COS-JAM
College of Science Joint Annual Meeting
Friday, May 4, 2018
Jordan Hall Galleria

1-1:45 pm: Poster Session I
1:45-2:45 pm: Oral Presentations I
2:45-3:30 pm: Poster Session II
3:30-4:30 pm: Oral Presentations II
4:30-5 pm: Reception and Awards

COS-JAM is part of the University of Notre Dame Undergraduate Scholars Conference. Please contact Xuemin Lu with any questions at xlu1@nd.edu.

For more information visit: science.nd.edu/cosjam
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<tr>
<th>Time</th>
<th>Session</th>
<th>Room</th>
<th>Chair/s</th>
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<td>01:00</td>
<td>Session: Poster session 1</td>
<td>Room: Jordan Hall Galleria</td>
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<tr>
<td>01:45</td>
<td>Session: Biology</td>
<td>Room: Jordan Hall Room 105</td>
<td>Chair/s: Xuemin Lu</td>
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<td>01:45</td>
<td><strong>Genomic characterization of the sparkleberry fly as the sister species to Rhagoletis mendax</strong></td>
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<td></td>
<td>Katherine Inskeep $^1$, Stewart Berlocher $^2$, Jeffrey Feder $^1$</td>
<td>1 Department of Biological Sciences, Notre Dame, United States, $^2$ School of Integrative Biology, University of Illinois, Urbana-Champaign, United States</td>
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<td>02:00</td>
<td><strong>Investigation of GRP78 Survival Mechanisms and ER stress in PDAC</strong></td>
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<td></td>
<td>Gabrielle Mungcal</td>
<td>University of Notre Dame, Notre Dame, United States</td>
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<td>02:15</td>
<td><strong>Expression Changes of Novel Genes in Cisplatin Treated Lung and Ovarian Cell Lines Reveal Relationships Across Disparate Cancer Types</strong></td>
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<td></td>
<td>Sawyer Williams</td>
<td>College of Arts and Letters- Environmental Sciences and Political Science, Notre Dame, United States</td>
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<td>02:30</td>
<td><strong>The Host Decoy Trap (HDT): exploiting visual, olfactory and thermal stimuli to improve surveillance of malarial mosquitoes in western Kenya</strong></td>
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<td>Xiaoyu Yu $^1$, Maurice Ombok $^2$, Nalie Bayoh $^2$, Frances Hawkes $^3$, Martin Geier $^4$</td>
<td>1 University of Notre Dame, South Bend, United States, $^2$ Kenya Medical Research Institute (KEMRI)/ Center for Disease Control and Prevention Research and Public Health (CDC), Kisumu, Kenya, $^3$ Natural</td>
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01:45 - 02:45  Session: ChemBiochem  Room: Jordan Hall Room 101  Chair/s: Dee Anne Goodenough-Lashua

01:45  Synthesis of hyperbranched polymers with post-functionalization specificity
Hannah Naguib, Xiaosong Cao, Haifeng Gao  University of Notre Dame, Department of Chemistry and Biochemistry, Notre Dame, United States

02:00  Adapting large scale and low cost genomics sample prep to microproteomics
Camille N Pierre, Matthew M Champion  University of Notre Dame, Notre Dame, United States

02:15  Effects of Supercharging and Solubility Tags on Protein Refolding & Solubility
Harisa Spahic, Matthew Klauer, Ian Walsh, Patricia Clark  Department of Chemistry and Biochemistry University of Notre Dame, Notre Dame, United States

02:30  Dissolved Nutrients And Greenhouse Gasses In A Midwestern Agricultural Stream: The Role Of Shallow Groundwater Inputs And Hyporheic Zone Exchange
Audrey Thellman, Martha Dee, Jennifer Tank  Department of Biological Sciences, University of Notre Dame, Notre Dame, IN 46616, United States

01:45 - 02:45  Session: Math & Physics  Room: Jordan Hall Reading Room  Chair/s: Tan Ahn
01:45  Decentralizing Cancer Care in Tanzania: A Facility Location Approach
Luke Maillie, Zoltan Toroczkai
Notre Dame Department of Physics, Notre Dame, IN, United States

02:00  Application of Machine Learning Techniques to Study ttH Events
Kaitlin Salyer
University of Notre Dame Department of Physics, Notre Dame, United States

02:15  Relating Topological Quantum Field Theories and Cut and Paste Invariants
Matthew Schoenbauer
University of Notre Dame, Notre Dame, United States, Indiana University, Bloomington, Bloomington, IN, United States

02:30  Performance Studies for the Proposed CMS L1 Track Trigger Upgrade
Patrick Shields
University of Notre Dame, Notre Dame, IN, United States

02:45 - 03:30  Session: Poster Session 2
Room: Jordan Hall Galleria

02:45 - 03:30  Session:
Room: Digital Visualization Theater

03:30 - 04:30  Session: Biology
Room: Jordan Hall Room 105
Chair/s: Jennifer Robichaud

03:30  Inducing Synthetic Lethality in Triple-Negative Breast Cancer using Combinatorial Drug Treatments
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<tr>
<td>03:45</td>
<td>Adenomatous Polyposis Coli regulates transcriptional activity of Epithelial Membrane Protein 2</td>
<td>Emily Abramczyk 1, Yingjia Ni 2, Bhavana Palakurthi 2, Siyuan Zhang 2</td>
<td>1 Department of Preprofessional Studies, Notre Dame, United States, 2 Department of Biological Sciences, Notre Dame, United States</td>
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<td>04:00</td>
<td>APC loss alters DNA damage repair in breast cancer cells</td>
<td>Jocelyn Gaona 1, 2, Alyssa Lesko 1, 2, Carolyn Ahlers 1, 2, Anna Lyons 1, 2, Jenifer Prosperi 1, 2, 3</td>
<td>1 Department of Biological Sciences, Harper Cancer Research Institute, University of Notre Dame, Notre Dame, United States, 2 College of Science, University of Notre Dame, Notre Dame, United States, 3 Department of Biochemistry and Molecular Biology, Indiana University School of Medicine – South Bend, South Bend, United States</td>
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<td>04:15</td>
<td>Inhibition of the Androgen Receptor N-Terminal Domain in Castration Resistant Prostate Cancer</td>
<td>Helen Streff 1, 2, 3, Scott Dehm 2, 3, Yingming Li 2, 3</td>
<td>1 University of Notre Dame, College of Science, Notre Dame, United States, 2 Harper Cancer Research Institute, Notre Dame, United States, 3 Department of Biochemistry and Molecular Biology, Indiana University School of Medicine, South Bend, United States</td>
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**Session: Physics**

Room: Jordan Hall Reading Room

Chair/s: Tan Ahn

03:30 - 04:30

**Atmospheric Pressure Plasma Jets for Biomedical Applications**

Elek Wellman, Ek Adhikari, Sylwia Ptasinska
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<tr>
<td>03:42</td>
<td><strong>Quantifying the Physics of the Second Maximum in I-band Type Ia Supernova Light Curves for Improved Cosmological Constraints</strong></td>
<td>Michael Foley</td>
<td>1, Ryan Foley</td>
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<td>03:54</td>
<td><strong>Investigating Implicit Bias in Letters of Recommendation for a High School Physics Camp</strong></td>
<td>Allison Olshefke, Micha Kilburn</td>
<td>University of Notre Dame Department of Physics, Notre Dame, United States</td>
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<td>04:06</td>
<td><strong>Analysis of Phase-Imaging Ion-Cyclotron-Resonance Mass Measurements at Argonne National Lab</strong></td>
<td>William Porter</td>
<td>1, Rodney Orford</td>
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<td>04:18</td>
<td><strong>Calculating Absolute Transition Probabilities for Deformed Nuclei in the Rare-Earth Region</strong></td>
<td>Anne Stratman, Clark Casarella, Ani Aprahamian</td>
<td>University of Notre Dame, Notre Dame, IN, United States</td>
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<tr>
<td>04:30 - 05:00</td>
<td><strong>Reception and Awards</strong></td>
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ABSTRACTS:

Friday, May 4th, 2018 - Jordan Hall Galleria - 01:00 - 01:45

Poster session - Poster session 1

Diurnal Rhythmic Behavior of Free-Ranging Brown-throated three-toed Sloths (Bradypus variegatus) in a Remnant of the Brazilian Atlantic Forest.

Dominic Acri 1, Diogo de oliveira Bezerra 2, Leandro Ricardo Rodrigues de Lucena 3, Antonio Rossano Mendes Pontes 4, Giles Duffield 1

1 University of Notre Dame, Department of Biological Sciences & Eck Institute for Global Health, Galvin Life Science Center, Notre Dame, IN, United States
2 Universidade Federal de Pernambuco, Centro de Ciências Biológicas, Departamento de Zoologia. R. Prof. Moraes Rego, 1235, Cidade Universitária, Recife, PE, Brazil
3 Universidade Federal Rural de Pernambuco, Campus de Serra Talhada, Departamento de Zootecnia. Av. Gregório Ferraz Nogueira, S/N, Serra Talhada, Pernambuco, CEP, Brazil
4 Instituto Nacional de Pesquisas da Amazônia - INPA, Núcleo de Pesquisas de Roraima - NPRR. Rua Coronel Pinto, 315, Centro, Boa Vista, Roraima, CEP, Brazil

Previous studies exploring the rhythmic activity of sloths of the Bradypus genus in undisturbed forests revealed either nocturnal or cathemeral patterns of activity. In the current study we wished to examine sloth behavior in a disturbed secondary forest habitat. In this study we evaluated activity pattern, time budget and rhythmic activities of brown-throated three-toed sloths living in the border of a highly disturbed forest fragment in northeastern Brazil. Observations were made over 29 days, and individual animal data analyzed as a series of 5-11 concatenated days. Three adults (2 females and 1 male) and 2 infants were studied. Observational data were collected in 15 min increments over the 24-hr day in the following categories: resting, moving, travelling, eating and grooming. Time series data were subjected to X2 periodogram, Fourier (Fast Fourier Transformation, FFT), cosinor and CircWave analysis, and revealed significant 24-hr rhythms in all behaviors in most circumstances. Unlike sloths located in undisturbed forest, this population exhibited primarily diurnal/day active patterns of behavior, with the center of gravity for each behavior occurring between ZT4 and ZT8. Furthermore, several behaviors were expressed in a bimodal pattern, with a morning (between ZT0-4) (and a late afternoon bout of activity (ZT8-12). These data suggest that with decreased predator presence and with a more ubiquitous food source, sloths adjust their temporal niche to daytime. Conversely, with elevated predator pressure and higher variability in food source locations, sloths tend to exhibit nocturnal patterns of activity.

Keywords: Sloth, Circadian, Behavior, Behavioral Ecology

Investigating the Extrinsic Effects of Tumor Microenvironment and Chemotherapy on Metastasis and Progression in PDAC

Madeleine Andreas 1, Ann Zeleniak 2,3, Reginald Hill 2,3
Pancreatic ductal adenocarcinoma (PDAC) is one of the most aggressive and malignant cancers. Most patients have a disease that is difficult to cure, and is almost always fatal. This difficult prognosis results from various factors, including inflammation and ER stress. In the GRP-78 mediated model of pancreatic cancer, the underlying mechanism of resistance is due to the Unfolded Protein Response (UPR). Sodium trans-(tetrachlorobis(1H-indazole)ruthenate(III)) (IT-139) is a novel small molecule inhibitor that impedes the action of GRP-78 in PDAC. While this treatment has recently been approved by the FDA as an orphan drug in treatment of PDAC, more research is needed to investigate the effect of IT-139 on PDAC at the cellular level. Furthermore, the role of MTSS1 was tested in PDAC in fibroblast-conditioned media. These cells are more likely to metastasize, and an overexpression of MTSS1 has been linked to a loss of this metastatic potential and increased survival. Here, we explore the effect of MTSS1 knockdown and IT-139 on the invasion and metastasis of PDAC cells. This data provides further insight into the effect of IT-139 and MTSS1 in PDAC, aimed at providing more effective treatment in patients with PDAC.

**Keywords:** Cancer, IT-139, Microenvironment, Metastasis, Pancreatic, GRP, Inflammation, Chemotherapy

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**Paclitaxel Effects on G2/M Arrest in APC Knockdown Cells Through Semi-Quantitative Protein Analysis**

Emily M. Astarita 1, Bronwyn J. Berkeley 2, Jenifer Prosperi 3

1 Department of Chemistry and Biochemistry, University of Notre Dame, Notre Dame, United States
2 Smurfit Institute of Genetics, School of Genetics and Microbiology, Trinity College Dublin, Dublin, Ireland
3 Department of Biological Sciences, Harper Cancer Research Institute, University of Notre Dame, Notre Dame, United States

**Adenomatous Polyposis Coli (APC)** is a tumor suppressor that is mutated or hypermethylated in approximately 70% of sporadic breast tumors with an inclination towards triple negative breast cancer (TNBC). Patients with TNBC often experience chemotherapeutic resistance when treated with traditional chemotherapy, such as paclitaxel. While paclitaxel acts by stabilizing microtubules, APC is also involved in regulation of microtubule stability through mechanisms that are not fully understood. These uninvestigated roles suggest that APC loss may have significant implications on the efficacy of paclitaxel in breast cancer treatment. We previously created APC knockdown cells (APC\textsuperscript{KD}) using the TNBC human breast cancer cell line, MDA-MB-157, and determined APC loss-of-function significantly increases resistance to paclitaxel. We hypothesized that varying microtubule stability in normal cells versus APC\textsuperscript{KD} cells may lead to a difference in cell cycle protein modulators during G2/M transition. Therefore, we profiled G2/M transition proteins Cyclin B1 and CDK1, including inhibitory (Thr\textsuperscript{14} and Tyr\textsuperscript{15}) and activating (Thr\textsuperscript{161}) phosphorylation sites on CDK1. Western blot analysis indicated an increase in Cyclin B1 and total CDK1 expression in APC\textsuperscript{KD} cells, with no changes in
phosphorylated CDK1. There was a selective increase in CDK1 Thr^14 and Thr^161 expression in PTX-treated APC^{KD} cells; however, both cell lines exhibited increased Cyclin B1 after PTX treatment. Cell cycle analysis using flow cytometry demonstrated increased cells in the G2/M phase for PTX-treated APC^{KD} cells compared to PTX-treated parent cells. Combined, these data suggest that, while APC^{KD} cells are able to evade PTX-induced apoptosis, APC status does not prevent G2/M arrest after 24 hour PTX treatment. Examination of these cell cycle protein modulators can further our understanding of paclitaxel resistance in APC^{KD} cells and help to identify a potential therapeutic target. Future directions include examining regulatory proteins upstream of Cyclin B1 and CDK1, and a time course of PTX treatment.

**Keywords:** Adenomatous Polyposis Coli, chemoresistance, paclitaxel

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**Expression of developmental commitment factors in the regenerating adult zebrafish retina**

Margaret Brecker, Manuela Lahne, David Hyde

*University of Notre Dame, Notre Dame, United States*

Retinal damage in zebrafish, but not mammals, induces Müller glia cell cycle re-entry to produce neural progenitor cells (NPCs), which transiently amplify before differentiating into both lost neuronal subtypes and those unaffected by the damage stimulus. The generation of all neuronal subtypes that were not lost to damage suggests that cell-fate specification follows a sequential order similar to retinal development. We assessed whether factors governing cell fate choices during development are expressed in a similar temporal fashion in retinal regeneration. We first examined NPC-expression of the bipolar cell commitment marker *vsx1* in light-damaged retinas, where only photoreceptors are lost. Here we demonstrate that several PCNA-positive NPCs co-expressed *vsx1:EGFP* relatively late in retinal regeneration. Commitment markers for ganglion (*atoh7*), amacrine (*ptf1a*), cone (*prdm1a*) and rod photoreceptors cells (*nrl*) were assessed by quantitative real-time PCR, all of which were upregulated prior to the onset of *vsx1:EGFP* expression. *prdm1a* expression increased before both *atoh7* and *ptf1a*, which displayed similar onsets of upregulation. In addition, *prdm1a* exhibited a second wave of increased expression following increased *atoh7* and *ptf1a* expression. Expression of *nrl* first decreased during photoreceptor death, but subsequently rose during the recovery phase. Similarly, commitment markers *otx2* and *crx*, which regulate both rod and cone photoreceptor differentiation, first decreased during photoreceptor cell death, but then were upregulated twice, first around the time of *prdm1a* upregulation and then again when *nrl* was upregulated. This suggests a role of these genes in differentiation of both cone and rod photoreceptor cells, respectively. We also began investigating the expression of downstream targets of both Atoh7 (*dlx2a, alcama*) and Ptf1a (*barhl2*). In summary, a subset of transcription factors driving subtype specification in development are also expressed in the regenerating retina, in a sequential manner that recapitulates what is seen in development.

**Keywords:**

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**Factors influencing the optical features of quartz glass capillaries**

Christian Bunker
The purpose of this research is to determine the ideal factors for a waveshifting quartz capillary to transmit ultraviolet light with minimum attenuation and maximum total light output. The total light output was obtained by measuring the output from a source at the far end of the capillary. The attenuation was determined by measuring the output as a function of distance as the source is moved away from the readout end, then dividing all data points by the total output to enable comparisons of percentage attenuation.

The factors investigated were reflective titanium coating, radiation and the presence of a ruby quartz end-cap. The results showed that the titanium coating alone had a beneficial effect on the capillaries, moderately increasing their output and leaving their attenuation unchanged. Two megarads of radiation alone had a detrimental effect on the capillaries, slightly decreasing their output and leaving their attenuation unchanged. Two megarads and the coating together had a beneficial effect on the capillaries, slightly increasing their output and leaving their attenuation unchanged. The introduction of the ruby quartz end cap had a mixed effect on the capillaries, drastically decreasing both their total output and attenuation. Finally, two megarads, the titanium coating, and the ruby quartz together had a mixed effect on the capillaries, drastically decreasing their output but effectively eliminating attenuation, such that the output was nearly the same at both ends of the capillaries.

The data allowed the conclusion that due to the greater importance of total light output, the addition of titanium coating alone was the best modification to the capillary, since this provided a good light output and an acceptable attenuation, while the other factors led to a good attenuation but an unacceptably low output.

**Keywords:** Optics, high energy, particle detectors

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**The Effects of Increasing Atmospheric CO$_2$ Levels on Tree Growth and Carbon Isotope Uptake**

Clare Buntrock, Kelly Heilman

McLachlan Laboratory, Notre Dame, United States

Over the last century, atmospheric CO$_2$ levels have increased by over 20%. The increase in atmospheric CO$_2$ drives climate changes such as varied precipitation and extreme temperatures that could impact the CO$_2$ uptake of trees and tree growth. While both climate changes and atmospheric CO$_2$ may impact tree growth and CO$_2$ uptake, the net effects of increased atmospheric CO$_2$ on tree growth is still unknown. To further investigate this, we studied how the growth-climate relationships and carbon isotope ratios in trees from Western Minnesota vary over three time periods: 1930s, 1950s, and 2000s. Tree cores from Bonanza Prairie were collected, annual tree growth crossdated, measured, and $\delta^{13}$C isotopic ratio were quantified using EA IRMS. The detrended growth data was then analyzed with the Palmer Drought Severity Index (PDSI) data from the National Climate Data Center and with atmospheric CO$_2$ levels collected from Mauna Loa Station over the selected time periods. The detrended growth data was also analyzed with $\delta^{13}$C isotope values to determine the correlation between growth and uptake in CO$_2$. $\delta^{13}$C becomes more related to the atmospheric CO$_2$ over time. In the 1950s, $\delta^{13}$C is only marginally related to CO$_2$ concentration ($R^2=0.131$, $p=0.6188$) but in the
2000s it is strongly related to atmospheric CO$_2$ ($R^2 = 0.7808$, $p = 0.0055$). Surprisingly, there was no significant correlation between PDSI and carbon isotope levels in the 1950s ($R^2 = 0.0601$, $p = 0.6039$) and in the 2000s ($R^2 = 0.0057$, $p = 0.8353$). However, there was a significant correlation between average growth and PDSI ($R^2 = 0.2455$, $p = 7.5645 \times 10^{-09}$). These results suggest that as atmospheric CO$_2$ increases, the carbon isotope levels also increase leading to trees that are less sensitive to drought because the trees require less water for the same carbon intake.

**Keywords:**

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**Screening of Sensor Histidine Kinases for Interactions with the ESX-1 System in *Mycobacterium marinum***

**Clare Cahir, Micah Ferrell, Patricia Champion**

*University of Notre Dame, Notre Dame, United States*

The bacterial pathogen *M. tuberculosis* causes an estimated 1.3 million deaths each year. In order to cause disease, the mycobacteria must be able to detect their environment within the host and subsequently secrete the necessary virulence factors via the ESX-1 system. Despite the central importance of this process in pathogenicity the sensor histidine kinase (HK) responsible for initiating this response remains unknown. Identifying protein-protein interactions between sensor histidine kinases and components of the ESX-1 system would provide insight into the regulation. To test for interactions, we cloned all eleven sensor histidine kinases and five core components of the ESX-1 system from the mycobacteria model organism *M. marinum* into vectors for bacterial 2-hybrid screening of *E. coli*. Each HK was evaluated for interaction with the five ESX-1 core components. Strong interactions were subsequently confirmed and quantified using $\beta$-galactosidase assays. Using this technique we have identified at least three specific HK-ESX interactions. We are now studying these interactions further using targeted gene deletions and biochemical assays in the *M. marinum* model.

**Keywords:** microbiology, bacterial genetics, infectious disease, virulence, tuberculosis

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**The effects of sea level and nitrogen on the growth of modern *Schoenoplectus americanus***

**Jethro Castillo, Georgi Saucedo, Jennifer Robichaud**

*Department of Biological Sciences, Notre Dame, United States*

Global environmental change (GEC) has resulted in sea level rise, and is predicted to cause further changes in the future. Sea level rise threatens many coastal ecosystems, including salt marshes, in part because of the impacts on native flora integral to those ecosystems. Meanwhile, these ecosystems have been recognized as providing important ecosystem goods and services to society, such as protection from storm surges. To preserve these ecosystems, and the resources they provide, it is important to understand how coastal ecosystem plants will respond to changing conditions. Using greenhouse experiments, old and modern genotypes of the marsh plant, *Schoenoplectus americanus*, were exposed to a variety of water levels, salinities, and
nutrient concentrations along with in combination with other species, such as Spartina, found in coastal marshes. For 6 weeks, plants were grown in replicate plots using a fully factorial design reflecting a combination of two environmental factors, with constant temperature and artificial light. Each week, new stems were counted and height of stems were measured. After 6 weeks, after a final measurement of height and width, all new biomass was collected and dried in order to estimate biomass. Data were analysed using a two-way Analysis of Variance. Results suggest that sea level rise, salinity, and nitrogen could alter plant growth of S. americanus, along with potential for competition with other plant species. This study has generated important information that will help in the development of new predictive models with which to evaluate the consequences of future GEC for coastal marsh ecosystems.

