore College, personal communication.
3D modeling of a thrombus for simulation of ultrasound-mediated thrombolysis

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Many diseases such as immune-mediated disease, neoplasia, infectious diseases and others are frequently complicated by thrombosis (de Laforcade 2010). In order to release the blockage, the researchers have developed treatments such as sonothrombolysis, mechanical dissolution of the thrombi using microbubbles mediated by ultrasound waves (Rubiera 2010). The microbubbles, pushed by ultrasound, can move through the thrombus and undergo radial oscillations that break apart the clot. Although the effectiveness of the continuous microbubble infusions has been studied (Hernot 2008), there is no research that models the clot structure.

The main aim of the research was to create a thrombus and obtain its fluorescence image to be used for development of a computer model to predict the microbubble parameters and trajectory within a given clot body. The 3D clot modeling is critical for determining of the effective ultrasound parameters and optimization of microbubbles dimensions.

Using laser confocal microscopy and FIJI image analysis program, we obtained images of blood clots and analyzed their internal structure. The fluorescent fibrinogen, one of the main components of a blood clot, enabled visualization of tangled network of fine threads. The spaces that formed within the protein scaffold are expected to act as pathways for microbubbles and thus help estimate the optimal microbubble dimensions.

For the future work, the 3D images of the clot that were taken during this project will be made into models using for 3D printing and computer programming.

Literature Cited

Illegal Crossing in South Africa

Pedestrian Activity and Accidents on Cape Town Freeways

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Abstract

Traffic fatalities are at some of the highest levels in the world in South Africa, at over 28 deaths per 100,000 (WHO 2013). These deaths have major impacts on both small communities and the country as a whole, especially when the primary-income earners are the ones injured or killed. Cape Town’s land use situation still reflects the legacy of apartheid that created it, which means that most research in other international countries does not apply adequately to the city. In order to begin to understand the problem so that governing bodies can begin to develop appropriate policies, three different research questions were developed:

• What is the relationship between accidents and crossing activity?
• How does the presence of legal crossing infrastructure impact pedestrian activity?
• How does surrounding land use affect pedestrian activity?

Both a spatial analysis and statistical analysis was performed using MATLAB and ArcGIS to answer these questions. It was found that there was no significant relationship between the number of accidents around a high pedestrian traffic point and the number of people crossing there ($R^2 < 0.1$ for a 500 meter buffer). There was also no statistically significant relationship ($R^2 = 0.03$) between the number of people crossing at a point and the distance to a legal crossing point (pedestrian bridge, crossroad with sidewalks, etc.). Furthermore, a function was developed that could predict where high pedestrian traffic would occur based on a variety of land uses in a given traffic zone, although it still needs some refinement ($R^2 = 0.34$).

Literature cited

Construction of a Diode-Pumped Nd:YAG Laser

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Abstract

The purpose of this experiment was to build an open-cavity laser that allows undergraduate students to understand the mechanisms and individual components required for lasing. The project was a continuation of Alexandra Werth’s E90 project this past semester. A typical laser is composed of (1) a resonant cavity; (2) a high reflector and output coupler; (3) a gain medium; (4) a pumping mechanism; (5) a laser beam. The gain medium, the Nd:YAG rod, was an yttrium aluminum garnet crystal. One side of the rod had an anti-reflection coating for 808 nm light (light coming from the diode laser) and a high reflection coating for 1064 nm (the desired wavelength). A diode laser was used as a pump to stimulate ground-state electrons to enter higher energy levels. A series of coupled lenses collimated and focused the beam, allowing the light to enter the rod as a point source. The light then traveled through the rod to the output mirror, where it entered a monochrometer and its power was recorded.

We encountered a series of complications with the original setup. Many of the original pieces were either too rigid or too unstable for adequate precision. Thus, most of the summer consisted of redesigning each component in the setup. Further problems encountered throughout this project included changing the lenses in the original experiment design due to inadequate focal lengths, redesigning mounts due to space constraints, researching methods to clean optical components with thin coatings on their exteriors, amongst other issues. After fixing each of the problems, we had to recalibrate the laser to account for the changes we made. This took a substantial amount of time, as each optical component had to be re-inserted into the apparatus. At this point in our research, we have not been able to generate substantial enough power to deem the apparatus lasing. Rather, we believe that there was not enough stimulated emission occurring within the resonant cavity and it was simply fluorescing. We hope to continue working on this project, as we believe we are very close to getting it lasing. Specifically, we want to explore the relationship between temperature and power to see if we can maximize the output power. We also wish to confirm the linearity of power and excitation rate, amongst other relationships in the laser model.

Literature cited


**eg6 is a gene involved in the Arabidopsis heat shock response**

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**Abstract**

As sessile organisms unable to migrate or translocate, plants must endure wide variations in temperature over the course of a single day. To cope with potentially damaging temperatures, plants have developed a robust system of heat tolerance in the form of basal thermotolerance mechanisms as well as protein-mediated heat response cascades induced in response to heat stress [1,2]. Previous research indicates regulation of the heat shock (HS) response pathway by a host of HS transcription factors, cyclic nucleotide gated ion channels (CNGCs) and kinases [2,3]. Although significant research as been done regarding the down stream heat response mechanism, little is known of the plant heat sensing mechanism and the specifics of signal transduction resulting in protein synthesis and acquired thermotolerance. This summer, we conducted research using the newly developed RootScope and other molecular techniques in order to characterize a previously identified HS response mutant, eg6. The RootScope is a microscope developed by our lab that can be used to visualize the HS response in Arabidopsis roots with high spatial and temporal resolution. This microscope was used to identify and characterize a mutant in an EMS-mutagenized pool of Arabidopsis plants bearing an unknown mutation in the HS response pathway (eg6). The RootScope was also used to further characterize a set of plants harboring defective copies of various HS responsive genes which, when in a single mutant background, showed no phenotype in traditional thermotolerance assays. As a proof of concept, the RootScope was able to successfully distinguish a phenotype in hsfa1d mutants, a line showing no phenotype in previous traditional thermotolerance assays [2]. With respect to the mutagenesis screen, preliminary results indicate that eg6 is a gene essential in the down-regulation of the Arabidopsis response to sub-lethal HS, as mutants have over expression phenotypes at temperatures ranging from 28°C - 40°C. Furthermore, eg6 appears to regulate genes under the control of the HSFA1’s as well as at least one HS regulated gene (GRF1) not under the control of the A1 family, indicating EG6’s situation upstream of the HSFA1’s in the Arabidopsis HS response pathway. Further experimental characterization is necessary in order to draw any conclusions regarding EG6’s exact function in the Arabidopsis HS response pathway, but pursuant to this goal, DNA is currently being sequenced with the objective of cloning the EG6 gene.

3. Fei Gao, Xiaowei Han, Jianhai Wu, Shuzhi Zheng, Zhonglin Shang, Daye Sun, Rengang Zhou, and Bing Li (2012). A heat-activated calcium permeable channel – Arabidopsis cyclic nucleotide gated ion channel 6 - is involved in heat shock responses. The Plant Journal, 70(6), 1056-1069.
Conservation of heart enhancers and cardiac gene expression patterns in Corella inflata and Ciona intestinalis

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Abstract

Enhancers are key regulators of gene expression; yet, the relationship between the structure of these important regulators and their evolution is little understood. To investigate this relationship, we studied early developmental cardiac enhancers of two species of tunicate, Corella inflata and Ciona intestinalis. Despite hundreds of millions of years of evolution and a high mutation rate, functional conservation of heart enhancers has been demonstrated between C. inflata and C. intestinalis. To determine whether the functional conservation translated to sequence level conservation of enhancers, we have begun analyzing the genome of the lesser known species, C. inflata. We first assembled the C. inflata genome using paired-end illumina data. We then isolated conserved heart enhancers, in particular we focused on FoxF, a gene necessary for heart progenitor cell migration in C. intestinalis. We performed sequence comparison of the C. inflata and C. intestinalis FoxF enhancers, and found conservation in both the composition and order of transcription factor binding sites. We tested the functionality of each of these binding sites using reporter analysis. Our results demonstrate both sequence-level and functional conservation of this enhancer. We plan to further characterize conserved heart gene expression patterns using in situ hybridization and to perform more sequence analysis using recently-collected RNAseq data to better characterize the relationship between enhancer function, structure and evolution.