**Keywords:**

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**Parasites and Interbirth Intervals in Amboseli Yellow Baboons**

Idaleen Ching, David Jansen, Elizabeth Archie  
*University of Notre Dame, Department of Biological Sciences, Notre Dame, United States*

Parasites are known to affect health in baboons, but it is unknown whether they affect fertility. Previous studies have produced conflicting findings on effects of parasites in mammals. Some studies have found that the fitness of an infected host is not affected by their levels of parasite infection, or that if they are, the host is able to offset the effect with little to no cost. Other studies have found increased parasite load during lactation and that infection lengthened interbirth intervals. In this study, interbirth intervals were used as a measure of fertility. We hypothesized that parasite infection lengthens interbirth intervals in baboons, and that those with a greater variety of parasites would have longer interbirth intervals compared to conspecifics with only one kind of parasite. We tested these hypotheses by analyzing long term data on parasites in Amboseli yellow baboons, which was collected using standard parasitology measures. We looked at data on the most common parasites found in the baboons, which includes *Trichurus trichiura*, strongyles, *Abbreviata*, *Strongyloides fulleborni*, *Enterobius vermicularis*, and *Streptopharagus pigmetatus*. We used mixed effect linear models in R analysis to look for associations between parasite load and fertility. We controlled for the fixed effects of the sex of the offspring, rank, primiparity, and age, and modeled baboon identity as a random effect. We expect to see an effect between parasite load and fertility. By looking at the relationship between parasites and fertility, we hope to learn more about whether hosts are compelled to make efforts to offset negative effects that parasites might have on their fitness.

**Keywords:**

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**Effects of Transfluthrin on *Ae. albopictus* Attraction to Oviposition Sites**

Sarah Denning  
*University of Notre Dame, Notre Dame, United States*
Dengue viruses cause an approximate 50-100 million annual infection worldwide[1]. Current prevention strategies rely on vector control. Specifically, pyrethroids, which are spatial repellents, have been studied as a new delivery system for vector control [2]. These chemicals are highly volatile at ambient temperatures. Transfluthrin is a type of pyrethroid and currently used in vector control products. It is important to study the effects of transfluthrin on many elements of mosquito behavior to better understand how it will affect populations of dengue vectors. A previous study found that exposure to transfluthrin results in a stronger attraction of *Aedes aegypti* mosquitos to oviposition sites with an attractant infusion [3]. The objective of the study was to measure the changes in attraction of gravid *Ae. albopictus* female cohorts to oviposition sites after exposure of transfluthrin at sublethal quantities. The response was measured with a bioassay and oviposition sites containing either an attractant infusion or only water. Oviposition sites were covered with “sticky screens” to catch mosquitoes that land. Initial data indicates that unexposed gravid *Ae. albopictus* were 12.82% more likely to be attracted to oviposition sites with attractant infusion. On the other hand, exposed gravid *Ae. albopictus* were 13.28% less likely to be attracted to oviposition sites with attractant infusion. Current findings imply that transfluthrin can influence mosquito behavior beyond preventing human biting. This chemical can further be used alone or integrated into other vector control systems.

References:


Keywords:

HPLC Verification of Paper Analytical Devices to Test for Low-Quality Albendazole

Heather DiLallo, Dr. Toni Barstis

*Department of Chemistry & Physics, Saint Mary's College, Notre Dame, United States*

Parasitic worm infestations are common to children of developing countries and are considered to be a roadblock to the social and economic development of these countries. Albendazole is a commonly used oral medication for the treatment of parasitic worm infestations. Because albendazole is a safe and effective medication, the World Health Organization (WHO) placed
albendazole, a benzimidazole carbamate anthelmintic, as an essential medicine, meaning that all people should have access to albendazole in sufficient amounts at all times. Unfortunately, in developing countries such as Nepal and China, the quality of this essential medicine is suspect. In an extensive sample collection study in Nepal in summer 2016, including 180 samples of albendazole, Barstis found that albendazole was often stored improperly and distributed past its expiration date. Additionally, DiLallo conducted a preliminary sample collection study in China in summer 2017, collecting 55 samples of albendazole in two diverse regions. China is one of the largest manufacturers of counterfeit medicines. This research focuses on the results of a general paper analytical device (PAD) used both in the field and the laboratory to screen for low-quality albendazole. These PADs are slightly larger than business cards, use colorimetric chemistry to screen for select ingredients, and can be completed in less than five minutes. A US Pharmacopeia validated method for HPLC, as well as an independent UPLC-MS method being developed at Saint Mary’s College, are being used to validate the PADs data. Additionally, a specific “Albendazole PAD” with semi-quantitative tests for albendazole and common excipients is being developed. Lastly, crystal structures of albendazole and some of its complexes have been obtained. All results will be presented.

Keywords:

Exploring the effects of global environmental change on the marsh plant, *Schoenoplectus americanus*

Sarah Duehren, Shannon O'Neil, Dominic Chaloner

University of Notre Dame, Notre Dame, United States

Global environmental change (GEC) has resulted in sea level rise, and is predicted to cause further changes in the future. Sea level rise threatens many coastal ecosystems, including salt marshes, in part because of the impacts on native flora integral to those ecosystems. Meanwhile, these ecosystems have been recognized as providing important ecosystem goods and services to society, such as protection from storm surges. To preserve these ecosystems, and the resources they provide, it is important to understand how coastal ecosystem plants will respond to changing conditions. Using greenhouse experiments, old and modern genotypes of the marsh plant, *Schoenoplectus americanus*, were exposed to a variety of water levels, salinities, and nutrient concentrations along with in combination with other species, such as *Spartina*, found in coastal marshes. For 6 weeks, plants were grown in replicate plots using a fully factorial design reflecting a combination of two environmental factors, with constant temperature and artificial light. Each week, new stems were counted and height of stems were measured. After 6 weeks, after a final measurement of height and width, all new biomass was collected and dried in order to estimate biomass. Data were analysed using a two-way Analysis of Variance. Results suggest that sea level rise, salinity, and nitrogen could alter plant growth of *S. americanus*, along with potential for competition with other plant species. This study has generated important information that will help in the development of new predictive models with which to evaluate the consequences of future GEC for coastal marsh ecosystems.

Keywords:
Comparing the Oral and Gut Microbiomes Across Populations of Long-tailed Macaques

Bailee Egan

University of Notre Dame, South Bend, United States

Studying the microbiome across sites of the body gives insight into the interplay between microbiomes at different locations and elucidates the mechanisms that shape their communities. The oral and gut microbiome present two distinct habitats for microorganisms. The oral cavity consists of variable surfaces, providing different ecological niches, while also being exposed to the external environment. On the other hand, gut microbiome is controlled by the host immune system as well as the highly-selective conditions of the intestines. Given the interconnection between the mouth and the intestines, it is possible that the sites share bacterial taxa but also retain unique taxa specifically adapted to that site. We used Illumina Hi-Seq to sequence the V4 region of the 16S rRNA gene in the feces and saliva of long-tailed macaques from Singapore and tested for differences in diversity, composition, and evenness between the oral and gut microbiomes at a population level. Results show that both sites share a majority of taxa, but the oral microbiome possesses a higher diversity than the gut microbiome while also showing greater evenness across samples.

Keywords:

Single-ion Conducting Polymer Electrolyte Characterization

Clay Elmore, Morgan Seidler

University of Notre Dame, Notre Dame, United States

We report how structural changes to lithium ionomers can drastically change the conductivity of cross-linking polymer electrolytes. Polyethylene glycol diacrylate (PEDGA) cross-linking monomers form a polymer backbone for the electrolyte of interest in these experiments. The substitution of different Lithium ion complexes, specifically lithium styrene sulfonate (LiSS), lithium (4-styrenesulfonyl) trifluoromethanesulfonylimide (LiSTFSI), lithium vinly sulfonate (LiVS), or lithium 3 sulfo-propyl acrylate (LiSPA), in the polymer structure has been shown to greatly affect the conductivity of our electrolytes. These effects are shown to be on the order of almost 2 orders of magnitude. The mobility of the lithium ions in the polymers is also an important characteristic to understand for our electrolytes, so we present a theoretical way to model this mobility as well as the effective number of charge carriers in our film. Computational predictions using Density Functional Theory (DFT) are currently being used to help model the effective number of charge carriers in these polymers. The method that is being employed here is the prediction of Raman shifts that lithium ions cause in polymer systems and then compare with experimental spectra. This presents a way to measure the effective number of charge carrying lithium cations. DFT has also been used to calculate relative dissociation energies of lithium cations from their tethered anions. These findings suggest that lithium ionomers are a potential solid state electrolyte to be used in future electronic fields such as energy transportation batteries.

Keywords: Polymer Electrolyte, DFT, Raman, Lithium Battery
The impact of rainfall on production of termites in southwest Western Australia

Nicole Gorman ¹, Peter Mawson ²

¹ University of Notre Dame, Notre Dame, United States
² Perth Zoo, South Perth, Australia

Rainfall is an influential environmental driver of many ecological processes. However, its effects on termite populations, especially those in mediterranean Australia, have been understudied. Past work has shown that Australian termites are not significantly affected by rain but are significantly affected by fire. This study uses collection data for two Western Australian termite species to determine how they are influenced by rainfall. While one species, Coptotermes acinaciformis raffrayi, was affected by rainfall immediately, the other species, Nasutitermes exitiosus, showed a lag in response to rainfall of approximately three months. These results indicate that termites are impacted by rainfall, but the magnitude and timing of the effects may be species- or location-dependent.

Keywords:

Microplastic Distribution Above and Below Large Dams in Indiana, USA

Margaret Hartlage, Whitney Conard, Katherine O'Reilly, Gary Lamberti

University of Notre Dame, Notre Dame, Indiana, United States

Microplastics (plastic particles <5 mm in size) pose environmental threats of unknown magnitude to aquatic ecosystems. Microplastics can enter aquatic systems through wastewater effluent, breakdown of plastic debris, precipitation events, and atmospheric deposition. If ingested by aquatic organisms (e.g., filter-feeders), microplastics and sorbed toxins can be transferred through the food web, thereby accumulating in predators. Previous studies have shown that sediment and other contaminants can accumulate behind large dams. Here we investigate whether and how dams affect microplastic distribution in flowing water. Water samples were taken upstream, downstream, and within the reservoirs of three dams in Indiana, USA. Samples were filtered and microplastics were quantified and classified. We expected to observe a higher concentration of microplastics upstream of dams than downstream due to settlement in the reservoir of less buoyant particles. Preliminary results suggest that microplastics are higher in concentration both in tributaries upstream of a reservoir and within the reservoir than downstream of a dam. Dam removal can be a controversial subject, but knowledge of microplastic transport past dams may contribute to decision-making.

Keywords:

The Effects of Seasonal Change on Parasite Load in Yellow Baboons

Abigail Herman, David Jansen, Elizabeth Archie

University of Notre Dame Department of Biological Sciences, Notre Dame, United States
In non-human primates, there have been mixed reports of the trends associated with host parasite load and seasonal change. Some studies have reported that primate parasite load increases during dry periods, others have found the opposite, with an increase during high rainfall periods; yet, others have found no significant change. Given the mixed literature, our research seeks to add depth to the understanding of how fluctuations in rainfall may affect the parasite burden in non-human primates. In this study we focus on seasonal changes in parasite load and what it can tell us about the interplay between host immune vulnerability and parasite transmissibility. Looking specifically at yellow baboons (*Papio cynocephalus*) from the Amboseli Ecosystem, we test two alternative hypotheses. First, if rain leads to increased parasite transmissibility, we predict that parasite load will increase from dry season to the wet season. Second, if baboon health deteriorates in the dry season, we predict that parasite load will increase from the wet season to the dry season. In order to test these hypotheses, we will test how parasite load fluctuates throughout and across the seasons, controlling for other factors known to explain inter-individual differences in parasitism. We will draw our data from a long-term data base which uses parasite count techniques of sedimentation and sugar-flotation. Utilizing R analysis, we will determine which hypothesis is correct based on the significant trends observed. Our analysis will merit insight into not only the overall seasonal trends, but specific dynamics within each season itself. Looking at the dynamics of change rather than just a seasonal comparison will give us a greater understanding of the relationship between the susceptibility a host has for infection and the parasite’s ability to transmit effectively.

**Keywords:**

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**Conflicts in Africa and Their Dependence on Dams**

Dunyeng Huh, Stefano Castruccio  
*Junior majoring in Applied Computational Mathematics and Statistics, Chuncheon, Korea, Republic of (South)*

The fear of ‘lack of water’ has led to a considerable number of armed conflicts of different severity in neighboring developing countries. This is most apparent in Africa, where most countries’ economy is predominantly agricultural, and hence heavily reliant on water resources. Not surprisingly, many of the strife and armed collision took place in the vicinity of a large water body such as rivers and lakes or dams.

This study will specifically concentrate on the studying the dependence between armed conflicts and the presence of dams. We will leverage an exhaustive dataset of more than two thousand African large dams and recently developed geotagged data on more than ten thousand violent conflicts. To observe the dependence, we would use difference-in-difference empirical strategy that compares the frequency of conflicts before and after the dams have been built. A statistical model to capture the spatial structure of the conflicts will also be deployed to assess the uncertainty around our conclusions. The study will allow us the study and even predict the conflicts that arise/ will arise due to the scarcity of water in African countries.

**Keywords:** Africa, Conflict, Dams, Dependence
Regulation and relevance of intercellular calcium signaling in Drosophila wing development

Francisco Huizar 1, Pavel Brodskiy 1, Qinfeng Wu 1, Dharsan Soundarrajan 1, Cody Narciso 1, Megan Levis 1, Danny Chen 2, Jamison Jangula 1, Teresa Brito-Robinson 1, Jeremiah Zartman 1

1 Department of Chemical and Biomolecular Engineering, Notre Dame, United States
2 Department of Computer Science and Engineering, Notre Dame, United States

Tissue morphogenesis during embryonic development is regulated by patterns of inductive signals. Recently, intercellular calcium transients (ICTs) were reported in the Drosophila wing disc during embryogenesis. However, how the functional significance of ICTs and how these signals are integrated to induce tissue patterning is not well understood. Calcium ions are known to be critical secondary messenger signaling components involved in numerous cellular processes. Here we demonstrate the impact of ICTs and calcium-related genes on wing size and shape through RNAi. Frequency of calcium signaling in vivo decreases as the wing disc matures. Upon observing calcium signaling ex vivo in the presence of a growth medium normally present in vivo, calcium signaling responded in a dose-dependent manner. This suggests that ICTs occur in vivo due to the tissue microenvironment providing chemical stimulus of varying concentrations. Inhibition of calcium-related genes resulted in defects in wing size, shape, and vein patterning of adult wings. Further, there was a reported reduction or elimination of in vivo ICTs upon inhibition of calcium-related genes. This led to the examination of ICTs during inhibition of genes involved in the Hedgehog morphogen pathway. Hedgehog related genes were shown to control frequencies of calcium oscillations uniformly in tissue and is required for spatial patterning of intercellular calcium oscillations. This led to the discovery of specific spatiotemporal signatures of ICTs during wing disc development. These results suggest that coordinated oscillations of ICTs function to assist in regulation of patterning and tissue growth during development in the Drosophila wing disc.

Keywords: calcium, morphogen, signal transduction, developmental biology

Role of Myosin Heavy Chain Genes during Interkinetic Nuclear Migration of Müller Glia in the Regenerating Light-Damaged Retina

Jacob Kalathoor, Manuela Lahne, David Hyde

Department of Biological Sciences, Center for Zebrafish Research, and Center for Stem Cells and Regenerative Medicine, University of Notre Dame, Notre Dame, IN 46556, Notre Dame, United States

Müller glia are retinal glial cells that serve as support cells for retinal neurons. In response to neuronal damage, Müller glia re-enter the cell cycle and produce neuronal progenitor cells (NPCs) that continue to proliferate and differentiate into damaged neuronal cell types. Müller glia and NPCs both undergo Interkinetic Nuclear Migration (IKNM), the movement of proliferating nuclei along the elongated cell body synchronized with cell cycle stages. Because myosin drives IKNM during retinal development, I examined expression patterns of myosin heavy chain genes myh9a, myh9b, and myh10 in light-damaged retinas to determine their potential role in IKNM during regeneration. Dark-adapted albino zebrafish were exposed to constant intense light for 0, 12, 24, 36, 48, 72, and 96 hours. At each timepoint, dorsal retinas were collected for RNA isolation, converted into cDNA, and used for quantitative real-time
polymerase chain reaction (qRT-PCR). I performed qRT-PCR using primers to *rhodopsin*, *pcna*, *myh10*, *myh9a*, and *myh9b*, as well as 18s rRNA as a control gene. Downregulation of *rhodopsin* expression throughout light-treatment confirmed that rod photoreceptor cells were dying due to light-treatment. Increased *pcna* expression beginning at 24 hours light-treatment (hLT) was consistent with the onset of Müller glia proliferation. Preliminary data suggest that different myosin heavy chain isoforms display distinct expression patterns. While *myh9b* expression was upregulated at 12 hLT and increased throughout light-treatment, *myh10* was initially downregulated, then upregulated from 36-96 hLT. The latter expression pattern is consistent with the onset of Müller glia IKNM. Guide RNAs (gRNAs) were designed to target exon 2 and exon 11 of *myh10*, to create mutations in the gene using the CRISPR system. These gRNAs were ligated into a pDR274 plasmid and confirmed through Bsa1 restriction digests and sequencing. The plasmid was *in vitro* transcribed to generate mRNA. The efficacy of the gRNA will be discussed through injection into one-cell stage embryos.

**Keywords:**

Combating Drug Resistant Tuberculosis: Development of a Paper Analytical Device to Monitor Patient Compliance with Isoniazid Therapy

Ian Kelly, Marya Lieberman, Madeline Smith

*Department of Chemistry and Biochemistry, University of Notre Dame, Notre Dame, United States*

Patient compliance in adhering to antituberculosis therapies involving treatment with isoniazid (INH) is historically poor and can lead to acquisition and further transmission of drug resistant forms of the disease. Developing nations are especially at risk, due to both increased disease prevalence and lack of resources to adequately oversee patient compliance to the prescribed drug regimen. This research aims to provide healthcare providers with a non-invasive, affordable, and easy to interpret method of monitoring patient compliance to antituberculosis therapy by developing paper analytical devices (PADs) to detect isoniazid in urine. Three different reactions were used to detect isoniazid in a synthetic urine solution, each exploiting a different reactive property of the drug to form a colored product indicating its presence in the analyte solution. The first reaction utilized the reactivity of the pyridine ring present in isoniazid and was based on an adaptation of the Arkansas Method to paper. Though this test was able to produce a highly specific response to isoniazid, it was not sensitive enough to detect the drug at concentrations commonly observed in patient urine, with a limit of detection (LOD) of 500-750µg/ml. The next test exploited the redox properties of isoniazid, using it to reduce iron to form Prussian blue. This method was shown to be the most sensitive (LOD= 5µg/ml) and was able to differentiate isoniazid from negative controls at concentrations lower than the observed literature value for the bottom 25% of patient urine concentration four hours after dose administration (18µg/ml). However, this test was subject to interference due to redox active agents found in urine, principally ascorbic acid. The third test presents an alternative method of detecting isoniazid using azo-coupling. This approach was observed to be more sensitive than the adaptation of the Arkansas Method (LOD=150µg/ml) and produces a colored product unique to isoniazid.

**Keywords:** Paper Analytical Devices, Isoniazid, Tuberculosis
Film characterization and reaction mechanism analysis of ultrathin films created by reactive gel deposition.

Patrick Lawler, Khachatur Manukyan
Nuclear Science Lab, Notre Dame, United States

A method was optimized for depositing and combusting a reactive gel onto substrates and the subsequent ultrathin films were characterized. Variables tested include: metal nitrate, fuel, solvent, substrate, phi value, amount, concentration, spin coat speed, substrate cleaning method, heating rate, heating final temperature, heating duration, and atmosphere. Copper nitrates were studied extensively due to their ease of handling and visible changes associated with phase changes. Films were characterized using High Resolution X-Ray Diffraction, Scanning Electron Microscopy, and Infrared and High Speed camera imaging. HR-XRD provided spectra that identified the composition of the thin films. This analysis indicated the reaction atmosphere’s significance in determining phase composition: in air, the films were metal oxides, whereas in argon the films were metals. Additionally, reactive gels were reacted partially and quenched mid-reaction in such a way that different intermediates of a reaction were arranged sequentially across the sample. Using HRXRD, obtained data on how the spectra changes as the reaction progresses. SEM allowed insight into the surface uniformity, grain size and structure, thickness, and porosity of our films. Imaging showed incredible uniformity across samples with minimal porosity in some cases. When that same protocol was conducted except that the film was heated in an argon environment, however, imaging showed particle sintering with cubic particle shape of two distinct sizes and significant porosity. The greatest finding associated with this research experiment involved the use of infrared and high speed camera imaging. With the cameras coupled and capturing the reaction as it proceeds, we were able to gain insight into the reaction mechanism and thermodynamics of the reaction. We found the copper nitrate solution reaction to have three main phases with an initial phase that changed before the reaction front, and that the reaction self-propagated.

Keywords: thin films, solution combustion, bone implant

The Impact of Aging on Tumor-Associated Collagen Cleavage

Annemarie Leonard 1, Emma Sheedy 4, Elizabeth Harper 1,3, Elizabeth Harper 1,3, Elizabeth Loughran 1,3, Yueying Liu 1, Jeff Johnson 1, Tyvette Hilliard 1, M. Sharon Stack 1

1 Department of Chemistry and Biochemistry, Notre Dame, United States
2 Department of Biological Sciences, Notre Dame, United States
3 Integrated Biomedical Studies Graduate Program, Notre Dame, United States
4 Department of Mathematics, Notre Dame, United States

Epithelial ovarian cancer (OvCa) is the most common subtype of ovarian cancer. OvCa often goes undetected until late metastatic stages of the disease, contributing to its high mortality rate. OvCa multicellular aggregates are exfoliated from the primary tumor and diffuse through the peritoneal cavity, where they adheres to and invades through the mesothelium in the collagen-rich extracellular matrix (ECM). Our lab has demonstrated that aged mice have increased tumor burden, which supports OvCa incidence data in the literature. To investigate biochemical factors
underlying the age-related metastatic success, structural properties of collagen from young versus aged mice were investigated. Collagen was selected because it has been demonstrated that OvCa cells preferentially bind to collagen over other ECM components. Furthermore, visualization of tumor invasion of peritoneal tissues using second harmonic generation (SHG) microscopy show that tumor cell: collagen interaction is an important early event in OvCa’s metastatic success. To test the hypothesis that age-related structural differences in collagen contributed to the increased age-related OvCa metastatic success, a study was designed using collagen extracted from the tails of young (3–6 months) and aged (20–23 months) C57BL6 mice. Once the collagen was purified it was analyzed through the following two methods: 1) Probing the age-related differences in the kinetics of collagen cleavage by matrix metalloproteinase (MMP)-1 and 2) Characterizing the invasion of OVCAR5 cells, a membrane type-1 MMP (MT1-MMP; MMP-14)-expressing cell line representative of OvCa, through aged and young collagen in 3D invasion chambers. Kinetic studies demonstrated that aged collagen was more effectively cleaved (lower Km) when compared to young collagen. This was confirmed in invasion studies, showing an increase in invasion of cells through aged vs young collagen. Future studies plan to investigate the biophysical properties and structural elements of young and aged collagen to elucidate the role of aging on OvCa metastasis.