Literature cited


Study of H$_2$TCPPSpm4 and ZnTCP Spm4’s stabilizing interaction with human telomeric DNA

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Abstract

In this work we investigate interactions between free-base porphyrin, TCP, and its Zn(II) derivative, ZnTCP, with human telomeric DNA, Tel22. The unique feature of the porphyrin under investigation is the presence of spermine arms that should confer better solubility and stabilizing ability to this molecule. Interactions between Tel22 and the porphyrins are studied using fluorescence resonance energy transfer (FRET), circular dichroism, UV-vis and fluorescence spectroscopies. UV and fluorescence titration data allowed determination of the binding constant which is $\sim 10^7$ and $\sim 10^6$ M$^{-1}$ for ZnTCP and TCP, respectively. Job plot data suggest high stoichiometry of 15 and 5 molecules of ZnTCP and TCP, respectively, per one molecule of DNA. The possible binding mode includes end-stacking of one porphyrin molecule onto the terminal G-tetrad of one quadruplex and subsequent aggregation of the other molecules. The aggregation is possible via $\pi$-$\pi$ stacking of porphyrin rings or interaction between spermine arms. The FRET melting studies indicate that to achieve effective stabilization (over 10 °C) of quadruplex structure, at least 12 equivalence of ZnTCP is required, while the same effect can be achieved with only 3 equivalents of TCP. The result is reconfirmed by CD melting for both porphyrins. FRET competition studies show that neither ZnTCP nor TCP is particularly selective for GQ structure when high excess of duplex DNA is present. Overall, our data indicate that TCP and ZnTCP are both capable of binding and stabilizing human telomeric DNA and could serve as potential anticancer drug candidates.
Identifying the connection between \textit{HSP17.6} expression and the thermotolerance response in \textit{Arabidopsis thaliana}

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Abstract

All organisms, especially plants, must have a well-adapted method of responding to stress under high temperatures. The thermotolerance response is mediated on a molecular scale by a network of heat shock proteins (HSPs), however many details involved with this system remain poorly understood. HSP17.6 is a heat shock protein that prevents polypeptide aggregation by binding to denatured proteins. By using \textit{HSP17.6} levels as a proxy for the subcellular thermotolerance response, we sought to determine whether higher \textit{HSP17.6} levels correspond to increased thermotolerance acquirement. We identified a mutant labeled \textit{eg6} with an ectopic response to heat. \textit{Arabidopsis thaliana} plants with the \textit{eg6} phenotype were assayed for thermotolerance and displayed improved thermotolerance in comparison to their wild type counterparts. These data suggest a possible direct link between augmented \textit{HSP17.6} levels and heightened thermotolerance. We also attempted to fuse the genomic \textit{HSP17.6} sequence to a green fluorescence protein (GFP) marker as a more precise method of monitoring \textit{HSP17.6} kinetics in response to heat. Presently, \textit{HSP17.6} genomic fragments have been cloned into a gateway entry vector and will be fused to GFP in a destination vector before transformation into a plant vector.
Abstract

This summer, I attempted to design an interactive sculpture that could also serve as a bench. I decided to mimic the shape of a Mobius Strip as I was drawn to its inverted yet upright nature. I believe that the shape of the Möbius Strip is most fitting for an interactive campus sculpture as its shape is a positive, philosophical reminder that life is not about dead ends or abrupt conclusions. Whether metaphorically up or down, the Mobius Strip aims to encourage viewers to continue and not be satisfied. I engaged with both Professor Meunier and Professor Everbach in designing a functional yet aesthetically pleasing bench. The materials and machines available to me greatly limited my designs, but also simultaneously taught me to adapt and that designing is a process and not about the first, idealistic solution. I decided to utilize the Mobius Strip’s centerline in order to limit outside dependence and cost. What is unique about the Mobius Strip is that not only is there one apparent side and one edge, but the centerline is always either a circle or an oval. By spacing out 47 assemblies of wooden blocks and plank around the center line about two inches apart and rotated 3.8 degrees from its preceding assembly, the top plank will become the bottom plank after 180 degrees rotation. Finally, I chose to insert a cable through the ends of the planks to preserve the smooth regularity and shape of the Mobius Strip.

However, before completion, the welding on one end snapped and the bar deflected under its own weight. I had not taken the dynamic movement of the bench and the increase of momentum, inertia, and stress under consideration and by connecting the planks to the blocks, the center rod deflected too much for the welding to keep it together. Since then however, I have constructed renderings on MultiFrame and have calculated the total moment, strain, stress, deflection, axial load, and reaction of different materials. I have decided to change from a rod to pipe in order to decrease the amount of deflection and stress. A reconstruction of my failed structure on MultiFrame showed that the steel 3/4” center rod deflected 10 inches. Now with stainless steel pipe, it should deflect no more than .6 inches under 275 pounds of ice, 825 pounds of self-weight, 220 pounds of longitudinal wind force, and five 150-pound ambitious climbers. Although initially discouraged, I will complete this bench. I plan to use my leftover funds to pay for the additional costs of the bench as it was my negligence and lack of understanding that caused it to fail. I want to complete the bench in order to give proper thanks to the Halpern Family.
Nswap2L: Heterogeneous Swapping for Cluster Computers

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Abstract

Most super computers these days are of a variety known as cluster computers. Cluster computers are built by combining many smaller computers, called nodes, and interconnecting them with a fast network so that they can communicate easily. Large jobs can be completed quickly by breaking them into small parts and assigning each node a part. Unfortunately, it is difficult to keep the workload even between all the nodes—it is often the case that some nodes will use all their main memory (RAM) while other nodes in the network have plenty of free RAM. Typically, when a computer fills up all its RAM, it will swap some memory from RAM onto a hard disk. This is convenient because hard disk space is much more cheap and abundant than RAM. The drawback is that hard drives are much slower.

Nswap provides an alternate method of swapping. Rather than send excess memory to the hard disk, Nswap finds a node in the network whose RAM has free space and sends the memory to be held there. Since network speed is much better than disk speed, this is a faster solution.

Nswap2L builds on Nswap, and chooses whether to swap memory to network RAM, hard disk, flash drive, or some other storage device. Though a prototype for Nswap2L has been built, there is not a fully implemented version, and there are design decisions that must still be made. Work was done to test out several new features for potential use in Nswap2L, including DMIO, discard, and multi-threading. DMIO would allow Nswap2L to easily add, remove, and swap to many devices. Discard is a Linux kernel feature that notifies a device driver when memory is no longer needed. Writing a multi-threaded device driver allows a computer to run it on multiple CPUs simultaneously. Testing was done on all three of these features and results indicate that all can be feasibly implemented in the full version of Nswap2L.

Literature cited

Tia Newhall and Douglas Woos,
Proceedings of IEEE Cluster Conference, Austin, TX, September 2011
Over the course of the summer Professor Carl Grossman and I learned to program a FPGA (Field Programmable Gate Array), hardware that will be used for high speed photon counting of molecular fluorescence. I learned to code in both Verilog and C++ in order to program the FPGA (Embedded Micro Mojo V3) to receive signals from a photodetector, record time stamps, which are signatures of the arrival of a photon, and send them to a computer for processing. These time stamps are then analyzed in real time to calculate a fluorescence correlation function, a very useful diagnostic in physical chemistry and biochemistry research.
Ranks of graphs over $\mathbb{Z}_2$

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Abstract
We define the $\mathbb{Z}_2$-rank of a graph $G$ to be the rank of its adjacency matrix over $\mathbb{Z}_2$. We show that the $\mathbb{Z}_2$-rank of $G$ is full if and only if the graph $G$ has an odd number of perfect matchings. We then compute the rank of $G$ over $\mathbb{Z}_2$ for a number of different graph families, including paths, cycles, wheels, complete graphs, complete bipartite graphs, and ladder graphs.

References
Constructing a LacZ Reporter Mycobacteriophage for Diagnosing Mycobacterium Tuberculosis

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Mycobacterium tuberculosis (Mtb), the causative agent of tuberculosis, continues to be a worldwide pandemic (estimates place global infection at 1/3), infecting 10 million new people a year and resulting in 2 million deaths annually [1]. With incidence of of multi-drug resistant strains of Mtb (MDR-TB) on the rise, developing an accurate and rapid way to identify and determine drug susceptibility of Mtb is a major priority to aide with control and treatment. The construction of a LacZ-DS6A reporter mycobacteriophage is described here. This new phage will be used to deliver the lacZ gene to Mtb, that will allow for the Mtb to appear dark blue when grown in the presence of X-gal. This reporter phage has the potential to be a powerful Mtb diagnostic tool as it will require little to no expensive equipment or training and is easily coupled with antibiotic screening to test for resistant bacilli.

LITERATURE CITED


Identification of transport controlling structures in geophysical fluid dynamics

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Abstract

We address the generation of controllable ocean-like flows in a laboratory setting. Geophysical fluid dynamics is the study of natural fluid flows on large physical scales, such as oceans, rivers, and the atmosphere. Geophysical flows are stochastic and aperiodic, but are known to exhibit coherent structures. In ocean flows, these time-dependent coherent structures, Lagrangian coherent structures (LCS) divide the flow into dynamically distinct regions (Haller and Yuan, 2000). LCS thus provide important global information regarding the dynamics and transport of such environments. For two-dimensional (2D) flows, ridges of locally maximal finite-time Lyapunov exponent (FTLE) values correspond to a good approximation of LCS (Shadden, et al., 2005).

Building upon previous work, we show that a low Reynolds number experimental flow tank is capable of producing repeatable and controllable coherent structures in 2D by analyzing surface flows using FTLE and Dynamic Mode Decomposition (DMD). Specifically, we consider the scenario where flow is generated by motors placed such that rotation occurs at a set distance under the surface. We describe the computation of the FTLE and show that the flow structure can be encapsulated by select dominant modes from the DMD analysis.

Literature cited


Synthesis and characterization of organometallic tungsten and molybdenum complexes as electrocatalysts

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Abstract

For centuries, we have used fossil fuels as our primary energy source. However, facing various problems caused by these non-renewable resources, the development of a sustainable and carbon-free energy system is demanded. Scientists proposed the notion of hydrogen economy in the early 1970s. As the name suggests, hydrogen gas, a chemical fuel, works as a great substitute for traditional energy storage method.

Electrocatalysts are molecules that use applied electrical potential to catalyze a chemical reaction. If the stored chemical energy in products is higher than the initial reactants, an energy storage method is created by the catalyzed electrochemical reaction. Thus, the development of fast, efficient, inexpensive, and durable electrocatalysts for interconversion of electrical energy and fuels is essential.