Keywords:

**In vivo screen identifies PYGO2 as a driver for metastatic prostate cancer**

Yanting Luo, Xin Lu, Xiaolu Pan, Chang-Jiun Wu, Rumi Lee, Xuemin Lu, William Morgenlander, Jacquelin Weinrich, Ronald A. DePinho, Y. Alan Wang

1. Department of Cancer Biology, The University of Texas MD Anderson Cancer Center, Houston, United States
2. Department of Biological Sciences, Center for Rare and Neglected Diseases, University of Notre Dame, Notre Dame, United States
3. Tumor Microenvironment and Metastasis Program, Indiana University Melvin and Bren Simon Cancer Center, Indianapolis, United States
4. Department of Genomic Medicine, The University of Texas MD Anderson Cancer Center, Houston, United States
5. Department of Biostatistics, Indiana University, Indianapolis, United States
6. Department of Biological Science, Wonkwang University, Iksan, Korea, Republic of (South)
7. Institute for Applied Cancer Science, The University of Texas MD Anderson Cancer Center, Houston, United States
8. Department of Pathology, The University of Texas MD Anderson Cancer Center, Houston, United States

Advanced prostate cancer displays conspicuous chromosomal instability and rampant copy number aberrations. The identity of functional drivers resident in many amplicons remain elusive. Here, a functional genomics approach was implemented to identify new prostate cancer oncogenes involved in disease progression. Through integrated analyses of focal amplicons in large prostate cancer genomic and transcriptomic datasets as well as genes upregulated in metastasis, 276 putative oncogenes were enlisted into an in vivo gain-of-function tumorigenesis screens. Among the top positive hits, we conducted an in-depth functional analysis on Pygopus family PHD finger 2 (PYGO2), located in the amplicon at 1q21.3. PYGO2 overexpression enhances primary tumor growth and local invasion to draining lymph nodes. Conversely, PYGO2 depletion inhibits prostate cancer cell invasion in vitro, and progression of primary
tumor and metastasis *in vivo*. In clinical samples, PYGO2 upregulation is associated with higher Gleason score and metastasis to lymph nodes and bone. Silencing PYGO2 expression in patient-derived xenograft models impairs tumor progression. **Lastly, PYGO2 is necessary to enhance the transcriptional activation in response to ligand-induced Wnt/β-catenin signaling.** Together, our results indicate that PYGO2 functions as a driver oncogene in the 1q21.3 amplicon and may serve as a potential prognostic biomarker and therapeutic target for metastatic prostate cancer.

**Keywords:** PYGO2, prostate cancer

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**Research Opportunities in the Galapagos**

*Cristina Mancini, Robin Seay, Carolina Ochoa, Alison O'Neil*  
*University of Notre Dame, Notre Dame, United States*

The Galápagos Islands are one of the most well-known examples of evolution and biodiversity. Following in Charles Darwin’s footsteps, fourteen Notre Dame students are selected each year to conduct research on the islands during fall break as part of the Galápagos practicum. Over the course of the semester, students learn about the natural and evolutionary history of the Galápagos in the classroom, and participate in community engagement (this year, with the South Bend Center for the Homeless). During their week in the Galápagos, students conduct independent research projects as they travel across several islands in the archipelago. In addition to research projects, students spend time observing flora and fauna while hiking, snorkeling, and exploring different towns. The practicum offers a hands-on way to experience the biology and culture of the Galápagos.

Topics for the independent research projects range from studies on plants and animals that call the islands home, to economic and cultural examinations of the Galápagos. Included are excerpts of four of the fourteen different projects carried out in Fall 2017: 1) The Impact of Invasive Species on Human Health in the Galápagos Islands, 2) Effect of sea surface temperature and pH on coral vitality in disturbed and pristine Galápagos reef systems, 3) Cultivating the Land of Darwin: Exploring the Possibilities of Sustainable Coffee Farming in the Galápagos Islands, and 4) Population Viability Analysis of the Galápagos Penguin. These projects demonstrate the breadth of educational value students acquire during their week in the Galápagos.

**Keywords:**

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**Kinetics and Substituent Effects of Oxygen Atom Transfer by Oxobis(amidophenoxo)osmium(VI)**

*Sean Markovitz*  
*University of Notre Dame, South Bend, United States*

Bis(amidophenolate) complexes (ap)$_2$OsO (ap = N-aryl-3,5-di-tert-butyl-2-amidophenoxide) transfer an oxygen atom to triphenylphosphine to form triphenylphosphine oxide. The reduced osmium complex exists as an equilibrium mixture of mono- and bis-phosphine adducts
(ap)$_2$Os(PPh$_3$) and (ap)$_2$Os(PPh$_3$)$_2$, and structural studies of the bis phosphine complex indicate that the amidophenoxides donate to the reduced osmium complex much more substantially than to the oxidized oxoosmium complex. UV-visible spectroscopy confirms that the reaction is first order in both phosphine and osmium oxo complex. Electron-donating substituents on the triphenylphosphine increase the rate, as expected, but substitution of the N-aryl group of the amidophenoxide has a remarkably small effect on the rate. Possible explanations for this small substituent effect in terms of the unique π bonding capabilities of the amidophenolate ligands will be discussed.

Keywords:

[Re]Evaluating the Cost of Electricity in Hospitals with Unreliable Energy - VSL/E Metric

Brady McLaughlin 1, Dr. Abigail Mechtenberg 1, Dr. Moses Musaazi 2, Dr. Lydia Nanjura 5, Dr. Mark Shrime 4

1 University of Notre Dame, Department of Physics and ND Energy, ESDD Research group, South Bend, United States
2 Makerere University, Kampala, Uganda
3 Ugandan Martyrs University, Fort Portal Campus, Fort Portal, Uganda
4 Harvard Medical School, Cambridge, United States
5 College of Engineering, Design, Art, and Technology, Kampala, Uganda

This research defines a new term called VSL/E based on value of a statistical life (VSL-$\text{USD}$) and energy failure based on electricity capacity shortages (kWh). Building upon four peer-reviewed research articles that highlight either a health care facilities’ published optimal energy design simulation or actual measured failure rates, we modeled nine VSLs based on three elasticities for four countries: Iraq, Ghana, Uganda, and Bangladesh. Results suggest that health care electricity costs should include not only typical levelized cost of electricity (LCOE: $0.03-3.00/kWh), but this new VSL/E ($5-500,000/kWh) analysis which is orders of magnitude larger and should not be ignored.

Keywords: Energy, Healthcare, Systems

Future projections of walnut-infesting fly distributions in response to a changing climate

Dung Nguyen, Mary Glover, Jeff Feder

University of Notre Dame College of Science Department of Biological Sciences, South Bend, United States

Global climate changes are a driving force of range shifts in many species, as each species seeks their own optimal climate condition. The walnut-infesting Rhagoletis suavis species group, including R. completa, R. boycei, R. suavis, and R. juglandis, have shifted their distributions since the 1980s. For instance, R. juglandis has moved up into a higher elevation in the Southwestern U.S. and came into contact with the the R. boycei. In the Midwestern region of
the U.S., R. completa has moved their range 200 miles eastward into the range of the R. suavis. Previous studies, using Species Distribution Models (SDMs), a useful predictive tool for modeling species distribution have shown climate change to be the major factor behind the walnut flies’ movements. We aimed to project future walnut fly distributions based on future climate scenarios of the year 2050 and 2070 using SDMs. While SDMs had been constructed previously for the four species using presence only data with pseudo-absence from background environmental data, this study will also incorporated true absence data collected across 83 sites for a more accurate model, using random forest regression for each species. Driven by climate changes, the shift in the walnut flies’ distributions had caused some species, such as the R. completa and the R. suavis, to come into contact. The overlapping range of the species increases the potential for competition, displacement, hybrid zones, and other evolutionary implications.

Keywords:

Through time and space: mapping Schoenoplectus americanus population change in the salt marshes of the Chesapeake Bay

Erin Nguyen
McLachlan Lab, University of Notre Dame, Notre Dame, United States

Recent studies have demonstrated that the common salt marsh sedge, Schoenoplectus americanus, possesses seeds that can be resurrected after a century-long dormancy by germinating seeds collected in sediment cores. Thus, sampled sediment cores can be used to understand population shifts across decadal scales. The objective of this study was to investigate changing S. americanus populations using seed abundance as a proxy for population estimates of S. americanus in the Chesapeake Bay. We propose that S. americanus populations would decline with sediment depth due to decomposition. The preliminary data suggests this is not the case, instead revealing the surprisingly heterogeneous character of these core samples, across both temporal and spatial scales. For example, in one sediment core, the top, or most modern, layer had an abundance of 6 seeds but the bottom, or most ancestral, had 226 seeds. Compare this to yet another core with a top layer abundance of 143 seeds and a bottom layer abundance of 0 seeds. The lack of a trend in population abundance may be reflective of various environmental factors from the marsh such as a nutrient or salinity gradient or distance inland. Currently we are determining germination rates of these old and modern seeds as a proxy for decomposition rates. These decomposition rates may help determine which environmental factors are most critical in determining how abundant S. americanus will be in a particular region in future studies.

Keywords: scirpus, sedge, salt marsh, population

Genomic profiling of photic-regulated genes in Anopheles gambiae and An. Coluzzii malaria mosquitoes
Mosquitoes of the *Anopheles gambiae* complex are major vectors of malaria in Africa. Our previous studies have revealed that patterns of behavior are regulated by photic stimuli and by the environmental light-dark cycle. Light presented during the night can affect the circadian clock and diel timing (Rund et al, 2013, *BMC Genomics* 14: 218), as well as suppress blood feeding (biting) and modulate flight activity in an acute and sustained manner (Sheppard et al, 2017, *Parasites and Vectors* 10:255). We have also revealed distinct strain-specific differences in the mosquitoes’ behavioral responses to light. To better understand the molecular basis for these sustained responses to light and how they are transduced in the eye and brain, we undertook a genomics analysis of mosquitoes exposed to a discrete photic stimulus presented during the early night. Adult female *An. gambiae* s.s. (Pimperena strain) and *An. coluzzii* (Mali-NIH strain) mosquitoes were exposed to a 10 min 300 lux pulse of white light at the onset of night and animals harvested at 30-minute intervals over a 2 hour period. RNA was extracted from mosquito heads and subjected to genome-wide high throughput RNA sequencing analysis. Differential gene expression (greater than or equal to 1.75-fold change up or down compared to dark [no light] controls) was observed in 401 and 351 genes of Pimperena and Mali-NIH mosquitoes respectively. Of these, 120 were shared between the two strains/species. Functional group analysis highlights genes involved in the circadian clock mechanism, feeding behavior, olfaction (smell), vision, and the Wnt signaling pathway (contributes to local signaling between neighboring cells). These data reveal a breadth of gene expression changes that likely underpin the coordinated responses of brain-behavior pathways to adapt to environmental change, including resetting of the mosquito circadian clock. A better understanding of these pathways that regulate time-of-day specific behaviors, that include human host-detection and blood-feeding, have implications for improving control of malaria transmission.

**Keywords:** Mosquito, Anopheles gambiae, circadian, light, genomics

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**The effect of increasing salinity levels on plant growth of old and modern *S. americanus* salt marsh plants**

Frederick Lockie, Liam Nugent, Jennifer Robichaud

*Department of Biological Sciences, Notre Dame, United States*

Global environmental change (GEC) has resulted in sea level rise, and is predicted to cause further changes in the future. Sea level rise threatens many coastal ecosystems, including salt marshes, in part because of the impacts on native flora integral to those ecosystems. Meanwhile, these ecosystems have been recognized as providing important ecosystem goods and services to society, such as protection from storm surges. To preserve these ecosystems, and the resources they provide, it is important to understand how coastal ecosystem plants will respond to changing conditions. Using greenhouse experiments, old and modern genotypes of the marsh plant, *Schoenoplectus americanus*, were exposed to a variety of water levels, salinities, and nutrient concentrations along with in combination with other species, such as Spartina, found in coastal marshes. For 6 weeks, plants were grown in replicate plots using a fully factorial design reflecting a combination of two environmental factors, with constant temperature and
artificial light. Each week, new stems were counted and height of stems were measured. After 6 weeks, after a final measurement of height and width, all new biomass was collected and dried in order to estimate biomass. Data were analysed using a two-way Analysis of Variance. Results suggest that sea level rise, salinity, and nitrogen could alter plant growth of S. americanus, along with potential for competition with other plant species. This study has generated important information that will help in the development of new predictive models with which to evaluate the consequences of future GEC for coastal marsh ecosystems.

**Keywords:**

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**Applying OMP and LASSO to Perform Sparse Variable Selection (Single and Double-Selection) on Financial & Economic Data**

*Joseph Pennacchio*

*University of Notre Dame, Notre Dame, United States*

A wide range of phenomena in the natural, mathematical, and economic sciences can be represented through a parsimonious, or “sparse,” representation in terms of a limited number of factors or causes. Prior knowledge about the underlying sparsity of a certain phenomenon can be leveraged in the context of regression to constrain the relationship among variables. Thus, sparse regression aims to look at a dataset with many observations and to explain as much as possible of the desired relationship with as few variables as possible. This study focuses on comparing the performances of two families of algorithms for sparse regression, Orthogonal Matching Pursuit (OMP) and Least Absolute Shrinkage and Selection Operator (LASSO) for econometric applications. The selected algorithms were first tested on synthetically generated datasets to verify their ability to capture the expected undersampling-sparsity phase transitions. Then, variable selection was performed using OMP and LASSO both for instrumental variables (IV)/two-stage least squares (2SLS) applications and for forecasting applications. For IV/2SLS, in addition to selecting instruments using OMP and LASSO analogously to the selection of the best predictors for the forecast, variable selection for the controls was performed in light of “least squares after double selection.” To compute valid standard errors associated with the estimated coefficients, the residual bootstrap was developed and tested. Cross Validation was used to ensure an appropriate balance between the simplicity and explanatory power of the models, sometimes demonstrating that sparse representations are not optimal. Throughout the process, parallel computing was used to improve the computational efficiency of the algorithms. Literature results were both reproduced and extended for the impact of eminent domain on economic outcomes and for the forecasting of industrial production. Finally, the results produced by OMP and LASSO are critically examined in light of the algorithmic differences between the two approaches.

**Keywords:**

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**Subcellular Localization of AIMP1**

*Eric Sah ¹, Christina Murphy ¹, Daniel Lee ², Margaret Schwarz ²*
Aminoacyl tRNA synthetase complex-interacting multifunctional protein 1 (AIMP1, also known as SCYE1, and EMAP II) is homologous across all species as a scaffold protein of multi-tRNA synthetase complexes (MSC) that supply tRNA synthetases for protein translation. However, in mammalian cells, the MSC is complex; AIMP1 is expressed at varying levels, but apparently with unclear functions beyond that of being a scaffold in the MSC. In line with playing a role in protein translation, initial studies reported AIMP1 to be expressed in the cytoplasm. However, we have shown that it was also found in other cellular compartments through other biochemical techniques: on the cellular surface and intracellularly in the nucleus of permeabilized cells (Liu, 2006). What fractions of AIMP1 exist then in which subcellular compartments is unclear. Utilizing immunocytochemistry, we hypothesized that a majority of AIMP1 would localize to the MSC in the cytoplasm of HEK293-T cells. Contrary to our expectations, not only did a small fraction of AIMP1 co-localize with QARS but also co-localize with Phalloidin (a marker of F-actin at the cell membrane). Visualizing the localization patterns of AIMP1 can then begin to provide insight into its unknown functions.

**Keywords:** AIMP1, Endothelial–Monocyte Activating Polypeptide II, MSC, localization

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**Painted (Chrysemys picta) and Snapping (Chelydra serpentina) turtles as indicators of mercury contamination in Great Lakes coastal wetlands and resultant human health implications**

Karl Schlaht, Katherine O'Reilly, Michael Brueseke, Gary Lamberti

*University of Notre Dame, Notre Dame, United States*

The presence of heavy metals, such as mercury (Hg), in aquatic environments as a result of anthropogenic activity (e.g., the burning of fossil fuels) represents a persistent management issue in the Laurentian Great Lakes. Organomercury compounds like monomethyl mercury biomagnify within food chains as animals consume contaminated lower trophic taxa. The bioaccumulation and biomagnification of Hg in freshwater fish has been well studied. However, these processes in freshwater turtles, especially those in the Great Lakes region, have not been thoroughly researched. In this study, we investigated the total mercury (THg) content in muscle and liver tissue of painted and snapping turtles collected from four Lake Michigan coastal wetlands. Our goals were to determine if 1) bioaccumulation varies by tissue type, 2) whether THg concentrations are related to environmental contamination, 3) the potential for freshwater turtles to be used as an indicators of wetland contamination due to their longevity, site fidelity and high trophic position, and 4) possible human health implications associated with wild-caught turtle consumption. Muscle and liver tissue were dissected out of euthanized turtles, then freeze-dried and homogenized to fine powders. THg was measured for each tissue type using CEST’s Direct Mercury Analyzer (DMA80, Milestone). Preliminary results show that snapping turtles have substantially higher Hg concentrations compared to painted turtles, likely as a result of greater body size or dietary differences. It is assumed that snappers occupy a higher trophic position. Additionally, both species displayed higher THg content in liver tissue compared to muscle tissue. Regarding environmental contamination, THg varied significantly by sampling site with two sites exhibiting substantially higher concentrations. Overall, results suggest that
freshwater turtles may serve a valuable role as indicators of wetland contamination and prompt concerns for human consumption of wild-caught turtle tissue in the Great Lakes region.

Keywords:

Identifying the source of parasitoids infesting western *Rhagoletis pomonella* using Cytochrome Oxidase-I sequence analysis

Nicholas Seifert¹, Glen Hood¹⁻², Meredith Doellman¹, Jeffrey Feder¹
¹ Department of Biological Sciences - University of Notre Dame, Notre Dame, United States
² Department of Biosciences, Rice University, Houston, United States

The apple maggot fly, *Rhagoletis pomonella*, is a model system for the study of sympatric speciation. Originally infesting native hawthorn plants (*Crataegus spp.*) in the eastern United States, the introduction of domesticated apples (*Malus domestica*) in the last 150 years caused a host plant shift, leading to rapid divergence. In the last 60 years, *Rhagoletis* flies were found infesting apples in the western United States. Genetic data shows that these populations were introduced from the east, as opposed to shifting from native western hawthorns. *Rhagoletis* flies are parasitized by a family of braconid wasps, with life cycles highly dependent on the host fly. The purpose of this study is to investigate the origin of the parasitoid populations infesting *R. pomonella* in the western United States. These parasitoid populations could either have been introduced with the flies, or they could have shifted from populations infesting the native snowberry fly, *R. zephyria*. *Cytochrome-oxidase I* sequences were collected from individuals of western populations of braconid wasps of the ornamental hawthorn (*C. monogyna*), black hawthorn (*C. douglasii*), and apple host races, and compared to those from parasitoids of both western *R. zephyria* and eastern *R. pomonella*. Haplotype analysis showed that the native parasitoid community infesting *R. zephyria* and the western parasitoids of *R. pomonella* are more closely related than either is to the eastern populations. This supports the hypothesis that western *R. pomonella* parasitoids evolved from native populations infesting *R. zephyria*. These findings also support the hypothesis of sequential speciation: the idea that ‘biodiversity begets biodiversity.’ In this case, addition of a new species had a multiplicative effect on a higher trophic level. The sequential speciation hypothesis could be a critical factor in explaining adaptive radiation and the origins of community biodiversity.

Keywords: Sequential Speciation, Cytochrome Oxidase-I, Rhagoletis pomonella

Electrical Feedthrough and Printed-Circuit Board Design for the ND Cube

Michael Serikow

*University of Notre Dame Department of Physics, Notre Dame, United States*

The ND Cube is an active target-detector, currently in the late-stages of design, that will be used to carry out low-energy nuclear physics experiments to study the structure of light radioactive nuclei. The ND Cube consists of a vacuum chamber with detector elements inside. The electrical data signals generated during experiments must be efficiently transferred from the electron detector inside to outside of the vacuum chamber. This has resulted in the need to design an electrical feedthrough that will connect the electron detector to a data acquisition system. The
feedthrough consists of a Printed-Circuit Board (PCB) and a vacuum flange on the chamber. PCB design and CAD modeling was used to create the feedthrough, which included designing an electron detector-to-PCB cable connection, the mechanism used to hold the PCB’s to the ND Cube, and the PCB’s themselves. With the finalization of these designs, their physical production can begin and the ND Cube will be closer to running its first experiment.

**Keywords:** Physics, Low Energy, CAD, PCB, Detector

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**Investigation and Detection of Metformin**

Chiara Smorada, Toni Barstis, Heather DiLallo

*Department of Chemistry & Physics, Saint Mary’s College, Notre Dame, IN, Notre Dame, United States*

Diabetes, a chronic condition affecting the body’s ability to process glucose, impacts individuals all around the world and leads to additional health risks such as heart disease or strokes. In the United States alone, diabetes affects millions of individuals. Most cases of diabetes have been identified as type II diabetes, and metformin has been identified as a primary prescription drug to treat type II diabetes. Metformin helps the body metabolize food and is believed to play a role in prevention of diabetes. When treating type II diabetes, maintaining the proper dosage of metformin is essential; however, metformin distributed in developing countries are suspect of being substandard. In response to the World Health Organization (WHO) and their emphasis on medicines as a global health issue, samples of metformin from Nepal were collected for analysis in the summer of 2016. Paper analytical devices (PADs) were used to screen for low quality metformin. This research focuses on improving the colorimetric tests on the PAD to detect the active pharmaceutical ingredient (API) metformin, studying the crystalline structures of the metformin colored complexes, and discussing the validation of the PADs results via high performance liquid chromatography (HPLC) analysis. All results will be given in this poster presentation.

**Keywords:**

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**Rare Earth Element Interactions with Uranium Dioxide**

Samantha Sutter, Amy Hixon

*Department of Civil Environmental Engineering and Earth Sciences, Notre Dame, United States*

Analysis of trace elements in nuclear material provide evidence on process history and provenance to compliment analyses for both nuclear proliferation and nuclear smuggling activities. Over time, materials will age through interactions with the surrounding environment and will no longer be in pristine condition. Deciphering aging processes will provide information on the changes nuclear materials undergo from time of production to time of sample collection. This study investigates the diffusion of trace rare earth elements (REE) in an aqueous environment with solid uranium oxide (UO$_2$), a common nuclear material, to establish how various ageing scenarios can lead to identification of definitive ageing signatures. We used batch sorption experiments to investigate the interactions of twelve REEs in solution with UO$_2$ as a function of pH (3-9), ionic strength (0.025 - 0.5 M NaNO$_3$), REE concentration (4 - 8.33...
ppm), and UO$_2$ concentration (5 - 50 g/L). Aqueous phase concentrations of the REEs were determined using inductively coupled plasma mass spectrometry (ICP-MS) and the surface morphology of UO$_2$ was examined using scanning electron microscopy (SEM). Typical cation sorption behavior is observed as sorption increases with increasing pH. Ionic strength plays a small influential role in REE element sorption, particularly at pH 7 - 8. Preferential sorption of lighter REEs is observed. Combined results indicate pH is the most influential factor in the aging of UO$_2$.