Our goal in our research is to take naturally occurring hydrogenases and existing electrocatalysts for hydrogen gas production as a prototype, design, synthesize, and characterize new electrocatalysts using tungsten and molybdenum as the central metal atom. We believe that modifications of these low-cost metal complexes are able to perform as well as the high-cost existing electrocatalysts.

Literature cited

Analysis of Sex-Based Differences in a Mouse Model of Stress-Induced Analgesia

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Abstract

Stress is known to enhance pain under chronic conditions, while acute periods of stress can suppress pain. Stress-induced analgesia (SIA) occurs when somebody experiences pain suppression during a stressful event. This phenomenon has been well documented in humans, particularly in soldiers and professional athletes. Recent studies have drawn attention to the presence of sex differences in animal research, including pain. Here, we investigated sex-based differences in a mouse model of SIA. Male and female mice were restrained to induce stress before receiving a formalin paw injection, a common inflammatory pain model. Behavioral assays were used to assess mechanical spontaneous behavior and mechanical hypersensitivity. On the molecular level, the signaling molecule extracellular signal-regulated kinase 1/2 (ERK1/2) was analyzed in the central nucleus of the amygdala (CeA) in the brain. The CeA is known to integrate information about stress and pain and ERK1/2 is phosphorylated (i.e. activated) three hours after formalin injection.
Patterns of genetic variation in the Australian Grey Fantail complex: 
*Rhipidura albiscapa* and *Rhipidura phasiana*

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Abstract


To answer questions on the genetic variation of the Grey Fantail complex within its Australian range, we sequenced mitochondrial genes ND2 and ND3 and the nuclear intron beta-fibrinogen intron 5 (Fib5) for 38 individuals of *R. phasiana* and the Australian subspecies of *R. albiscapa*. These sequences were edited and aligned with seven additional sequences from Nyari et al. (2009). Maximum parsimony and maximum likelihood analyses were performed on this data.

Our results indicated that *R. phasiana* and Australian populations of *R. albiscapa* were monophyletic, but were not sister taxa. However, *R. albiscapa* as a whole was found to be polyphyletic because the Melanesian subspecies *R. a. brenchleyi* was not sister to the Australian subspecies. With some exceptions, Australian *R. albiscapa* grouped into three taxonomically and geographically coherent clades: (1) *albiscapa* (Tasmania), (2) *keasti* and *alisteri* (eastern Australia), and (3) *preissi* and *albicauda* (western Australia). Our results support the evolutionary distinctiveness of *R. phasiana* relative to *R. albiscapa* (Ford 1981, Nyari et al. 2009). Within *R. albiscapa*, the southern forms *alisteri*, *preissi*, and *albicauda* are not sister taxa (contra Ford 1981), but instead span the entire genetic diversity of Australian *R. albiscapa*.

Literature Cited

Assessing the efficacy of owl pellets in reconstructing small mammal diversity

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Abstract

In order to better understand the limitations of the fossil record and how it biases our knowledge of the past, it useful to examine what or who is involved in preserving fossils. This study looked specifically at present-day owls and their pellets, which are a rich source of paleontological data. Owl pellets from different owl species were collected from meadow complexes throughout Yosemite National Park. In the lab, the pellets were dissected, and the remains were identified based on teeth morphology and dental formula. Based on our data, we constructed a food web that characterized the strength of predator prey interactions as well as the selectiveness of different owl species. Using museum trapping records from online databases, we then compared our pellet data to the collective trapping data and found that neither pellets nor trapping alone captured all of the known small mammal diversity. This suggests that employing both methods in conjunction might more accurately represent biodiversity in present-day populations. Moreover, these results demonstrate some of the pitfalls of taking fossil data at face value; reconstructions of past populations based on the fossil record include some but definitely not all individuals present in historic populations.
Investigating the role of miRNAs in osteogenic differentiation of progenitor cells

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Abstract

Musculoskeletal diseases are typically painful and debilitating, albeit non-life-threatening conditions that affect bone, cartilage, tendon, and ligament. The goal of skeletal regenerative medicine research is to manipulate mesenchymal stem cells (MSCs) to differentiate into a variety of cell types, including osteoblasts (bone cells). One of the factors that affect the differentiation is the micro-RNA. Micro-RNAs (miRNAs) are small noncoding RNAs that regulate gene expression by base-pairing with complementary sequences of messenger RNAs and thereby inhibiting their translation. Previous studies have found that regulate the expression of mesenchymal lineage-specific genes. In order to investigate the role of miR-218, 140, and 101a in osteogenic differentiation of progenitor cells, MC3T3 cells were cultured and transfected with pCAG-GFP/RFP plasmid construct with miRNA-encoding sequences. The cells were introduced to osteogenic cocktail and were harvested at 72 hours and 10 days. For downstream analysis, RNA was extracted and was reverse transcribed. Transcript levels of bone marker genes were quantified via mRNA and miRNA qPCR. Upon analysis of gene expression for bone markers, no statistically significant changes in the expression were found. Even though this study was inconclusive of the role of miR-218, 140, and 101a in osteogenic differentiation, data and previous studies indicate that it is likely that miRNAs still partake in the differentiation process. The major limitation of this study was achieving overexpression of the miRNA’s of interest. For future studies, it would be crucial to reassess the method of transfection. Furthermore, western blot technique may also be used to investigate whether the detected mRNA level translates to the protein level. It would also be ideal to develop a genetic mouse model to study the effect of miRNAs in vivo and also use miRNA-treated MSCs in a fracture repair model.

Literature cited

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Optimization of the extraction of myclobutanil from solid samples by HPLC

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Abstract

A simple method for extracting myclobutanil from solid agar media is proposed. Myclobutanil is classified as a triazole fungicide, a common anthropogenic chemical used in agriculture and landscaping, and can be detrimental to species other than the fungi intended when applied largely. Separation is one of the most important prerequisites towards investigations of its environmental behaviors. The separation of the myclobutanil from solid media was analyzed using high-performance liquid chromatography (HPLC). Modifications of the extraction solvent, internal standard, and separation conditions were performed to optimize the extraction of myclobutanil. Recoveries for analytes ranged from 35.7-98.7%. The method presented allows a fast, quantitative determination of triazole fungicides in agar media and has the potential to assess temporal changes in triazole fungicides via microbial biodegradation.

Literature Cited

Designing a Polarizing Variable Angle Spectrometer
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Advisors: Prof. Nader Engheta, Dr. Brian Edwards

An apparatus to measure the angular dependence of light scattering from a gold sphere at varying wavelengths, or perform angular resolved spectroscopy, in order to probe the fundamental properties of gold nanoparticles is designed and tested. This information is important because metallic nanoparticles have many different applications in medical imaging, targeted medicinal delivery, and electronics, such as photovoltaic cells. Gold nanoparticles, in particular, have extensive applications, and so was the focus of the testing here. Mie theory is the generally accepted way to predict how light scatters off of a sphere; however in considering the case of a metallic sphere, there are more complicated interactions to consider. When the incident light hits the nanoparticle, the free electrons in the metallic structure are excited by the temporary local field generated by the incident light’s electric field and begin to oscillate, generating an electromagnetic field of their own. This field can be decomposed, in the same way that a signal can be composed into sine waves using a Fourier series, into a linear combination of the electric and magnetic fields from electric and magnetic dipoles, quadrupoles, and higher order poles. Initial testing looked for the higher order electric and magnetic poles that manifest in the scattered light and found that the device is capable of taking angular resolved measurements to find those higher order poles at various wavelengths for gold nanoparticles with a diameter of approximately 400 nm.
Trichomes, Latitude and Climactic Variability

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The evolution of plasticity itself is not well understood (Fusco & Minelli 2010). While the ‘climactic variability hypothesis’ has garnered support as a solid theoretical basis (Molina-Montenegro et al. 2012; Maldonado et al. 2011), there is still no consensus that this is in fact the correct mechanism (Overgaard et al. 2011). In the genus Campanulastrum, varying light levels in the maternal generation have been correlated to the phenotypes and plasticity and of the offspring (Galloway & Burgess 2009; Galloway & Etterson). Furthermore, the climactic variability hypothesis, which states that higher temperature variability at higher latitudes may determine greater phenotypic plasticity with latitude, forms a strong basis for the theory of plasticity evolution. To this end, recent experiments on the Campanulastrum appear to have supported this theory.

I began working with Dr. Laura Galloway, an expert on maternal effects on plasticity who has been using Campanulastrum for a great deal of time. I decided to examine trichomes (epidermis hairs) in the select plants in relation to the latitudinal location of their parents. The theory behind the selection of trichomes posits that as latitude increases (following the climactic variability hypothesis), trichomes will show a discernable pattern towards one end of the latitudinal spectrum because of their function to aid with regulation and environmental interaction of the Campanulastrum. We began with 21 distinct parental populations of Campanula that formed a tight latitudinal transect from the panhandle of Florida to southern Michigan. Seeds were collected from these 21 populations and planted at Mountain Lake Biological Station in enclosed outdoor fields. Once the plants fully bolted, a single mature leaf from the same position on each healthy plant was harvested. Densities and lengths of trichomes along the adaxial side of the leaf were taken in several exact locations for every leaf and composited.

Surprisingly, the data we recovered showed a very different picture than previous models predicted. Trichomes were often thought to aid against herbivory, reduce water loss via transpiration, and provide shade to certain parts of the leaf to protect delicate tissue; these factors each would predict the plants at the southernmost part of the transect to have the greatest trichome density and length. However, precisely the opposite occurred. Length showed a strong association increasing with latitude linearly. Density took a U-shaped trend in which southernmost and northernmost populations had the highest densities and central populations had some of the lowest. These results suggest that the trichomes may be serving a function entirely apart from the traditional narrative. Namely, the data suggests that the trichomes are in fact acting as protection from frost as the northernmost latitudes have the greatest densities and lengths. Furthermore, the fact that the central and northern populations have the most diverse and varying phenotypes bolsters the climatic variability hypothesis.

Literature Cited:


Conceptum: an Online Platform For Developing Modular Concept Inventories

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Abstract

Concept Inventories (CIs) are short, multiple-choice exams that evaluate a student's understanding of core concepts of a particular course. They are particularly adept at evaluating how effective a professor is at teaching material via comparing pre- and post-course scores. However, CI development requires significant overhead: the current state of the art calls for an intensive, 6-step process (Adams, 2). As a result, there are few CIs available for academic use, despite their effectiveness. Additionally, the CIs that do exist are made for a set curriculum; CIs for courses with modular content (like a data structures & algorithms CS course) remain undeveloped.

Our research is devoted to solving this problem by implementing an online platform for developing, deploying, and evaluating a modular concept inventory. This open-source software will allow any number of collaborators to come together and build a CI for a much lower cost. Additionally, the tool will be able to manage, administer, and iteratively improve CIs after they are created. Our web tool will be modular, so that researchers can use it to explore different methods of creating CIs, as well as use the standard process to create them. Our hope is to greatly accelerate the production of CIs, as this will prove to be a great benefit for the pedagogical community.

Literature Cited

Diastereoselective Synthesis Directed by Planar Iron(0) Tricarbonyl Diene Complexes

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For many years, the Paley laboratory has been developing synthetic methods that employ an element of planar chirality to direct the stereochemistry of incipient chiral centers. A chiral auxiliary is used to install planar chirality by diastereoselectively preparing an iron(0) tricarbonyl diene unit. The iron tricarbonyl fragment creates steric hindrance, restricting nucleophilic addition along the periphery of the diene, thus allowing for the control of stereochemistry at those positions.¹

Azaspirocycles are cyclic compounds where a nitrogen atom is attached at the carbon atom junction of two different rings, known as the “spiro center.”² The Paley lab has successfully completed diastereoselective syntheses of azaspiroycles using the planar chiral iron(0) tricarbonyl complexes. Unfortunately, the approach involved isolation of a compound – an imine – that was surprisingly unstable. In fact, even in dilute conditions a large portion of the material would typically be lost at this step before subsequent transformations could be undertaken. A new approach was thus designed to develop an alternative synthesis of an azaspirocycle. The stannylcupration of electron-poor alkynes that the Paley lab has been using to form precursors to the diene complexes was extended to include an alkylnyl acetal. This product, which also contained a suitably protected amine, was carried through a number of subsequent steps to afford the aldehyde derived from deprotection of the acetal. Unfortunately this aldehyde was completely resistant to the reactions we planned to use to complete the azaspirocycle synthesis.

We also undertook a related project involving the use of an alternative chiral auxiliary. Nearly all of the strategies used in the Paley lab have employed chiral sulfoxides; unfortunately these have proven difficult to remove and/or manipulate after the desired transformations. Instead an oxazolidinone was employed. The use of this auxiliary would have great benefits: chemical yields for the preparation of the precursor dienes are higher, and there are improvements in the selectivity of the installation of the iron(0) tricarbonyl unit. Furthermore, removal of the auxiliary via acid-catalyzed hydrolysis is anticipated to be easier to accomplish. Our current work combines the alkylnyl acetal precursor with the oxazolidinone auxiliary. The acetal group of the iron(0) tricarbonyl diene complex prepared in this way was converted to an alkylidene malonate to be used as a precursor for diastereoselective additions, revisiting a methodology used in the sulfoxide series.³ Addition to this will provide a new stereocenter with excellent selectivity and this will enable us to design more elaborate systems for future syntheses of natural product sub-units.

References
The parameter geography of multisite protein post-translational modification

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Abstract

Multistability – the existence of multiple steady states in a dynamical system – is thought to undergird complex decision-making processes in mammalian cells. But given a dynamical system, the number and nature of its steady states depends on the numerical values of its parameters, and different types of dynamical behavior may be encountered as the parameters are varied (i.e., as “parameter space” is traversed). Because of the nonlinearity of biological systems and the high dimensionality of the corresponding parameter spaces, it is difficult to elucidate the “geography” of any such parameter space. Here, we integrate several new developments in mathematics and theoretical biology that enable us to map the parameter space of a two-site post-translational modification (PTM) system. We begin by using (under assumptions of a physiologically realistic enzymology) a “linear framework,” built out of results in graph theory and linear algebra, to simplify and non-dimensionalize a nonlinear differential system of 13 variable concentrations into a polynomial system of two variable (normalized) concentrations and eight generalized parameters. Second, we solve the equations using efficient homotopy continuation methods implemented in Bertini and Paramotopy, two recently developed tools in numerical algebraic geometry, thereby mapping the parameter space of the system. Given the combination of model reduction via the linear framework, sampling techniques, and specialized numerical algorithms, we find that (with probability one) multistability vanishes with sufficiently low substrate relative to enzyme; there exists a multistable region of full measure that grows monotonically as substrate increases; and the multistable region is connected but not convex.
FABelbow: an FAB elbow angle computation program

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Abstract

One of the simplest structural determinants of the antibody FAB (fragment, antigen-binding) is the elbow angle – the angle between the pseudo-dyad axes of rotation between the constant and variable domains of an FAB. Given the growing wealth of static structural data on FABs available on the Protein Data Bank, the relationship between the elbow angle and the primary sequence of an FAB; the conformational dynamics of the elbow angle; and the viability of the elbow angle as a structural determinant in wide-search molecular replacement techniques are all of great interest. To efficiently perform these analyses, we have developed a robust, standalone elbow angle computation software package named FABelbow that can reliably calculate elbow angles without stringent agreement in sequence numbering, chain labeling, and chain identification. In summary, FABelbow assigns DSSP secondary structure elements to each residue in a given FAB, then computes the domain limits by identifying the most likely linker region for each chain using sequence alignment and the secondary structure assignments. Once the domain limits have been identified, FABelbow runs TM-align, a structural alignment program, to perform a structural alignment between the variable domains and between the constant domains, then uses the resulting rotation matrices to compute the corresponding pseudo-dyad axes of rotation. These two axes intersect at either of two explementary angles, one of which is chosen to be the elbow angle of the FAB; this decision is based on an auxiliary structural alignment (again performed using TM-align) between the FAB and a reference FAB with a defined elbow angle.
Mechanistic aspects of thrombolysis using inertial cavitation induced by ultrasound on microbubbles

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Abstract

Thrombi (blood clots) are currently a leading cause of death, particularly in the elderly, given that they lead to various common fatal diseases such as heart attack and stroke; however, despite how prevalent they are in causing deadly complications, there are no approved procedures that can safely and efficiently target and dissolve a clot. Recent research (Xie 2005) has shown that pulsed ultrasound has dissolutive effects on a thrombus in the presence of microbubbles and/or tPA (a protein that breaks down thrombi); however, little progress has been made on studying the actual mechanism by which dissolution occurs apart from speculation that the inertial cavitation and radial oscillations tear apart the fibrin ropes in the clot matrix (Weiss 2013).

The main purpose of the research was to look into the mechanistic aspects of sonothrombolysis. We looked specifically at in vitro dissolution of clotted porcine blood inside a 10% gel by pulsing a solution of DEFINITY® microbubbles and isotonic water against the clot with a 1.1 MHz ultrasound and observing cavitation of the microbubbles at 20 MHz. Due to variability in clot formation many trials rendered inconclusive data; nevertheless, trials in which the clot formed a complete blockage of the path indicated that the microbubbles collectively make their way through the clot gradually from point a to point b rather than thrombolysing at different locations.

In the future we hope to reduce variability in the thrombi so that results will be more constant, as well as to devise a method by which we can monitor the rate of dissolution in real-time. Ultimately with enough information on the mechanism of sonothrombolysis, the sonothrombolysis will become a common and effective clinical procedure.

Literature cited


Children Prefer Diverse Samples for Inductive Reasoning in the Social Domain

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Abstract

Inductive reasoning is an important tool by which children usefully generalize their limited experience to more comprehensive knowledge. We investigated children’s ability to evaluate inferences—appreciating that diverse evidence is more informative than non-diverse evidence for making generalizations about a property of a category. In previous studies, which tested reasoning about biological properties and animals, children did not demonstrate spontaneous preference for diverse information (Lopez, et al., 1992; Gutheil & Gelman, 1997; Li, et al., 2009; Rhodes, Brickman, & Gelman, 2008; Rhodes, Gelman, & Brickman, 2008).

We hypothesized that children would be able to use the diverse sample preferentially if the distinction between the diverse and the narrow sample was evident, for example when reasoning about people. Social categories like race and gender are highly salient (Kinzler, et al., 2010) and inform children’s inferences and decision-making in other domains of reasoning. Second, prior research has focused on biological properties of animals. In the present study, rather than asking about biological properties, children reasoned about toy preferences, whose variability across entities they should be more familiar with.

Children were given samples of either animals or people. In both conditions, children evaluated evidence for making generalizations about internal properties and about toy preferences. We found that, as in past literature, children did not prefer diverse evidence when reasoning about animals or biological properties. However, when generalizing about people’s toy preferences, 5- to 7-year-olds selected diverse samples over the non-diverse ones. This provides the most compelling evidence to date of young children’s spontaneous use of diversity-based information.