**Keywords:**

Identification of low quality and counterfeit antimalarial pharmaceuticals chloroquine, doxycyline, primaquine using Surface-enhanced Raman Scattering (SERS)

Emma Tackman, Michael Trujillo, Jon Camden

*University of Notre Dame, Notre Dame, United States*

Counterfeit antimalarial pharmaceuticals are a problem worldwide with negative public health implications that cannot be overstated. Here, SERS-based techniques to detect low quality and counterfeit antimalarial drugs in commercially available tablets were developed. Spectra for pure chloroquine, primaquine, and doxycycline are presented. Additionally, SERS signal from the desired drugs in the presence of excipients common in pharmaceutical caplets were successfully obtained. A ‘red shirt’ study was also performed where identified low quality and counterfeit formulations presented as unknowns were identified. These data in conjunction with promising results from a portable SERS spectrometer suggest that SERS is a viable technique for on-site analysis of drug quality.

**Keywords:** antimalarial pharmaceuticals, counterfeit detection, nanotechnology, surface-enhanced Raman spectroscopy

Sorption of U$_{60}$ Clusters and Strontium to Ion-Exchange Resins


*University of Notre Dame, Environmental Actinide Chemistry Laboratory, Notre Dame, United States*

The current generation of nuclear reactors produce energy through fission of uranium-235. When fuel assemblies are removed from a nuclear reactor, approximately 95% of the uranium remains with additional contribution from various fission products, which hinder the chain reaction needed to sustain fission in the reactor. Plutonium Uranium Recovery by Extraction (PUREX) is a solvent extraction process most commonly used to recover uranium and plutonium from used nuclear fuel. This requires dissolving the spent fuel rod in concentrated acid and employs harsh organic chemicals in a complex solvent extraction scheme. The discovery of uranyl peroxide nanoclusters (e.g., U$_{60}$) provides an opportunity to develop new, environmentally-friendly recovery methods. Our goal is to use ion exchange resins to recover the uranyl peroxide nanoclusters from the spent fuel matrix and separate them from the fission products (e.g., Sr, Ba, Nd, Cs). We have two ways to accomplish this task: use an anion
exchange resin to remove the uranium, in the form of $U_{60}$ nanoclusters, or use a cation exchange resin to remove the fission byproducts from solution, allowing $U_{60}$ nanoclusters to pass through the column. To test these two methods, we used batch sorption tests to determine which sorption isotherm model best describes the uptake of $U_{60}$ to an anion exchange resin and Sr to a cation exchange resin. Small angle X-ray scattering (SAXS) and Raman Spectroscopy were used to confirm the presence of the $U_{60}$ clusters in the presence of the resins. Inductively coupled plasma optical emission spectroscopy (ICP-OES) was used to measure the equilibrium concentrations of $U_{60}$ and Sr. If both of these experiments are successful, then we will have demonstrated a novel approach to used fuel reprocessing that may replace the environmentally-taxing method of liquid extraction (PUREX).

**Keywords:** sorption, nanocluster, nuclear, resin

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**Heat Shock Protein Response to Treatment with Triple Combination Formulation**

Anna Volk $^{1,2}$, MD Suhail Alam $^{1,2}$, Kasturi Haldar $^{1,2}$

$^{1}$ University of Notre Dame, Notre Dame, United States

$^{2}$ Boler-Parseghian Center for Rare and Neglected Diseases, Notre Dame, United States

Niemann-Pick Type C (NPC) is a rare neurodegenerative disorder caused by mutations in the NPC1 or NPC2 gene. Earlier study in the lab developed a triple combination formulation (TCF) for treatment of NPC, which includes a histone deacetylase inhibitor, vorinostat (Vo), 2-hydroxypropyl-$\beta$-cyclodextrin (HPBCD) and polyethylene glycol (PEG). Treatment with TCF enhances the expression of Npc1 at transcript and protein level in the brain of Npc mice. However, fold change in NPC1 protein was 2-3 fold higher than the elevation in Npc1 transcript. Heat shock proteins (HSPs) act to stabilize proteins and assist in proper protein folding. Therefore, we hypothesized that there was amplification of NPC1 due to the higher chaperone activities of HSPs in TCF-treated mice. Quantitative PCR was used to examine transcript levels of six selected heat shock proteins in liver and brain of healthy control mice injected with TCF. Additionally, protein for HSP70 was examined through western blotting. The transcript level of Hsp90, Hspb1, Hspa5 and Hspa4 remain unchanged at one and four hours post-TCF treatment, whereas Hsp70 (Hspa1b) and Hspa8 were reduced by 11-12 and 2-3 fold, respectively, in liver 4 hours post-TCF treatment but are unchanged 1 hour post-TCF treatment. Immunoblotting showed a slight increase in the HSP70 protein. To understand the global effects of TCF treatment, genome-wide gene expression analysis was conducted using RNA-seq in the liver of drug-injected mice. The result showed modulation in the expression of multiple heat shock proteins. Similar to qPCR, RNA-seq studies also showed a 10-fold and 2-fold reduction in the Hsp70 and Hspa8 transcript levels. A detailed analysis of transcriptomic data is in progress and is expected to provide insights into mechanism of TCF action. This study suggests TCF modulates the expression of multiple heat shock proteins and could potentially be involved in elevating the NPC1 protein after chronic treatment.

**Keywords:** Rare Diseases, Niemann Pick Type C, Heat Shock Proteins
**Combination of antimicrobial peptides and nanoparticles to inhibit bacterial growth on orthopedic implants and surgical instruments**

Margo Waters, Veronica Kalwajtys  
*College of Science, Notre Dame, United States*

In a time where we are facing an antibiotic resistance crisis, it is necessary to develop non-conventional antimicrobial substances. One possible route is the development of antimicrobial peptides on nanoparticles. The overall goal of our project is to determine if antibacterial peptides linked to antibacterial nanoparticles can completely inhibit bacterial growth. If we are successful, these particles have the potential to be coated onto orthopedic implants and surgical instruments, among others. The combination of antimicrobial peptides with nanoparticles will help to prevent infections following a surgery, thereby preventing the over-use of antibiotics. This could potentially decrease the development of antibiotic resistance in bacteria.

In this study, we have been investigating a newly developed nanospheres@cores class of nanoparticles with either a 65nm or 130nm silica core which has been conjugated with anisotropic nanospheres consisting of gold with a thin silver layer (3-5nm). In additional testing, we then linked a polymer to the silver-layer to test our potential of linking complex organic molecules to our particle. Four clinically relevant bacterial species were chosen as test organisms: *Staphylococcus aureus* USA300, *Pseudomonas aeruginosa* FRD1, *Enterococcus faecalis* (isolated from joint infection material), and *Corynebacterium striatum* (isolated from joint infection material). The nanoparticles’ antimicrobial effects were first tested on bacterial growth in/on different liquid and solid media. Subsequently, different implants coated with the nanoparticles will be screened for their antimicrobial effects as well as stability of the nanoparticles on the surface. The final phase would be to test these particles for cytotoxicity on human tissue.

Initial results have indicated a slowdown in growth in all species when they were tested against the nanoparticles alone, with *Corynebacterium striatum* reacting with the greatest sensitivity. Results were even more promising when the polymer was linked to the nanoparticle. The polymer@nanoparticle combination completely inhibited the growth of *Corynebacterium striatum*.

**Keywords:**

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**Expression of the atoh7 gene signals ganglion cell commitment and differentiation during adult zebrafish retina regeneration**

Grace Zhou  
*Hyde Lab, South Bend, United States*

Damage to the mammalian retina leads to permanent vision loss and blindness, whereas the damaged zebrafish retina is able to undergo a regenerative response. Damage in the zebrafish retina induces Müller glia to re-enter the cell cycle to produce neuronal progenitor cells (NPCs). NPCs continue to proliferate before differentiating into the lost neurons. Recently it was observed that cells not damaged in light treatment are also produced in the regenerating
retina, leading to the hypothesis that retinal regeneration could follow a developmental sequence where ganglion and amacrine cells are produced before photoreceptor cells. The *atoh7* gene is required for ganglion cell commitment and if retinal regeneration follows a developmental sequence then *atoh7* expression should be upregulated in the light-damaged retina. Thus, dark-adapted albino Tg[*atoh7:GFP*] zebrafish were light-damaged for up to 96 hours and retinal sections were immunostained for the proliferation marker PCNA and for GFP to investigate the *atoh7:GFP* expression pattern. PCNA was expressed in the outer and inner nuclear layer (ONL & INL, respectively) starting at 36 hours of light damage (hLD) and peaked at 72hLD. In contrast, *atoh7:GFP*-positive cells were first present at 60 hLD while its expression peaked at 72 hLD in both the ONL and INL, the same timepoint when the maximal number of PCNA-positive cells were observed. To investigate whether *atoh7:GFP*-positive cells differentiated into ganglion cells, retinal sections were co-labeled with the mature amacrine and ganglion cell marker HuC/D. Beginning at 72 hLD and throughout the rest of light treatment, a few *atoh7:GFP*-positive cells co-labeled with HuC/D in both the INL and ONL suggesting that a subset of *atoh7:GFP*-positive cells either differentiated into ganglion or amacrine cells. In summary, the ganglion cell commitment marker *atoh7* is expressed in the regenerating retina, suggesting that differentiation during retinal regeneration might mimic development.

**Keywords:**

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**Friday, May 4th, 2018 - Jordan Hall Room 105 - 01:45 - 02:45**

Oral session - Biology

**Genomic characterization of the sparkleberry fly as the sister species to Rhagoletis mendax**

Katherine Inskeep 1, Stewart Berlocher 2, Jeffrey Feder 1

1 Department of Biological Sciences, Notre Dame, United States
2 School of Integrative Biology, University of Illinois, Urbana-Champaign, United States

The Rhagoletis pomenella species complex includes separate host races infesting apple and hawthorn fruits, as well as separate species such as the blueberry- and deerberry-infesting R. mendax and the snowberry-infesting R. zephyria. We hypothesized that the undescribed sparkleberry fly represents a separate species from R. mendax because of the complete separation between each taxon’s host fruiting times. Our objective was to identify whether R. mendax and the sparkleberry fly are genetically distinct on a genome-wide basis and to locate these two taxa on the continuum from host race to species. R.mendax and sparkleberry pupae were collected from sympatric sites across their co-occurring range in the southeastern United States. DNA extracted from these samples was processed with restriction site associated DNA (RAD) sequencing. Along with earlier collections of northern R. mendax populations, these data were analyzed with a bioinformatics pipeline. Trimmed reads were aligned to the R. zephyria draft genome, and single nucleotide polymorphisms (SNPs) were then called and filtered. It was observed that R. mendax and sparkleberry fly populations cluster distinctly across their geographic ranges. Negligible gene flow was quantified between the two taxa, as expected given the clear separation in emergence time of adult flies on their different host fruit. Comparison of allele frequency differences between R. mendax and sparkleberry flies with
known host race and species pairs within the complex shows sister species level differentiation, indicating that these taxa deserve separate species status. By correlating these findings with variation associated with emergence time disparity, we will understand how natural selection creates new species in the R. pomonella complex on such a rapid time scale.

**Keywords:** evolution, sympatric speciation, gene flow

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**Investigation of GRP78 Survival Mechanisms and ER stress in PDAC**

Gabrielle Mungeal  
*University of Notre Dame, Notre Dame, United States*

As Pancreatic ductal adenocarcinoma (PDAC) continues to provide a grim diagnosis for all those affected, more effective treatments prove to be increasingly necessary. The inefficacy of current treatments is partially due to PDAC’s high levels of chemoresistance, a characteristic the Hill lab has previously shown to be closely associated with GRP78. Expressed in high levels by chemoresistant PDAC, GRP78 acts as a molecular chaperone and alleviator of ER stress. Through inhibition of GRP78, in combination with Gemcitabine (GEM) and IT-139 treatment, the Hill lab mouse model displayed decreased chemoresistance and extended survival times. Despite decreased cell survival, tumors were still present, suggesting that in the event of GRP78 inhibition, other mechanisms impacted chemoresistance. We sought to further examine these mechanisms in two ways: inhibition of HSP70 family members by treatment with VER-155008 alongside GEM and treatment with Bortezomib (Bort), a proteasome inhibitor, in combination with IT-139 as opposed to GEM. For the HSP70 studies, cell survival assays demonstrated increased cell death following both VER treatment and combination GEM/VER treatment. To assess GRP78 levels, western blot analysis was performed. Contrary to the anticipated outcome, western blot analysis indicated increased GRP78 expression post-VER and GEM/VER treatment, a finding further supported by decreased ThT fluorescence in the same samples. Apoptotic assays however showed an upregulation of Death receptor-5, indicating that compensatory mechanisms play a role in cell survival following GRP78 inhibition. For the Bort studies, cell survival assays displayed significantly increased cell death, but no showed impact on unfolded protein burden or GRP78 expression as compared to GEM. Future experiments will involve further elucidation of the mechanisms behind chemoresistance, as well as possible applications to other metastatic forms of cancer that have been closely linked with GRP78.

**Keywords:** cancer, chemoresistance, PDAC, GRP78, HSP70

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**Expression Changes of Novel Genes in Cisplatin Treated Lung and Ovarian Cell Lines Reveal Relationships Across Disparate Cancer Types**

Sawyer Williams  
*College of Arts and Letters- Environmental Sciences and Political Science, Notre Dame, United States*

Lung and ovarian cancers will lead to over 168,000 deaths in the United States in 2018. Despite extensive research into the genetic nature of these types of cancers individually, broader relationships between the cancers are not as well understood. Cisplatin, a platinum-based drug which affects DNA replication, is used in the treatment of both lung and ovarian cancers. The
The goal of this research was to gain a more complete understanding of the relationship between lung and ovarian cancer treatment by examining the expression profiles of genes in cisplatin treated cell lines. Utilizing the Expression Atlas, a continually developing database of gene expression information created by the European Bioinformatics Institute, genes with significant expression changes following cisplatin treatment in ovarian cancer cells were identified. These genes were then evaluated in comparably treated lung cancer cells to identify similarities and differences. This study identified genes where expression changes were in discordant directions between treated lung and ovarian cells, where changes were in concordant directions with variable degree, and where there was little or no expression change in one of the tissues. Interestingly this study identified three genes, MMP12, FAM9C and MEF2C, which showed large expression changes in ovarian cancer cells but no detectable expression in treated lung cancer cells. These results suggest underlying gene expression relationships between lung and ovarian cancer cisplatin treatment and reveals further research directions which could lead to more effective tissue-specific treatments of cancer with cisplatin.

Keywords: gene expression, lung cancer, ovarian cancer, cisplatin

The Host Decoy Trap (HDT): exploiting visual, olfactory and thermal stimuli to improve surveillance of malarial mosquitoes in western Kenya

Xiaoyu Yu 1, Maurice Ombok 2, Nabie Bayoh 2, Frances Hawkes 3, Martin Geier 4

1 University of Notre Dame, South Bend, United States
2 Kenya Medical Research Institute (KEMRI)/ Center for Disease Control and Prevention Research and Public Health (CDC), Kisumu, Kenya
3 Natural Resources Institute, University of Greenwich, Chatham, United Kingdom
4 Biogents AG, Regensburg, Germany

Background: Human Landing Catches (HLCs) are been the gold standard for collection of blood-feeding Anopheles. However, several ethical concerns exist concerning the potential exposure of collectors to mosquito-borne pathogens, and possible biases based on collector skills. Many surveillance programs in sub-Saharan Africa focus on indoor monitoring of malaria vectors. However, outdoor-biting may play an important role in residual malaria transmission as this behavior does not overlap with the commonly indoor interventions, like long-lasting insecticidal nets (LLIN) and indoor residual spraying (IRS). This project aimed to evaluate the performance of two versions of a novel mosquito odor-baited sticky trap, Biogents’ HDT (BG-HDT) and Original HDT (O-HDT), in sampling mosquitoes outdoors. The hypothesis is that a trap that emits human odor, is visually conspicuous and heated to human body temperature will catch a reasonable proportion of the number of mosquitoes that would land on a host with the same characteristics.

Results: No significant difference was found in the number of outdoor Anopheles (An.) collection among the three methods. However, species composition varied significantly between HLC and HDTs, revealing important differences in behavior of Anopheles species. Significantly higher numbers and relative proportions of An. arabiensis were caught in HDTs than in HLC, but higher numbers and proportions of An. gambiae were caught by HLCs than by HDTs. Sporozoite infection rates were 5.56% (1/18) in HDTs and 0.90% (1/111) in HLC. In
addition, the effect of heat was tested by comparing an unbaited HDT with the BG-HDT and O-HDT, and the unbaited one had a significantly lower capture than HLC (p=0.00004).

**Conclusions:** Consistent outdoor risk of malaria is further proven by this study. To better monitor that risk, the HDT is a potential candidate to replace HLC outdoor, since they had similar performance in catching *Anopheles*. Moreover, the importance of heat is proven for host-location of the *Anopheles*.

**Keywords:** Anopheles, mosquito trap, exophily, host

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Friday, May 4th, 2018 - Jordan Hall Room 101 - 01:45 - 02:45

Oral session - ChemBiochem

**Synthesis of hyperbranched polymers with post-functionalization specificity**

Hannah Naguib, Xiaosong Cao, Haifeng Gao

*University of Notre Dame, Department of Chemistry and Biochemistry, Notre Dame, United States*

The ease and convenience involved in the one-pot syntheses of hyperbranched polymers using the CuAAC mechanism makes these polymers ideal starting points for the construction of a variety of polymeric macromolecules. However, due to the irregularity of their final structures inherently resulting from their step-growth mechanism, improving the uniformity of the molecular weights of hyperbranched polymers becomes a parameter desirable to regulate. The copolymerization of a trifunctional B3 core with an AB2 monomer using copper catalyzed azide-alkyne cycloaddition (CuAAC) polymerization techniques produces a hyperbranched polymer with a molecular weight in the hundreds of thousands as well as a sophisticated, layered architecture, and thousands of dangling reactive groups. Such dangling groups, in addition to peripheral azide groups from the AB2 monomer, are then available for post-functionalization modifications. When consecutively integrated, copolymerizations and post-functionalizations provide greater accessibility to a broad range of desired hyperbranched polymers both in molecular weight and surface functionalities. It is known that thiolene reactions exhibit high conversions, and thus, such reactions highlight the versatility and applicability of post-functionalizations of copolymers. Due to the diversity of thiols readily available, a variety of functional groups are able to be appended to the surface of hyperbranched polymers via this thiolene mechanism. The development of multi-layered hyperbranched polymers introduces the ability to change the properties of the polymer, especially concerning solubility, which has promising applications in topics such as drug delivery methods and encapsulations.

**Keywords:**

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**Adapting large scale and low cost genomics sample prep to microproteomics**

Camille N Pierre, Matthew M Champion

*University of Notre Dame, Notre Dame, United States*
The overall yield of microproteomic digests for mass spectrometry has been an ongoing concern in the proteomics community. A variety of procedures are available, including in-solution, in-gel, and filter aided sample prep (FASP). These all have distinct advantages and disadvantages. An ideal sample protocol will couple harsh detergent-based sample denaturation with complete removal of these and other contaminants prior to analysis, typically mass-spectrometry proteomics. It should also have commercial reproducibility, and operate with multiple sample types. The FASP protocol utilizes a high molecular weight cutoff filter to perform digestion, and provides a means of removing detergents, salts, and very high and low weight contaminants. This protocol has become a standard for proteomics sample preparation, and has been adapted to suit a variety of specific conditions. However, the protein losses associated with FASP are inconsistently reported, and the procedure is time-consuming, expensive, and has a high failure-rate. There is a need for a simple, very inexpensive, reproducible sample preparation method. We have developed a new protocol that utilizes the filtering and ionic-binding properties of DNA miniprep columns to solve these issues. Samples can be prepared in very high (>5%) concentrations of detergents (SDS) followed by rapid binding and removal of contaminants without the time consuming urea steps associated with FASP. We first tested on a digest of BSA, and then on whole cell lysates. The new workflow is extremely quick and easy to perform, and results show that the minipreps perform as well or better than the FASP for samples in the mid-µg range. When analyzed by mass spectrometry, the consistency of results for the new protocol was provisionally confirmed better than that of the FASP protocol. Additionally, DNA miniprep columns are available in commercial bulk for less than $0.50 ea (US). Our results and protocol development will be discussed.

**Keywords:** miniprep, microproteomics, FASP, mass spectrometry, sample prep

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**Effects of Supercharging and Solubility Tags on Protein Refolding & Solubility**

Harisa Spahic, Matthew Klauer, Ian Walsh, Patricia Clark  
Department of Chemistry and Biochemistry University of Notre Dame, Notre Dame, United States

Protein aggregation occurs when intermolecular interactions among unfolded, misfolded, and folded proteins supersede the interactions between the protein and surrounding solution. Green fluorescent protein (GFP) is prone to aggregation. Solubility in GFP could be enhanced through two methods: (1) supercharging the protein by mutating neutral amino acids on the surface of the native protein structure to charged residues or (2) attaching a solubility tag to the protein by including a highly soluble protein at one terminus of the polypeptide chain. YKB is derived from GFP and contains three half-domains (Y, K, and B) which can fold to form YK or KB. YK and KB are kinetically stable variants of GFP which possess distinct spectrometric properties, but the unfolded half-domains (B and Y, respectively) may interact and thus decrease YKB’s solubility. Here we test the effects of supercharging on the folding yield of YKB and its two precursor proteins, yellow fluorescent protein (YFP) and cyan fluorescent protein (CFP). Supercharging did not affect the protein’s secondary structure as measured by far-UV circular dichroism spectroscopy; however, the fluorescent properties of the proteins were altered. Subsequently, the B half-domain of YKB was supercharged to produce YKB+. Preparation of YKB+ yielded lower amounts of soluble protein than preparation of YKB, and spectrometric analysis of YKB+ indicates that the supercharged B half-domain was unable to participate in folding. We hypothesize YKB+ was unable to fold to form KB+ because the positive charges prevented competitive folding of the supercharged B half-domain. Additionally, we test the
effects of attaching Protein G, a solubility tag, to the N-terminus of YKB. The solubility tag increased the amount of soluble YKB; however, the fluorescent yield of YKB was decreased. We hypothesize the presence of Protein G at the N-terminus either prevents chromophore formation despite the decrease in aggregation.

Keywords:

**Dissolved Nutrients And Greenhouse Gasses In A Midwestern Agricultural Stream: The Role Of Shallow Groundwater Inputs And Hyporheic Zone Exchange**

Audrey Thellman, Martha Dee, Jennifer Tank

*Department of Biological Sciences, University of Notre Dame, Notre Dame, IN 46616, United States*

Land use change and the associated application of synthetic fertilizers to agricultural fields in the Midwestern U.S. have altered the cycling of bioavailable nutrients in aquatic ecosystems. The subsequent biogeochemical processing of dissolved reactive nutrients make stream networks important sources of greenhouse gasses (GHG) that possess a high global warming potential in the modern atmosphere. To mitigate excess nutrient export from the agricultural landscape, best management practices (BMPs) have been developed to increase the physical retention or assimilation of nutrients on the terrestrial zone adjacent to streams. We compared dissolved nutrient and GHG concentrations from the shallow groundwater and hyporheic zones of a conventional trapezoidal agricultural channel to those of two BMP treatments (two-stage ditch and forested buffer strip) within the same watershed, seasonally. We found that the shallow groundwater and the hyporheic zones of both the two-stage and forested sites were significant sources of methane (CH$_4$) and ammonium (NH$_4^+$-N) to the stream. Further, we found that nitrous oxide (N$_2$O) concentration of tile drain efflux was significantly greater than that of stream and groundwater, suggesting that the primary source of N$_2$O in this watershed is production within soils of adjacent agricultural fields. Our study seeks to parse apart the relative contribution of groundwater and hyporheic zone to the dissolved nutrient and GHG budget of an agricultural stream in the context of active BMPs. By gaining a more accurate estimation of the role that these BMPs assume in surface-subsurface interactions, we can better understand reach-scale nutrient dynamics in these critical watersheds.