Literature Cited

Analysis of early heart asymmetry in *Ciona intestinalis*

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Abstract

Humans’ bilaterally symmetric appearance disguises the asymmetric body plan that underlies their growth and health. Diseases resulting from defects in asymmetric development can result in congenital heart defects and lead to death. However, very little is known about the origins of these diseases and how to prevent them. Here, we use the simple chordate *Ciona intestinalis* to develop an understanding of early mechanisms determining heart asymmetry. In *Ciona*, it is known that neurula rotation, or the spinning of the embryo inside its chorion layer, contributes to left-right asymmetry. Additionally, disruption of nodal signaling is known to impact asymmetry. Yet, asymmetries contributing to heart formation in *Ciona* remain unknown. Here we show that *Ciona* has right-sided, asymmetric heart formation. We also demonstrate that disrupting neurula rotation randomized heart asymmetry but inhibiting nodal signaling had no effect. These findings suggest that there is a nodal-independent mechanism, downstream of neurula rotation, crucial in heart asymmetry. Further research will reveal this mechanism and begin to uncover the underlying causes of human, heart-related asymmetry defects.

Literature Cited:


Analysis on the Role of Cell Free DNA As Diagnostic Tool For Sonic Hedgehog Subtype Medulloblastoma

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Abstract

Medulloblastoma refers to the tumor inside the cerebellum that is normally responsible for coordination and movement of the trunk. There exist four different subtypes of the disease, among which Sonic Hedgehog is known for its higher mortality. It involves an error in one or more genes along the Sonic Hedgehog pathway that controls the development of the cerebellum. The current therapy relies on conventional techniques which all pose risks for dangerous complications. However, scientists have devised safer treatment called targeted drug therapy that can inhibit the activity of SMO gene inside the pathway to halt the over-growth of granule cells. Nevertheless, the drug only works for Sonic Hedgehog subtype not for other kinds. Therefore, physicians need to correctly identify the target population. Yet, obstacle still exists.

The diagnostic mechanism primarily involves an invasive procedure such as open biopsy. Our project was focused on analyzing the blood test as a potential source for safer diagnostics. According to various sources, the intact tumor cells can become necrotic eventually spilling their contents into the nearby bloodstream including their cell-free DNA. If we can detect the significant amount of these DNA inside the blood, we can trace their origins to the Sonic Hedgehog subtype tumor cells. The model we used was flank tumor model meaning that we removed parts of spontaneous tumor from the brain of mouse and injected them onto the flank of immune-deficient mouse. The source of tumor cell free DNA is more definite in the flank tumor model than in spontaneous model, where the difference between tumor and normal cell free DNA becomes ambiguous.

The findings indicated that we can detect noticeable degree of tumor cell-free DNA inside the blood of flank models using the probe. Thus, the blood test can be a useful tool to identify Sonic Hedgehog subtype medulloblastoma. We can apply these findings to the clinical samples only when the complex molecular profile of human medulloblastoma is carefully analyzed so that the specific marker for tumor cell free DNA can be invented.
Laser-Induced Fluorescence of Boron Monoxide (BO)

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Abstract

Two diboride compounds with high melting points, ZrB₂ and HfB₂, are promising candidates for use on the exteriors of hypersonic vehicles, which travel in extreme temperature and high particle flow environments. While these compounds do not melt below 3000°C, they do oxidize in these environments to form boron monoxide (BO). By electronically exciting the BO formed in a sample with a laser, it is possible to quantitatively determine the BO formation rate and oxidation rate of the sample.

This study determined the electronic transition moment function of the BO B²Σ⁺ state, which is necessary for this quantitative detection. Ground state boron monoxide was created from a series of reactions inside a quartz reactor cell, and then pumped to the BO B²Σ⁺ (v = 1) electronic-vibrational state. Its emissions were then measured with a spectrometer. From the relative peak intensities of the emissions from this state, it was determined that the electronic transition moment function decreased with increasing r-centroid value.

Literature cited

Jasplakinolide prevents spatial memory deficits following brief sleep deprivation

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Abstract

Sleep deprivation impairs the formation of hippocampus-dependent memories. However, the molecular mechanisms by which sleep loss perturbs the consolidation process are unclear. Consolidation after learning is dependent plasticity of dendritic spines in the hippocampus. The Abel Lab found that there was a 38% reduction in dendritic spines after brief sleep deprivation (Havekes et al., in press). Actin polymerization is critically required for memory consolidation and forms the structural component of dendritic spines.

Jasplakinolide (JASP) is a potent polymerizer of actin in vivo. Previous work (Huang et al. 2013) demonstrated that JASP enhances contextual fear memory in the mouse hippocampus, indicating that actin polymerization is an essential mechanism for the consolidation of long-term memory. Since hippocampal-dependent spatial memory is consolidated during sleep, sleep deprivation following learning prevents memory formation.

I performed a pharmacological experiment using JASP to assess whether this drug is able to prevent spatial memory deficits following brief sleep deprivation. For this experiment, an object placement recognition (OPR) paradigm was used in which mice were trained to learn the spatial orientation of three objects. Twenty-four hours later, mice are exposed to the same three objects, one of whose position is changed. Spatial memory is assessed by measuring increased exploratory behavior for the object in a novel location. Half the mice were sleep deprived after the training period. Sleep deprivation perturbs consolidation of the spatial orientation memory, so mice that were sleep deprived showed no memory of spatial location. However, mice that were sleep deprived but were injected with JASP after training showed spatial memory. These findings indicate that JASP prevents spatial memory deficits following brief sleep deprivation. Future studies should look to identify the biochemical mechanism by with JASP is inducing actin polymerization and thus preventing memory deficits.

Literature cited

1. Havekes et al. In press
Impact of social network position on reproductive behaviors in forked fungus beetles (*Bolitotherus cornutus*)

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Abstract

Social networks explain the evolution of animal behavior by juxtaposing the role of the individual’s phenotype with the larger social structure of the population. Evidence shows that these networks can describe a variety of population trends, including reproductive behaviors. We investigated a population of wild forked fungus beetles for one day to determine if an individual’s position in the network, in relationship to its conspecifics, affects its reproductive behaviors and vice versa. The number of courtships attained by males correlated positively to strength and betweenness, while the number of courtships attained by females correlated positively to strength. Both strength and betweenness are measures of network centrality. These results suggest that centrality is experiencing sexual selection, but individual-level behaviors may affect the network metrics. Further research on this topic will hopefully clarify the impact of the individual-level behaviors.

Literature Cited

Downing, B.C. and Royle, N.J. 2013. "Animal Social Networks." eLS.
The interpersonal stress of strongly disliking someone and angrily ruminating about negative interactions produces physiological stress symptoms that endanger health and happiness over time. We hypothesized that negative interpersonal stimuli would create stress but that stress would be reduced by practicing compassion meditation with a smartphone app. Participants (7 female, 4 male) provided pictures of and narratives describing familiar people they strongly disliked. Heart rate, respiration, and eye movement were monitored while they viewed these stimuli. Before compassion training, listening to dislike narratives produced an increase in heart rate compared to impersonal narratives (average increase=4.24bpm, t=2.97, p<0.05, n=7). Eye tracking data indicated that more time was spent looking at disliked than liked faces, which correlates with increased heart rate (n=9, r=0.53). Participants were then instructed to practice short daily meditation exercises on the app for three weeks. Preliminary data indicate that after using the app, stress response during dislike narratives was reduced. These results suggest that practicing compassion meditation with an app can help to alleviate the stress of difficult interpersonal relationships.
Trajectory Optimization for Robotic Manipulators Using Multigrid CHOMP

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Abstract

I worked under Siddhartha Srinivasa to integrate Matt Zucker's Multigrid CHOMP with the Personal Robotics Lab's robotic planning environment. This consisted of integrating an implementation of Multigrid CHOMP with collision detection and constraint handling, and extending it to include several modifications explored in the literature, including: Hamiltonian Monte Carlo method and momentum updates, goal set CHOMP, task space region constraints, and joint limit constraints. For non-constrained cases, the new CHOMP module reduces planning time by 90% on average over the current module, and for constrained cases the speedup is even greater.

In addition, I integrated CHOMP with NLopt, a nonlinear-optimization library, hoping to improve upon CHOMP's current optimization method of gradient descent. This modification enables trajectory optimization using numerous other algorithms that have not previously been applied to trajectory optimization. Optimization can proceed in two stages: 1) a global optimization algorithm searches the state space widely for areas of low cost and 2) a local optimizer refines the solution returned from global optimization.

Literature cited


Hydrogen Synthesis via Electrode Functionalization

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Abstract

The past few decades have revealed a growing interest in the development of alternative energies to fossil fuel combustion. The conversion of hydrogen gas’ chemical energy into electrical energy has the potential to become a new sustainable and environmentally friendly candidate. In order for this technology to be developed, efficient ways to synthesize hydrogen must be established. One such method looks at how certain nickel complexes can mimic the reaction pathway behind hydrogenase enzymes. In order to maximize these molecules’ efficiencies, this project looks at how the nickel complexes can be bound to electrodes via electrografting procedures. These procedures occur via nucleophilic substitution of pyridines, or via radical reactions of alkynes.

Different nickel complexes were synthesized with pendant amines containing either pyridine groups or alkyl groups. Their catalytic activity for hydrogen production was measured through electrochemical studies. The nickel complexes whose pendant amines included pyridine rings were not successfully synthesized due to unknown side reactions. The other complexes (with alkyl groups attached to the amines) that were synthesized showed no catalytic activity. Electrochemical studies show that the nickel complex, once reduced to Ni(I) from Ni(II), undergoes an unknown reaction with the pendant alkyne. Upon further reduction to Ni(0), the complex forms an as-yet unidentified polymer. We verified these results and assumptions by examining how simple nickel complexes reacted to alkynes in a solution.
The Effect of Variations in Diet and Environment on C. elegans

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Abstract

Although prior work has characterized the effect of diet on physical and developmental phenotypes, many questions connecting diet, the environment, and behavior remain. We used C. elegans as a model organism to test the effect of alternative diets on behavior and the neuromuscular system. We tested 10 different species of bacteria, including the standard E. coli OP50 strain as a control. Most of the alternate diets resulted in significant developmental delays and reduced brood size. We looked more closely at worms fed diets of Pseudomonas and Brachybacterium. Introducing C. elegans to a lawn of Pseudomonas caused a swelling behavior and aggregating phenotype, likely caused by a biophysical property of the biofilm formed by Psuedomonas. A diet of Brachybacterium causes a significant developmental delay in single worms that is partially remedied when the worms are in a group. Our data suggest that Brachybacteria may produce a toxic molecule that induces a pheromone to be released by worms, and that groups of animals are better off than animals in isolation. Taken together, our results further highlight the importance of diet and environmental factors in animal lifestyle and behavioral choices, and suggest a role for social behavior in promoting selective fitness.

Literature Cited


MacNeil and Walhout, Food, pathogen, signal: The multifaceted nature of a bacterial diet, 2013, Worm Volume 2 Issue 4
The Effect of Model Parameters on Residual HIV Load

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Abstract

Many researchers have analyzed the dynamics of the Human Immunodeficiency Virus (HIV) \textit{in vivo} in attempts to curate a deeper understanding of the virus. The purpose of this work was in the same vain: to conduct an exploratory data analysis involving data from an HIV research study. The project aimed to 1) model differential equations that describe the virus \textit{in vivo}, 2) observe how the residual viral load responds with respect to the drug efficacy, and 3) find which parameters of the equations will lead to a viral load above detectable viral threshold of 50 virions per mL. Blood sample data retrospectively obtained from 12 patients with diagnosed HIV constituted the primary dataset of this project [1]. Consistent with the design of an \textit{interruption} study, samples were taken during drug treatment and drug interruption. From this data, a Monte-Carlo Markov-Chain (MCMC) technique was used to generate data points from a set of differential equations [2].

The block schematic program Simulink proved to be an effective tool to model differential equations. Sampling the MCMC data points via this model provided ample data to analyze. The drug efficacy was the target parameter to discover its relationship to the viral load. The most telling observation was how different each patient responded to drug effectiveness. This was expressed at the point where the viral load is below detection level of 50 virions per ml, a level where the virus is in such small concentrations that it cannot be of extreme harm. For some patients, the viral load was controlled at this detection level corresponding with a low drug efficacy value, and for others the viral load was controlled at a significantly higher drug efficacy value.

Surprisingly, when looking at all parameters across all patients, there was one parameter that overtly affected the residual viral load. Isolating data exemplars above the detectable viral load level and also above corresponding drug efficacy value yielded one parameter correlated with a higher residual viral load. A particularly high value of the death rate of infected cells parameter corresponded with higher residual viral loads. For other parameters, there was too much interdependency to confidently identify trends in the residual viral load.

Literature cited

Communication Complexity of the Multiparty Pointer Jumping Problem

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Abstract

In standard computer science theory, one often focuses on problems where a computer has data and wants to use this data to compute an answer to a question. However, this does not encompass all of the interesting problems that occur. Consider the following situation: There are two or more agents attempting to solve a problem together. The catch is that each agent has data that is disjoint from the rest, and must then communicate their information to each other. The trivial solution would be for each agent to communicate all of their information to each other, and then solve the problem as usual; however, in problems with a large amount of data, the runtime for this protocol is very large. The field of communication complexity focuses on finding efficient protocols for solving various of these problems.

In this poster, we focus on the Multiparty Pointer Jumping Problem. We take the previous bound found by Brody et al [1] and improve it to $CC(MPJ) = O\left(\frac{n \log n}{\log \log n}\right)$. While constructing the protocol, we also extend the Erdős-Renyi random graph model to include dependence. We believe this extension to be of independent interest in mathematics.

References

Zero Diagonal Minimum Rank of Graphs

Jorin Schug

Abstract

Given a graph $G$, we can associate a family of zero-diagonal real symmetric matrices $S_0(G)$ with it using the same nonzero pattern as the graph’s adjacency matrix. The zero-diagonal minimum rank of the graph $mr_0(G)$ is the minimum of the ranks of all the associated matrices. On this poster, we first introduce the concepts needed to define the zero-diagonal minimum rank of a graph. After presenting some known results, we present some new calculations done this summer. Finally, we generalize one of those calculations to describe a theorem about the zero-diagonal minimum rank of a cone on a graph and some some applications of that theorem.

References


Lentiviral SLIT1 shRNA plasmid validation:
an exploration of the genetic basis of vocal learning
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Abstract

Vocal learning, the ability to produce novel vocalizations, has evolved independently in eight
animal groups including humans and songbirds (Petkov and Jarvis, 2012). All vocal learners share
one neuroanatomical hallmark that is never found in vocal non-learners: a direct neural projection
from the cortex to the brainstem used during production of vocalizations. A direct pathway allows
for finer movements of the larynx or syrinx and thus greater control over vocalizations (Jarvis,
2004).

One gene potentially responsible for this difference between vocal learners and vocal non-learners
is slit1. Slit1 is known to be involved in axon guidance in vertebrates (Andrews et al., 2006). Given
slit1 is down-regulated in the cortical motor output region of vocal learners but not vocal non-
learners, it was then hypothesized that this down-regulation of slit1 is necessary to permit the
formation of a direct neural pathway (Arriaga et al., 2012).

To test this hypothesis, the Jarvis lab has undertaken a series of experiments involving genetic
manipulation of slit1 expression in vocal learners (songbirds) and vocal non-learners (mice)
through the use of two lentiviruses designed to either cause overexpression of slit1 or knock
expression down with shRNA. In the following experiment, we validated that our lentiviral slit1
plasmid correctly alters SLIT1 protein levels in HEK cells, allowing use of slit1 lentiviruses in in vivo
injections in the brains of live birds and mice.

Literature cited

Andrews, W., Liapi, A., Plachez, C., Camurri, L., Zhang, J., Mori, S., Murakami, F., Parnavelas, J.G.,
Sundaresan, V., and Richards, L.J. (2006). Robo1 regulates the development of major axon
tracts and interneuron migration in the forebrain. Development 133, 2243–2252.

System Has Some Features Similar to Humans and Song-Learning Birds. PLoS ONE 7, e46610.


Petkov, C.I., and Jarvis, E. (2012). Birds, primates, and spoken language origins: behavioral
Hooking and Sheeting: strategies used by *Haminoea vesicula* to maintain stability on different substrates

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Abstract

Many marine gastropods face the challenge of adhering to substrates under adverse flow conditions. Some species live on both solid and sedimentary substrates, although how these substrate generalists resist detachment from materials with fundamentally different mechanical properties is not well studied. We used field observations and flow tank experiments to compare the capabilities and tactics of *Haminoea vesicula*, an opisthobranch gastropod, when exposed to destabilizing flow on its native sand and eelgrass. Velocities of outgoing and incoming spring tides in the tidal creeks and over and within eelgrass beds where *H. vesicula* live at False Bay, San Juan Island, WA ranged from 1 to 30 cm/s. In a flow tank, snails’ response to current depended on substrate and orientation. On eelgrass, snails moving into flow maintained their position at velocities exceeding 40 cm/s, but were more vulnerable when facing away from or sideways to flow (falling off at mean velocities of 25 and 32 cm/s respectively). In the latter orientation, snails often rotated into flow by hooking onto the leading edge of eelgrass with the anterior edge of their cephalic shield. In this position, snails resisted flows exceeding 40 cm/s. Snails crawling on sediment and exposed to turbulent flow drew sediment-encrusted mucus sheets dorsally, completely ensheathing their bodies. “Sheeting” significantly increased snails’ effective weight and ability to resist flow. On sand, snails ensheathed in sediment were least stable in the sideways orientation compared to those facing into or away from flow (mean velocities of 13 vs. 20 and 23 cm/s). Experiments on sandpaper indicated that snails were destabilized on sediment due to failure of adhesion of the sedimentary layers beneath them rather than their attachment to the sand.
Light Evoked Responses from Ensembles of Ganglion Cells in Mouse Retina

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Abstract:

The multielectrode array (MEA) is a group of tightly spaced electrodes that allows simultaneous collection of action potentials from hundreds of ganglion cells at a time. This is ideal for the study of ganglion cells in the retina, as it allows one to see how all the cells are working together to send visual information to the brain. Using different types of stimuli, the characteristics of each cell's receptive field can be determined. This can be used to identify the mosaic of these fields tiling the retina (1).

Each cell can be classified as responding to light onset (ON), offset (OFF), or both (ON/OFF). Directionally selective cells can then be further identified using a moving bars stimulus. Furthermore, the specific location of the cell's receptive field can be determined using a white noise stimulus and spike triggered averaging (2).

In order to easily classify each of these characteristics from hundreds of ganglion cells at a time, huge amounts of data must be collected. In order to efficiently collect and process this data, we designed multiple programs on MATLAB. The goals of my summer was to build the physical set up and write these programs so that the MEA could easily be used by anyone in the lab for any purpose.