Keywords: biogeochemistry, agriculture, greenhouse gas, nutrients, groundwater, hyporheic zone

**Friday, May 4th, 2018 - Jordan Hall Reading Room - 01:45 - 02:45**

Oral session - Math & Physics

**Decentralizing Cancer Care in Tanzania: A Facility Location Approach**

Luke Maillie, Zoltan Toroczkai

*Notre Dame Department of Physics, Notre Dame, IN, United States*
Cancer is becoming increasingly prevalent among populations in developing countries, yet access to cancer care remains scarce and highly centralized. Using Tanzania as a case study, we approach the problem of decentralizing cancer care as a facility location problem, asking which existing health facilities are optimally located such that if capacity for cancer care was added to these facilities, the travel distance for population to the nearest available site of cancer care would be minimized. We utilize publicly available GIS data along with ArcGIS, a geographic information system. We do not seek to develop a precise strategy for decentralizing cancer care in Tanzania, but instead aim to illustrate the utility of an algorithmic approach to this optimization problem.

Keywords:

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**Application of Machine Learning Techniques to Study ttH Events**

Kaitlin Salyer  
*University of Notre Dame Department of Physics, Notre Dame, United States*

At the Large Hadron Collider in Geneva, Switzerland, protons are collided at speeds just shy of the speed of light in order to find answers about the most fundamental building blocks of the universe. One of the many possibilities that can result is the production of a Higgs Boson with a top quark-antiquark pair, which are called “ttH events”. These are very rare events, especially in cases where these particles decay leptonically. We are particularly interested in studying these extremely rare particle decays, as they may hold important information that will help us better understand Higgs Bosons and top quarks individually, as well as how they interact together. The rarity of these events necessitates the usage of machine learning (ML) algorithms to maximize the accuracy of separating ttH events from a huge amount of very similar-looking events. The strength of the ML algorithms is determined by how well they are trained, which requires large amounts of simulated information and a collection of variables for the algorithm to use as guidelines for analysis. Past and current investigations focus on pushing the limits of these algorithms with the intention of making them better at selecting the most interesting events to study this particularly rare and exciting process.

Keywords:

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**Relating Topological Quantum Field Theories and Cut and Paste Invariants**

Matthew Schoenbauer  
*University of Notre Dame, Notre Dame, United States*  
*Indiana University, Bloomington, Bloomington, IN, United States*

In this presentation we shall be concerned with a relation between topological quantum field theories (TQFTs) and cut and paste invariants. These cut and paste invariants, or SK invariants, are functions on the set of smooth manifolds that are invariant under the cutting and pasting operation. There are also weaker invariants, called SKK invariants, whose values on a manifold depend on both the cut and paste class and the gluing diffeomorphism. Here we investigate a surprisingly natural group homomorphism between the group of invertible TQFTs and the
group of SKK invariants and describe how these groups fit into an exact sequence. We conclude in particular that all positive real-valued SKK invariants can be realized as restrictions of invertible TQFTs.

**Keywords:**

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**Performance Studies for the Proposed CMS L1 Track Trigger Upgrade**

Patrick Shields  
*University of Notre Dame, Notre Dame, IN, United States*

The Large Hadron Collider (LHC) at CERN will be upgraded in the mid-2020s to produce collisions at higher rates, and therefore the Compact Muon Solenoid (CMS) detector will require an upgrade in order to handle the accompanying increase in collision data. This upgrade involves implementing a system capable of reconstructing charged particle tracks from the detector in real time, known as a Level-1 (L1) Track Trigger. In order to study the expected performance of such a trigger system, a simulation code has been developed which is capable of running the proposed reconstruction algorithm over simulated collision events. Performance is typically characterized in terms of tracking efficiency. The tracking efficiency is the fraction of simulated particle tracks successfully reconstructed by the L1 trigger. Measuring the efficiency in the simulation reveals problems that can be prevented in the actual trigger by solving them in the code. This research focuses on the effects of including stricter requirements in forming reconstructed tracks. While stricter requirements cut down on the amount of overall data that needs to be processed, requirements that are too strict will result in efficiency losses. The goal of this research is to determine the strictest requirements we can make with minimal efficiency loss.

**Keywords:**

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**Friday, May 4th, 2018 - Jordan Hall Galleria - 02:45 - 03:30**

Poster session - Poster Session 2  
**Reliability and Validity of the Cogstate Cognigram for Concussion Testing in Amateur Female Boxers**

Claire Alexander, Nathan Rose  
*University of Notre Dame, Notre Dame, United States*

Concussion testing is often criticized for its subjective procedures, and identification of sports-related concussions is complicated by the desire for athletes to continue participating. The conflict between a desire for continued participation in the sport and the risk of exacerbating a head injury can make an already subjective procedure vulnerable to bias. Computerized cognitive testing to inform concussion diagnosis has been developing over the past few decades, but insufficient research has been done to validate the efficacy of these tests for identifying the presence of sports-related concussion. The current study examined the CogniGram, a new, brief set of cognitive tests, to see if the measures were associated with reported symptomatology.
related to concussion in boxers. We examined the reliability and validity of the CogniGram by comparing it to established computerized cognitive testing on members of a women’s boxing club. The CogniGram and other cognitive testing occurred before and after sparring and participation in a boxing tournament. Test-retest reliability of the Psychomotor Function and Attention composite measure of the CogniGram was strong (r=0.710, p<0.001); test-retest reliability for the Learning and Working Memory composite measure was more moderate (r=0.413, p=0.015). Overall, the Cognigram had very limited correlation with other measures of cognitive function or concussion-related symptomatology. Limitations of the study, especially small sample size, demonstrate the need for further investigation, but the CogniGram seems to require further development and validation.

**Keywords:** Cognigram, Concussion, Concussion Testing, Computerized Cognitive Testing, Neuropsychology

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**Inquiry-Based Laboratory Course: Current Status and Future Improvement**

Aleah Appling  
*McLachlan Lab, Notre Dame, United States*

The McLachlan Research lab is collaborating with the General Biology B lab course to further develop the ecology component in the lab following upcoming changes to the general biology laboratory courses. This curriculum change prompted an opportunity for the McLachlan lab to incorporate more of our current NSF funded research involving the phenotypic response of marsh plants, resurrected from the last 100 years, to changing environmental conditions such as salinity, carbon dioxide, and nutrients.

As the McLachlan lab has worked with the instructors of the General Biology B lab, we have focused on a number of questions to determine how to create an inquiry-based course. How can lab courses be more authentic to the true scientific process? How can lab courses allow undergraduates to contribute to and benefit from current research being done on campus? And how well do lab courses prepare students to ask their own research questions?

We implemented a pre- and post-survey for students in the lab course to assess the current state of the course, gauge the interests and science careers goals of the students, and evaluate the overall confidence in lab skills and the scientific process. We received 220 responses to the pre-survey. When asked about general confidence in lab and research skills, females were on average 14% less confident in all skills than males. Students also ranked fieldwork as the ideal scientific approach they are interested in, however, ranked environmental (which arguably involves the most fieldwork) as a scientific application they are least interested in. At the conclusion of the course we will give the post-survey to assess if participation in the course influenced students understanding and future goals. The insights we gain from these pre- and post-surveys will then be used to further refine and develop the future general biology course.

**Keywords:** ecology, research, undergraduate, inquiry-based, laboratory, survey
Comparing Matlab's ODE Solvers in a Model of Sap Flow and Tree Growth

Logan Arnold

University of Notre Dame, Notre Dame, United States

Tree growth depends critically on the hydrophysiology of the organism, specifically water loss by leaf transpiration and water uptake by roots. A time lag in this process causes stem diameter to oscillate daily. Steppe et al. (2005) developed a system of ordinary differential equations (ODEs) that incorporates both stem growth and daily diameter fluctuation and connects these radial changes to plant hydraulics within individual trees. This type of model is necessary to simulate tree growth accurately, but these equations may be difficult to solve in realistic simulations due to the long time scales of tree growth, and it is presently unknown what numeric algorithms are best for this system. The goal of this project was to apply state-of-the-art numeric techniques to find the solution to these ODEs that represents the best tradeoff between accuracy and speed. This system of equations was implemented in a Matlab script and solved using a variety of Matlab’s built-in ODE solvers over a timespan of four days. Both stiff and nonstiff solvers were used with relative error tolerances ranging from $10^{-12}$ to $10^{-1}$. Normalized root mean square error was used to compare the results across solvers.


Keywords:

Aminoacyl tRNA synthetase complex interacting multifunctional protein 1 binds Glutamyl-Prolyl-tRNA Synthetase and Scaffold Protein Aminoacyl tRNA synthetase complex interacting multifunctional protein 3 of the Multi-tRNA Synthetase Complex

Margaret Schwarz 1, Daniel Lee 1, Seamus Bartlett 2

1 Indiana University School of Medicine, South Bend, Indiana, United States
2 University of Notre Dame, Notre Dame, Indiana, United States

Higher eukaryotes have developed extensive compartmentalization of amino acid (aa) - tRNA coupling through the formation of a multi-synthetase complex (MSC) that is composed of eight aa-tRNA synthetases (ARS) and three scaffold proteins: aminoacyl tRNA synthetase complex interacting multifunctional proteins (AIMP1, 2 and 3). Lower eukaryotes have a much smaller complex while yeast MSC consists of only two ARS (MetRS and GluRS) and one ARS cofactor 1 protein, Arc1p (1), the homolog of the mammalian AIMP1. Arc1p is reported to form a tripartite complex with GluRS and MetRS through association of the N-terminus GST-like domains (GST-L) of the three proteins (2). Mammalian AIMP1 has no GST-L domain corresponding to Arc1p N-terminus. Instead, AIMP3, another scaffold protein of 18 kDa composed entirely of a GST-L domain, interacts with Methionyl-tRNA synthetase (MARS) (3) and Glutamyl-Prolyl-tRNA Synthetase (EPRS) (4). Here we report two new interactions between MSC members: AIMP1 binds to EPRS and AIMP1 binds to AIMP3. Interestingly, the
interaction between AIMP1 and AIMP3 complex makes it the functional equivalent of a single Arc1p polypeptide in yeast. This interaction is not mapped to AIMP1 N-terminal coiled-coil domain, but rather requires an intact tertiary structure of the entire protein. Since AIMP1 also interacts with AIMP2, all three proteins appear to compose a core docking structure for the eight ARS in the MSC complex.

**Keywords:** aminoacyl tRNA synthetase, RNA-protein interaction, transfer RNA (tRNA)

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**Self-assembly of secreted bacterial virulence proteins into macroscopic, rope-like fibers**

Lourdes Brea $^{1,2}$, Kristopher Murray $^1$, Jennifer Starner $^1$, Patricia Clark $^{1,2}$

$^1$ University of Notre Dame, Notre Dame, United States  
$^2$ Eck Institute for Global Health, Notre Dame, United States

While protein aggregation and amyloid formation are well-known for their detrimental effects on protein function, protein aggregation can also be used by prokaryotes, eukaryotes, and fungi for beneficial, functional roles (Chiti et al., 2006; DePas et al., 2012; Dobson, 2003). For example, secreted bacterial virulence proteins have been shown to self-assemble into macroscopic, rope-like structures (Xicohtencatl-Cortes et al., 2010). These structures could provide a biofilm-type environment, protecting bacteria from external forces and supporting their survival. These protein ropes have been proposed to enhance the pathogenesis of Gram-negative bacteria. However, the mechanism to create a micro-environment within which secreted proteins assemble into structures and shelter bacteria from their macro-environment is poorly understood. In order to shed light upon this phenomena, we tested the ability of diverse proteins to self-assemble into macroscopic, rope-like structures. Autotransporter virulence proteins are of particular interest, as they were the first proteins shown to form ropes and are associated with pathogenesis in a wide variety of Gram-negative bacteria that cause diarrheal and other infectious diseases in the developing world, including *E. coli*, *Shigella* and *Yersinia*. Rope or biofilm formation has been achieved with a number of proteins, including EspP and OmpF. Further studies are being performed to develop a more complete understanding of the conditions under which the protein ropes form, the forces that are driving this rope formation, and the biological significance of these ropes.

**Keywords:**

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**Observing Leptin's Impacts on Locomotor Activity in Hyla versicolor and Xenopus laevis**

James Capella  
*University of Notre Dame, Notre Dame, United States*

Leptin, a hormone involved in energy expenditure, may have significant impacts on the mating behaviors of various anuran amphibians. The males of species such as *Hyla versicolor* and *Xenopus laevis* engage in energy-expensive calling behavior to attract mates. Locomotor activity is a reliable indicator of energy expenditure, and an easily observable measure in
behavioral experiments. For this experiment, we evaluated the effects of exogenous leptin on the locomotor activity of adult *Hyla versicolor* and tadpole *Xenopus laevis*. Adult *Hyla versicolor* were injected with either a solution of 100ug leptin in 100ul saline or a control of 100ul saline. Tadpole *Xenopus laevis* were injected with either 5ug of leptin in 5ul saline, or a control of 5ul saline. Adults were placed in a square arena and tadpoles were observed in a 22 cm diameter bucket. For each experiment, the animals were videotaped for 5 minutes, and locomotor activity was measured with a manual tracking plugin on imageJ. We found that leptin had no significant impact on the frequency of movements in adult *Hyla versicolor*. In addition, leptin did not significantly increase or decrease the total distance moved in either adult *Hyla versicolor* or tadpole *Xenopus laevis*. Ongoing research is investigating the relationship between leptin and other aspects of anural amphibian mating behavior, such as call frequency and phonotaxis.

**Keywords:** leptin, locomotor activity, hyla versicolor, xenopus laevis

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**Synthesis and Characterization of Triptycene-containing Polysulfones for Gas Separation Membranes**

Joseph Aboki, Tanner Corrado, Lukas Cepkauskas  
*University of Notre Dame, Department of Chemical and Biomolecular Engineering, Notre Dame, United States*

Polysulfones are widely used commercially in membrane-based gas separation processes due to their ease of synthesis, low cost, as well as excellent thermal and mechanical stability; however, there is significant room for improvement of polysulfone membrane performance through innovative molecular design. Our group has recently developed phenolphthalein-based polysulfone membranes which showed good permeability and selectivity compared to previously reported commercial polysulfone membranes. In this project, a series of new polysulfone membranes have been synthesized from a standard diphenylene sulfone with either triptycene and/or phenolphthalein as the bulky bridging unit in the polymer backbone. The composition and morphology of this new series of polysulfones were systematically varied to investigate the influence of the rigid, bulky triptycene and/or phenolphthalein units as well as the arrangement on the fractional free volume, chain rigidity, permeability and selectivity of the membrane. The incorporation of the triptycene unit in polysulfones is expected to further increase the fractional free volume and chain rigidity of the membrane which will lead to even improve gas transport properties.

**Keywords:**

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**Identification and Characterization of Antimicrobial Compounds in Quercus rubra L.**

Patrick Cunniff, Robert Stanley, Jeanne Romero-Severson  
*University of Notre Dame, Notre Dame, United States*
For thousands of years, nature has served as an effective source of medicinal agents. In fact, of the 252 drugs that the World Health Organization designates as basic and essential, 11% are exclusively of plant origin and a significant number of others were synthesized from natural plant precursors (Rates, 2001). For this reason, plant natural products could be a key source for novel antibiotics. Our prior research of Quercus rubra L. (Northern Red Oak) has shown that the acorns contain compounds with specific antimicrobial activity against gram positive bacteria, including methicillin resistant Staphylococcus aureus (MRSA). Compounds were extracted from the acorns using a gradient of solvents of increasing polarity, and a number of the initial extract fractions exhibited activity against MRSA. Activity assay guided Medium pressure liquid chromatography (MPLC) and high pressure liquid chromatography (HPLC) has been used to further separate these fractions with the intent of isolating individual compounds responsible for the activity seen in the acorns. In addition to tannic acid, which has been known to have antimicrobial activity, our research to this point has found active compounds present in ethyl acetate, 70% ethanol, and water fractions exhibit activity and have not been previously classified. Our further research will utilize elucidation methods such as nuclear magnetic resonance (NMR) and Mass Spectroscopy to identify these unclassified active compounds. Minimum inhibitory concentrations (MICs) and biofilm inhibitory activity of these compounds will also be determined, and the compounds will be tested for synergetic activity with other known antibiotics.

Keywords: antibiotics, natural products, drug discovery

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Early Stages of Lung Adenocarcinoma Tumorigenesis are Characterized by Dyslipidemia and a Shift from M1 to Pro-Tumoral M2 Macrophages

Johannes Fahrmann 2, Nese Unver 2, Samir Hanash 2, Edwin Ostrin 2, Shane Davitt 1

1 University of Notre Dame (Biological Sciences), Notre Dame, United States
2 Department of Clinical Cancer Prevention, The University of Texas MD Anderson Cancer Center, Houston, United States

While approximately 90% of lung cancers are related to smoking, cessation of smoking does not eliminate risk for developing lung cancer later in life, and as no major risk markers exist to predict lung cancer genesis and development this area remains an important field of research. Plasma samples from human patients with solid pulmonary nodules underwent untargeted metabolomics. Lysophosphatidylcholines 16:0 and 18:0 (LPCs 16:0 and 18:0) were significantly reduced in males that progressed to lung cancer compared to those who did not. A murine model with an inducible KRAS mutation was created using the Cre recombinase system. Untargeted metabolomics were conducted on the mice and matched littermate controls at 4, 6, 14 and 28 weeks. Males demonstrated a significant reduction in systemic LPC and its precursor, phosphatidylcholine, levels in the cases compared to controls at 6 weeks. Soluble phospholipase A2 (sPLA2) converts PC to LPC and arachidonic acid, so sPLA2 activity was assayed, and in males, sPLA2 activity was lower when LPC and PC levels were lower than controls (6 weeks) than when LPC and PC levels were near control levels (14 weeks). Due to role of PC-derivatives in inflammatory pathways, the role of macrophages became relevant. Immunohistochemistry demonstrated that at 14 weeks case mice had a much higher number of macrophages surrounding the tumor relative to control mouse tissue, supporting the importance of macrophages in the early stages of tumorigenesis. Flow cytometry analysis of the KRAS mouse model indicated a shift from cells with M1 surface markers to cells with M2 markers comparing
controls to cases, and PCR analysis indicated that murine macrophages treated with an LPC
gradient have a corresponding reduction in the M1 marker inducible nitric oxide synthase. The
importance of macrophages and other immune cells in tumorigenesis continues to be of interest.

**Keywords:** Cancer, Lung, Adenocarcinoma, Metabolomics, Tumorigenesis, Macrophage, Immune, Early

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**One Man's Junk is another Man's Insulation**

Benjamin Pamachena, Jake Dixon

*John Young Middle School, Mishawaka, United States*

Currently, recreational vehicle companies throw away window and door cutouts because they
think it is scrap material. The cutouts are the extra material that is cut out of the walls during
construction of the motorhomes and trailers. The scrap material is filling up landfills when they
do this. By recycling this material, we can help the environment.

Our group was wondering if the cutouts could provide suitable insulation for residential homes,
and compare it to the other forms of insulation such as cellulose, fiberglass, styrofoam, and
siding insulation. In addition, our group decided to find the heat resistance or R-value of each
material to determine the best insulation to use in housing. Our group predicted the cutouts
would be the best type of insulation.

In this experiment, we took our selected insulation and placed it in between two plywood
boards. After we placed the selected material in between the two boards, we preheated it with a
heating fan for 20 minutes. Finally, we measured and graphed the hot and cold sides as they
were being heated by the fan for every 2 minutes over a course of 18 minutes. Then we took the
averages and compared them to each other.

After finishing the experiment, we found that the wall material had the second to worst R-
value than the other materials. One of the reasons we think it had a poor R-value was the fact that it
had some aluminium inside of it. Aluminium is a conductor of heat and not an insulator. Since
the R-value was similar to the styrofoam, it makes the cutouts a feasible insulation. Our science
fair project contributes to the environment by potentially reducing the amount of trash in
landfills by recycling wall insulation to use in attics and for other insulation applications.

**Keywords:**

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**The effects of nitrogen concentration and evolutionary age on Schoenoplectus americanus growth**

Abigail Epplen, Quinn Scallon, Kristin Lewis

*Department of Biological Sciences, Notre Dame, IN, United States*

Global environmental change (GEC) has resulted in sea level rise, and is predicted to cause
further changes in the future. Sea level rise threatens many coastal ecosystems, including salt
marshes, in part because of the impacts on native flora integral to those ecosystems. Meanwhile,
these ecosystems have been recognized as providing important ecosystem goods and services to society, such as protection from storm surges. To preserve these ecosystems, and the resources they provide, it is important to understand how coastal ecosystem plants will respond to changing conditions. Using greenhouse experiments, old and modern genotypes of the marsh plant, *Schoenoplectus americanus*, were exposed to a variety of water levels, salinities, and nutrient concentrations along with in combination with other species, such as *Spartina*, found in coastal marshes. For 6 weeks, plants were grown in replicate plots using a fully factorial design reflecting a combination of two environmental factors, with constant temperature and artificial light. Each week, new stems were counted and height of stems were measured. After 6 weeks, after a final measurement of height and width, all new biomass was collected and dried in order to estimate biomass. Data were analysed using a two-way Analysis of Variance. Results suggest that sea level rise, salinity, and nitrogen could alter plant growth of *S. americanus*, along with potential for competition with other plant species. This study has generated important information that will help in the development of new predictive models with which to evaluate the consequences of future GEC for coastal marsh ecosystems.

**Keywords:**

The Role of Lysophosphatidic Acid in Regulation of Lipogenesis in Ovarian Cancer Cells

Emily Franz1,2, Meghan Conroy1,4, Jing Yang1,2, and M. Sharon Stack1,2,3

Emily Franz

*Harper Cancer Research Institute, Notre Dame, United States*
*Department of Chemistry and Biochemistry, Notre Dame, United States*
*Department of Biological Sciences, Notre Dame, United States*
*Department of Preprofessional Studies, Notre Dame, United States*

Ovarian cancer (OvCa), the leading cause of death from gynecological malignancy, presents a unique mechanism of intra-abdominal metastasis. Obesity and excess accumulation of adipose tissue are known risk factors for several types of cancer progression, including high grade serous ovarian cancer (HGSOC). Meta-analyses support a link between increased body mass index and enhanced ovarian cancer risk. Our recent study of tumors grown in mice on control diet relative to western diet (40% fat) showed a striking increase in nuclear-localized sterol regulatory element binding protein 1 (SREBP1) and increased intracellular lipid content. SREBP1 is a master transcriptional regulator of *de novo* lipogenesis that can induce metabolic reprogramming of tumor cells. SREBP1 is synthesized in the ER and transported to the Golgi via SREBP cleavage-activating protein, where it undergoes regulated proteolysis by site-1-protease and site-2-protease. Mature SREBP1 is then released from the membrane, translocates to the nucleus, and binds sterol regulatory elements to activate expression of target genes. Lysophosphatidic acid (LPA), a lipid mediator, is highly expressed in ascites of ovarian cancer patients. LPA regulated diverse biological processes such as proliferation, migration and invasion of cancer cells. Our previous data showed that LPA-treated ovarian cancer cells exhibit enhanced lipid accumulation. Here we investigate that LPA-mediated SREBP1 expression and activation of downstream target genes by qPCR, Western Blot, and immunofluorescence in 3 HGSOC cell lines, OVCAR3, OVCAR5, and OVCAR8, respectively. Varied gene expression were observed due to LPA treatment. These results suggest that LPA plays a role in regulating tumor *de novo* lipogenesis through activation of SREBP1-regulated transcriptional pathways in
ovarian cancer cells. This investigation may provide critical insight into the obesity risk factor associated with OvCa metastasis through the role of LPA/SREBP1 axis that influences both tumor and host cells, and provide a potential target for clinical cancer treatment strategies.

Keywords:

Performance Studies for the Proposed CMS L1 Track Trigger Upgrade

Kevin Greif, Justin Dragoo
University of Notre Dame, Notre Dame, United States

The Large Hadron Collider (LHC) at CERN will be upgraded in the mid-2020s to produce collisions at higher rates, and therefore the Compact Muon Solenoid (CMS) detector will require an upgrade in order to handle the accompanying increase in collision data. This upgrade involves implementing a system capable of reconstructing charged particle tracks from the detector in real time, known as a Level-1 (L1) Track Trigger. In order to study the expected performance of such a trigger system, a simulation code has been developed which is capable of running the proposed reconstruction algorithm over simulated collision events. Performance is typically characterized in terms of tracking efficiency. The tracking efficiency is the fraction of simulated particle tracks successfully reconstructed by the L1 trigger. Measuring the efficiency in the simulation reveals problems that can be prevented in the actual trigger by solving them in the code. This research focuses on the effects of including stricter requirements in forming reconstructed tracks. While stricter requirements cut down on the amount of overall data that needs to be processed, requirements that are too strict will result in efficiency losses. The goal of this research is to determine the strictest requirements we can make with minimal efficiency loss.

Keywords: High-energy physics, Large Hadron Collider, CMS, L1 Trigger

Detecting INDELs to Obtain Aaop1 Mutant Line of Aedes aegypti

Caitlin Harrington
Biological Sciences, Notre Dame, United States

*Aedes aegypti* is the primary vector for dengue fever, yellow fever, and zika virus. Understanding the phototransduction cascade of these mosquitoes could lead to strategies for vector control. The *Aaop 1* gene in *Ae. aegypti* codes for the rhodopsin Aaop1, important in photoreceptors in *Ae. aegypti* adult mosquitoes. The goal of our study is to produce *Aaop1* mutant *Ae. aegypti* lines through targeted genome editing using CRISPR-Cas9 technology. *Ae. aegypti* eggs expressing Cas9 have been injected with an *Aaop1* gRNA that guides the CRISPR-Cas9 protein to produce a double stranded break in the DNA at the ATG site of the target gene. This cut can then be repaired through non-homologous end joining (NHEJ). Insertion/deletions (INDELs) may occur as a result of NHEJ and effectively knock out the *Aaop1* gene. Screening for INDELs through PCR is an efficient way to identify G1 mosquitoes that are potential *Aaop1* mutants. Genomic DNA from individual G1 injected mosquitoes is PCR amplified to 125 and 130 base pair fragments containing the *Aaop1* cut site and run on a 3% agarose gel. Our results show that we are able to distinguish a 5 base pair difference in DNA
fragments, suggesting we have the ability to detect INDELs of at least 5 base pairs. Once an INDEL is found, the DNA is sequenced to confirm the presence of a mutation before establishing the mutant line. Creating an Aaop1 mutant line of Ae. aegypti mosquitoes will lead to further studies in behavior, vector competence, and disease transmission.

**Keywords:**

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**Reconstructing the Paleoenvironment of Late Jurassic Period with Stable Isotope Analysis on Belemnite Rostra**

Simian Huang

_University of Notre Dame, Notre Dame, United States_

Sundance Sea was an inland sea that existed in North America from middle to late Jurassic. Marine inundation created an irregularly shaped Jurassic Western Interior Seaway in which the Sundance Formation was deposited. Fossils records have shown the presence of diverse marine species, among which the specimens Pachyteuthis densus is the most abundant. However, the marine environment of the Sundance Sea remains unknown. In order to fill in the knowledge gap, his study aims to reconstruct the paleoenvironment of Jurassic Sundance Sea to better understand the habitat of a variety of species. Stable isotopes (δ^{18}O and δ^{13}C) analysis would be conducted on belemnite rostra to accomplish this goal. Previous researches have shown that the composition of belemnites rostra is in equilibrium with the ambient water. In addition, rostra of belemnites are generally resistant to diagenetic alteration. These features make belemnites rostra a great tool for paleoclimate analysis.

**Keywords:**

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**Virtual Enrichment of Protein Termini by Differential Labeling**

William Huffman

_University of Notre Dame, Notre Dame, United States_

Proteins represent the terminal step in the central dogma. Proteins perform virtually all cellular functions, and are dynamically regulated in expression, stability, localization and activity. Proteins are polymers comprised of amino acids and typically have an amino (N) and carboxy (C) terminus. The composition of the N-terminus is especially important, and can direct the protein to a location in the cell, determine the rate of degradation of the protein and other potential roles in the cell. Alterations in the amino acids at the N-terminus can have serious effects on an organism or pathogen. Termini represent a small portion of a total proteins and therefore are difficult to study without enrichment and purification. This is typically done by taking advantage of the difference in exposed charged termini present on proteins vs. peptides generated during an experiment. Here we have developed multiple strategies to directly enrich protein termini from protease-digested cell lysates directly in a mass spectrometer. This obviates the need to perform any biochemical isolation, instead developing chemical properties of non-terminal peptides which reduce their detection efficiency. We synthesized a reagent with N-terminal specificity which converts internal peptides to polyanionic sulfonic acids, which causes them to ionize less efficiently on the mass spectrometer. We utilized dry ball-mill synthesis of
the NHS-ester of benzosulfonic acid with N,N’-Disuccinimidyl carbonate (DSC). The solutions were tested and analyzed by MALDI-MS. The labeled peptide had poor retention on reverse-phase and ionization properties which suggest a dual mechanism for enrichment, both chromatographic and in the gas-phase. The process for enrichment of whole proteomes is progressing.

Keywords:

How does duckweed...

Grace Jones

ND Regional Science Fair, Notre Dame, United States

Duckweed

Keywords:

Novel Combination Therapy for High-Risk Alveolar Rhabdomyosarcoma with CDK4/6 & Wee1 Kinase Inhibitors

Melanie Justice 1, 2, Simin Kiany 1, Eugenie Kleinerman 1

1 Division of Pediatrics, The University of Texas MD Anderson Cancer Center, Houston, United States
2 University of Notre Dame, Notre Dame, United States

Rhabdomyosarcoma is a childhood soft tissue sarcoma of skeletal muscle. It has two histologic subtypes, with alveolar rhabdomyosarcoma (ARMS) having the worse prognosis. ARMS patients who present with metastasis only have a 15% EFS, and unfortunately, this outcome has not improved significantly in 30 years. However, recent work has shown that for Rb+ adult sarcoma cells, the CDK4/6 inhibitor palbociclib is synergistic with the Wee1 kinase inhibitor AZD1775 through reversible cell cycle arrest. Our study now seeks to find a novel combination therapy for children with RMS based on the hypothesis that in pRb+ ARMS cells, sequential treatment with palbociclib followed by the Wee1 kinase inhibitor MK-1775 will result in synergistic response for tumor cell death. Using patient-derived metastatic ARMS cells and cell cycle analysis, we proved that palbociclib induces reversible G1 arrest in pRb+ ARMS cells. We determined the most effective palbociclib dosage for inducing G1 arrest in two ARMS cell lines, as well as the optimal recovery time that allowed one line of ARMS cells to synchronize in S/G2 in order to be more vulnerable to MK-1775. While the data combining palbociclib and MK-1775 is not available yet, this preliminary data is promising that sequential treatment with palbociclib and MK-1775 will be synergistic. Finally, this study is innovative because the calculated timing for the sequential addition of the drugs takes full advantage of their mechanistic properties. It also focuses on a novel combination that has never been studied before in rhabdomyosarcoma, a childhood cancer that needs new therapeutic approaches.

Keywords: cancer, therapy, rhabdomyosarcoma, CDK4/6, Wee1, cell cycle
The Effect of Mesothelin Expression on the Ultrastructure of Mouse Peritoneum

Brooke Kowalski¹, Tyvette Hilliard¹,², Elizabeth Loughran¹,²,³, Sharon Stack¹,²

¹ Department of Chemistry and Biochemistry, Notre Dame, United States
² Harper Cancer Research Institute, Notre Dame, United States
³ Integrated Biomedical Sciences Graduate Program, Notre Dame, United States

Ovarian Cancer (OvCa) is the leading cause of death from gynecological cancers in US women. In 2017, there was an estimated 22,440 new diagnoses of OvCa of which 14,080 (~63%) women died from the disease. Poor survival is due to diagnosis at late stage when metastasis to the abdominal cavity has occurred. OvCa metastasis involves the detachment of the OvCa cells from the primary tumor, migration of cells by ascites fluid, and adhesion to and penetration through the mesothelial cell layer of organs in the abdominal cavity including the peritoneum. Mesothelin is a 40 kDa protein that is normally expressed on the surface of mesothelial cells and is expressed at abnormally high levels in several carcinomas including ovarian. The exact role of mesothelin is not yet fully understood as mesothelin knockout mice do not display an abnormal phenotype. However, there is some evidence to suggest that mesothelin is involved in OvCa cell adhesion by binding to the OvCa antigen CA-125. Mesothelin wild type and knockout mice were used to investigate the role of mesothelin in the ultrastructure of the peritoneum. A peritoneal ex vivo assay using peritoneal tissues from mesothelin wild type (WT) and knockout mice (KO) and CA-125 negative human OvCa cell line OvCa433 MT1 and CA-125 positive OvCa cell line OvCa 433 was performed. Scanning electron microscopy (SEM) was conducted on ex vivo tissue explants and normal peritoneal tissues. Mesothelin WT ex vivo peritoneal tissues displayed more defined mesothelial cells compared to KO peritoneal tissues. In normal peritoneal tissues, mesothelin WT tissues displayed relatively elongated microvilli compared to mesothelin KO tissues. The ultrastructural differences between mesothelin WT and KO tissues demonstrated by SEM could further explain mesothelial-ovarian tumor cell adhesion seen in OvCa metastasis.

Keywords:

The Importance of Nucleic Acid Sensing Pathways in Host Response to Mycobacterium avium Infection

Nicholas Kiene, Alexandra Tatarian, Jeffrey Schorey, Yong Cheng

Department of Biological Sciences, Center for Rare and Neglected Diseases and Eck Institute for Global Health, University of Notre Dame, Notre Dame, IN 46556, Notre Dame, United States

Mycobacterium avium is a ubiquitous, non-tuberculous mycobacterial pathogen that may infect immune-compromised hosts, such as HIV patients and individuals with underlying lung disease such as cystic fibrosis patients. Like other mycobacterial infections, M. avium is difficult to treat and often imparts significant patient morbidity. To improve therapeutics and patient outcomes in M. avium infections, it is necessary to understand mechanisms of infection and the host immune responses. Previous work has established that Mycobacterium tuberculosis (M.tb) can induce certain immune responses, which are dependent on secreted M.tb RNA. Here, we address whether M. avium, like its M.tb counterpart, may also secrete RNA and characterize downstream effects on host immune activation. Interestingly, induction of interferon-beta (IFN-β) in mouse bone marrow-derived macrophages (BMMs) after M. avium infection was observed.
by quantitative Real-time PCR during a time course experiment with an expression peak at 8 hours. To assess the underlying mechanisms of IFN-β induction during *M. avium* infection, we determined the role of various host genes including RIG-I, MAVS, TBK-1, IRF-8, STING and MyD88, which are all linked to host nucleic acid sensing pathways. In response to individual gene knockout or knockdown of sensing pathway proteins, IFN-β expression was significantly reduced relative to control infected BMMs, implicating a dependence of these sensing proteins on IFN-β production. Meanwhile, a bacterial CFU assay was employed to discern the importance of nucleic acid sensing pathways for *M. avium* survival in BMMs. Finally, we found that *M. avium*-infected macrophages may release extracellular vesicles (EVs) containing mycobacterial RNA, suggesting a possible role for EVs as a carrier of mycobacterial components to activate neighboring uninfected host cells. Together, these findings illuminate compelling insights into host-pathogen interactions in *M. avium* and potentially other mycobacterial diseases.

**Keywords:** mycobacteria, RNA, immunology, bacteriology, infection

**Variable Odor Preferences in Rhagoletis Flies: Implications for Sympatric Speciation**

ShinHae Kim ¹, Cheyenne Tait ¹, Meredith Doellman ¹, Charles Linn ², Jeffrey Feder ¹

¹ Department of Biological Sciences, University of Notre Dame, Notre Dame, United States
² Department of Entomology, New York State Agricultural Experimental Station, Cornell University, Geneva, United States

Olfactory preference has a direct influence on evolution and speciation of animals that use smells to locate mates or oviposition sites in nature. Rhagoletis pomonella (Diptera: Tephritidae) utilizes olfaction to track volatile chemical compounds emanating from its host fruits, apple and hawthorn. It is hypothesized that sympatric speciation occurred between the host races because of the differences in their host fruit odor discrimination, which resulted in reproductive isolation, with each host race isolated on the “island” of their own fruit. Studies of *R. pomonella* infesting apple and hawthorn fruits have found that each host race is attracted to their own host fruit, and avoids non-natal fruits. To understand the genetics of host fruit preference in Rhagoletis, we first phenotyped them for their differential odor preferences. In a flight tunnel, apple and hawthorn flies from Grant, Michigan were placed in holding cages with the open end of the cage facing upwind, one meter from the odor source consisting of synthetic fruit odor mixture. During the 1 minute exposure to the odor compound, the behaviors of the flies were scored as: 1) taking flight; 2) upwind flight; and 3) reaching source. Apple flies showed that they had significantly higher preference for sources releasing the apple blend than hawthorn. Similarly, hawthorn flies showed stronger preference for hawthorn blend than for apple blends. Tests with apple and hawthorn flies collected from Cassopolis and Lansing, Michigan produced similar results. Also, it has been found that a moderate proportion of apple and hawthorn flies are broad responders that are able to recognize and orient to more than one blend. By extracting the DNA and analyzing the genetic difference between flies with variable responses, we can better understand the basis for odor preferences, and, eventually, how choice behaviors can drive evolutionary events.

**Keywords:** Sympatric speciation, odor preference, Rhagoletis pomonella, olfaction
How will water flow rate affect the time between sparks produced by a Kelvin Electrostatic Generator?

Cole Klinedinst

*Discovery Middle School, Granger, United States*

This experiment was about building and testing a Kelvin Electrostatic Generator, which is a type of electric generator from 1867 that uses falling water and no moving parts to create small sparks. The problem being solved was "How will water flow rate affect the time between sparks produced by a Kelvin Electrostatic Generator?" It was hypothesized that if the amount of water going through the generator is raised, the electricity produced will increase. Also, time between sparks will decrease by 15% every time the flow rate increases by 10%. The procedure begins with building the generator. To find the flow rate for testing, place two cups under the nozzles and hold them for one minute. Measure the ml output and fine-tune the flow rate. Record the times between sparks for 15 sparks. Repeat at five different flow rates. The results partially proved the hypothesis. The prediction that more water equals lower time between sparks was correct. The predicted percents were off by 18.92%. During this experiment, much was learned about properties of electricity and traveling of ions, among other things.

**Keywords:**

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Can I Guess Your Password?

Arda Kurama

*Discovery Middle School, Granger, United States*

This project aims to inform people on how to have a safer cyber life by answering the question: “what type of password is easiest to hack?” The hypothesis is that a completely random password made of letters, numbers, and punctuation would be hardest to crack because it uses all characters. To test this hypothesis, a Python 3 password cracking code from Science Buddies was altered and enhanced. Then, sample passwords were created, converted into MD5 hash, and tested in mixed order. The constants were the computer, code, and password length. The independent variable was the password and the dependent variable was the number of guesses to hack the password. The hypothesis was found to be incorrect. The pronounceable random password (created with only letters and is pronounceable) took more guesses than the completely random password for the following reason. The Brute Force attack was used to guess both passwords. This method spins a 74 character dial, from a-z, A-Z, 0-9, then punctuation, in order. The code took a longer time to guess the pronounceable random password because this password started with the letter t while the completely random password started with the letter m, which is earlier on the dial. It is concluded that more sample passwords should be tested to generalize the findings. Password length was found to be critical as it can increase the time to guess exponentially. Passwords with only numbers are weak. Finally, common dictionary words can be guessed nearly instantaneously, whether long or short.

**Keywords:**
Assessing the Genetic Diversity of Bur Oak (*Q. macrocarpa*) Across its Range

William Langbo, Warren Chatwin, Jeanne Romero-Severson

*University of Notre Dame Department of Biological Sciences, Notre Dame, United States*

**Background.** Bur Oak (*Quercus macrocarpa*) is a large economically important hardwood tree found in eastern and central North America. Anthropogenic influences have affected the native range and distribution of this species. Few studies have been conducted on this species, and the most recent range-wide study was conducted with a limited geographic sampling using allozymes in 1990. Improved techniques for assessing genetic diversity present a need for reassessment of genotypic variance across the range of *Q. macrocarpa*. Our objective is to preliminarily assess genetic diversity of *Q. macrocarpa* across its geographic range in order to obtain a better understanding of its genotypic variation and geographic population substructure. We hypothesize that *Q. macrocarpa* will show high levels of genetic diversity between individuals with low levels of genetic differentiation across its range.

**Method.** In 2015, we collected 462 samples, representing the geographic range of *Q. macrocarpa*, from four provenance plots and extracted DNA from each sample. In spring 2017, we employed a targeted sequencing technique to selectively capture ~500 EST-SSR microsatellite sequences from a screening panel of 11 *Q. macrocarpa* samples representing its entire geographic range. These samples were sequenced and then processed using multiple bioinformatics programs. Currently, we are assessing the quality, consistency, and polymorphism of each EST-SSR. We then will select the 16 most informative EST-SSR sequences which will be used to genotype all 462 samples.

**Future Plans.** The data will be analyzed using the Bayesian analysis program STRUCTURE to assess the population substructure of *Q. macrocarpa*. For future studies, we will use climate data (www.worldclim.org) to identify possible relationships between genotype and specific climate variables. This relationship will be useful in informing predictive models of range shifts of *Q. macrocarpa* under climate change.

**Keywords:** Quercus macrocarpa, Trees, Genetics, Genetic Diversity, EST-SSR, Oak,

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Extinction and Long-Term Survival in Crinoids

Elizabeth Lawler

*University of Notre Dame, Department of Biological Sciences, Museum of Biodiversity, Notre Dame, United States*

The Paleozoic Era was a time of great change, evolutionarily, geologically, and climatically, culminating with the Permian extinction 252 million years ago. At this time, about 96% of marine species went extinct, including much of the crinoid class and other members of the echinoderm phylum. The crinoid species that survived further diversified into the more than 600 species that are alive today. The purpose of my research was to examine the fossil collection from Notre Dame’s Museum of Biodiversity to see if morphological changes in crinoids from before and after the Permian extinction could be mapped. Investigations based on fossil
evidence suggest that the initial echinoderm species that survived were those that were lightly calcified, had active control of their circulation, and had elaborate gas exchange mechanisms. In addition, they seemed to be more flexible and motile than the species that died out. This, in conjunction with theories that the oceans at the end of the Permian period were stagnant and ridden with carbon dioxide, suggests that the increased mobility and ability to exchange gases at an upregulated rate would offer a significant evolutionary advantage. As sea levels dropped around this time as well, the more mobile marine beings would have been able to travel into deeper water, as today’s crinoids are able to survive at multiple water depths from very shallow to relatively deep. Overall, given the limited number of species that are preserved as fossils, conclusions drawn from extinct to extant species should be evaluated with caution.

**Keywords:**

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**Characterizing and Predicting of Harmful Dust Storms in Saudi Arabia**

Eric Lee  
*College of Science Department of Applied and Computational Math and Statistics, Notre Dame, United States*

Saudi Arabia experiences frequent dust storms that have calamitous impacts on the environment, economy, and health of the general population. Prolonged exposure to dust-sized particles carry along infectious diseases and causes numerous long-term health effects such as pulmonary and respiratory diseases. Sandstorms can also tear through agricultural landscapes to accelerate processes of land degradation and desertification. The United Nations has calculated that storms account for losses of over 12 billion dollars in GDP every year across the Middle East. Additionally, in the past 15 years the country has seen a significant rise in the severity and occurrence of these storms due to human and environmental factors. This project aims at characterizing and predicting the behavior of dust particles in Saudi Arabia using measurements of Aerosol Optical Depth (AOD) at various locations over the past 5 years. We characterize the hourly behavior of AOD using a time series model with a daily functional nonparametric structure, and aim at leveraging over multiple site measurements to provide accurate, spatially resolved forecast of dust storm occurrence.

**Keywords:**

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**Generation of transgenic lines for cell-specific analysis of TNFα receptor 1a during zebrafish retinal regeneration**

Anne Lentino, Leah Campbell, David Hyde  
*Center for Stem Cells and Regenerative Medicine, Center for Zebrafish Research, Department of Biological Sciences, University of Notre Dame, Notre Dame, United States*

Photoreceptor cell death leads to permanent retinal damage in mammals. However, the damaged zebrafish retina can regenerate via a population of Müller glia in the inner nuclear layer (INL). Following exposure to constant intense light, Müller glia proliferate to generate neuronal progenitor cells that amplify, differentiate, and replace the neurons lost to damage. Tumor Necrosis Factor-alpha (TNFα) was shown to be necessary and sufficient to induce this process.
in the zebrafish retina. A likely receptor for TNFα on the Müller glia is Tumor Necrosis Factor Receptor Superfamily 1a (Tnfrsf1a). In order to investigate the role of Tnfrsf1a in retinal regeneration, I generated two zebrafish Tet-On response lines for inducible, cell-specific expression of Tnfrsf1a: (1) a full-length Tnfrsf1a as a control and (2) a truncated Tnfrsf1a as a dominant negative, which dimerizes with the wild-type receptor and prevents activation in the presence of TNFα. Using multisite Gateway cloning, I generated vectors containing the tetracycline response element (TRE) upstream of the full or truncated forms of tnfrsf1a, both with a self-splicing P2A-EGFP tag and Tol2 sites for transposase-mediated genome integration. Constructs were microinjected along with transposase mRNA into either albino$^{b4/b4}$ or Tg(rlbp1a:rtTA$^{FLAG}$); albino$^{b4/b4}$ embryos at the one or two-cell stage. The transgenic rlbp1a:rtTA$^{FLAG}$ line was previously developed with a FLAG epitope-tagged reverse tetracycline-controlled transcriptional transactivator (rTA) driven by the retinal-binding protein 1a (rlbp1a) promoter for Müller glia-specific expression. The albino$^{b4/b4}$-injected fish were raised to adulthood for generation of transgenic lines, while the Tg(rlbp1a:rtTA$^{FLAG}$); albino$^{b4/b4}$-injected fish were treated with doxycycline (to induce expression of the tnfrsf1a construct) for 24 hours at 5 days post fertilization (dpf) and analyzed for GFP expression in the INL. Results on the retinal expression pattern in both the mosaic embryos and F1 progeny from the transgenic lines will be presented.

Keywords: zebrafish, retina, regeneration, TNFα

Transcriptional regulation of Epithelial Membrane Protein 2 by Adenomatous Polyposis Coli

Anna Lyons1, 2, Alyssa Lesko1, 2, Carolyn Ahlers1, 2, Jocelyn Gaona1, 2, Jenifer Prosperi1, 2, 3

1 Department of Biological Sciences, Harper Cancer Research Institute, University of Notre Dame, Notre Dame, IN, United States
2 College of Science, University of Notre Dame, Notre Dame, IN, United States
3 Department of Biochemistry and Molecular Biology, Indiana University School of Medicine, South Bend, IN, United States

The Adenomatous Polyposis Coli (APC) tumor suppressor is a multifunctional scaffolding protein implicated in various cellular processes. Our lab has demonstrated that APC knockdown (APC$^{KD}$) in Madin Darby Canine Kidney (MDCK) cells leads to atypical cyst shape, abnormal polarity, and increased migration. The lab also made the novel observation that APC loss results in increased expression of epithelial membrane protein 2 (EMP2). Previous studies demonstrated that EMP2 knockdown in APC$^{KD}$ cells results in decreased cyst size and restored polarity, establishing a novel association between APC and EMP2 and suggesting new role of EMP2 in polarity regulation. This study examines how APC transcriptionally regulates EMP2 and the implications of this interaction on cyst size and polarity. Transcriptional activation of EMP2 was previously examined using bioinformatics, DNA/protein arrays, and luciferase reporter assays. EMP2 promoter screens determined potential binding sites for E2F transcription factor 1 (E2F1) and signal transducer and activator of transcription 1 and 3 (STAT1 and 3). APC$^{KD}$ cells displayed increased expression of STAT1 and E2F1 and transcriptional activity of STAT3, indicating these as possible transcriptional regulators of EMP2 mediated by APC. Preliminary studies demonstrated significant difference in CREB1...
binding between APC$^{\text{KD}}$ and MDCK cells. E2F1 was shown to weakly bind to the promoter in all cell lines. No significant difference between APC$^{\text{KD}}$ and MDCK controls was observed. Ongoing experiments will determine binding of STAT1 and STAT3 to the EMP2 promoter. Current studies are validating the role of these transcription factors in EMP2 expression, as mutation of the E2F1, STAT1 and STAT3 promoter-binding sites should decrease expression in EMP2 promoter driven assays. In future studies, transcription factors identified through ChIP will be manipulated. Cyst size, polarity, and EMP2 expression will be evaluated. A better understanding of the interaction between APC and EMP2 will further elucidate the molecular mechanisms driving APC-mutant cancers.

**Keywords:** Adenomatous polyposis coli, breast cancer, tumorigenesis, polarity

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**Characterizing Uranium Behavior at the Solid-Solution Interface**

Noreen Maloney, Meena Said, Amy E Hixon  
CEEES department at Notre Dame, Notre Dame, United States

Understanding the behavior of nuclear material in its surrounding environment can provide insight into its mobility as well as its chemical and physical properties. Interactions with inorganic and organic ligands, behavior at the mineral-water interface, and environmental fate and transport underscore the importance of constraining the behavior of the nuclear material under relevant conditions. Through multiple avenues, we aim to better constrain the behavior uranium exhibits under various conditions in both the solid and aqueous phase.

The first project aims to observe interactions between UO$_2$ solid material and aqueous metal impurities commonly found during the nuclear fuel cycle. When specific metal(s) – namely Pb, Ca, and Cr – are introduced, incorporation, secondary mineral phase formation, and morphological changes on the surface of UO$_2$ may be observed. Inductively coupled plasma mass spectrometry (ICP-MS) will be used to quantify the concentration of elements in solution while scanning electron microscopy with energy dispersive spectroscopy (SEM-EDS) will provide high-resolution images to understand the physical and chemical changes on the UO$_2$ solid surface.

The second project aims to understand the potential desorption processes of uranium from a mineral surface, such as iron oxide. It is known that in the presence of H$_2$O$_2$, preferred cations, and alkaline pH conditions, uranyl peroxide nanoclusters preferentially form in solution. These clusters are unique due to their high solubility and distinct size fraction, having applications in separations and waste remediation. The primary objective of this study is not only to observe desorption of uranium from a mineral surface but the speciation of uranium in solution. Inductively coupled plasma optical emission spectroscopy (ICP-OES) will be used to quantify elemental concentration in solution, and electrospray ionization mass spectrometry (ESI-MS) will confirm the presence of clusters in solution.

**Keywords:**
**Preparation and chemistry of the stereoselective Bis(aminophenoxide)osmium(VI) oxo ligand BdanH₄**

Timothy Mikulski, Seth Brown  
*University of Notre Dame, Notre Dame, IN, United States*

Bis(amidophenoxide)osmium(VI) oxo complexes have been shown to have interesting reactivity with oxygen atom acceptors. In order to probe the stereoselectivity of such compounds, an optically active bis(aminophenol) ligand, BdanH₄, was prepared. Optically active (R,R)-Butane diol reacts with isatoic anhydride form (2R,3R)-2,3-butanediylidianthranilate. This product then reacts with 3,5 – di-tert-butyl catechol to form (2R,3R)-2,3-Butanediyl-di-N (2-hydroxy-3,5-di-tert-butylphenyl)anthranilate (BdanH₄). Finally, BdanH₄ and OsO(OCH₂CH₂O)₂ react in benzene with heat to yield (Bdan)OsO. This product is a five-coordinate osmium organometallic species with a reactive oxo ligand. The formation of (2R,3R)-2,3-butanediylidianthranilate is confirmed by NMR and X-ray crystallography, while the BdanH₄ is confirmed by NMR. Structural analysis of the diastereomers of (Bdan)OsO, as well as attempts to prepare diastereomerically pure samples of the compound, will be discussed.

**Keywords:**

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**Emergence of intermediate wing phenotypes in secondary contact zones within Rhagoletis suavis species group**

Anthony Molinaro, Mary Glover, Jeffrey Feder  
*University of Notre Dame, Notre Dame, United States*

Species are moving in response to climate change, causing previously isolated species to come into contact. This secondary contact can have many implications, including the evolution of reproductive isolation, hybridization, and local extinction. The walnut-infesting *Rhagoletis suavis* species group are thought to have speciated in geographic isolation in the United States, resulting in unique wing patterns for each of the four indigenous species. Currently, there are multiple regions where *Rhagoletis suavis* species co-occur, including *Rhagoletis juglandis* and *Rhagoletis completa* in New Mexico. In the lab, these two species are able to successfully mate and lay eggs, but heterospecific eggs have a lower hatching rate. To determine if *R. completa* and *R. juglandis* might be hybridizing in secondary contact zones, we analyzed the wing morphologies from both isolated and co-occurring sites for intermediate wing patterns. There was no difference between *R. completa* in isolated and co-occurring sites. We observed that *R. juglandis* in co-occurring sites appeared more similar to *R. completa* than *R. juglandis* in isolated sites, indicating a potential imbalance in reproductive isolation. In conclusion, the secondary contact of two geographically isolated species of walnut flies has resulted in the emergence of an intermediate wing pattern for one species, but not the other. A future genetic study of walnut flies could reveal if hybridization is the cause for this phenotypical convergence. Understanding what is happening at these co-occurring sites is important because instances of secondary contact are expected to increase as species continue to move in response to climate change.
Towards Second-Generation Total Syntheses of Microtubule Stabilizing Agents Dactylolide & Peluroside

Michael Mulligan

University of Notre Dame, Notre Dame, United States

Poster Presentation

Towards Second-Generation Total Syntheses of Microtubule Stabilizing Agents Dactylolide & Peluroside

Michael Mulligan

College of Science

Chemistry

Jeff Henry, Department of Chemistry and Biochemistry

Isaac Chogli, Department of Chemistry and Biochemistry

Advisor: Dr. Richard Taylor, Dept. of Chemistry and Biochemistry, Director of Notre Dame-California

Polyketides are a group of secondary metabolites produced by many species of bacteria and fungi that have historically served as an important source of inspiration for novel drugs. Dactylolide and peluroside are two such polyketides that demonstrate activity against several cancer cell lines through a microtubule-stabilizing mechanism. The efficiency of microtubule-stabilizing agents (MSA’s) in targeting actively dividing cells has been based upon the taxanes and epothilones. Zampanolide is a promising drug candidate demonstrating cytotoxicity in the nanomolar range and is known to bind to the taxane pocket of β-tubulin. Dactylolide is a polyketide with micromolar toxicity that has been isolated from Dactylospongia sp. and has a similar structure to zampanolide. Peluroside is another polyketide natural product that has an alternate microtubule-stabilizing mechanism demonstrating the possibility of these two drugs being used cooperatively to treat cancer patients. Each of these targets have been previously prepared in our laboratory. The goal of this project is to create new routes to each structure that provide the targets and analogues with improved efficiency.

Keywords:

Reed it and Weep: Ancestral Kicks Modern's Grass in the Presence of Spartina

Eva Napierkowski, Aishwarya Natarahan, Jennifer Robichaud
Global environmental change (GEC) has resulted in sea level rise, and is predicted to cause further changes in the future. Sea level rise threatens many coastal ecosystems, including salt marshes, in part because of the impacts on native flora integral to those ecosystems. Meanwhile, these ecosystems have been recognized as providing important ecosystem goods and services to society, such as protection from storm surges. To preserve these ecosystems, and the resources they provide, it is important to understand how coastal ecosystem plants will respond to changing conditions. Using greenhouse experiments, old and modern genotypes of the marsh plant, Schoenoplectus americanus, were exposed to a variety of water levels, salinities, and nutrient concentrations along with in combination with other species, such as Spartina, found in coastal marshes. For 6 weeks, plants were grown in replicate plots using a fully factorial design reflecting a combination of two environmental factors, with constant temperature and artificial light. Each week, new stems were counted and height of stems were measured. After 6 weeks, after a final measurement of height and width, all new biomass was collected and dried in order to estimate biomass. Data were analysed using a two-way Analysis of Variance. Results suggest that sea level rise, salinity, and nitrogen could alter plant growth of S. americanus, along with potential for competition with other plant species. This study has generated important information that will help in the development of new predictive models with which to evaluate the consequences of future GEC for coastal marsh ecosystems.

**Keywords:**

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**Effect of Parasite Burden on the Survival of Yellow Baboons (Papio cynocephalus)**

Elise Paietta, David Jansen, Elizabeth Archie

*University of Notre Dame, Notre Dame, Indiana, United States*

Parasites are thought to exact a significant toll on animal health and survival. Parasite levels have been found to be enhanced by drought. Drought alone brings with it many imposing hardships to wildlife populations including loss of habitat, reduced food sources, and migration. This study aims to look at the effect that parasites have on individual survival during a drought. To accomplish this aim, we will use data on yellow baboons (Papio cynocephalus) from the Amboseli Baboon Research Project, a long-term population study, which experienced a drought in 2016-2017. We hypothesize that increased parasite load, diversity, and richness will result in high mortality rates in the baboon population during the drought. The parasites Trichuris trichiura, strongyles, Abbreviata caucasica, and Streptopharagus pigmentatus will be examined for this study. The additional hypothesis that the drought caused reduced habitat and food quality will also be explored. Standard parasitological techniques will be used to measure parasite burdens in the baboons. We will combine this information with data on survival to test our hypotheses. Few studies have combined multiple factors, especially parasites, to investigate the effects of a drought on a specific population. This study will help to bring insight to the transmission of infectious agents among a wild population during a time of great environmental stress.

**Keywords:**
Speciation in plant-feeding insects: Characterizing *Rhagoletis zephyria* eclosion timing using Pool-seq analysis

Lydia Piendel, Meredith Doellman, Jeff Feder

*Department of Biological Sciences University of Notre Dame, South Bend, United States*

Characterizing the genetic basis for differing traits is essential for a deeper understanding of the process of speciation. Speciation among plant-feeding insects often involves variation in life history timing; for example, flies of the *Rhagoletis pomonella* species complex differ in eclosing timing. *R. pomonella* has become a model for sympatric speciation, with a well documented recent host shift from hawthorn to earlier fruiting apples. The genetic basis of variation in eclosion timing within these host races has been established through the identification of associated loci, some of which also show divergence between host races. *R. zephyria*, another species in the complex, shows substantial, but not fixed genetic differences from *R. pomonella*. Unlike other taxa within the complex, the availability of the *R. zephyria* host fruit, snowberry, broadly overlaps with fruits preferred by *R. pomonella* (apple and hawthorn). We hypothesized that loci associated with eclosion variation within *R. pomonella* should also show differences between early and late eclosing *R. zephyria*. However, unlike the case of the apple and hawthorn host races, we do not expect these loci to show large differences between *R. pomonella* and *R. zephyria*. In an extreme phenotyping approach, we extracted genomic DNA and sequenced pools of early and late eclosing *R. zephyria* using Illumina HiSeq. The resulting sequences were trimmed for quality, aligned to the *R. zephyria* draft genome, and single nucleotide polymorphisms (SNPs) were called and filtered. We identified SNPs showing differences between early and late eclosing *R. zephyria*, largely overlapping with those previously associated with eclosion timing in *R. pomonella*; however, these same loci did not differentiate *R. zephyria* from *R. pomonella*. Our results shed light on the role of life history timing in insect speciation, and invite further investigation of eclosion timing in the *R. pomonella* species complex.

**Keywords:** speciation, life history timing, eclosion, pool-seq

Spectroscopic Characterization of Perovskites for Improved Solar Energy

Elisabeth Kerns, Rebecca Scheidt, Prashant Kamat

*Radiation Laboratory, Department of Chemistry and Biochemistry, Notre Dame, United States*

Viable alternative energy sources must be developed to combat increasing atmospheric carbon dioxide levels. Basic science research on potential solar cell constituents may elucidate next-generation solar energy sources. Here, materials characterization research was carried out on perovskite solar cells. Cesium lead bromide served as the light absorbing layer in perovskite solar cells. The electron transfer mechanism from cesium lead bromide to conductive titanium dioxide, which acts as an electron transport material, to generate current was probed through absorbance spectroscopy and transient absorption spectroscopy. Cesium lead iodide perovskites were also characterized in order to further investigate the electron transfer from materials with different band gaps. Further experiments will study cesium lead bromide and cesium lead iodide with x-ray photoelectron spectroscopy and scanning electron microscopy.

**Keywords:**
Examining a Novel High Throughput Method for Manufacturing Copolymer Membranes for Water Purification Applications

Mauricio Segovia Pacheco

University of Notre Dame, South Bend, United States

Higher performance and more efficient desalination and water treatment must be discovered, developed, and implemented to meet the increasing global demand for clean water. Previous work has demonstrated the potential of self-assembled, copolymer membranes as part of the solution to the impending water crisis. Equipped with both high density arrays of well-defined nanopores and tunable chemical functionalities, these membranes show promise of being able to efficiently purify non-traditional water sources at low energy demands. Poly(trifluoroethyl methacrylate-oligoethylene glycol methacrylate-glycidyl methacrylate)-coated [P(TFEMA-OEGMA-GMA)-coated] membranes are of particular note because they are amenable to facile surface and pore functionalization methods. In this study, we compared electrospray (E-spray), a conventional technique for producing such membranes, to piezoelectric transformer induced electrospray (PT-spray), a novel technique. Conventional E-spray utilizes high DC voltage and micro-scale capillaries while PT-spray utilizes a milli-scale piezoelectric crystal and low AC voltage to deposit the polymer solution on a substrate. E-sprayed and PT-sprayed membranes were manufactured using a systematically varied series of conditions, functionalized for metal ion capture, and analyzed for performance in order to compare the two membrane fabrication methods. Membrane performance was evaluated by measuring hydraulic permeability and copper ion uptake. This study found that PT-sprayed membranes demonstrated a permeability of $235 \pm 32 \, \text{L m}^{-2} \, \text{hr}^{-1} \, \text{bar}^{-1}$ and a copper ion uptake of $264.1 \pm 29.9 \, \text{mg Cu}^{2+}/\text{g polymer}$, closely matching the permeability, $243 \pm 94 \, \text{L m}^{-2} \, \text{hr}^{-1} \, \text{bar}^{-1}$, and copper ion uptake, $262.7 \pm 21.0 \, \text{mg Cu}^{2+}/\text{g polymer}$, achieved by E-sprayed membranes. However, PT-sprayed membranes only required one-sixth of the manufacturing time. This suggests that mass production could be achieved more readily with the PT-spray technique. With further optimization, the PT-spray technique shows promise for implementation in industrial scale production of high-performing, polymeric membranes for water treatment applications.

Keywords:

Thermodynamic trajectories and fission yields for neutron star merger nucleosynthesis

David Shaw

University of Notre Dame, Notre Dame, United States

The gravitational observation of a neutron star merger (NSM) and the optical observations of its subsequent kilonova indicate that such mergers definitely contribute to the abundance of heavy elements in the galaxy. These elements with atomic number greater than that of iron ($Z=26$) cannot be produced via nuclear fusion as can the lighter nuclei. Instead, they require other mechanisms such as the rapid neutron capture process, known as the r-process. Because of the neutron-rich seed nuclei, extreme thermodynamic conditions, and high flux of free neutrons,
NSMs are believed to be important astrophysical sites of the r-process. In order to assess the viability of NSMs for r-process nucleosynthesis, nucleosynthesis abundances in the post-merger environment must be calculated and compared to the observed abundances of the heavy elements in our galaxy. To allow for such a prolonged nucleosynthesis calculation, we cleaned and extended in time the temperature and density data from a NSM simulation using both numerical equation of state tables and idealized analytical models. In addition, we used a nuclear fission code to determine the statistical yields of fission products and promptly emitted neutrons for over a thousand different isotopes. We used these inputs to inform the nuclear reaction network called PRISM in calculating the abundances of the r-process elements in the wake of a NSM. Finally, we compared the resulting abundances to the observed abundances in our solar system to determine the likelihood that NSM r-process nucleosynthesis is responsible for the current quantity of heavy elements.

Keywords:

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**Zebrafish as a Model for Niemann Pick Type C Disease (NPC)**

Lillian Spatz  
*University of Notre Dame Department of Biological Sciences, Notre Dame, United States*

Niemann Pick Type C Disease (NPC) is a lysosomal storage disorder characterized by progressive Purkinje cell death and motor coordination defects, such as ataxia, tremors, difficulty swallowing, and difficulty moving the eyes up and down. NPC is caused by point mutations in NPC1 and NPC2, which ultimately lead to defects in cholesterol trafficking and the observed lysosomal engorgement. Our lab proposes a model in which StARD9, a novel transmembrane kinesin localized to lysosomes, functions as a genetic modifier of NPC and aids in the export of lysosomal cholesterol. To test our model, in vitro and in vivo studies of StARD9 knockouts have been conducted. We expect the loss of StARD9 to manifest in symptoms mimicking the histological and behavioral abnormalities detected in NPC patients because loss of StARD9 would result in defective cholesterol transport. StARD9 -/- mice have several neurodegenerative defects that parallel NPC, including twitching, seizures, and progressive Purkinje cell death. I expect mutant zebrafish with a point mutation in StARD9, which leads to a premature truncation of the protein, to display similar phenotypes, such as a decrease in Purkinje cell number over time and abnormal swimming behavior and startle responses. Should this be the case, many of the benefits that are inherent to zebrafish research could be applied to the NPC disease research community. Production of a zebrafish model for NPC will enable more efficient treatment analysis compared to the mouse model system and provide our lab with additional insights into the timeline for NPC progression. Characterization of the zebrafish StARD9 -/- model will serve to complement the cell culture and mouse models for NPC.

Keywords:
Characterization of the Molecular Mechanism of IFN-β Production in Host Cells during a *Mycobacterium avium* Infection

Nicholas Kiene, Yong Chen, Alexandra Tatarian  
*University of Notre Dame, Notre Dame, United States*

*Mycobacterium avium* primarily affects individuals with compromised immune systems or with lung disease such as Cystic Fibrosis. It is very closely related to *Mycobacterium tuberculosis*, the causative agent for tuberculosis. The incidence of *M. avium* infection has been increasing in recent years in the United States and in other countries such as Japan. However, we still lack an understanding what is responsible for this increase and for what makes *M. avium* pathogenic in susceptible individuals. The current study was designed to investigate whether *M. avium* releases its RNA into the cytosol of host cells and thus activates the corresponding host RNA signaling pathways. We first isolated the cytosolic total RNA from Raw 264.7 cells post *M. avium* 104 infection, and the presence of *M. avium* RNA in the cytosolic fraction was confirmed by performing quantitative Real-time PCR analysis. To identify the host signaling pathways activated by released *M. avium* RNA, we measured IFN-β production using quantitative qRT-PCR (RNA-level) and ELISA (protein-level) in mouse bone marrow-derived macrophages. To determine what pathway was involved in this RNA-mediated production of IFN-β we used macrophages from knockout mice or siRNA to knock-down gene expression. Our results demonstrate that the *M. avium*-induced IFN-β production by macrophages relies on RIG-I, MAVS, TBK1, IFR7, MYD88, and STING, indicating a complicated regulatory network for the type I interferon production of host cells in the context of *M. avium* infection. Our study provides new information about *M. avium* pathogenesis which we hope can be used for the development of anti-*M. avium* vaccines and treatments.

**Keywords:** *M. avium*

Discovering Ancestry-Informative Chloroplast Markers in Chestnuts (*Castanea*)

Matthew Valenti, Jeanne Romero-Severson, Warren Chatwin, Will Langbo, Aaron Long  
*University of Notre Dame, Notre Dame, United States*

There are eight species of Chestnut tree, *Castanea*, all of which are capable of hybridizing with each other and producing viable offspring, which makes the task of identifying ancestry by morphology next to impossible. This is an issue for chestnut breeders because of the lack of records on the ancestry of their trees or cultivar identity. To combat this problem, my research seeks to identify interspecific genetic differences in the chloroplast genome using ancestry-informative markers. Chloroplast inheritance, being entirely maternal, simplifies the process of identifying hybrid ancestry if the chloroplast origin is different than the presumed species identity. By identifying 15-20 informative markers, I will be confident in my ability to differentiate between the species chloroplasts. As a starting set, I am using markers that have already proven to be informative, meaning they revealed interspecies differences, in other species of the Fagales, the order that includes chestnuts, oaks, and walnuts. I have created a preliminary screening panel that contains samples from all eight chestnut species. Using this panel I have tested six markers thus far and am in the process of testing more. The amplified regions of interest are being sequenced at the Notre Dame Genomics and Bioinformatics Core Facility. The results are aligned using ClustalW and analyzed in Sequencher 5.2. Once I have
a confident set of markers, I will begin testing them on twig samples that have been sent us to
by chestnut growers from around the country. Ultimately, I seek to create a protocol using these
markers that can be used to quickly determine the ancestry of trees sent to us by chestnut
breeders for further use in breeding programs across the country.

Keywords:

An Exploration of Gene AMIGO2 in Ovarian Cancer Metastasis

Kelly Volk 1,4, Eric Lee 3,4, Katie Santanello 3,4, Leigh Campbell 3,4, Yueying Liu 1,4, Zonggao
Shi 1,4, Xuejuan Tan 2,4, Jing Yang 1,4, Siyuan Zhang 2,4, M. Sharon Stack 1,4

1 Department of Chemistry and Biochemistry, Notre Dame, IN, United States
2 Department of Biological Sciences, Notre Dame, IN, United States
3 Department of Pre-Professional Studies, Notre Dame, IN, United States
4 Harper Cancer Research Institute, Notre Dame, IN, United States

Ovarian cancer is often fatal due to aggressive metastasis and late-stage diagnosis. Late stage
diagnosis (stage III) is largely due to gastrointestinal symptoms initially not considered a threat;
this leads to prolonged diagnosis at a metastatic stage in which the cancer cells have detached
from the primary tumor and attached to organs in the peritoneal cavity. Once diagnosed in stage
III, women only have a 39% five-year survival rate. To identify genetic factors that contribute
to ovarian cancer metastasis, our laboratory has generated cells from parental human ovarian
cancer cells OVCAR8, selected in vivo for intra-peritoneal (IP) metastatic potential (termed IP
cells). IP cells are created by alternating in vivo and in vitro growth cycles. After the third
iteration of in vivo tumor growth, the resulting cancer cells are referred to as OVCAR8 IP3, and
are used for further studies. OVCAR8 IP3 cells have demonstrated increased adhesion,
invasion, and in vivo tumor growth compared to OVCAR8 parental cells, indicating a more
aggressive and metastatic phenotype. To explore potential therapeutic targets, we used next
generation RNA sequencing to identify genes that differ between the parental OVCAR8 and
OVCAR8 IP3 cells. This procedure exhibited that OVCAR8 IP3 cells have significant genetic
differences from their parental OVCAR8 counterparts. Of a panel of genes found to display
substantial upregulation in the IP3 line, this study focuses on the gene AMIGO2. This gene of
interest is thought to play a role in tumor metastasis, as it has been shown to be heavily
associated with the coding of cell adhesion molecules. Using qPCR amplification, we confirmed
positive trends for AMIGO2 expression in OVCAR8 IP3 cells compared to parental OVCAR8
cells. To define the role of AMIGO2 in ovarian cancer metastasis, siRNA silencing of AMIGO2
is underway. Modifications of AMIGO2 could potentially have therapeutic applications in the
future for ovarian cancer patients.

Keywords:

Investigating the effects of ivermectin on the mortality, fecundity, and behavior of
Aedes aegypti and Anopheles minimus mosquitoes

Robert Wozniak
The goal of this research project is to provide a novel, comparative analysis on how ivermectin impacts the mortality, fecundity, and behavior of *Ae. aegypti* and *An. minimus* mosquitoes, which are responsible for the transmission of various viral and parasitic diseases, including dengue fever, chikungunya, yellow fever, and malaria. Vector control methods are needed to prevent transmission of these diseases, especially within the tropics of Central and South America, Africa, and Asia, where millions of people have been infected or are at risk of infection. Existing data regarding the effects of ivermectin on *Ae. aegypti* mosquitoes suggests that the semisynthetic drug induces adult mortality and decreases the hatch rate of eggs through different mechanisms. To determine the LC$_{50}$ for both species of mosquitoes, various concentrations of ivermectin were provided to female mosquitoes through a membrane blood-feeder system as well as via treated sugar-feeding stations. To evaluate the effects of ivermectin, the number of surviving mosquitoes, their fecundity, and the viability of their resulting eggs were monitored and compared to the matched control group cohorts. A behavioral analysis was completed on those that survived the ivermectin from both sugar and blood feeds using a HTSS assay system, topical repellent (PMD), and the LoliTrack behavior tracking software. This research project is still in the process of being completed. If the results demonstrate a significant reduction in *Ae. aegypti* and *An. minimus* survival, fecundity, or egg-vitality after being introduced to ivermectin, it can offer new strategies to combat mosquito-borne diseases, specifically in endemic regions.

**Keywords:** Aedes, Anopheles, Mosquito, Ivermectin

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**The Optimization of the Geometry of the High Efficiency Total Absorption Spectrometer (HECTOR)**

Jack Wurzer, Rebeka Kelmar, Nathan Cooper, Craig Reingold, Orlando Gomez, Patrick Millican, Patrick Tinsley, Matthew Chamberlain, Anna Simon

*University of Notre Dame, Notre Dame, United States*

To better understand stellar nucleosynthesis processes, numerous nuclear reaction cross sections must be measured. These cross sections typically yield low values, therefore requiring highly efficient measurement techniques. A γ-summing detector consisting of sixteen separate NaI(Tl) segments, known as the High Efficiency Total Absorption Spectrometer (HECTOR), was designed to efficiently measure these reaction cross sections. This research studied the effect that the geometric placement of a radioactive source inside of HECTOR had on the efficiency of the γ detection. The results found that the ideal placement of the radioactive source, in this case Cobalt-60, to maximize detection efficiency was approximately 4 cm from the center of HECTOR due to the segmentation of the detector. In the future, this study will determine the optimum placement of a source on the outside of one of the segments of HECTOR to further examine the detecting properties of the device. By better understanding the characteristics of this novel γ detector, HECTOR, and maximizing its efficiency, several nuclear reaction cross sections can be properly measured to better understand stellar nucleosynthesis processes.

**Keywords:**
Weak polyelectrolyte complexation driven by associative charging

Aristotle Zervoudakis

University of Notre Dame, Notre Dame, United States

Weak polyelectrolytes are relevant for a wide range of fields; in particular, they are useful in the creation of “smart” materials for chemical separations and drug delivery. The charges on weak polyelectrolytes are dynamic and sensitive to the surroundings, causing polymer chains to adopt environmentally responsive conformations. Currently, there exists no comprehensive picture of this behavior, particularly where polymer–polymer interactions have the potential to affect charging properties significantly. In this study, we elucidate the novel interplay between weak polyelectrolyte charging and complexation behavior through coupled molecular dynamics and Monte Carlo simulations. Specifically, we investigate a model of two equal-length and oppositely charging polymer chains in implicit salt solution represented through Debye–Huckel interactions. The charging tendency of each chain, along with the salt concentration, is varied to determine the existence and extent of cooperativity in charging and complexation. Strong cooperation in the charging of these chains is observed at large Debye lengths corresponding to low salt concentrations, while at lower Debye lengths (higher salt concentrations), the chains behave in apparent isolation. When the electrostatic coupling is long-ranged, we find that a highly charged chain strongly promotes the charging of its partner chain, even if the environment is unfavorable for an isolated version of that partner chain. Evidence of this phenomenon is supported by a drop in the potential energy of the system, which does not occur at the lower Debye lengths where both potential energies and charge fractions converge for all partner chain charging tendencies. The discovery of this cooperation will be helpful in developing “smart” drug delivery mechanisms by allowing for better predictions for the dissociation point of delivery complexes.

Keywords:

Friday, May 4th, 2018 - Digital Visualization Theater - 02:45 - 03:30

Seeing the Invisible: Real-time Vector Fields in Planetarium Domes

Patrick Link 1, Keith Davis 2

1 University of Notre Dame, Notre Dame, United States
2 University of Notre Dame, Notre Dame, United States

One of the most difficult aspects of physics education is building the intuition for abstract ideas. Every electricity and magnetism student has to learn about electric fields, and how a charge creates a field that permeates space and influences other charged objects. While fields are often illustrated on a flat board or paper, real-world fields are three dimensional, challenging new student’s visualization skills. I will demonstrate real-time fulldome visualizations of electrostatic fields produced with Dr. Keith Davis and used for teaching courses at the University of Notre Dame. The presentation will include a discussion of my work at the Digital
Visualization Theater as an undergraduate student, the development of the Python code to generate these visuals, and choices about color, vector length and vector density to best illustrate the concepts for inexperienced physics students. Finally, I will explain how the framework created during this project can be used to visualize other topics in the dome, including gravitational fields, magnetic fields, and electrodynamics.

Keywords:

Friday, May 4th, 2018 - Jordan Hall Room 105 - 03:30 - 04:30

Oral session - Biology

Inducing Synthetic Lethality in Triple-Negative Breast Cancer using Combinatorial Drug Treatments

Emily Abramczyk ¹, Yingjia Ni ², Bhavana Palakurthi ², Siyuan Zhang ²

¹ Department of Preprofessional Studies, Notre Dame, United States
² Department of Biological Sciences, Notre Dame, United States

Triple-negative breast cancer (TNBC) constitutes 15-20% of all breast cancer cases but presents few possibilities for treatment, with chemotherapy remaining the main option. Demand for more therapeutic options has led to the use of targeted drug treatments in tandem with chemotherapy to specifically target cancer cells. Yet, TNBC cells exhibit drug resistance by upregulation of redundant signaling cascades to circumvent effects of the drug. TNBC cells overexpress epidermal growth factor receptor 1 (EGFR1), but treatment with lapatinib (anti-EGFR1) is only moderately effective. We aim to overcome drug resistance by using combinatorial therapies to target redundant pathways in TNBC that exhibit synthetic lethality. Genetic screening of TNBC cells has identified the CDK 4/6 pathway as a potential complement to anti-EGFR1 treatments, and effectiveness of abemaciclib (CDK 4/6 inhibitor) increases when used with inhibitors of other transmembrane kinases in the same family as EGFR1. To assess the efficacy of combination therapy using lapatinib and abemaciclib, MCF10DCIS.com cells were used to model early stage noninvasive triple-negative breast cancer and treated with drug monotherapies and combinatorial therapy. MTT cell viability assays indicated increased synergy and effect fraction for combination therapies. Flow cytometry demonstrated that combination therapy had a significant increase in cells arrested at the G1 phase compared to the lapatinib monotherapy, though cell cycle arrest for the combination therapy was approximately equal to the abemaciclib monotherapy. Western blotting confirmed downregulation of pEGFR, pAKT, pRb, and DEDD following combinatorial treatment, while lapatinib only decreased pEGFR and pAKT expression and abemaciclib decreased pRb and DEDD expression. This combined downregulation of protein expression indicates the success of combination therapy in targeting EGFR1 and CDK 4/6 redundant signaling pathways, highlighting the potential of this combination therapy to both offer a more targeted course of treatment and reduce the potential for lapatinib resistance often observed in the monotherapy.

Keywords: breast cancer, combinatorial therapies, synthetic lethality
Adenomatous Polyposis Coli (APC) is a tumor suppressor that regulates polarity proteins. Epithelial structure and intracellular signaling are disrupted by the loss of apical-basal polarity and act as an early marker for tumor development. In 3D Matrigel culture, we illustrated that APC knockdown (APC<sup>KD</sup>) in Madin-Darby Canine Kidney (MDCK) cells resulted in inverted polarity and increased cyst size. The novel observation that epithelial membrane protein 2 (EMP2) expression was increased upon APC loss was made through microarray analysis. EMP2 knockdown in APC<sup>KD</sup> cells normalized cyst size and apical polarity, suggesting a previously unknown role for EMP2 in the regulation of cyst development. Here, we investigated the mechanism by which APC transcriptionally regulates EMP2 expression. As the increase of EMP2 expression is at the mRNA level, we examined transcriptional regulation of EMP2 using bioinformatics, transcription factor DNA/protein arrays, and luciferase reporter assays. EMP2 promoter screens (ConTra v2 webserver) identified binding sites for signal transducer and activator of transcription 1 and 3 (STAT1 and 3), and E2F transcription factor 1 (E2F1). Compared to controls, APC<sup>KD</sup> cells exhibited increased expression of STAT1 and E2F1 (DNA/protein arrays) and STAT3 activation was increased (reporter assays). These studies identified STAT3, STAT1, and E2F1 as possible APC-mediated transcriptional regulators of EMP2, and we are currently confirming this through reporter assays. CREB, revealed through other studies to be the only known transcriptional regulator of EMP2, was unchanged in APC<sup>KD</sup> cells, and is being used as a control for reporter studies. We will continue to examine the transcriptional mechanism of EMP2 regulation through ChIP assays and reporter assays using wild-type and mutant EMP2 promoter constructs. Future studies will investigate if transcriptional activity affects polarity. By understanding the interaction of APC and EMP2 and the influence on apical polarity, we will identify the key players in APC disease progression.

**Keywords:** Adenomatous Polyposis Coli, transcription, polarity, breast cancer

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**APC loss alters DNA damage repair in breast cancer cells**

Stephanie McClintock<sup>1, 2</sup>, Casey Stefanski<sup>1, 2</sup>, Kaitlyn Keffler<sup>1, 2</sup>, Jenifer Prosperi<sup>1, 2, 3</sup>  
<sup>1</sup> University of Notre Dame, College of Science, Notre Dame, United States  
<sup>2</sup> Harper Cancer Research Institute, Notre Dame, United States  
<sup>3</sup> Department of Biochemistry and Molecular Biology, Indiana University School of Medicine – South Bend, United States

Breast cancer is the second leading cause of cancer deaths in U.S. women. Many of these deaths are attributed to chemotherapeutic resistance. Thus, understanding the process of chemoresistance will help develop novel approaches to combat breast cancer. The *Adenomatous Polyposis Coli (APC)* tumor suppressor is silenced or mutated in up to 70% of sporadic breast
cancer; however, the effects of APC loss on chemoresistance has not been elucidated. Using the $Apc^{Min/+}$ mouse crossed to the Polyoma middle T antigen (PyMT) transgenic model, we demonstrated that APC loss decreased doxorubicin-induced apoptosis. We also showed that APC loss activated STAT3 causing increased multidrug resistance protein 1 (MDR1) expression. Here, we hypothesize that APC loss causes increases doxorubicin efflux and DNA damage repair. First, we show that APC loss increased MDR1 activity as measured by calcein flux. To determine whether MDR1 inhibition restores doxorubicin-induced DNA damage, a combination treatment of doxorubicin and the MDR1 inhibitor, Valspodar, restored doxorubicin sensitivity in MMTV-PyMT;$Apc^{Min/+}$ cells compared to control. In addition, we showed a decrease of γH2AX, a marker of damaged DNA, in doxorubicin treated MMTV-PyMT;$Apc^{Min/+}$ cells suggesting a decreased damage due to increased drug efflux via MDR1 or to increased DNA damage repair. As APC binds to Topoisomerase IIa, we also show no change in the degree of Topoisomerase IIa inhibition (via doxorubicin and etoposide) in MMTV-PyMT;$Apc^{Min/+}$ compared to control. To test the hypothesis that APC loss affected DNA damage repair, the longevity of doxorubicin-induced DNA damage was measured in MMTV-PyMT;$Apc^{Min/+}$ and MMTV-PyMT;$Apc^{+/+}$ cells treated with doxorubicin or in combination with Valspodar suggesting increased DNA damage repair. Future studies will measure DNA damage repair pathway efficiency via reporter plasmids and measure downstream signaling of yH2AX. Through understanding of APC's role in DNA damage repair, we can ascertain combination therapies to overcome chemoresistance.

**Keywords:** APC loss, DNA damage, DNA damage repair

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**Inhibition of the Androgen Receptor N-Terminal Domain in Castration Resistant Prostate Cancer**

Helen Streff $^{1,2,3}$, Scott Dehm $^{2,3}$, Yingming Li $^{2,3}$

$^{1}$ University of Notre Dame, College of Science, Notre Dame, United States

$^{2}$ Department of Laboratory Medicine and Pathology, University of Minnesota-Twin Cities, Minneapolis, United States

$^{3}$ Masonic Cancer Center-University of Minnesota, Minneapolis, United States

Prostate cancer claims 26,000 American lives each year despite its 99% 5-year survival rate. The androgen receptor (AR) is an important transcription factor in prostate cancer. Thus, therapies for metastatic prostate cancer typically aim to inhibit the AR through chemical androgen deprivation. However, this is not curative, because prostate cancer cells can become resistant to such therapies and progress to castration resistant prostate cancer (CRPC). In CRPC, AR alternative splicing occurs, giving rise to AR variants that lack the ligand binding domain (LBD). Because these AR variants retain the transcriptionally active N-terminal domain (NTD), inhibiting the AR NTD may be a more promising approach for developing new therapeutics. A high-throughput screen of 100,353 compounds led to the identification of four potential inhibitors of the AR NTD. Cell growth inhibition by these compounds was tested using a crystal violet assay on two prostate cancer cell lines which are driven by the AR or AR splice variants (LNCaP and 22Rv1, respectively), and as controls, we tested two prostate cancer cell lines that lack expression of the AR (PC-3 and DU145). The results indicate that three compounds successfully target the AR. Additional studies are warranted to characterize the AR NTD.
specificity of these compounds, which could lead to new therapies that improve the lives of men with advanced CRPC.

Keywords:

Friday, May 4th, 2018 - Jordan Hall Reading Room - 03:30 - 04:30

Oral session - Physics

Atmospheric Pressure Plasma Jets for Biomedical Applications

Elek Wellman, Ek Adhikari, Sylwia Ptasinska
Radiation Laboratory and Department of Physics, Notre Dame, United States

Atmospheric pressure plasma jets (APPJs) are currently being investigated for their potential use in clinical medicine. The components of the ignited plasma, including radicals, charged particles and photons cause necrosis and/or apoptosis within exposed cells. Previous studies have shown that atmospheric pressure plasma (APP) may be used to control cell adhesion, stimulate tissue ablation, tissue sterilization, blood coagulation, wound healing, and induction of apoptosis in cancer cells. The mechanisms by which APP produces these effects are not fully understood, but the output of the APPJ has been demonstrated to create reactive oxygen species (ROS) and reactive nitrogen species (RNS) within the target solution which cause DNA damage. The DNA damage in turn causes cell necrosis and apoptosis.

Many reactive oxygen species are created by the components of the ignited plasma, but hydrogen peroxide specifically has been believed to be particularly harmful to DNA. Thus, the effect of the presence of hydrogen peroxide within the APPJ and target solution on DNA damage was evaluated. Agarose gel electrophoresis was utilized to evaluate the DNA damage in regards to single and double strand breakage. Our results show that when hydrogen peroxide is added to the feed gas of the APPJ, an increase in DNA damage is not observed. The results are compared to the utilization of APP combined with H2O which demonstrated a lack of toxicity of hydrogen peroxide to DNA. Furthermore, addition of hydrogen peroxide to a solution of plasmid DNA induces negligible damage as compared to exposure of APP. Further research is needed in order to establish which product of APP primarily causes DNA damage.

Keywords: atmospheric pressure plasma, DNA damage, hydrogen peroxide

Quantifying the Physics of the Second Maximum in I-band Type Ia Supernova Light Curves for Improved Cosmological Constraints

Michael Foley 1, Ryan Foley 2, Peter Garnavich 3

1 University of Notre Dame, Notre Dame, IN, United States
2 University of California Santa Cruz, Santa Cruz, CA, United States
3 University of Notre Dame, Notre Dame, IN, United States
Type Ia supernovae are important cosmological distance indicators, particularly in the measurement of $H_0$ and dark energy. Their use relies on the precise fitting of light curves in different bandpass filters to extract intrinsic parameters of the supernova, such as stretch and color. The I-band (infrared) is an important filter in these analyses as luminosity variations and dust extinction are reduced in this band compared to bluer bands. However, the I-band possesses a poorly constrained feature that is not present in bluer bands - a second peak in the supernova light curve that occurs roughly 20-30 days after the first maximum. This limits the effectiveness of light curve fits, forcing analyses to weight against this band. To remedy this, we use data from the Open Supernova Catalog and the Foundation Supernova Survey to determine correlations between the time and magnitude of the second maximum and other known parameters, including peak luminosity, dm15, and ejecta velocity. This work could help improve distance measurements of Type Ia supernovae and provide important information about the physics of the explosion.

**Keywords:** supernovae, cosmology, astrophysics

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**Investigating Implicit Bias in Letters of Recommendation for a High School Physics Camp**

Allison Olshefke, Micha Kilburn  
*University of Notre Dame Department of Physics, Notre Dame, United States*

Academic fields whose practitioners emphasize aptitude over hard work have fewer women Ph.D.’s. This is true in physics, which both emphasizes brilliance and has one of the lowest percentages of women Ph.D.’s. In this study, 1,725 teacher recommendations for high school applicants to the Physics of Atomic Nuclei summer program were analyzed for possible gender biases. Text supplied by teachers was examined for gender differences based on coding schema from prior research. This study compares the qualitative and quantitative assessments of the recommendations for consistency across gender to determine whether a discrepancy exists at the high school level as an invisible barrier for female students pursuing STEM opportunities. Results indicate that male and female students who were rated equivalently on the quantitative portion of the application had significantly different frequencies of key terms that previous studies identified as indicators of gender bias in letters of recommendation for STEM positions in the qualitative portion. Recommendation letter writers and reviewers should be aware of the impact that language choice can have on a student’s application for a physics program. Further research should be done to investigate the these biases in other high school contexts.

**Keywords:** letters of recommendation, gender, physics education research

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**Analysis of Phase-Imaging Ion-Cyclotron-Resonance Mass Measurements at Argonne National Lab**

William Porter $^1$, Rodney Orford $^{2,3}$, Trenton Kuta $^1$, Ani Aprahamian $^1$, Guy Savard $^{2,4}$, Jason Clark $^2$
In the realm of nuclear physics, the mass of a nucleus is less than that of its constituent protons and neutrons, due to the binding energy of the nucleus. Thus, further studies into nuclear structure are warranted, and are especially relevant for nuclear astrophysics in the study of the r-process. The primary contemporary tool for determining the mass of an ion with high precision is the Penning trap. One of the newest methods for increasing the precision of Penning trap mass measurements is known as the Phase-Imaging technique. Using this technique, the measurement of nuclear masses is accomplished by measuring the cyclotron frequency of the isotopes circling within the trap. Using time-dependent position measurements, the phases of the circling ions are used to determine the cyclotron frequency and, subsequently, the nuclear mass. I will report on the measurements of several neutron rich nuclear masses in the rare earth region from Argonne National Lab's Canadian Penning Trap facility.

Keywords:

Calculating Absolute Transition Probabilities for Deformed Nuclei in the Rare-Earth Region

Anne Stratman, Clark Casarella, Ani Aprahamian
University of Notre Dame, Notre Dame, IN, United States

Absolute transition probabilities are the cornerstone of understanding nuclear structure physics in comparison to nuclear models. We have developed a code to calculate absolute transition probabilities from measured lifetimes, using a Python script and a Mathematica notebook. Both of these methods take pertinent quantities such as the lifetime of a given state, the energy and intensity of the emitted gamma ray, and the multipolarities of the transitions to calculate the appropriate $B(E1)$, $B(E2)$, $B(M1)$ or in general, any $B(\sigma\lambda)$ values. The program allows for the inclusion of mixing ratios of different multipolarities and the electron conversion of gamma-rays to correct for their intensities, and yields results in absolute units or results normalized to Weisskopf units. The code has been tested against available data in a wide range of nuclei from the rare earth region (28 in total), including $^{146-154}$Sm, $^{154-160}$Gd, $^{158-164}$Dy, $^{162-170}$Er, $^{168-176}$Yb, and $^{174-182}$Hf. It will be available from the Notre Dame Nuclear Science Laboratory webpage for use by the community.

This work was funded by the University of Notre Dame College of Science and the National Science Foundation under contract number PHY-1419765.

Keywords: Nuclear physics, computational physics

Friday, May 4th, 2018 - Jordan Hall Reading Room - 04:30 - 05:00

Reception - Reception and Awards