Literature Cited:


An examination of structural and functional brain differences across the autism spectrum during affective language processing

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Abstract

Previous experiments have examined the neurodevelopmental-based cognitive deficits of autism spectrum disorder (ASD), which include impairments in social cognition, emotion comprehension, and language processing (Sucksmith, Roth, & Hoekstra, 2011). Structural brain abnormalities (Just, Cherkassky, Keller, Kana, & Minshew, 2007) as well as irregular functional activity in frontal-parietal and ACC networks (Just et al., 2007; Mundy, 2003; DiMartino, Shehzad, Kelly, Roy, Gee, Uddin, Gotimer, Klein, Castellanos, and Milham, 2009) have been linked to ASD, suggesting that autistic individuals lack the executive control and social inferencing abilities of neurotypical individuals. The goal of the present study was to examine structural and functional differences across neurotypical young adults who vary in autistic characteristics, measured by the autism quotient (AQ), during performance on an fMRI emotional inferencing task.

Although we predicted that individuals with higher AQ scores would demonstrate less functional activity in response to affective linguistic stimuli, it was found that more autistic individuals’ brains were more active in regions belonging to cognitive control and default mode networks. Our results indicate that more autistic individuals find the task of comprehending emotional content in conjunction with forming an inference challenging, and they consequently must employ greater cognitive resources to perform accurately. Future research is in order to determine if our emotional inferencing paradigm is representative of real-world phenomena.

Literature cited


Abstract

The Horde architecture, first developed by Modayil, Sutton, et al in 2011, uses unsupervised reinforcement learning to make a complicated environment easier to understand by separating the action-state space of interaction into numerous action-state pairs, each of which is assigned an independent learning agent within the Horde. However, training the Horde takes both a considerable amount of time, even within a simple virtual environment, and by itself does not provide any means of applying the learned knowledge to performing some task within the robot’s environment. Therefore, it becomes necessary to ask how the Horde can be made more efficient, both in terms of its training period and how the knowledge resulting from its training can be utilized in a task-completing situation.

Efforts to refine the Horde’s efficiency took the form of multiple experiments conducted with variations in the virtual environment, amount of sensors available to the robot, amount of actions available to the robot, amount of steps trained, and which selection of demons was being trained. To better represent the information being gathered, a tilecoding method was implemented which discretizes the sensor data being collected, and this tilecoding was also tested with the Horde to yield the best performance from the smallest possible time period of training. These virtual experiments cleared up the capabilities of the Horde as it exists currently in virtual simulation and the results provided a guide on how to optimize the Horde’s performance in different situations.

Literature Cited

Quantifying CSO reduction by backyard rain gardens

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Abstract

Combined sewer overflow (CSO) occurs in municipalities with combined sewers (storm water and sewage are combined) when rainstorms cause sewer volumes to exceed processing capacity. Excess raw sewage is then expelled from CSO outfalls into a body of water. Cleveland is one such city, with CSOs directly into creeks, rivers, and Lake Erie. In accordance with United States and State of Ohio v. Northeast Ohio Regional Sewer District (2010), the NEORSD is now responsible for diverting 44 million gallons of storm water per year using green infrastructure.

Green infrastructure is used to control high water volumes by mimicking natural hydrological systems. In order to explore the impact of many small backyard rain gardens on CSO reduction, Cleveland Botanical Garden is installing nine rain gardens on vacant lots in Cleveland, Gary, and Buffalo in fall 2014. Equipment and methods to estimate storm water capture were tested and evaluated on an existing rain garden at the Botanical Garden. A LIDAR sub-watershed model was utilized to calculate the catchment area of the rain garden. Weather data were gathered to track precipitation and estimate evapotranspiration using the Penman-Monteith equation. Soil moisture probes were installed to corroborate storm water capture, as well as investigate the movement of water within the soil. While data analysis is ongoing, preliminary results show the setup to be suitable for remote monitoring of rain garden performance.
Induced protease inhibitors by suite as a plant defense response in Solidago altissima

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Abstract

Plants must often defend themselves against a multitude of herbivores and both serine and cysteine protease inhibitors are a method of defense. Protease inhibitors (PI) hamper the ability of insects to digest necessary amino acids, which results in stunted herbivore development and less damage to plants overall. Using tall goldenrod (Solidago altissima) and its many respective herbivores as a model system, we investigated how plants defend themselves against various herbivores with differing feeding guilds.

Our main hypothesis was that species-specific induction of PIs made the most sense as a cost saving mechanism. By only producing the necessary PIs when an herbivore attacked, the plant would not waste energy producing these costly PIs, presumably leading to greater fitness. However, we also had an alternate hypothesis that plants could have guild-specific induction, as the benefit would be a more diversified resistance to multiple herbivores, as well as a possible synergistic effect.

After conducting protein assays our results indicate that instead of species or feeding guilds, suites are how plants organize their PI defenses. Suites are groups of herbivores that were visually documented by Maddox and Root (1990) to induce a consistently similar plant response, with disregard to guilds and taxonomy. Our chemical data confirms the existence of suites, although it is unknown what brings vastly different insects of different orders to induce a similar plant response.

Furthermore, choice feeding assays were done to discover how previous herbivores affect current herbivores. Our results indicate that herbivores tend to prefer plants damaged by herbivores of other suites. Without further replicates we cannot definitively conclude this, but it does suggest that plants may tailor their defenses to a specific suite and inadvertently make themselves more susceptible to other suites.

Literature cited

Physical properties and structural preferences of isoeugenol: a computational study

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Abstract

Over time, plants have adapted flavor and scent molecules that are often used to attract pollinators or provide natural protection against ultraviolet radiation, herbivores, and pathogens. Isoeugenol (C_{10}H_{12}O_{2}) is a phenylpropene of particular interest, a scent molecule having the essence of clove. Isoeugenol consists of an aromatic ring with three substituents: a propenyl group, a hydroxy group, and a methoxy group. Ab initio computation was used to examine the structures and dynamics of the geometric isomers of isoeugenol. All calculations, including ground state optimization and frequency calculations, excited state calculations (CIS and TD-DFT), transition state calculations, and potential energy scan calculations were performed using Gaussian 09 through the supercomputing system Trestles under XSEDE.

Isoeugenol was found to have six relevant trans conformers and eight relevant cis conformers. The two lowest energy minima of both geometric isomers correspond to a structure in which the hydrogen of the hydroxy group points towards the oxygen of the methoxy group, forming a stabilizing intramolecular hydrogen bond. In all other conformers, the hydrogen of the hydroxy is pointing away from the methoxy group and thus the stabilization provided by the intramolecular hydrogen bond is lost and, as a result, these conformers are all significantly higher in energy (>1000 relative cm^{-1}) than the two lowest energy conformers of each geometric isomer.

The potential energy scans taken of (E) and (Z)-isoeugenol calculated the lowest energy path a substituent takes when rotating 360 degrees. Potential energy scans of the methoxy torsion, hydroxy torsion, and propenyl torsion were taken and fit with a truncated Fourier expansion. The calculated ground state minima and transition states were found along the paths proposed by the potential energy scans, further validating the accuracy of the calculations. Further studies should include recording the fluorescence excitation and emission spectra of isoeugenol and comparing these spectra to the ab initio results in order to correctly make vibronic assignments.

Literature Cited


Preliminary Investigation of Proton Dose Range Verification Using Monte-Carlo PET Simulations

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ABSTRACT

Using the simulation software Geant4 Application for Emission Tomography (GATE) we investigated two primary isotope channels' (Carbon-11 and Nitrogen-13) contribution to the dose of radiation deposited by protons onto a 1x20x1 cm box of HU35 (a synthetic material similar to brain white-matter). A virtual UFPTI Gemini PET Scanner was used to detect the isotope distribution inside the source with particular attention being paid to the PET machine’s ability to detect the weaker Nitrogen-13 signature (~5% the intensity of the Carbon-11) when combined with the Carbon-11 signature. These preliminary results indicate PET’s ability to distinguish the two signatures both in detected coincidences and in the Sinograms constructed by the PET machine. This is promising that further investigation and quantification of isotope behavior will lead to higher-resolution dose-range verification with PET.
Polypyridyl Ru complexes as G-quadruplex DNA ligands

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Hexacoordinated polypyridal Ru(II) compounds have been demonstrated to interact selectively with G-quadruplex (GQ) DNA. Eleven Ru compounds with the general formula [Ru(bpy)$_2$L]$^{2+}$ and [Ru(phen)$_2$L]$^{2+}$ (where bpy is 2,2-bipyridine, phen is 1,10-phenanthroline, and L is an experimental polypyridal bidentate ligand) were studied as G-quadruplex binders. These compounds were subjected to FRET stabilization and selectivity tests using human telomeric DNA. The most effective Ru compounds were characterized in greater detail using UV-vis and fluorescence spectroscopy. Bpy or phen ligands did not have a significant impact on GQ binding, suggesting GQ interaction is mostly due to the experimental ligand, L. The “light switch” properties of the Ru compounds were also studied; all compounds displayed “light switch” effect but with varying degree of efficiency.
Identifying Biomarkers of Response to checkpoint kinase 1 (Chk1) in SCLC

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Purpose: Small cell lung cancer (SCLC) is an aggressive malignancy with approximately 30,000 new diagnoses annually and a 2-year survival rate of 5%. Proteomic and mRNA analyses have identified DNA repair proteins, such as Chk1 and PARP1, that are enriched in SCLC and thus have potential as therapeutic targets. In this study, we evaluate the activity of Chk1 inhibitors, SCH-900776, LY-2603618, and LY-2606368, in the presence and absence of cisplatin or a PARP1 inhibitor, AZD 2281 (olaparib), to investigate the efficacy of potential combinatorial treatment options, and to determine potential biomarkers that may help predict response to treatment.

Experimental Design: Inhibition of SCLC proliferation by single agent and combinatorial drug treatments was assayed \textit{in vitro} via Cell Titer Glo assay. Drug sensitivity was correlated with protein expression by reverse phase protein array (RPPA).

Results: We observe high single agent activity of LY-2606368 in SCLC, with greater \textit{in vitro} sensitivity to LY-2606368 than cisplatin and olaparib. Response to treatment with LY-2606368 in combination with cisplatin or olaparib was found to be additive in SCLC cell lines. Sensitivity to Chk1 inhibitors was associated with elevated basal expression levels of pro-apoptotic proteins whereas resistance was associated with high levels of pAKT and other PI3K pathway proteins.

Conclusion: Novel Chk1 inhibitor, LY-2606368, shows striking activity in SCLC. Pro-apoptotic proteins, which are overexpressed in SCLC, serve as potential markers for drug sensitivity.
Characterization of Growth and Oil Degradation of Gamma-proteobacteria: *Marinobacter* EN3

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Abstract

Oil degrading bacteria are ubiquitous throughout marine environments. Gamma-proteobacteria of the genus *Marinobacter* were commonly found at oil contaminated sites along the coast of the Gulf of Mexico after the Deepwater Horizon spill in 2010. The particular strain *Marinobacter* EN3 was isolated from contaminated beach sands at Pensacola beach in Florida after the spill (Kostka et al. 2011). The growth patterns and oil degradation capability of *Marinobacter* EN3 were assessed. Growth was measured as a function of total cellular protein and by genome copy number. The percent of total hydrocarbons degraded was evaluated at various time points over a 14 day period by GC-FID measurements. The two growth methodologies resulted in closely aligned classic growth curves for growth on crude oil. *Marinobacter* EN3 exhibited near constant levels of cell density in peptone. Overall growth was greater in oil treatments, though this may be due to differences in total carbon present. After 14 days, 22.9% of total hydrocarbons in the oil were degraded. Thus *Marinobacter* EN3 likely only possesses the enzymes to degrade a fraction of the total hydrocarbons. Only by understanding bacterial physiology and growth patterns in relation to crude oil presence and degradation, can inroads by made into new treatments and technologies for future spill management.

Literature cited

Permutation entropy analysis of dynamical plasma turbulence

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Abstract

The statistical character of turbulence in the plasma wind-tunnel configuration at the Swarthmore Spheromak Experiment (SSX) and the solar wind is evaluated using ordinal pattern-based measures of complexity. The SSX MHD wind tunnel measures fluctuations in magnetic field, velocity, and density as highly magnetized spheromaks of plasma evolve dynamically into a relaxed state. Flow speeds are measured with a visible light array. \( \dot{B} \) and \( B \) time series for 3 spatial directions recorded by a 16-channel, high-resolution probe array embedded in the chamber are analyzed using the permutation entropy and Jensen-Shannon statistical complexity. By calculating the position of signals on a complexity-entropy plane as in [1], the degree of stochastic, periodic, or chaotic dynamics can be evaluated. Complexity-entropy positions of SSX signals are compared to those of turbulent fluctuations in the solar wind and the Large Plasma Device (LAPD), and it is found that the dynamics in the SSX plasma source are more truly turbulent than those in the LAPD but less stochastic than fluctuations in the solar wind.

Literature cited

The Use of Image Segmentation to Calculate Brain Tissue and Cerebrospinal Fluid Volume

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Abstract

In developed countries Magnetic Resonance (MR) imaging is mainly used for diagnosing medical problems. MR images have a greater range of intensity differences and therefore can show better contrasts between tissues, which is useful for brain images. However, due to the large cost associated with installing and operating MRI machines, Computed Tomography (CT) machines are primarily used in developing countries. Since most image analysis software is made in developed countries, these software packages are catered towards MR images. Therefore, there is a high need for image segmentation software for CT images in developing countries.

The purpose of the project was to develop a software program that would quickly, efficiently, and reliably perform image segmentation on CT brain scans. The program would segment and calculate the volume of brain tissue and cerebrospinal fluid. The program will then be used in a trial to analyze the use of a new procedure for treating infants with post-infectious hydrocephalus in Africa.

This program will be used in measuring the effectiveness in a new procedure for treating infants with post-infectious hydrocephalus. The use of shunts to treat hydrocephalus is not effective in areas in Africa. This is because shunts have to be replaced often and that it not always possible in Africa. Therefore, two new procedure are being tested: Endoscopic Third Ventriculostomy and Choroid Plexus Cauterization. This program will be used to measure how well these new procedures are in reducing fluid volume buildup.

References


Phytoplankton cell growth under fluctuating light regimes

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Abstract

Light functions as an essential resource for photosynthetic organisms to grow and perform physiological functions. The goal of this research project is to determine how the perturbations in light sources (intensity/frequency) can alter the photosynthetic production and growth rates of phytoplankton. Any understanding of phytoplankton ecology and predictions about how environmental changes will affect marine ecosystems comes down to what factors control growth and photosynthesis, and how variations in those factors affect the community. In vivo fluorescence, primarily through chlorophyll a light emission, will be used to determine growth rates of phytoplankton cultures incubated in batch culture mode under constant temperature and varying light levels with conditions. Samples will be run through Tau-Turner and PAM Fluorometers to determine fluorescence as a measure of chlorophyll concentration. Data on how phytoplankton respond to light fluctuations will provide a better understanding of how species respond to fluctuations of light in the ocean, and how that will affect communities.

Literature cited


Dufresne, A. et al. (2003), Genome sequence of the cyanobacterium Prochlorococcus marinus SS120, a nearly minimal oxyphototrophic genome, Proc. Natl. Acad. Sci. USA 100, 10020-10025.


Biologists have developed a good understanding of genetic coding regions, but the function of regulatory DNA, known as enhancers, remains poorly characterized. 3 to 4 hour *Drosophila* embryos are a convenient system to study since active genes, their regulatory elements, and regulators are well known. *Krüppel* is expressed at this stage in a single stripe that is driven by two enhancers, called shadow enhancers. I studied the rules governing the regulation of *Krüppel* enhancers by a particular transcription factor, Hunchback, and found that Hunchback represses one of *Krüppel’s* shadow enhancers, but acts as either a repressor or an activator in the other depending on its concentration.
Abstract

Many astrophysicists are currently studying gravitational waves, a phenomenon which was predicted by Einstein and which is central to our current understanding of gravity, but has never yet been definitively observed. Recently, the BICEP2 team in Antarctica has published work on the detection of gravitational waves from the very early universe and the Planck Satellite has upcoming data that may shed some light on the issue. This summer, I studied the theoretical effects of gravitational waves on space and the systems they pass through, by developing code to simulate the event and its results, which explores a novel method of gravitational wave detection. Unlike BICEP2 and the Planck team, I focused on gravitational waves produced by galactic or stellar binary mergers, rather than the early universe. A gravitational wave is a tensor, but we express the small force the wave exerts as a vector quantity, and this can be used in conjunction with the Gaussian perturbation equations and to predict the small changes in orbital parameters that result from the interaction of a binary system with a gravitational wave. Some of the perturbations we see are periodic, which average out to zero over time, but there are also secular perturbations predicted, and these build up over time. The advantage of investigating the secular perturbations is that they are more easily detectable in principle, which is significant when observers look for extremely small signals such as these. I also investigated non-Einsteinian theories of gravity and the differing types of gravitational wave polarization predicted by these alternate theories, as well as modeling the effects of Einsteinian polarizations of gravitational waves on a ring of test particles in space, to specify how we can use precise observations of binary systems to distinguish between these various theories of gravity.
Comparison of Headache Characteristics in Children who do and do not meet Revised Criteria for Pseudotumor Cerebri Syndrome

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Abstract
Pseudotumor cerebri syndrome (PTCS) is a condition where a patient has increased pressure of the cerebrospinal fluid. This condition causes permanent vision loss in 10% and headaches in 91% of children who have it. While headaches are the most common symptom for patients with PTCS, headache characteristics (i.e. headache quality, duration, and severity) have not been previously compared between patients who do and do not meet the diagnostic criteria for PTCS. The objective of this study was to compare headache characteristics between a control group and three other study groups made up of pediatric patients who meet different criteria for pseudotumor cerebri syndrome (PTCS). To do this, a retrospective chart review was used to collect information on the headache characteristics for migraine and tension-type headaches as defined by the International Classification of Headache Disorders. This research resulted in two main findings. 1) A lumbar puncture, used for mainly diagnostic purposes, provided temporary headache relief in a majority of patients both meeting the criteria for PTCS and currently not meeting the criteria for, but with symptoms suggestive of, PTCS (Intracranial Hypertension). 2) A large portion of patients with Definite PTCS and Intracranial Hypertension had a similar spread of headache classifications, with the majority meeting criteria for migraine headaches. In conclusion, both patients with Definite PTCS and Intracranial Hypertension are experiencing mostly migraine headaches. With expansion, including continued data collection, particularly in regards to the control group, this research could lead to a prospective study and the ultimate creation of a prediction rule that could improve the ability to diagnose, and subsequently treat, headaches that are suggestive of, but not meeting criteria for, PTCS.

References: