The College of Science Joint Annual Meeting is part of the 5th annual University of Notre Dame Undergraduate Scholars Conference. The intent of the Undergraduate Scholars Conference is to highlight the research achievements of all undergraduates to the Notre Dame community, including students, staff, and faculty.
COLLEGE OF SCIENCE - JOINT ANNUAL MEETING

Schedule and Abstracts
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Schedule – Applied and Computational Mathematics and Statistics

Poster Presentation
2:30 - 3:30 p.m.

Oliver Kernell - *Investigating Discretizations of Tumor Models*
Schedule - Biological Sciences

Oral Presentations I
1:00 - 2:30 p.m.  
Jordan Room 105

Moderator: Clarissa Mertens

1:00 Gary Lamberti, Chair, Dept of Biological Sciences - Opening remarks
1:05 Rachel Cotton - Leishmania inhibits ETS-mediated transcription in host macrophages
1:25 Alexander Metoxen - Maturation and Localization of Rhodopsin in Mosquito Photoreceptors
1:45 Marilyn Blasingame - Development of an environmental DNA assay to detect the yellow fever mosquito, Aedes aegypti
2:05 Kate Augustine - Investigating the prairie-forest transition within Illinois and Wisconsin using General Land Office surveys

Poster Presentations
2:30 - 3:30 p.m.  
Jordan Galleria

Alexandra Below, Matthew Collins, Taylor Boland, Patrick Fagan, and Rachel Rogers - Mechanism of cell death in ECM detached Bcl-2-MCF-10A cells
Erin Boyle - A Sensitized Screen for Genes that Interact with Bag--Of--Marbles in the Lymph Gland of Drosophila melanogaster
Alexandria Brumfield - Molecular Genetic Analysis of STARD9, a Novel Membrane-Associated Kinesin Implicated in Membrane Tubulation and Cholesterol Transport
Nicholas Burley - The Role of Retinoid X Receptor-Alpha in C1q-dependent Clearance of Apoptotic Cells
Joseph Cannova - Screening Mycobacteria marinum Mutants for Iron Sensitivity and the Role of Iron Transport in Virulence
Stephen Elser - Associations between taxonomic groups in a lake community impacted by an invasive species
Tylor Gauger and Danielle Guilfoyle - The Effects of Formalin and Ethanol on Parasite Egg Morphology, Prevalence and Diversity in Fecal Samples From Wild Elephants
Henry Gens - Production of recombinant therapeutic proteins in transformed silkworms
Stephanie Jones - C1q-dependent upregulation of MerTK and its role in proinflammatory signaling
Allison Kress, Matthew Esparza, Emily Siebert, and Michael Nokes - The Role of ARF1 in coatamer recruitment in Toxoplasma gondii.
Kristen Laricchia - Chloroplast Haplotype Diversity and Distribution in Butternut (Juglans cinerea)
Katherine Lenkiewicz - The effect of temperature on ovipositional behavior of the invasive mosquito Aedes japonicus japonicus
Amelia McCready - A plate based assay for novel genes involved in mycobacterial cell wall transport and biogenesis
Martha McGraw - Localization of GM1 in Salmonella Infected NPC Cells
Harrison Mooers - Iroquois Transcription Factors Direct Patterning and Development of the Zebrafish Kidney Nephron
Young Moon - Investigating Opsin Trafficking in Anopheles gambiae: Elucidating Light Adaptation in Mosquito Vision
Patrick O'Hayer - Analysis of TNFα receptor signaling within the regenerating zebrafish (Danio rerio) retina
Joseph Paik - Discovery of Novel Antibiotics against Bacterial Diseases
Kevin Park - Macroinvertebrate diversity in agricultural streams: comparison of two-stage vs. channelized streams in northern Indiana, USA
Michael Petravick - Sox2 Expression in the Regenerating Zebrafish Retina
Whitney Preisser - The Effect of Parasitic Nematode Infections on Body Condition in Wild Savannah Baboons (Papio cynocephalus)
Cameron Pywell - Targeted disruption of the Inhibitor of DNA binding 2 (Id2) gene results in a circadian clock and metabolic phenotype
Robert Ring, Pablo Quan and Ian Trudell - Characterizing tree biodiversity and the environmental context of woodlots on the University of Notre Dame campus
Erika Rivera - A PCR-based assay to detect Culex quinquefasciatus eDNA in aquatic habitats
Manuel Rocha - Characterization of Aaop3 Expression Patterns and Transport Mechanism
Ariane Rodriguez - Exosome targeting of mycobacterial proteins GroES and Antigen85b
Mona Rodriguez - Knowledge, health behaviors and risk perceptions about human papillomavirus (HPV) among female college students who have not been vaccinated against HPV
Matthew Sarna - Regulation of quorum sensing and swarm motility for the bacterium Pseudomonas aeruginosa
Matthew Schirtzinger - Assessing seed banks at increasing soil depth: Effects on seed viability and implications for ecosystem recovery
Alexandra Searle, Meryl Pax, Aaron Steele, Adam Harshbarger, and James Hodgens - Role of Adiponection in Clearance of Immune Complexes and Apoptotic Cells
Brian Semanek - Identification of Wolbachia in Papilio glaucus and Papilio canadensis
Donna Shrader - Evidence for seedborne transmission of growth-promoting bacteria in mung bean seeds
Matthew Smith - Modeling the effects of possible interventions on lost productivity due to the spread and prevalence of seasonal influenza at the University of Notre Dame
Roger Smith - Predicting Antimalarial Mode of Action from Gene Expression Signatures
Suzanne Spitzer - A Hierarchy of Health: Dominance Rank and Parasite Load in Wild Male Baboons
Emily Spulak - The Influence of Sex and Age on Patterns of Parasitism in Wild Baboons
Kevin Towle - Utilizing ecological niche modeling to analyze local climatic adaptation within the endangered Karner blue butterfly species
Daniel Williams - Impact of European Settlement and Land Management on Ohio Forests
Timothy Yee - Sensitized screen for enhancers of mutant dorsal vessel phenotypes in Drosophila
Sue Yi - Characterization of Niemann-Pick Type C Diseased Mice
Kyunghee Yu - Determination of synergism or antagonism between common antimalarial drugs and non-antimalarial drugs using HB3 and Dd2 strains of Plasmodium falciparum
Victoria Zellmer - Tissue culture study on the effect of the EGFR-inhibitor gefitinib on the UMUC-5 bladder carcinoma cell line
Kathleen Zenker - Viability of Self Fertilization in Schoenoplectus americanus

Oral Presentations II
3:30 - 5:00 p.m. Jordan Room 105

Moderator: Katie Pieper

3:30 Paul Baranay - Metassembler: Improving de novo genome assembly
3:50 Antoinette Pusateri - Biochemistry of Antigen Presentation in the GI Tract during colitis
4:10 Kevin Towle - The effect of trematode parasitic manipulation (Microphallus sp.) on crayfish host behavior
4:30 Charles Xu - Spider web DNA: a novel source of noninvasive and environmental genetic material
Schedule - Chemistry and Biochemistry

Oral Presentations  
1:00 - 2:30 p.m.  
Jordan Room 101

Moderator: Steven Wietstock

1:00 Jason Kopec - Synthesis and Characterization of Molybdenum Complexes of 2,2'-bis(2-hydroxyphenylamino)biphenyl for Use in Nonclassical Oxygenation Reactions
1:15 James Baker - Mitsunobu Synthesis of a Monobactam Using the FMOC-Protecting Group
1:30 Andrea Palazzolo - BTZ Scaffold Simplification: Stopping Mycobacterium Tuberculosis dead in its Tracks
1:45 Meghan Courbanou and Katrina Cuisson - Chemically Triggered Release from Liposomes
2:00 Mark Fraser - Development of a Pro-Apoptotic Anti-Hepatitis C Virus Trans-Splicing Group I Intron
2:15 Michael Hur - The Effect of Conus Parius on NMDA-Stimulated Intracellular Calcium Influx and Downstream CREB Phosphorylation

Poster Presentations  
2:30 - 3:30 p.m.  
Jordan Galleria

Nicholas Arnold - Pd/InI Mediated Synthesis of Glutamic Acid Derivatives
James Catalino - Synthesis of Diverse Ionic Liquids for CO₂ Capture and Sequestration
Malcolm Chan - Propargyl Aldehydes as Dielectrophiles in Triyne Formation and Propargyl Iodide Synthesis
Frances Crowell, Andrew Anderson, and Carl Brophy - A Simple Method for Assigning Structure of 1,2,3-Triazoles
Michael D'Netto - Determine dose response to chemotherapeutics and identification of ARID3B interacting proteins in epithelial ovarian cancer cells
Lisa Edwards - Rainbow CdSe Quantum Dot Solar Cell
Tiffany Fan - The Synthesis of Amides and Hydrazones via the Use of Organophosphorus Activation
Sean Fitzgerald - Access Functional Star Polymers with Controlled Nanostructures
Justin Hintz - Rainbow Solar Cell
Kathryn Kraft - Towards the Synthesis of Phosphoramides and Sulfonamides via Organophosphorous Activation
Mark Leong - Synthesis and catalysis of location-specific cobalt nanoparticles supported by carbon nanotubes for Fischer-Tropsch Synthesis
Sean Liebscher and Travis Marshall-Roth - Non-classical Oxygen Atom Transfer Reactions Involving Oxo(molybdenum(VI))bis(catecholate) and Pyridine-N-oxides
Elizabeth Loughran - Composition of the Vg1 Localization RNP Complex in Xenopus Oocytes
Michelle Lundholm - *Asymmetric Ketone Hydrogenations by Ruthenium Noyori Catalysts: A Computational Study*

Grace Meikle - *Synthesis of Yellow, Orange and Red CdSe Quantum Dots on TiO₂ Nanoparticles Using SILAR Method*

Rick Morasse - *Synthesis and Characterization of CdSe Nanosheets*

Amanda Randolph - *Lewis-Acidity and Non-Classical Redox Reactions of Tris(3,5-di-tert-butylcatecholato)molybdenum(VI)*

Elizabeth Robbins, Mary Bevilacqua, and Jimmy Firth - *Developing Simple Colorimetric Verification Tests for Antibiotics on PADs (Paper Analytical Devices)*

William Taylor - *Functionalization of Deltahedral Germanium Clusters*

Laura Thelen, Susan Barr, and Kerry Bauer - *The role of over-expressed nucleoporin Nup62CL mRNA on disease progression and metastasis in colorectal cancer cells*

John Vernon, Brennan Kruszewski, Megan Schlitt, Dayna Smith, and Michelle Tin - *Cell Phone Use and its Effects on Brain Function*

Tanya Watts - *Associating Cell Lines with the Ascending or Descending Colon Using a Panel of Genes*

Zachary Wehrmann - *Quantitative Analysis of the Cholesterol-Lowering Effects of Various Drugs in Niemann-Pick Type C Fibroblasts*
Schedule - Physics

Oral Presentations I  
1:00 - 2:30 p.m.  

Moderator: Jacek Furdyna

1:00 John Brems - *The effect of X-ray induced radiation on DNA and poly-L-arginine*
1:15 William Cantrell - *Construction and Development of an Electron Radiator for DNA Damage Studies*
1:30 Benjamin Coffey - *Development and Species Characterization of Atmospheric Pressure Plasma Jets*
1:45 Joseph Levri - *Plasma Surface Cleaning*
2:00 James Yurkovich - *Treatment of SCC-25 oral cancer cells with non-thermal atmospheric pressure plasma jet*

Poster Presentations  
2:30 - 3:30 p.m.

Mitchell Faulk and Mason Faulk - *Alternative Galaxy Classification Methods*
Ryan Ketterer and David McKenna - *An Optical Atomic Clock in Neutral Silver*
Patrick Marino and Rachael Creager - *Analyzing Potential Tracking Algorithms for the Track Trigger Upgrade to the Silicon Tracker of the Compact Muon Solenoid*
Giuseppe Passucci and Julie Cass - *Study of the Effects of Varying Beta Decay Rates in Cold and Hot r-Process Simulations*
Nancy Paul - *Move over Superman! Nuclear Physics Tackles Krypton With Neff*
Roland Perkins, Patrick Bedard, Mason Faulk, and David Howe - *Building a Bragg Detector*

Oral Presentations II  
3:30 - 5:00 p.m.  

Moderator: Jacek Furdyna

3:30 Thomas Catanach - *Atmospheric Corrections and Periodic Variations at Project GRAND*
3:45 Colin Littlefield - *Discovery of a Wolf-Rayet Star from Detection of its Photometric Variability*
4:00 Stanislava Sevova - *+ γγ Event Production at the Tevatron*
4:15 Kevin McDermott - *Potential Tracking Algorithms for the Trigger Upgrade to the Compact Muon Solenoid*
4:30 Timothy O'Brien - *Studying W + Charm Production at the Large Hadron Collider*
4:45 Patrick Mooney - *Development of a Superconducting Solenoid Spectrometer for the 12C+12C Fusion Reaction at Astrophysical Energies*
Schedule – Spirit of Science Award Winners

Poster Presentations
2:30 - 3:30 p.m.  Jordan Galleria

Darius Balsara - Which Household Pollutant is most harmful to Aquatic Life: The Effect of Various Pollutants on the Survival Rate of Daphnia
Dinuka Cooray - The Effect of Tin and Radiation on the Death of Simulated Cancer Cells
Abigail Erickson - The Effects of Acidification and Temperature on Decalcification
Joshua Leady - Bugging Around With Magnets: An Analysis of Strength of a Horseshoe Magnet on the Velocity of a Magnet
Jeffrey Strycker - Solar Power vs. Shading
Megan Wyse - Mixin’ It Up
ABSTRACTS – APPLIED AND COMPUTATIONAL MATHEMATICS AND STATISTICS
Poster Presentation

*Investigating Discretizations of Tumor Models*

Oliver Kernell  
College of Sciences  
Applied and Computational Mathematics and Statistics  
Advisors: Andrew Sommese and Wenrui Hao,  
Dept. of Applied and Computational Mathematics and Statistics

Tumor growth models are free boundary problems: the boundary of the tumor is the free “boundary.” Adding such details as a necrotic core, angiogenesis, reasonable laws for nutrient flow lead to challenging systems of partial differential equations that cannot be analytically solved. In addition to continuum models, there are cellular level models based on probabilistic simulation and models mixing the two approaches. This research is based on the continuum models with a second goal of devising new numerical methods to solve free boundary problems. The discretization of the systems of partial differential equations arising in the above models often lead to extremely large (several thousand variables and equations) systems of polynomial equations. There are numerical and symbolic approaches to solving systems of polynomials. For more than one variable and for all but very small systems, parallel algorithms based on numerical continuation are the only currently feasible approach for computing all of the physically meaningful solutions of polynomial systems. This approach, implemented in Bertini, requires the finding of all complex solutions to the system of equations. Choice of moving grids, stencils, and formulae for approximation of derivatives are critical to the numerical investigation of tumor models. For this project, a very coarse grid was taken over certain solutions producing a few select grid points. Between consecutive points, a finer grid was computed in order to produce many more grid points. After all points between each consecutive set of coarse points were found, homotopy continuation was used to track those solutions to the actual solutions of the original equation. These were tracked solutions, because although the solutions were found with other solutions of the equations, they were not computed from the boundary points of the entire system and are therefore not necessarily correct. After the creation of the grid, a new system was used to generate grid points. Using the Chebyshev Polynomials, a grid was computed that allowed more points near the boundary of the tumor in order to more accurately model the boundary. Using this method of creating grid points we hope to successfully model the growth of tumors.
Leishmania inhibits ETS-mediated transcription in host macrophages

Rachel Cotton
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Biological Sciences
Advisor: Mary McDowell, Dept. of Biological Sciences

Leishmania major is a protozoan parasite transmitted by the bite of a female phlebotomine sand fly. L. major metacyclic promastigotes invade immune cells, primarily macrophages, dendritic cells, and neutrophils causing skin lesions that can be quite disfiguring and leave substantial scarring. L. major evades immune detection by inhibiting production of IL-12 in host macrophages, and furthermore by inhibiting the subsequent activation of host macrophages by other stimuli like lipopolysaccharide (LPS). Leishmania has been shown to inhibit IL-12p40 at the transcriptional level, but the mechanism by which this occurs has yet to be elucidated. The murine IL-12p40 promoter has been well characterized and includes binding sites for ETS, C/EBPβ, NF-κB, and GATA family transcription factors. In this investigation we specifically interrogate the role of the ETS binding site in mediating transcriptional inhibition by L. major. Using murine macrophages transfected with a luciferase reporter construct fused to a TNFα-derived ETS binding sequence, we can quantify the level of ETS-mediated transcription in infected and uninfected cells upon stimulation. Preliminary results indicate that L. major infection inhibits binding at the ETS promoter element. Ongoing studies include assessing the localization of ETS family transcription factors upon L. major infection by Western Blot, and using RT-PCR to quantify the level of transcription of genes encoding ETS family transcription factors.
Maturation and Localization of Rhodopsin in Mosquito Photoreceptors

Alexander Metoxen
College of Sciences
Biological Sciences

Matthew Leming, Dept. of Biological Sciences
Advisors: Joseph O'Tousa and Michelle Whaley, Dept. of Biological Sciences

The *Aedes aegypti* mosquito is a diurnal species that is a vector for the transmission of the yellow fever and dengue fever viruses. A study of the genome identified ten opsins, which are differentially expressed in photoreceptor cells across the retina. The long-wavelength-sensitive rhodopsin Aaop1 is a major rhodopsin, expressed in all R1-R6 photoreceptor cells and the vast majority of R8 photoreceptor cells. Polyclonal antibodies generated against an amino acid sequence found at either the carboxyl terminus or the amino terminus of the Aaop1 peptide show differential localization patterns. Under light conditions, the antibody against the carboxyl terminus identifies Aaop1 populations sequestered from the light-sensitive rhabdomeric membranes that are localized to multi-vesicular bodies (MVBs) located within the cytoplasm of the photoreceptor cells. The antibody against the amino terminus identifies the same Aaop1 populations as the carboxyl terminus antibody under light conditions, but the amino terminus antibody does not detect Aaop1 in the rhabdomeric membranes under dark conditions. Western blot analysis of Aaop1 shows two distinct populations of Aaop1 at slightly different molecular weights that exist at varying ratios throughout the day. Based on these results, we propose a novel model that newly synthesized Aaop1 is localized in MVBs of the photoreceptor cytoplasm, and matures when the amino terminus of the Aaop1 peptide is removed, signaling for localization to the rhabdomeric membranes. This mechanism for the maturation and localization of photosensitive pigments within the mosquito photoreceptor cells provides a means for modulating light sensitivity during the daily light-dark cycle.
Oral Presentation I

*Development of an environmental DNA assay to detect the yellow fever mosquito, Aedes aegypti*

Marilyn Blasingame  
College of Sciences  
Biological Sciences and Russian  
Diane Lovin and Paul Hickner, Dept. of Biological Sciences  
David Chadee, Dept. of Life Sciences, University of West Indies  
Advisor: David Severson, Dept. of Biological Sciences

*Aedes aegypti*, the primary vector of yellow fever and dengue viruses, is a mosquito species of global health significance. Approximately 2.5 billion people are at risk for dengue fever, a tropical and subtropical disease for which there is no vaccine, so the most effective way to control dengue transmission is surveillance and control of *Ae. aegypti* populations. The ultimate objective of this research is to develop a simple and quick PCR-based assay to detect the presence of *Ae. aegypti*, through amplification of environmental DNA (eDNA) in breeding sites. We hypothesize that a sufficient quantity and quality of DNA is shed into the environment as the mosquito proceeds through its aquatic life cycle such that it can be detected by PCR-based amplification. Since the organism’s DNA is present in the environment where the organism lives, eDNA sampling is different from other methods of species identification because it is not necessary to find a whole organism to confirm its presence. eDNA detection will help to accurately and quickly locate populations without the difficulty of correctly identifying the species using classical methods. We have successfully developed an *Ae. aegypti* specific assay using a mitochondrial gene sequence. Breeding container water from laboratory-reared mosquitoes at different concentrations per liter has been used to test the specificity and overall effectiveness of this assay. Our research thus far has shown that it is possible to confirm the presence of 5 larvae per liter, which is an approximate mitochondrial amplicon concentration of 100 fg/ul ($1 \times 10^{-13}$ g/ul). Development of this technology will enhance surveillance strategies for *Ae. aegypti* and will provide the basis for similar assays for other vector species.
In order to understand how forest ecosystems will respond to global environmental change, we have to understand the relationship between vegetation structure and environmental conditions such as temperature, precipitation, and soil. Of particular interest is the boundary between forests and open prairie, as these two ecosystems vary widely in their ecological and economic functions. There is currently little consensus, however, about what environmental factors determine tree density in a particular location. In the United States, the boundary between prairies and forests extends eastward into Wisconsin and Illinois in an area that is known as the prairie peninsula. This area was extensively surveyed by the General Land Office (GLO) in the 1800’s, providing a record of vegetation composition and tree density prior to widespread landscape change by European settlement. Here, we take advantage of this unique dataset to examine the relationship between temperature, precipitation, and soil factors on tree density at this prairie-forest boundary. Based on a GIS analysis of environmental factors in Illinois and Wisconsin, we selected a subset of townships in these states to gather data on tree density using the GLO survey notes. We aim to present a spatial analysis of these data to determine how this suite of environmental factors correlates with tree density. This analysis has the potential to clarify factors determining prairie-forest boundaries that could be used to understand how forest ecosystems will respond to global change. Additionally, this work contributes to the development of a regional historical vegetation dataset that will be used as an improved baseline for terrestrial ecosystem models.
Understanding the mechanisms of cell death has many implications regarding homeostasis and tumorigenesis. Normal epithelial cells require attachment to the extracellular cellular matrix (ECM) in order to receive cell signals necessary for survival. Upon detachment from the ECM, cells undergo detachment-induced apoptosis, termed anoikis. Previous studies have shown that in non-tumorigenic mammary epithelial (MCF-10A) cells, caspase activation occurs approximately 48 hours after ECM detachment. However, when the anti-apoptotic protein Bcl-2 is overexpressed in MCF-10A cells, caspase activation is inhibited, yet these cells still ultimately die. These studies suggest an alternate cell death mechanism acting independently of the apoptotic pathway that must be evaded for long-term survival after ECM detachment. In this study, we hypothesize that this death is due to a recently elucidated form of programmed necrosis, termed necroptosis. In order to determine whether necroptosis is involved in ECM-detached cell death when apoptosis is inhibited, MCF-10A-Bcl-2 cells will be treated with necrostatin, a small molecule inhibitor of necroptosis, and viability will be assessed. To further elucidate if necroptosis is occurring, a co-immunoprecipitation approach will be utilized to determine if RIP1 and RIP3 are interacting, as RIP1/RIP3 complexes are indicative of necroptosis. Because previous studies have found an association between elevated levels of reactive oxygen species (ROS) and necroptosis, a viability assay will be performed on MCF-10A cells expressing Bcl-2 that have been treated with Trolox and necrostatin to determine if necroptosis and ROS levels are related. Finally, 3D cell culture experiments will be carried out in the presence of necrostatin to determine if necroptosis is involved in luminal clearing during mammary morphogenesis. These studies should determine if necroptosis plays a role in detachment-induced cell death under conditions when apoptosis has been blocked, as is the case in many forms of metastatic cancer. Ultimately, understanding this process of necroptosis may allow for novel cancer therapeutics to be developed that will more efficiently target and kill apoptosis-resistant cancer cells.
Poster Presentation

*A Sensitized Screen for Genes that Interact with Bag--Of--Marbles in the Lymph Gland of Drosophila melanogaster*

Erin Boyle  
College of Sciences  
Biological Sciences  
Dawn Weseli, Dept. of Biological Sciences  
Advisor: Robert Schulz, Dept. of Biological Sciences

*Bag-of-marbles (bam)* is a gene that causes an overproliferation of differentiated cells in the lymph glands. A sensitized screen of the third chromosome was performed in order to identify genes that interact with bam. The screen has essentially been completed, and has thus far identified a region that induced lamellocytes in 34% of the MSN-F9 mcherry;;Df(3L)ED217/e`bamΔ86 third instar larva. Smaller deficiencies in this region have been screened and 12 potential genes that may be responsible for the increased interaction have been identified and are currently being screened. Many of the potential genes are possible translation factors and studies such as chromatin immunoprecipitation could be performed in order to identify how this gene interacts with other proteins and with DNA in promoting lamellocyte induction. The gene could also regulate *bam*, perhaps in conjunction with other proteins with mechanisms that could be explored. In addition, a deficiency region of the third that appears to repress bam induction of lamellocytes has been found. The genes in this region will also be screened in order to identify the gene responsible for repression. Further studies may be done to identify the function of the gene and its role in blood cell development. In addition, when the gene is identified, the lymph glands of the heterozygous *bam* and unknown gene larva will be dissected and mounted on a slide in order to obtain a more accurate count of the amount of lamellocytes induced in the lymph gland by this interaction. Furthermore, using antibodies or fluorescent tags for the product of the unknown gene, dissected lymph glands of the unknown gene larva, as well as heterozygous *unknown gene-bam* larva, could be imaged to determine expression patterns.
NPC disease is a rare autosomal recessive neurodegenerative disease induced by mutations in either NPC1 or NPC2 genes. 95% of NPC patients suffer from mutations in NPC1, a large multi-pass transmembrane protein shown recently to bind cholesterol (Infante et al., 2010). Defects in cholesterol transport are recognized in NPC disease, however the contributions of cholesterol binding by NPC1 are not understood completely. Live-cell imaging of membranes containing NPC1 reveals that, in contrast to wild-type NPC1, mutant NPC1 membranes fail to project dynamic tubular NPC1 membranes. This suggests that membrane tubulation is a critical aspect of cholesterol transport and that the proteins responsible for tubulation are targets for therapeutic intervention. Comparing membranes containing wild-type NPC1 to membranes containing I1061T NPC1, we identified STARD9 as a cholesterol-binding protein present in wild-type NPC1 membranes but missing in mutant NPC1 membranes. The StARD9 gene encodes a 4700 amino acid transmembrane protein containing an N-terminal kinesin motor domain and a C-terminal START (StAR-related lipid transfer) lipid-binding domain. These features suggest that STARD9 is a membrane protein with a cytoplasmic microtubule motor activity. To test these hypotheses, we used cDNA cloning to produce a construct encoding the complete 4700 A.A. protein. This was accomplished using existing cDNA constructs and de novo cDNA cloning. We also engineered catalytic mutations into the nucleotide-binding pocket of STARD9 to inactivate ATPase activity. Using shRNA to deplete cells of NPC1 activity, we observe accumulations of cholesterol that mimic NPC disease. This suggests that NPC1 plays an important role in cholesterol transport. Wild-type NPC1 was capable of rescuing shRNA-based depletion of STARD9. Mutant STARD9 constructs were not capable of rescuing shRNA depletion of STARD9. These studies suggest that STARD9 is an essential membrane-associated motor protein required for tubulation of lysosomal membranes. Activation of membrane tubulation is suggested as a mechanism to stimulate cholesterol efflux.
Failure to clear apoptotic cells leads to the development of autoimmune diseases, such as systemic lupus erythematosus (SLE). Complement component C1q has been shown to be crucial in the clearance of apoptotic cells in both mice and humans, but the mechanism of its action is relatively unknown. Previous studies demonstrated that C1q enhances the expression of Mer tyrosine kinase (Mer), a member of the TAM family of receptor tyrosine kinases. Furthermore, the interaction between C1q and Mer was required for C1q-dependent uptake of apoptotic cells. Nuclear receptors induce expression of Mer and other engulfment proteins, therefore we tested the hypothesis that C1q-triggered expression of Mer was dependent on nuclear receptor signaling. The nuclear receptors liver x receptor-alpha (LXRα), peroxisome proliferator activated receptor-gamma (PPARγ), and peroxisome proliferator activated receptor-delta/beta (PPARδ/β) form heterodimers with retinoid x receptor-alpha (RXRα), and regulate expression of engulfment proteins and engulfment of apoptotic cells. Therefore, we used an RXRα antagonist to determine if nuclear receptors were required for C1q-dependent upregulation of Mer. Bone marrow derived macrophages (BMDM) were treated with the RXRα antagonist HX531, and C1q-dependent Mer expression and function was assessed. HX531 inhibited C1q-dependent expression of Mer as determined by Western blot. Furthermore, HX531 inhibited C1q-dependent engulfment of apoptotic cells. The result suggests that C1q-dependent uptake of apoptotic cells acts through an RXRα-dependent pathway to stimulate Mer expression and function. Future studies are aimed at identifying binding partners for RXRα that are required for C1q-dependent functions.
Mycobacterium tuberculosis, the causative agent of human tuberculosis disease, poses difficult global challenges, especially in particularly poor nations. The pathogen infects one in three people worldwide and accounts for millions of deaths per year. Of particular concern is concurrent infection with HIV, which increases mortality considerably. Furthermore, the emergence of M. tuberculosis strains resistant to multiple first and second line antibiotics, some of which are totally resistant to all available antibiotics, poses a serious threat to the health of the world as a whole and drives our study of M. tuberculosis. By characterizing the method of M. tuberculosis pathogenesis, alternative methods for treating tuberculosis might be developed. To study the mechanism of M. tuberculosis pathogenesis, an ongoing transposon screen of Mycobacterium marinum has contributed to the characterization of the ESX-1 secretion system, which is essential in active infection. Immunoprecipitation experiments on known components and substrates of this secretion have revealed interactions with known ESX-3 iron transport pathway components. Strains lacking genes required for iron transport fail to grow on iron deficient agar. Using the transposon strain collection derived from the aforementioned screen, the sensitivity to the presence of iron will be tested in a parallel screen in which mutants are grown on complete and iron deficient media. The screen is currently being optimized but has strong potential in further unveiling the mechanism of secretion and how it contributes to virulence. We expect to identify mycobacterial strains bearing defects in iron uptake to better understand how these systems interact with the ESX-1 secretion system.
Invasive species can impact their recipient ecosystems in a variety of ways, including disrupting nutrient cycling and lowering biodiversity. Invasive species that are generalists, meaning they thrive in a large range of ecological conditions and utilize many different resources, have the potential to have wide-reaching impacts. Multiple generalist crayfish species have established invasive populations outside their native range, including rusty crayfish (*Orconectes rusticus*), which are well established in our study region in northern Wisconsin. Once rusty crayfish are introduced to a lake, the richness of macroinvertebrates, snails, aquatic plants, and other crayfish species decreases. Here, I examine the impact the presence of rusty crayfish has on snails in areas with different levels of aquatic plant richness and abundance. I hypothesized that lakes with high abundance and richness of plants will have a higher abundance and richness of snails in lakes with similar crayfish densities. The data used in this survey were collected by the Lodge Lab as part of a long term, multi-lake survey encompassing 11 lakes over 25 years. The most recent data collected from 2011 will be the focus of this project. The lakes represent four different categories of crayfish density: always high, always low, decreasing and increasing, where the increasing and decreasing describe population trends since the first survey in 1987. Individual lakes were separated into sectors at which snail, aquatic plant, and crayfish data were collected. At the whole-lake scale, there was a positive relationship between plant and snail richness (p<0.0001, R^2=0.912), and negative relationships between crayfish density and snail richness (p<0.01, R^2=0.567), plant richness (p=0.017, R^2=0.484), and plant abundance (p=0.029, R^2=0.430). There was no significant relationship between snail abundance and crayfish density (p=0.240) or between snail and plant abundance (p=0.066). Further analysis will consider interactions between plants and snails as a response to crayfish density. By reducing biodiversity and altering the food web, rusty crayfish display direct and indirect effects at the whole-lake scale. These effects can impact ecosystem services such as recreational fishing and have implications for management as well as ecology.
To date, few studies have been completed that compare the merits of different preservatives for measuring parasite burdens in fecal samples. Currently, there are two preservatives used for fecal samples: ethanol and formalin. Formalin is the most common preservative for parasitology, but ethanol is more compatible with genetic techniques. While formalin maintains the morphology of parasite eggs, it destroys any genetic material. Conversely, ethanol is able to preserve genetic material, but was suspected to distort the morphology of the egg. The purpose of this study is to ascertain whether formalin or ethanol is a better preservative, as determined by the number, diversity, and morphology of parasite eggs found in the feces. We expected that the count and diversity of eggs found in each preservative would be consistent, whereas the morphology of the eggs would vary. The trade-offs of each preservation method have implications in determining their usage in further experiments. The fecal samples used in this study came from thirty African elephants that are part of the Amboseli Elephant Research Project (AERP), located in Amboseli National Park, Kenya. Each fecal sample was preserved twice, once in formalin and once in ethanol. This allowed for the cross-analysis of egg morphology, prevalence and diversity between the different preservatives. We found that samples in both formalin and ethanol had similar parasite egg counts. The species diversity was also relatively uniform; trematode eggs and three types of strongyle eggs were observed across all samples. Additionally, the eggs preserved in ethanol did not show any morphological differences from the eggs preserved in formalin. The results of this study indicate that future research on elephant parasite eggs will be able to utilize the ethanol preservation method because the morphological integrity of the eggs is not compromised while the genetic material remains intact.
Anticancer monoclonal antibodies (mAbs), such as Rituximab, Cetuximab and Herceptin, provide a compelling option for therapeutic intervention, but unfortunately current methods of production through hybridoma generation and culture are costly and inefficient. The transgenic silkworm system, however, is an effective “bio-reactor” for protein production, and offers a relatively inexpensive, scalable method of alternative production. In order to produce recombinant anticancer mAbs in a silkworm system, pXL-BacII plasmids expressing gene products for chimeric and humanized anticancer mAbs specific to CD20, EGFR, and HER2, and DsRed marker protein, were cloned as the first step in the process. The mAb recombinant genes contained unique nucleotide sequences for the heavy and light chains based on current FDA-approved therapeutic mAbs separated by a short, ‘self-cleaving’ FMDV 2A peptide sequence for high-level translational expression of full-length antibodies from a single open reading frame. The recombinant gene product sequences were inserted in the multiple cloning site between the 5’ and 3’ inverted terminal repeat segments of the plasmid for effective employment in the piggyBac transposon/transposase system. Two sets of plasmids were constructed for each mAb product, with either the Fibroin Heavy Chain or p25 promoter for localization of gene product in the silk. All plasmids contained the DsRed transformation reporter protein driven by the eye-specific 3xP3 promoter. Following construction, the plasmids are to be tested in Bombyx mori strain pnd-w1 silkworm silk gland cells in a DNA bombardment assay to test for successful gene introduction and expression in the silkworm system.
Efficient clearance of apoptotic cells and dampening of proinflammatory cytokine production is required for prevention of autoimmunity. Deficiencies in complement component C1q are associated with a failure to clear apoptotic cells and autoimmunity, and we are investigating the mechanism by which C1q regulates these functions in macrophages and dendritic cells (DC). We recently demonstrated that C1q upregulates expression of Mer tyrosine kinase (TK), a receptor on the membrane of macrophages and DCs that mediates apoptotic cell clearance and proinflammatory signaling. The goal of this study was to investigate the contribution of C1q-dependent upregulation of MerTK to proinflammatory signaling. To measure proinflammatory signaling, we stimulated mouse bone marrow-derived macrophages (BMDM) and immature DC (iDC) with lipopolysaccharide (LPS), an inflammatory trigger, and measured tumor necrosis factor-alpha (TNF-α) production by ELISA. As expected, BMDM responded to LPS with a dose-dependent increase in TNF-α production. Treatment of BMDM with C1q for five hours prior to addition of LPS resulted in an increase in LPS-dependent TNF-α production. This increase occurred independently of MerTK because MerTK-deficient macrophages responded to C1q with a similar increase in TNF-α. Treatment of BMDM with C1q resulted in increased expression of the Mer ligand Gas6, a bridging molecule that links apoptotic cells to phagocytes by binding to phosphatidylserine on the apoptotic cell and MerTK on the macrophage. Similar to C1q, recombinant Gas6 increased LPS-dependent TNF-α production by both BMDM and iDCs. This is contrary to previous studies in other cell types demonstrating that Gas6-dependent MerTK signaling dampens proinflammatory cytokine production. As expected, apoptotic cells (AC) dampened LPS-dependent TNF-α production; however, C1q did not regulate this process because treatment with ACs suppressed TNF-α production equally in C1q- and control-treated macrophages. The results of this study suggest that, although C1q may act through MerTK to enhance phagocytosis, C1q does not act through Mer under these conditions to suppress production of the proinflammatory mediator TNF-α. Further examination of the roles of Mer and Gas6 in the pathway through which C1q prevents an autoimmune phenotype could play a pivotal role in future treatment options for patients with autoimmunity.
Poster Presentation

The Role of ARF1 in coatmer recruitment in Toxoplasma gondii

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Toxoplasma gondii is an obligate intracellular parasite that must produce, package, target, and secrete proteins in order to invade host cells. Coatomer protein (COP) binding regulates protein targeting in mammalian cells. When activated by GTP, the conformation of ADP ribosylation factor 1 (ARF1) allows it to form vesicles through coatomer recruitment. Our research focuses on determining whether this process holds true in T. gondii. We hypothesize that ARF1 is responsible for the recruitment of coatomer TgßCOP. To test this, we treated T. gondii with the drug brefeldin A (BFA). In most cells, BFA disrupts ßCOP localization by targeting the SEC7 region of the ARF-GEF complex and thus deactivating ARF1 (Zeghouf, et. al, 2005). In our treatment of T. gondii, ßCOP was not disrupted as it does in other cells. Instead, ßCOP localized in the Golgi region in a less distinct and more rounded shape than it localized in untreated cells. These results suggest that protein trafficking in T. gondii differs from that of mammalian cells. Because BFA targets a specific region of the ARF/GEF complex, we hypothesize that either the ARF1 or GEF of T. gondii is different from that in most other cells. To test whether ARF1 is used to recruit TgßCOP, mutants representing the different conformations of ARF1 were designed, and the effect on ßCOP localization and intensity was observed in transfected parasites. Parasites expressing the negative mutant, T31N, showed a decrease in intensity of ßCOP localization. Parasites expressing the positive mutant, Q71L, showed an increase in intensity of ßCOP localization. These results suggest that ARF1’s role in TgßCOP recruitment is consistent with normal protein trafficking rules. Therefore, we hypothesize that T. gondii’s resistance to BFA arises due to a novel GEF sequence.
Poster Presentation

*Chloroplast Haplotype Diversity and Distribution in Butternut (Juglans cinerea)*

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The American butternut (*Juglans cinerea* L.) is a species of walnut tree distributed throughout much of the eastern United States and southern Canada. The tree is currently threatened by the fungal disease butternut canker which has decimated the species throughout its native range. Population genetics offers insight into the diversity and migration history of the tree, which can aid in conservation decisions and in understanding the reaction of the species to an unstable climate. After the last glacial maximum 18,000 years ago, *J. cinerea* began to recolonize northward as the Pleistocene glacier receded. Analysis of haplotype diversity in the maternally inherited, non-recombinant chloroplast allows for the reconstruction of these migration routes. It is expected that chloroplast diversity will be decreased along a south-north gradient as a result of a founder effect as trees repopulated suitable habitat in the north. The diversity and biogeographical distribution of haplotypes was determined across several populations, with approximately 20 samples taken from each site. Intergenic regions of the chloroplast were amplified using primers designed in closely related tree species and sequenced to determine sites of polymorphism. Fourteen single nucleotide polymorphisms were discovered among eight intergenic regions, constituting nine haplotypes. Analysis of the prevalence and distribution of the haplotypes across the native range will provide information on the population dynamics of *J. cinerea*. A decrease in haploype richness along the latitudinal gradient suggests recolonization through the founder effect, while a deviation from this distribution suggests alternative migration patterns.
Oviposition site selection is an important determinant of local species distribution. Where site selection incurs potential costs to offspring survival, oviposition choice can also influence population size. We examined the effect of water temperature on female egg-laying choice in the invasive mosquito vector, *Aedes japonicus japonicus*, which shows a tolerance for cold temperatures but is associated with a wide temperature range of aquatic habitats. Mosquitoes 7-8 d post-bloodmeal were exposed to concurrent water bodies of low, medium and high temperatures and allowed to select oviposition sites. Ovipositional activity was assessed over a 48 hr period to determine female site preference. To determine whether female oviposition preference along our thermal gradient coincides with optimal offspring fitness, or if maternal choice shows a mismatch to offspring fitness, eggs were then randomly re-distributed to among water temperature treatments and allowed to develop through adulthood. Thus, for a subset of eggs, we also tested if eggs reared in their natal treatment were preconditioned to natal temperatures. Results of our study contribute to our understanding of the spatial distribution of *Ae. japonicus* across multiple scales.
The World Health Organization estimates that one in three people worldwide are infected with *Mycobacterium tuberculosis*, the causative agent of Tuberculosis. As Tuberculosis becomes ever more prevalent, there is an increasing need for effective treatments against this global pathogen. Despite the fact that Tuberculosis is such a common disease, many of the mechanisms underlying infection are still not well understood. The ESX-1 secretion system is necessary for Tuberculosis infection and is conserved across many mycobacterial species. We have developed a new plate-based assay utilizing a knockout library to identify genes involved in ESX-1 secretion. This screen was performed in *Mycobacterium marinum*, a model system for *Mycobacterium tuberculosis* which contains the ESX-1 system. Using this screen, multiple genes of interest were identified. Our preliminary findings for one mutant *M. marinum* strain, 54E9, suggests that this strain exhibits novel properties when lysing red blood cells yet exhibits classical ESX-1 secretion for ESAT6/CFP10. In addition this strain demonstrates increased virulence. We are further determining the mechanism underlying these interesting phenotypes. We hope that further study will reveal more about 54E9 and other ESX-1 genes and thus help us to better understand the virulence pathways of tuberculosis.
Neimann Pick type C (NPC) disease is a rare lysosomal storage disorder caused by a mutation in either the NPC1 or NPC2 gene. The precise molecular and cellular players involved in lipid trafficking defects in NPC disease are still unknown. A loss in function of either the NPC1 or NPC2 proteins results in a harmful accumulation of lipids, including GM1 ganglioside and unesterified cholesterol in the early endosome/lysosome of NPC1-deficient cells. Previous studies have found that Salmonella typhimurium recruits host cholesterol to its Salmonella containing vacuole (SCV) in NPC cells. The objective of this study was to determine how other lipids, especially GM1, are sequestered and distributed in Salmonella infected wild type (WT) and NPC cells. NPC and WT cells were infected with Salmonella and an immunofluorescence assay was performed to observe the organization of GM1 in Salmonella infected and uninfected cells. The results show that GM1 is not concentrated to the SCV in NPC cells. This is a surprising finding since cholesterol does accumulate in the SCV and cholesterol and GM1 share the same trafficking route in cells. One possibility is that deficiency in NPC inhibits GM1 movement by Salmonella in NPC cells.
Zebrafish embryos form a pronephric kidney made of nephrons with two proximal and two distal segments, similar to mammals, and thus represent a powerful genetic system to study nephron segmentation. Previous studies have shown that Iroquois transcription factors (irx) genes, irx1a and irx3b, are expressed in zebrafish nephrons. We recently demonstrated that irx3b is essential for formation of one distal segment named the distal early (DE). However, the function of irx1a and its relationship to irx3b are unknown. Using whole-mount in situ hybridization, we found that irx1a transcripts were specifically localized to the DE segment after the onset of irx3b expression. This suggests that irx1a acts downstream of irx3b. To investigate the epistatic relationship between these factors, we knocked down irx3b by microinjecting an antisense morpholino into 1-cell stage wildtype zebrafish embryos. irx3b morphants failed to generate irx1a transcripts, demonstrating that irx3b activity is required for irx1a expression. Conversely, morpholino knockdown of irx1a had no effect on irx3b expression and did not disrupt nephron segmentation. Taken together, these data suggest irx1a may act downstream of irx3b. To further explore the functions of irx1a and irx3b, we performed a concomitant knockdown experiment. Embryos co-injected with both morpholinos resulted in a segment pattern identical to irx3b knockdown. Moreover, this knockdown resulted in a morphant distal tubule but wildtype proximal tubule, perhaps suggesting that other irx genes compensate for the loss of irx1a and irx3b in different parts of the pronephric kidney. To address this question, we conducted whole-mount in situ hybridization experiments for irx2a, irx4a and irx5b, and found transcripts for these genes in proximal and distal tubule segments. More research is necessary to elucidate the response of these genes to the loss of irx1a and irx3b. Studying these genetic programs holds significance for better understanding the conserved genetic pathways that direct nephron development, and thus may provide useful insights into congenital and acquired kidney diseases in humans.
The mosquito *Anopheles gambiae* is an important tropical disease vector that may use visual input for behavioral activities that underlie its role in disease transmission. *An. gambiae* possesses 10 opsins, photosensitive G proteins that initiate the phototransduction cascade, each of which are optimized for different wavelengths of light. Our lab previously characterized the opsins of *Aedes aegypti*, and the long-wavelength opsin1 was found to move in and out of the fused rhabdom in response to ambient light conditions. The movement of opsins into the rhabdom likely increases visual sensitivity in low-light conditions. We investigated whether a similar process occurs in *An. gambiae*. The localization and the level of the long-wavelength opsin Agop1 in *An. gambiae* at specific times was determined using whole mount, frozen section, and Western blot analyses with polyclonal antibodies generated against Agop1. Data obtained from the Mali strain of *An. gambiae* showed that Agop1 was found in the cytoplasm as well as in the rhabdomere one hour before dusk. This is unlike *Aedes aegypti* where all opsin1 is in the cytoplasm before dusk. In addition, the rate of movement of *An. gambiae* opsin1 out of the rhabdom and into the cytoplasm appeared to be slower than in *A. aegypti*. Opsin1 protein level in *An. gambiae* in a 24-hour period also seems to differ from that of *A. aegypti*. This difference in op1 trafficking and protein level possibly reflects the nocturnal behavior of *An. gambiae* and the diurnal crepuscular behavior of *A. aegypti*. 
Poster Presentation

**Analysis of TNFα receptor signaling within the regenerating zebrafish (Danio rerio) retina**

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Constant intense light induces photoreceptor apoptosis within the adult albino zebrafish (*Danio rerio*) retina. In response to this damage, Müller glial cells divide, giving rise to neuronal progenitor cells that transiently amplify and migrate to the outer nuclear layer where they differentiate into new photoreceptors. Recent work in the Hyde lab demonstrated that this regeneration process is initiated by Tumor Necrosis Factor Alpha (TNFα) signaling. Dying photoreceptors express TNFα as a trans-acting signal that is required for Müller glia to begin proliferating. It is likely that TNFα binds a transmembrane receptor on Müller glial cells and activates an intracellular pathway to initiate the regenerative cell division. However, there are 7 unique TNFα receptors (TNFRSF members) within the zebrafish genome and it is unknown what receptor(s) functions within this signaling pathway. I hypothesized that expression of the relevant TNFα receptor will increase as the TNFα signaling pathway is activated. To identify the TNFα receptor that initiates Müller glial cell division, gene specific RT-PCR and qRT-PCR were conducted using RNA isolated from both control retinas and light-damaged retinas. TNFRSFα mRNA expression levels were significantly higher in light-damaged retinal tissue relative to controls. Furthermore, immunohistochemical analysis indicated that TNFRSFα is expressed by Müller glia at the time when they begin dividing. This is consistent with preliminary data that TNFRSFα binds TNFα in the light-damaged retina. To confirm this spatial expression of TNFRSFα, I will immunolocalize TNFRSFα in the Tg(gfap:EGFP) transgenic line, which expresses EGFP in all Müller glia. If I confirm that TNFRSFα is expressed in the Müller glia, I will perform morpholino-mediated knockdown of TNFRSFα protein expression to determine if this receptor is required to initiate Müller glial cell division.
One of the serious problems related to poverty in third world countries is the prevalence of infectious diseases. Considering the fact that there are millions of deaths attributed to bacterial infections in third world countries, it is desperate that we invent cheap, but effective antibiotics that can be distributed throughout third world countries. Furthermore, the global spread of pathogens and the rapid rise of antibiotic resistance make the discovery of novel antibiotics an important concern. Cholera, which was caused by *Vibrio cholerae*, could be eradicated by distribution of clean water. Many organizations and companies attempted to increase distribution of clean water in third world countries by inventing new treatment systems that are cheap and can be easily distributed in poor countries. While Cholera is one of the diseases that are prevalent in third world countries and can be eradicated with proper distribution of clean water, there are many other diseases that are caused by bacteria and are difficult to get rid of. Peptide-based antibiotics have recently given light as an existing new avenue of antibiotic research. We screened several candidate antibiotics for activity against a major pathogen.
Conversion of wetlands, forests, and prairies to agricultural lands has been occurring in the midwestern United States since the 1800s. As a result of this conversion, many of the headwater streams in the region consist of channelized agricultural drainage ditches. These ditches were designed to improve drainage of agricultural plots by redirecting the flow from tile drains that underlie the fields and facilitate rapid drainage. Historic management practices in agricultural streams have emphasized water transport, maintained by costly dredging, more than the effects of altered hydrology on water quality and aquatic biota. This management emphasis combined with annual fertilizer application has resulted in high inorganic nutrient and sediment loads in these streams. One innovative management method that has been implemented to mitigate these disturbances is the two-stage ditch. Two-stage ditches employ lateral benches (miniature floodplains), constructed on each side of the stream, to increase water residence time during high-flow events. This strategy results in decreased water velocity enabling increased biological nutrient transformation rates and deposition of sediments. Therefore, two-stage ditches have the potential to increase biodiversity by improving water quality via reductions in nutrient and sediment export. To improve our understanding of concurrent effects on biodiversity in these systems, we compared the benthic macroinvertebrate assemblages of four streams located in northeastern Indiana having two-stage reaches, with their respective upstream reference reaches. All streams were characterized by warm summer water temperatures (mean ± SE = 20 ± 1.3°C), highly variable turbidity (56 ± 65.6 NTU), rapidly fluctuating discharge (76 ± 12 L/s), small sediments (49 ± 8.8% ≤ 2 mm), and high dissolved inorganic nutrient concentrations. Macroinvertebrate richness ranged from 18-31 taxa per study reach and was dominated by Physidae (30% of total), Caecidotea (23%), Chironomidae (11%), and Gammarus (7%). Taxa richness of macroinvertebrates (P = 0.75), Simpson’s D (P = 0.22), and Shannon’s H (P = 0.37) did not differ between reach types, suggesting that watershed effects of agriculture dominated reach-level mitigations in terms of macroinvertebrate diversity. Future research will compare results from macroinvertebrate assemblages to analyses of fish diversity.
Damaging the zebrafish (*Danio rerio*) retina with intense light causes photoreceptor cell death and subsequent regeneration of the rod and cone photoreceptor cells. In response to damage, Müller glial cells located in the inner nuclear layer (INL) divide asymmetrically to produce a population of neural progenitor cells (NPCs). NPCs eventually migrate to the outer nuclear layer (ONL) where they differentiate to replenish the lost photoreceptors. This study presents preliminary data of the spatial and temporal patterning of the Sox2 protein during the regeneration response. Sox2 is a transcription factor required for cells to maintain an undifferentiated state. Immunohistochemistry staining shows Sox2 is expressed in the INL amacrine cells and Müller glial cells of the undamaged retina. Qualitative real-time PCR (qRT-PCR) and immunohistochemistry show Sox2 expression is strongly up-regulated after 36 hours of light treatment, which corresponds to the time when Müller glial cells reenter the cell cycle. Between 51 and 68 hours of light treatment, Sox2 expression is enriched in early-stage NPCs, and then is down-regulated in late-stage NPCs between 68 and 96 hours of light treatment. These findings suggest Sox2 is important for the maintenance of undifferentiated Müller glial cells as they proliferate and serves as a marker for early-stage NPCs.
Parasitic infections are commonly assumed to have a negative effect on their hosts; however, to date we lack information on the effects of parasitic infections on wild animals. Gastrointestinal nematode parasites commonly infect wildlife and may cause anemia and decreased nutrient absorption, leading to poor body condition. I am currently testing the hypothesis that individuals with higher diversity and burden of gastrointestinal parasites have worse body condition than individuals infected with few parasites. Specifically, using standard parasitological techniques on fecal samples collected from yellow baboons (Papio cynocephalus) in Amboseli National Park, I am quantifying the type and number of parasites infecting individuals. I will then compare these data on parasite diversity and load with visual estimates of body condition data, collected by researchers of the Amboseli Baboon Research Project. I expect to find an inverse relationship between the number of parasite species and the body condition of the individual, as well as between the total number of parasites and body condition. The results of this study are important because confirmation of the presence of an inverse relationship between parasitic infection and host body condition will provide some of the first data on the physical costs of parasitic infections in wild primates. Additionally, results from this study would provide a solid foundation for future studies involving parasitic infections and host condition.
Targeted disruption of the Inhibitor of DNA binding 2 (Id2) gene results in a circadian clock and metabolic phenotype.

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Id genes comprise a family of four genes encoding rhythmically expressed HLH transcriptional inhibitors. Our earlier studies have focused on the role of Id2 in the circadian system, and data indicated that Id2 contributes to input pathways (photoentrainment), core clock function (interaction with the bHLH clock components CLOCK and BMAL1) and output pathways (regulation of liver clock controlled genes [CCGs]) (Duffield et al 2009 Curr Biol 19:297-304; Hou et al 2009 JBC 284:31735-45; Ward et al 2010 JBC 285:38987-39000). Furthermore, Id2--/ mice are lean with low white adipose tissue (WAT) density and lower lipid content in the liver, and have altered expression of liver genes associated with lipid metabolism (e.g. Ppargc1a/PGC-1a), including disruption of the normal phase of CCG rhythms (Hou et al 2009). Here we expand on our studies to explore the metabolic phenotype in the Id2--/ mouse, and its relationship to the circadian system. Id2--/ and WT littermate control mice were tested at ZT4-ZT6 for tolerances to intraperitoneal injected glucose and insulin. Male Id2--/ mice exhibited increased glucose tolerance and an enhanced response to insulin challenge. Mice were maintained on a 12:12 LD cycle and wheel running behavior, general activity and feeding activity were monitored. Whilst there was no difference found in the relative quantities of food consumed in the light versus the dark phase of the LD cycle, the Id2--/ mice exhibited a greater quantity of feeding activity during the late night phase (ZT21-ZT23). This shift in the feeding cycle may be related to the altered phases of metabolic CCGs in the liver we observed in earlier studies. Finally we examined the quantity of glucose uptake in vivo by PET-FDG imaging at ZT6-ZT9 and found that Id2--/ mice show higher levels of uptake in the interscapular brown adipose tissue (iBAT), suggesting a higher level of iBAT metabolic activity and thermogenesis. These results are consistent with ID2 contributing to the regulation of both glucose and lipid metabolism, the development of WAT and iBAT, as well as in the circadian control of metabolism.
Ongoing urbanization contributes to the fragmentation of natural habitats, creating remnant forest patches within an urban environment such as the University of Notre Dame (ND) campus. These woodlots need to be evaluated to identify areas with the most potential to preserve or restore biodiversity. In this study, we compared the tree biodiversity, soil characteristics, and abiotic factors of five woodlots on the ND campus to the managed area around Jordan Hall (JH) and the Warren Woods (WW), a mature beech-maple forest. The point-centered quarter method (PCQM) and the Shannon Index of biodiversity were employed to characterize tree density, dominance, and species diversity. Soil samples were analyzed for their physical and chemical properties (moisture content (%), organic carbon (%), pH, and nitrate and phosphate concentrations (mg/L)). To characterize the abiotic factors, light (mol m\(^{-2}\) s\(^{-1}\)), humidity (%), temperature (°F), and wind speed (m/s) were measured. Our results show that, for trees, there were significant differences in density, dominance, and species diversity between JH, WW, and the ND woodlots. WW exhibited the highest tree density, while the ND woodlots fell in between and JH had the lowest. There were also significant differences in soil pH and phosphate concentration between JH, WW, and the ND woodlots. Our results show that the sites constitute a continuum of ecological conditions reflecting human influence, ranging from the minimally impacted WW to the highly managed JH. Each ND woodlot can be placed along this continuum, identifying its potential for preserving or restoring biodiversity. From this classification, recommendations could be made to the University of Notre Dame as to which woodlots should be given the highest priority for protection. Future research will characterize additional factors, such as invertebrate biodiversity, to provide a more complete picture of the biodiversity of the ND woodlots.
A PCR-based assay to detect Culex quinquefasciatus eDNA in aquatic habitats

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*Culex quinquefasciatus* is an important vector of several human pathogens including West Nile virus (WNV) and *Wuchereria bancrofti*, a filarial worm causing the majority of lymphatic filariasis (LF). Because effective human vaccines for WNV and LF have not been developed, controlling mosquito populations remains an important factor in the prevention of these diseases. Here we describe a simple PCR assay to detect *Cx. quinquefasciatus* in aquatic habitats by amplifying a region of the mitochondrial genome from environmental DNA (eDNA). We predict that as the mosquito develops, a sufficient quantity of DNA is shed into the water to detect using PCR amplification. Primers specific to *Cx. pipiens/Cx. quinquefasciatus* were designed to amplify a 172 bp region in the mitochondrial gene, cytochrome oxidase subunit 1 (CO1). We tested the assay on three concentrations of larvae (100, 50, 10 larvae/liter) using mosquitoes reared in the laboratory. One liter of water was filtered to capture the eDNA. DNA was then extracted from the filter for PCR amplification. The assay was then tested on water collected from sites in Trinidad to assess its utility for detecting mosquitoes in the field. Detection of the target was observed in our laboratory samples suggesting that the eDNA protocol was effective. Further research will allow us to determine the threshold level of mosquito concentration needed for detection.
Aedes aegypti is the mosquito vector for dengue and yellow fever. The visual system of Ae. aegypti may play a significant role in behavioral aspects, including host seeking strategies. Visual transduction is initiated by G-protein coupled receptors (GPCR) known as rhodopsins embedded in a light sensitive organelle called the rhabdomere. Ae. aegypti has ten predicted rhodopsin genes, classified into five different groups based on sequence similarity: long-wavelength, short wavelength, UV-sensitive, a pteropsin, and Aaop10. Aaop3 is a long-wavelength opsin ($\lambda_{\text{max}} > 500$ nm) that had not been previously characterized.

Immunofluorescence was used to examine the expression patterns of Aaop3 in different light and dark conditions. An antibody recognizing an epitope on the N-terminus of Aaop3 was used to stain whole mounted retinas. Imaging of these retinas shows that the antibody detected Aaop3 in cytoplasmic vesicles in light conditions, but failed to detect Aaop3 in the dark samples. Previous data from the laboratory has shown that rhodopsins localize to the rhabdomere in dark conditions. Because the Aaop3 antibody cannot detect the epitope in dark samples, we propose that the N-terminus of Aaop3 is modified during the maturation process as it is transported to the rhabdomere.
Exosomes are 30-90nm vesicles involved in intercellular communication. They are formed through the fusion of the multivesicular body (MVB) with the plasma membrane and release of the intraluminal vesicles as exosomes. The MVB is a compartment formed by the invagination of the late endosomal membrane leading to the formation of these intraluminal vesicles (ILVs). Previous studies from our laboratory indicated that during a macrophage infection some mycobacterial components are trafficked to MVBs and released on exosomes. The first proteomic analysis of exosomes isolated from *Mycobacterium tuberculosis* H37Rv- infected macrophages identified forty-one mycobacterial proteins including antigens ESAT-6, Antigen 85 complex, GroES, MPT64, MPT63 among others. How these mycobacterial proteins are transported from the phagosome or endocytic vesicle to the MVB and onto the ILVs is presently unclear. To begin to answer this question recombinant Antigen 85b and GroES will be expressed in *E. coli* as a His-fusion protein and purified using a nickel column. Once purified, recombinant protein will be added to naïve macrophages and the exosomes isolated and examined for the Antigen 85b and GroES. To define the motifs required for trafficking to the MVB/exosomes, proteins will be altered via site directed mutagenesis and macrophages will be exposed to the mutated proteins. The exosomes released from these cells will be examined for the presence of mutated Antigen 85b and GroES. It is hypothesized that certain mutations will result in an inability of Antigen 85b and GroES to target to the exosome.
Using a cross-sectional design, a self-administered survey was administered to college students enrolled in selected general education courses at two public universities. The survey was administered to 2 cohorts of students, once during 2008 and once in 2010. The surveys generated a total of 811 female respondents (n=441 in 2008 and n=370 in 2010). The study focused on 380 unvaccinated females (n=259 in 2008 and n=121 in 2010) as they remain at risk of HPV related health outcomes. Respondents who reported no prior doses of the HPV vaccine were classified as “unvaccinated.” Descriptive and bivariate analyses were used to assess differences in selected health behaviors, perceived risk and knowledge of HPV between 2008 and 2010. The combined sample of unvaccinated females (n=380) was primarily white (70%) and ages 18-19 (63%). Alcohol, binge drinking, and sexual activity was relatively common in both years. In 2008 51% (n=131) and in 2010 53% (n=64) reported a prior pap smear and approximately 10% of this group had an abnormal pap smear. Most perceived their risk of HPV acquisition as low (75%). Knowledge about HPV related health condition, transmission, and prevention was variable and several HPV related questions demonstrated significant decreases in knowledge and awareness. Substantial gaps in knowledge exist including misperceptions about acquiring and passing HPV infection among college females not vaccinated against HPV. Perceived safety of the vaccine also demonstrated a significant decrease. These knowledge gaps may lend themselves to educational interventions designed to empower college females to complete the HPV vaccination series as a health promoting/risk reduction strategy.
Pseudomonas aeruginosa is a ubiquitous bacterium that is an opportunistic pathogen responsible for a wide variety of infections, such as those in skin burn wounds or the cystic fibrosis lung. Two fundamental processes involved in P. aeruginosa pathogenesis are the formation of structured multicellular communities called biofilms and the use of intercellular signaling known as quorum sensing. A link between biofilm formation and quorum sensing is the motility mode known as swarming, in which bacteria coordinate their movement as active quorum sensing groups prior to biofilm formation. This study sought to establish a surface growth model to describe the induction of quorum sensing and swarming motility. The model uses differing concentrations of agar to mimic hard and soft growth surfaces for P. aeruginosa colonization. It was found that during early stages of swarming, cells grown on hard and soft agar have highly similar population sizes, despite soft agar swarms covering a much greater surface area. Therefore, although the production of the P. aeruginosa surfactant, rhamnolipid, aids the spreading of cells into larger swarms on soft agar, it does not present a growth advantage until later stages of swarming. During later growth stages, a clear growth advantage is observed for these thinly spread soft agar swarms, and the population size is an order of magnitude greater than that of hard agar swarms. The focus of current research is to elucidate the underlying genetic factors responsible for the distinctive fractionated tendril patterns that develop on soft agar. Prior work in our group suggests that quorum sensing is inhibited upon hard agar surfaces, which prevents rhamnolipid production required for surface colonization. Our hypothesis is that an upstream regulator acts to suppress quorum sensing on hard surfaces, preventing activation of genes associated with rhamnolipid synthesis. As preliminary steps to identifying and characterizing this theoretical suppressor, a transposon mutagenesis and screen were performed to isolate mutants that acquired the ability to swarm on hard agar surfaces. Future work will involve cloning and characterizing the mutant genomic regions disrupted by transposon mutagenesis to reveal the genes responsible for suppression of quorum sensing on hard surfaces.
Poster Presentation

*Assessing seed banks at increasing soil depth: Effects on seed viability and implications for ecosystem recovery*

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Aquatic plant (i.e., macrophyte) populations are important to both the abiotic conditions and the communities of invertebrates, fish, and other organisms in freshwater systems. However, introduced species such as the rusty crayfish (*Orconectes rusticus*) can destroy these populations, effectively altering the ecosystems. One method for restoring macrophytes utilizes the natural seed banks, which can regenerate the plant community following a disturbance. The object of this study was to determine if the seed banks in northern oligotrophic lakes would be adequate to support macrophyte regeneration following invasion. I hypothesized that viable seeds are present at increased depths, but that species richness declines with depth. I collected soil samples from four sites in Tenderfoot Lake and separated them into three depth strata: 0-5 cm, 5-10 cm, and 10-15 cm. I tested for seed viability using tetrazolium assays, a chemical method that detects the presence of active tissue in excised seed embryos. The results showed that viable seeds are present in deeper substrates, but the percent viability significantly decreased with substrate depth (p < 0.001). Species richness was found to peak at the intermediate soil depth. This was likely due to seed accumulation, as this was also the depth with the most seeds present. Within the seed bank many common species were underrepresented. The only well-represented species were bull rushes, which are high in toughness and low in nutrition. This makes them a poor food source, so they are not usually affected by invasive crayfish. Species documented as susceptible to pressure from invasive species did not show high abundance in the seed bank. Thus, it is unlikely that the seed bank would be able to restore a macrophyte community that accurately represents the historic composition of the lake. However, the presence of viable seeds at greater depths means that in places with a more vibrant seed bank there is potential for use in ecosystem restoration.
**Role of Adiponectin in Clearance of Immune Complexes and Apoptotic Cells**

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C1q, a defense collagen, is known to enhance phagocytosis in two distinct ways. The first is via the “mer pathway”, an indirect clearance method in which C1q acts to upregulate Mer and Gas6, enhancing their ability to phagocytose apoptotic cells. The second is via the “antibody pathway”, in which C1q acts to activate phagocytes, which leads to the direct clearance of immune complexes. While the existence and implications of these pathways are well-known, the specific mechanisms by which they act are unclear and have proven difficult to target.

Adiponectin, a structurally similar defense collagen to C1q, has been well characterized for its involvement in metabolic pathways. However its function in the immune system is unknown. Based on its structural similarity to C1q, as well as its known ability to clear apoptotic cells, we hypothesize that adiponectin may also regulate one or both of the phagocytosis pathways. To determine if adiponectin regulates the “antibody pathway,” bone marrow derived macrophages (BMDM) will be activated with a control protein, C1q, or adiponectin and phagocytosis of antibody opsonized erythrocytes will be measured by microscopy. Gas6 is a Mer ligand that is synthesized in response to C1q. A Gas6 ELISA will be performed to determine if adiponectin, similar to C1q, regulates gene expression required for clearance of apoptotic cells. Additionally, we will perform a Western blot to assess Mer expression following treatment with C1q or adiponectin. The determination of adiponectin’s involvement in the Antibody and Mer pathways could identify adiponectin as a tool to better understand the mechanisms of the pathways. Unlike C1q, many of adiponectin’s receptors have already been characterized. This may enable the discovery of target receptors for C1q and therein a better understanding of autoimmune inflammatory diseases such as Lupus, opening up the possibility of cures and more effective treatments.
Wolbachia is a genus of bacteria that is estimated to infect 50-60% of all arthropods and can change the reproductive systems of its victims, which can lead to male killing and feminization. While this endosymbiotic bacterium is believed to infect most species of insects, few cases have been reported for Papilionids, a large family of butterflies that consists of roughly 550 species. Here I screened two species from the Papilionidae family (swallowtail butterflies), *Papilio glaucus* and *Papilio canadensis* for infection of *Wolbachia*. Both historic samples, caught approximately thirty years ago, and recently caught samples, caught within the last three years were selected from a state-wide latitudinal transect that dissected the center of Wisconsin. The abdomen tip of each butterfly was tissualyzed and extracted, followed by a PCR in which a 16S, hcpA and a *Wolbachia*-specific primer were used on each sample. Each sample was then sequenced and compared to known sequences related to *Wolbachia*. I found that while some samples were infected with a bacterium, none appeared to be *Wolbachia*. This may be due to lack of infection with *Wolbachia*, or it may be due to divergence in the target site – primers are not adequate for this strain and lead to a false negative for infection. Given the prevalence of this bacterium in arthropods, whatever the reason for a lack of infection the result is interesting. If these species are truly not infected with *Wolbachia*, it raises the interesting question; what is it about these species that keep them from becoming infected? Future studies will include attempting to identify what type of bacteria is present in the species if it is not *Wolbachia*. 
Interspecific competition plays a key role in determining the composition of bacterial communities in their respective niches. Plants have been shown to specifically recruit plant growth-promoting bacteria to occupy the niche of their root systems. We hypothesize that growth-promoting bacteria may also be transmitted through the seed and that these bacteria confer immunity from plant pathogens by secreting bacteriocins, which are ribosomally-produced antimicrobial peptides that target specific bacterial competitors. Here, we examine mung bean (\textit{Vigna radiata} (L.) R. Wilczek) (common bean sprout) seeds for the presence of internalized bacteria and investigate the antibiotic properties of these bacteria. Mung bean sprout seeds were surface-sterilized, and the bacteria present in ground plant material were cultured in the laboratory. Both gram-positive and gram-negative organisms (none of which were rhizobacteria) were isolated and identified to family or order through 16S rDNA sequencing. Antagonistic relationships between these isolated organisms and selected pathogens were tested by toxicity assay and co-culture with known pathogens. In addition, this project involves whole-genome sequencing with Illumina MiSeq, which serves both to more specifically identify the isolated organisms and also to reveal putative bacteriocin (peptide antibiotic)-encoding genes. In light of the recent \textit{E. coli} outbreak in bean sprouts in Germany, this work may serve to identify naturally-produced antibiotics that inhibit the growth of plant pathogens and human pathogens, as well as a novel mechanism for the transmission of protective microorganisms.
Influenza has a long history of seasonal epidemics and causes between 250,000 and 500,000 deaths globally each year (WHO 2003). Although mortality due to influenza is not as prevalent in the First World as in less developed nations, morbidity and consequent loss of productivity are still of great concern. Through better understanding the spread of influenza, better responses can be implemented to address these concerns and minimize lost productivity. One response already being implemented is an annual vaccine administered prior to the influenza season, which peaks in mid-late winter. This study looks at influenza within several subpopulations of the University of Notre Dame through the development and subsequent calibration of an SVEIR model using data from a variety of sources, including publicly available data, data provided by the Notre Dame Health Center, and governmental disease-monitoring programs already in place. The population of the University was divided into three subpopulations (students, faculty, and staff) and the impact of influenza was evaluated in terms of lost productivity to each of the three groups. The stability of the model was analyzed and the efficiencies of different interventions were evaluated, including that of the annual vaccine campaign on campus. This study specifically assesses the prevalence and spread of influenza within the Notre Dame community and how these affect productivity therein. The model produced can help to inform decisions on vaccination strategies and other attempts to minimize lost productivity in the future.
Predicting Antimalarial Mode of Action from Gene Expression Signatures

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Malaria is a mosquito-borne infectious disease caused by a parasite of the genus *Plasmodium* that is responsible for approximately one million deaths each year, affecting mostly young children and pregnant women. The mechanisms of action of antimalarial drugs are largely unknown. Here, we test the idea that exposure of parasites to drugs results in gene expression changes in several genes, leaving behind a unique signature that reflects the drug mechanism of action. Comparing the gene expression profile of drugs targeting a specific pathway with those of other pathways may define relationships between the drugs. This signature of gene expression would be unique to drugs targeting a given pathway of the parasite. To test this idea, we exposed malaria parasite cultures to drugs that target different pathways and measured gene expression levels using microarrays. For each pair of drugs, we computed the correlations between the gene expression levels of parasite cultures obtained after perturbations by the drugs for a period of 2 hours. Consistent with our hypothesis, we found that drugs targeting the same metabolic pathways do confer similar changes on gene expression. We also applied a network view of the pairwise relationships between the effects of the drug on gene expression and uncovered complex effects of some drugs. For instance, the network approach confirmed that the anti-cancer drug methotrexate has effects on both the folate and DNA damage repair pathways. In addition, the approach predicted a novel and an unexpected relationship between chloroquine and 5-Fluorouracil. We are currently extending this idea using more drugs targeting distinct pathways to develop a system that could aid the discovery of the mechanism of action of current and future anti-malarials.
A Hierarchy of Health: Dominance Rank and Parasite Load in Wild Male Baboons

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Previous research suggests that differences in social status can influence individual health. For instance, several studies have found correlations between social status and measures of health such as parasite load, body condition, and immune response. Male savannah baboons are no exception; in male baboons, *Papio cynocephalus*, an individual’s position in the social hierarchy has an effect on his reproductive success, stress level, and access to resources, and any or all of these factors may affect parasitism and immune function. For instance, low-ranking males are often older with high levels of social stress and reduced access to the best resources; these males may be more susceptible to parasite infection. On the other hand, high-ranking males have higher measures of immune-suppressing testosterone, but also have generally lower stress levels and greater access to high-quality resources, which may lead these males to have lighter parasite loads. The alpha male is perhaps the exception – he experiences high levels of energetic stress associated with maintaining dominance and as a result might be expected to have a heavier parasite load than other high-ranking males. I am currently testing these hypotheses using data on social status and parasite loads in wild, male baboons living in Amboseli National Park, Kenya. The results of this study will provide further insight into the health-related costs and benefits of social dominance for individuals living in complex hierarchical societal structures and could present more comprehensive information about individual disease risk.
The health-survival paradox describes a robust pattern whereby women experience greater longevity but higher rates of illness throughout their lives than men. To date, we do not understand the evolutionary origins of the health-survival paradox, or whether there is evidence for this paradox in non-human primates, such as baboons. Specifically, while we know that female baboons typically live longer than males, we do not yet know whether males or females exhibit greater rates of disease or parasitism as they age. To test whether the health-survival paradox occurs in baboons, I am currently testing the prediction that female baboons bear higher parasite loads than males throughout old age. This is done through standard float and sedimentation procedures performed on fecal samples collected from known-age wild baboons studied by the Amboseli Baboon Research Project (ABRP), near Amboseli National Park, Kenya. I will use these samples to quantify parasite load and burden in individuals, and to calculate age and sex-specific rates of parasite diversity and burdens. If my prediction is supported, I should find higher parasite loads and burdens in females, as compared to same-aged males. On the other hand, if baboons are like many other mammals, my results may show that males have higher parasite diversity and burdens than females. If the health-survival paradox is found to occur in wild primates, such as baboons, it could lead to two important insights. First, this could provide important insight into the understanding of the evolutionary origins of this paradox. Second, because the health-survival paradox plays an important role in determining differences in health and longevity in humans, baboons could serve as a useful model for human disease, parasite infection and aging.
Utilizing ecological niche modeling to analyze local climatic adaptation within the endangered Karner blue butterfly species

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The Karner blue Butterfly (*Lycaedides melissa samuelis*) is a federally listed endangered species whose historic range once spread from Maine to Minnesota, but has since been extirpated from many of these locations. The current Karner blue range has been constricted to include only fragmented, extant populations in Wisconsin, Minnesota, Michigan, New York, and Indiana. The goal of this study is to utilize a population-specific approach to ecological niche modeling to assess the potential of local adaptation within Karner blue and to determine if modeling algorithms are limited by small, fragmented populations. We used climate envelope modeling software MaxEnt, a machine learning algorithm that uses presence only point location data to describe the current occupancy of a species, to construct predictive maps of future geographic distribution. A range-wide dataset of Karner blue presence points was collated from state Department of Natural Resources records, for a total of 898 presence points. Environmental layers used in modeling included BIOCLIM variables (biologically informative surrogates derived from climate data) from the Canadian Centre for Climate Modeling and Analysis (CCCMA) A2 current and 2080 layers, Advanced Very High Resolution Radiometer (AVHRR) land cover, Moderate Resolution Imaging Spectroradiometer (MODIS) vegetation continuous fields, and IPCC Major Soil Classifications. In 2080, MaxEnt predicts an almost complete displacement from the current range with a strong northward range shift. Population-specific models differ in both predicted geographic extent as well as variables of highest percent contribution in future habitat suitability. Range wide response curves showed multiple peaks in climatic variables that are population-specific. The MaxEnt model was further optimized by addressing environmental layer autocorrelation through Random Forest analysis and Principle Components Analysis. Cluster analyses will be used to quantify the most accurate categorization of occurrence points into distinct populations. Results to date suggest that ecological niche range-wide outputs for fragmented ranges should be analyzed with caution and could inform management efforts on population-specific strategies.
This study uses county maps of Ohio forests tree species composition at the time of European settlement (1800-1820) to reconstruct the forests of the region at a time of minimal human land management and examine the factors influencing the shift to present day forest species. Ohio is an interesting region because the area is situated at a critical geographic transition from western prairie to hardwood forest in the East that can experience significant tree species shifts as a result of the advancement or recession of the prairie-forest boundary. This study uses Public Land Survey witness tree records to produce a reconstruction of Ohio vegetation that can then be compared with current USDA Forest Service records to determine how forests have changed since European settlement and the extensive land management that accompanied settlement. Only one percent of pre-settlement forest still remains in Ohio, which has allowed for substantial recolonization by completely different species. Because of extensive land clearance and drainage for agricultural use and fire suppression, it is expected that patches of the prairie peninsula extending eastward from the Great Plains have been replaced by closed forest. Removal of large areas of swampland in Northwestern Ohio also provides the opportunity to examine how the human driven ecosystem shift influences vegetation.
The *Drosophila* gene *tinman* (*tin*) encodes a transcription factor essential for the specification of the dorsal mesoderm as well as for the diversification of differentiated cardiac cells. The vertebrate homologs of *tin*, Nkx2-3 and Nkx2-5, are likewise necessary for heart development. This homeobox gene binds to consensus sequences in the cardiogenic mesoderm, thereby allowing these cells to respond to cardiac induction signals. Complete loss of *tin* function in *Drosophila* leads to the absence of all structures derived from the dorsal mesoderm, e.g., the dorsal vessel, visceral muscles, and dorsal body wall muscles. Using the allele, we conducted a sensitized screen of second chromosome deficiencies to discover genes that may interact with *tin*. Such an interaction may suggest that these genes have novel roles in cardiogenesis.

Through fluorescence microscopy, stage 16 *Drosophila* embryos were screened for phenotypes showing enhancement of the mutant phenotype. Our screen reveals that the deficiency region Df(2R)ED2457 contains two genes with potential epistatic relationships to *tin*: CG8370 and CG30095. Cardioblast hyperplasia was most frequently observed in CG8370 mutants, and both a patent heart region and cardioblast hyperplasia were most commonly observed in CG30095 mutants. While CG8370 has no known molecular function, sequence analysis indicates that CG30095 may possess oxidoreductase activity. Although the mutant phenotypes were weak, characterization of these genes would include determination of expression patterns, analysis of promoter sequences, and phenotypic examination of mutant alleles across several stages of *Drosophila* development.
Niemann-Pick Type C (NPC) is a genetically inherited, fatal neurodegenerative disorder. 95% of NPC cases are caused by a defect in the NPC1 protein while 5% of the cases are caused by a defect in the NPC2 protein. The disease is characterized by widespread intracellular accumulation of unesterified cholesterol and other lipids. While Miglustat is being used in some countries, there is currently no FDA approved treatment in the U.S. Hydroxypropyl-β-cyclodextrin (HPβCD) has been undergoing several tests in mammalian models, such as the Balb/cnih NPC / NPC1 knock-out mice, in which the NPC1 protein is truncated. In order to further characterize the disease progression of NPC as well as the effects of HPβCD, sets of Balb/cnih NPC / and NPC+/- mice were treated with 0.4mg/kg HPβCD in 0.9% saline while matching sets of NPC-/- and NPC+/- mice were treated with 0.9% saline to serve as controls. Injections were given three times a week beginning from 25 days old. The organs were harvested at about 35, 42 and 78 days old. Immunohistochemistry with calbindin was used to identify Purkinje cells in the brains. Quantification of these purkinje cells demonstrated that asymptomatic NPC mice had Purkinje cell counts equal to that of heterozygotes. However, NPC mice clearly have Purkinje cell degradation with disease progression and cyclodextrin treatment in mice does not seem to have an effect on Purkinje cell death.
Determination of synergism or antagonism between common antimalarial drugs and non-antimalarial drugs using HB3 and Dd2 strains of Plasmodium falciparum

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Several non-antimalarial drugs for common human disease exert antimalarial activity, by themselves and in combination with other antimalarial drugs. This study was conducted in two steps: first, individual IC50 values of eight non-antimalarial drugs including ivermectin (anti-worm), indinavir (antiretroviral), rifampin (anti-tuberculosis), tetracycline (antibiotic), fluconazole (antifungal), levofloxacin (anti-tuberculosis), sulphaemethoxazole (antibiotic), and streptomycin (antibiotic) and two antimalarial drugs, chloroquine and artemisinin, were determined against HB3 and Dd2 strains of Plasmodium falciparum. Ivermectin, indinavir, rifampin, and tetracycline were selected for further isobologram analysis in combination with chloroquine and artemisinin. Among initially planned eight combinations, four of them were completed to be tested. Rifampin behaved slightly antagonistically with chloroquine in both parasite strains. The combination of ivermectin with chloroquine showed antagonistic relationship in both parasites. Ivermectin in combination with artemisinin showed additive relationship in HB3 but slight antagonism in Dd2. Tetracycline and chloroquine combination behaved additively in both parasites.
An estimated 73,510 new cases of bladder cancer will be diagnosed in 2012 in the United States, in addition to the 14,880 deaths. Despite these figures, treatment for bladder carcinoma remains relatively untouched and expensive. Deregulation of microRNAs (miRNAs) has been a reported hallmark of several cancers, including bladder cancer. A systems biology approach was implemented to study gene modulation and cell signaling pathways by the EGFR inhibitor gefitinib in bladder tumors in rat models. A series of MTS proliferation assays were completed on the UMUC-5 bladder carcinoma cell line, which confirmed its sensitivity to gefitinib. RT-qPCR confirmed that increased expression of the miRNA let-7c decreases the proliferation of gefitinib-treated bladder carcinoma cells. This tissue culture work was collaborative research as a working model for “prevention drug trials” (Yan et al. 2012).
Poster Presentation

Viability of Self Fertilization in Schoenoplectus americanus

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In the marsh sedge Schoenoplectus americanus, evolution over the last one hundred years is clearly visible in samples germinated from seeds found deep in marsh cores. Though S. americanus is also able to grow clonally, sexual reproduction and the resulting seeds are the true fuel for evolutionary change. Understanding the mechanisms of this reproduction is key for understanding its past evolution and future evolutionary potential. Thus, this study examined whether S. americanus could viably self-fertilize. Inflorescences were isolated and hand pollinated, and the pollen and seeds of each were collected. The seeds were tested for viability by germination and tetrazoleum assay. It was found that there is no difference in the ability to produce seeds from self versus cross-fertilization using a binomial test with a p value of 1.0. With this information, it is now possible to study the variation and heritability of the range of phenotypic traits observed, and assess the potential for further evolution in Schoenoplectus americanus.
Researchers can choose from any of several programs for de novo assembly of genomes using second-generation sequencing data, such as SOAPdenovo, Velvet, and ALLPATHS-LG. These programs assemble the genome by constructing, simplifying, and walking a graph of read sequences; however, because assemblers can differ substantially in implementation and function, it is frequently the case that one assembly program or one set of assembly parameters can correctly assemble a difficult region of the genome, whereas others cannot.

To exploit this fact, here we present a method we call metassembly, which combines multiple assemblies to produce a single draft genome that is superior to all its contributing assemblies. Our implementation of this technique is available as a Python package called Metassembler. Metassembler employs Nucmer to align assemblies to each other and detect gaps between contigs in one assembly, which can be closed by “patching” sequence from the other assembly into the gap. Metassembler can also detect and correct localized misassemblies using assembly forensics signatures to decide which assembly is correct.

Metassembler was employed as part of our submission to the Assemblathon 2 competition, which challenged researchers from across the world to use the same set of sequence data to create the best possible de novo assemblies of three vertebrates: a fish, a bird, and a snake. Our preliminary results show that Metassembler substantially improves the quality, contiguity, and accuracy of the genomes under consideration. While a variation of this technique was previously used to improve several fly genomes, we believe this work represents the first use of this technique both for vertebrate-sized genomes and for assemblies created from short-read sequencing. By enabling researchers to perform metassembly in a straightforward and efficient fashion, we hope to improve the overall quality of assemblies produced by researchers across the world.

Presently, we are working to apply Metassembler to the parrot data sets from the Assemblathon 2 competition. We are also in the process of using Metassembler to improve assembly of the *Anopheles gambiae* mosquito genome.

More information about the Metassembler package and method is available online at [http://metassembler.sf.net](http://metassembler.sf.net)
Crohn’s Disease and Ulcerative Colitis are two types of immune mediated inflammatory diseases of the gastrointestinal (GI) tract collectively called Inflammatory Bowel Diseases (IBD’s). Dysfunctional immune response due to a combination of environmental and genetic factors leads to development of IBD. Critical for maintaining proper regulation of the mucosal adaptive immune system is antigen presentation, where cells of the GI tract display antigen, in the context of Major Histocompatibility Complex (MHC), to a subset of immune cells called T cells. Our lab is interested in understanding the biochemistry of antigen presentation in the GI tract. Antigen Presenting Cells (APC’s) present peptide-MHC as either native protein processed into a deep endosomal compartment, type-A conformer, or as degraded protein exogenously exchanged at the APC surface, type-B conformer. Each conformer activates distinct T cells. The pathologic consequence of type-B presentation may be that a distinct subset of the T cell repertoire, type-B reactive T cells, may potentiate disease. Therefore, we aimed to examine if type-A and type-B conformers are presented in a normal and colitis setting. We hypothesized that antigen presentation during colitis leads to presentation of the type-B conformer. To test this hypothesis, IL-2 cytokine was detected via ELISA following stimulation of T cell hybridomas with APCs presenting Hen Egg Lysozyme (HEL) 48-61 peptide bound to I-Ak MHC (IAk-HEL48-61) as a self-antigen. 3A9 hybridomas recognize both type-A and type-B conformer, 11A10 hybridomas only recognize type-B conformer and C3F6 hybridoma was a negative control. APC’s were derived from the Spleen, Mesenteric Lymph Node, and Peyer’s Patch of healthy and colitic mice. Colitis was induced by treating with 3% DSS in drinking water of the mice for 7 days. Results indicate significant differences in IL-2 production by T cells specific for type-A versus type-B conformer. These results suggest that antigen presentation is limited to the biochemically distinct type-A conformer in both healthy and colitic animals. Future work will be directed toward antigen presentation exogenous orally derived antigen in healthy and colitic animals.
Parasite-host interactions are important ecological drivers and have important implications on host behavior. However, little research has examined the effect of parasitic manipulation within the context of invasion biology. Certain parasites are capable of manipulating host behavior to increase the chance of transmission to the next host by increasing risk to predation, further propagating the parasite life cycle. A new trematode parasite, *Microphallus* sp., has been found in Northern Wisconsin and Michigan lakes, and is prevalent in the three dominant crayfish species (*Orconectes rusticus*, *Orconectes propinquus*, and *Orconectes virilis*), which are intermediate hosts for the parasite. Previous research has shown that *Microphallus* sp. infection can alter the competitive ability of the host. Therefore, we examined the effect of *Microphallus* sp. in different crayfish species to determine if parasite infection alters risk taking behavior in the presence of a predator. We were also interested in determining the factors that drive infection levels in natural environments. Infected and uninfected crayfish from all three species were collected from the field, as well as substrate cores to determine the relationship between abundance of the first intermediate host, a snail, and infection levels. Infected and uninfected specimens were offered a worm resource and a shelter, and the time to food acquisition was recorded. Trials included the presence and absence of a small mouth bass predator. We found that *Microphallus* sp. infection does not alter risk taking behavior in the presence of a predator. Infected and uninfected crayfish obtained food at the same rate when predators were absent. We also found that infected and uninfected *Orconectes rusticus* were significantly slower to obtain food in the presence of a predator. Concurrent studies show that *Microphallus* sp. infection reduces shelter use and competitive abilities in some species but not in others. Therefore, these results suggest that *Microphallus* sp. parasitic manipulation may be behavior-specific, where the direct manipulation of risky behavior is not altered but indirect effects of competitive abilities may increase parasite propagation. Further research on how *Microphallus* sp. alters crayfish behavior is needed to understand how this parasite may influence the success of invasive rusty crayfish.
Oral Presentation II

*Spider web DNA: a novel source of noninvasive and environmental genetic material*

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Biological Sciences and Chinese  
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Genetic analysis is now a common method for studying populations of wild organisms and the ecosystems they are a part of. Noninvasive genetic sampling – collection of naturally shed material such as hair or feces to obtain DNA from one species – has become increasingly important, especially for rare organisms such as invasive or endangered species. Environmental genetic sampling – collection of bulk environmental material such as soil or water to obtain DNA from many species – is increasingly used to describe species richness of an ecosystem. Here, we report a novel source of both noninvasive and environmental genetic material: spider webs. Using species-specific polymerase chain reaction (PCR) we successfully amplified and sequenced mitochondrial cytochrome oxidase I (COI) DNA of western black widow (Lactrodectus hesperus) from web obtained from the black widow exhibit at the Potawatomi Zoo. Additionally, DNA fragments of COI from spider prey (Rhagoletis pomonella) were successfully detected from the web of yellow-sac spider (Cheriacanthium inclusum) using a universal invertebrate PCR assay. These results demonstrate the utility of spider web as a source of DNA from both the spider (noninvasive genetics) and the local insect community (environmental genetics). Because spider webs are easily collected, composed of adhesive silk, and last a relatively long time in the environment, they are an excellent source of noninvasive and environmental genetic material. Spider web noninvasive genetics has immediate use for identification of pest and endangered species of spiders. Spider web environmental genetics has immediate use for insect biodiversity assessment, particularly of flying insects. Our future work will apply next-generation sequencing to spider web DNA to yield a more comprehensive genetic snapshot of local biodiversity. Quantification of genetic material may also lead to a rough estimate of the relative abundance of different insects.
ABSTRACTS – CHEMISTRY AND BIOCHEMISTRY
Oral Presentation

*Synthesis and Characterization of Molybdenum Complexes of 2,2’-bis(2-hydroxyphenylamino)biphenyl for Use in Nonclassical Oxygenation Reactions*

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Advisor: Seth Brown, Dept. of Chemistry and Biochemistry

The use of catalysts to mediate the transfer of electrons from fuel sources is of great interest. Bis(aminophenolate) ligands have been shown to be capable of one-electron transfers generating metal complexes of organic radicals. We have explored the chemistry of molybdenum with 4,4’-bis(tert-butyl)-2,2’-bis(3,5-di-tert-butyl-2-hydroxyphenylamino)biphenyl (tBuClipH4) with the hope that the oxo groups bound to molybdenum would be able to mediate the two-electron transfer between a fuel source and the electron-depleted organic ligand, resulting in the restoration of the catalyst.

MoO2(acac)2 reacts with tBuClipH4 to form a C2-symmetric cis-dioxo complex (tBuClipH2)MoO2 retaining the NH protons of the ligand. This compound reacts with Lewis bases such as pyridine and 3,5-lutidine with loss of water to form a mono-oxo molybdenum complex (tBuClip)Mo(O)(L); x-ray crystallography of the lutidine adduct indicates that the compound has a cis-β structure. Dynamic NMR data suggests that ligand exchange occurs via a dissociative mechanism ($\Delta H^\ddagger = 21.4 \pm 0.7$ kcal/mol, $\Delta S^\ddagger = 18 \pm 2$ cal/mol•K for pyridine exchange) but without symmetrization of the tBuClip ligand environment. Cyclic voltammetry of the pyridine adduct reveals redox activity in the range studied.

Attempts have been made to isolate the molybdenum complex of the doubly oxidized ligand, (tBuClip2-)MoO2 by reaction of (tBuClipH2)MoO2 with N-methylmorpholine-N-oxide (NMO). This is an unusual example of nonclassical oxygen atom transfer, where the oxygen atom is transferred from NMO to the metal but the oxidizing equivalents are transferred to the ligand. NMR spectroscopy suggests that (tBuClip2-)MoO2 does form at room temperature, but is quickly oxidized to produce MoO3 and the fully oxidized biphenyl bridged bis(iminoquinone). Dilution of the reaction reduces the degree of overoxidation and permits in situ formation of (tBuClip2-)MoO2. This compound reacts with dimethylphenylphosphine to form the phosphine oxide and a molybdenum oxo complex of the reduced ligand, supporting the formulation of the compound and closing a two-way cycle of non-classical oxygen atom transfer. UV-Vis spectroscopy experiments of (tBuClip2-)MoO2 formation and degradation provide insights into the mechanism by which these oxidations occur, and therefore, will continue to be the focus of future research.
A previously unused synthetic route for the production of monobactams is described. The utility of this synthesis is the ability to form monobactams starting from simple amino acids while maintaining flexibility for the placement of alternative substituent groups on various parts of the molecule. Central to this synthesis is the use of the FMOC protecting group. Previously, this kind of synthesis has been limited to the t-Boc protecting group (which is removed under acidic conditions) or the Cbz protecting group (which is removed using hydrogenolysis). Since the FMOC group is removed under mildly basic conditions, it allows for greater flexibility within the other parts of the molecule. The key step in the synthesis is the intra-molecular cyclization reaction using Mitsunobu conditions. The target molecule is an oxamazin – a monocyclic β-lactam with an N-O bond coming out of the ring – that is substituted at the 3 position.
Oral Presentation

_BTZ Scaffold Simplification: Stopping Mycobacterium tuberculosis dead in its Tracks_

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Tuberculosis affects \( \frac{1}{3} \) of the world’s population; in 2009 alone, the World Health Organization reported 9.4 million new cases of tuberculosis. Of these new cases, 1.1 million people were also HIV positive. Current medication proves inadequate for the treatment of this coinfection. The drug–drug interactions lead to sub-therapeutic concentrations of antiretrovirals necessary for HIV treatment. Benzothiazinones, a class of compounds with a novel mechanism of action, have been shown to be potent and specific to _Mycobacterium tuberculosis_ with an MIC 20-fold lower than Isoniazid. The structure of BTZ043 is depicted in Figure 1. The increased potency of this compound would allow for a reduced treatment period, helping to prevent the development of resistance. Through the simplification of this scaffold, the components necessary for potency can be determined. Starting from aldehyde sharing many structural similarities to BTZ043 as seen in Figure 1, many pathways were attempted for the addition of the BTZ tail, thought to be required for recognition. In the first pathway the BTZ tail could be coupled to the structure following the oxidation of the aldehyde to the carboxylic acid. Both Jones Oxidation and the Pinnick Oxidation were attempted, but the carboxylic acid failed to be synthesized in either case. Next, oximes were formed through the addition of a hydroxylamine. This synthesis proceeded in high yields with easily isolatable products. These products were then dehydrated to form the nitrile, which is at the same oxidation state as the carboxylic acid. Various mechanisms were attempted for the dehydration, but none were successful. Each of these simple oximes created were characterized and tested against a broad panel of bacteria. The benzyl analogue showed significant potency against _Mycobacterium vaccae_. More analogues were synthesized for testing based on these results.
Administration of water soluble drugs encapsulated within the interior of liposomes has been shown to increase drug efficacy and reduce toxic side effects relative to conventional drug administration. Current FDA approved liposome based drug delivery systems rely on passive leakage which make it difficult to deliver the correct dosage of drug. To improve delivery efficiency, triggered release liposome systems have been developed to deliver contents upon exposure to external stimuli including temperature, pH, light, and ultrasound. Reported herein is the development of a novel chemically triggered release system. Triggered release experiments demonstrate rapid leakage of tracer molecules (carboxyfluorescein, glucose) from a liposome system upon treatment with a non-toxic chemical trigger under physiologically relevant conditions. The chemical trigger is a Zn(II)-dipicolylamine coordination complex and mechanistic studies indicate that leakage is induced by association of the trigger with a phosphatidylserine target molecule that is in the liposome membrane.
Hepatitis C Virus exists as a positive sense single stranded RNA virus. These viruses are extremely variable along their genome, and therefore exist within patients as numerous genotypes. By targeting conserved regions of the HCV Internal Ribosome Entry Site (IRES) with a trans-splicing Group I Intron containing an apoptotic factor as the 3’ exon (modified BID, Procasparase 3, or Procasparase 8), a reconstructed IRES can stimulate translation of these modified proteins. After these proteins are translated, their modified cleavage sites will be cleaved by the HCV encoded NS3/4a serine protease, insuring activation of an apoptotic cascade which terminates viral replication within the cell. Several anti-viral group I intron constructs were designed and constructed targeting a variety of target sites within the HCV IRES sequence to determine the best ones to use for efficient cleavage and splicing-specific expression of the pro-apoptotic protein. Of these, many were determined to provide efficient activation of the intron-derived gene product following splicing. Splice product was confirmed by RT-PCR in transient expression assays in transfected Huh 7.5 cells. This intron, coupled with the several pro-apoptotic genes, will be used to generate cells that are incapable of supporting productive infection by HCV.
Oral Presentation

The Effect of Conus Parius on NMDA-Stimulated Intracellular Calcium Influx and Downstream CREB Phosphorylation

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The N-methyl-D-aspartate receptor (NMDAR) is a voltage-dependent glutamate receptor that is permeable to Ca\(^{2+}\) ions. Activation of these receptors can elicit cellular responses and modify neuronal function. In neuropathologies, such as ischemic stroke and Alzheimer’s disease, excessive receptor activation causes excitotoxicity and cell neuronal death; hence the development of NMDAR antagonists has gained much interest in recent years. Marine cone snails, of the genus *Conus*, have been documented to synthesize a wide variety of peptide toxins known as conantokins that are selective inhibitors of NMDARs. This research project set out to study both the effects of a particular set of conantokins, designated as *Conus Parius* 1, 2, and 3 (Con Pr 1, 2, and 3) on NMDA-stimulated intracellular Ca\(^{2+}\) influx in mature rat hippocampal neurons and the effect of these conantokins on CREB activation at serine 133 due to the known modulation of downstream CREB phosphorylation by intracellular calcium.

Real-time Ca\(^{2+}\) imaging was used to compare the intracellular Ca\(^{2+}\) levels before and after the exposure to Con Pr 1, 2, and 3 utilizing day in vitro (DIV) 12-14 rat hippocampal neurons. It has been demonstrated that Con Pr 1,2, and 3 effectively diminished intracellular Ca\(^{2+}\) influx that is dependent on the time of incubation and concentration of the peptide. Immunoblotting data has shown that Con Pr 2 and 3 decreased P-CREB (Ser133) levels without affecting total CREB levels.

This project was designed towards the better understanding of the conantokin structure function relationship with NMDA receptors and the broader implications of understanding the neurobiological and biochemical mechanisms that are exhibited by patients with neurodegenerative diseases. Data generated will aid towards a better understanding of how Conus parius functions as an antagonist and aid in rational drug designing that is able to correct specific NMDAR excitotoxicity without globally perturbing other receptor functions.
Amino acid derivatives represent an important class of potent therapeutic agents and precursors. N-hydroxy derivatives of amino acids, in particular, are found in a range of medically useful compounds, such as the antibiotic myobactin. We set out to develop a novel synthesis of an isotopically labelled, N-hydroxy derivative of glutamic acid. The acylnitroso Diels-Alder reaction of tert-butyl hydroxycarbamate with cyclopentadiene and periodate produced (1S,4R)-tert-butyl 2-oxa-3-azabicyclo[2.2.1]hept-5-ene-3-carboxylate (Boc-cycloadduct) (1). Pd/InI mediated electrophilic addition to the Boc-cycloadduct can result in a mixture of three different products, a 1,4 anti product of R-tert-butyl cyclopent-2-enyl(hydroxy)carbamate, a 1,4 syn product of R-tert-butyl cyclopent-2-enyl(hydroxy)carbamate, and a 1,2 anti product of tert-butyl cyclopent-3-enyl(hydroxy)carbamate. Attempts at D labeling via electrophilic Pd/InI addition resulted in the 1,4 product of R-tert-butyl cyclopent-2-enyl(hydroxy)carbamate (2), void of any deuteration. Oxidative cleavage of the 1,4 product (2) through ruthenium (III) chloride and sodium periodate produced the N-hydroxy-glutamic acid (3). The difficulty inherent in isotopic labeling in the Pd/InI reaction highlights potential unknown mechanisms of action. Future work aims to incorporate the D label via use of deuterated solvents, and to improve yields by changing the leaving group (Boc) on the cycloadduct.
The combustion of fossil fuels for energy results in 86% of anthropogenic greenhouse gases. Due to availability, cost and high investment in infrastructure, fossil fuels will likely remain the world’s primary energy source for many years. Since it is virtually impossible to change the human activity that causes these challenges, the aim of scientific research has become the reduction of greenhouse emissions. The objective of Carbon Capture and Sequestration (CCS) technology is to design and synthesize a class of compounds that can selectively remove CO$_2$ from a mixture of gases and be regenerated with minimal energy cost. The Brennecke and Schneider groups at Notre Dame have demonstrated that aprotic heterocyclic anions have high affinity for CO$_2$, and suggest them as viable CCS materials. The goal of this investigation is to design and synthesize a regenerative, low cost ionic liquid that will undergo selective CO$_2$ capture with zero parasitic energy consumption. Practical future applications of a successfully synthesized CCS material would allow CO$_2$ separation under ambient airflow. Such a compound would have far-reaching consequences on the international effort to manage Earth’s CO$_2$ concentrations. Once a desired ionic liquid is synthesized, it is characterized using primarily nuclear magnetic resonance (NMR). This compound is then tested for CO$_2$ capture by bubbling CO$_2$ gas into the compound and examining NMR chemical shifts to determine if a reaction has taken place with the material. After identifying a promising ionic liquid, its physical and chemical uptake of CO$_2$ is tested through collaboration with the Department of Chemical and Biomolecular Engineering. In the research conducted with the assistance of COS-SURF, the primary target anion was determined too problematic to synthesize. Two other target anions were obtained but failed to reach complete ion exchange with respective cations. However, since the period of this investigation, the lab group has experimented with an anion with ideal enthalpy of binding of CO$_2$ and that does not have the synthetic complications of the aforementioned anions. Focus of research has now turned to designing a cation that will allow for the best viscosity with this anion for potential future commercial use.
Aldehydes are one of the most common organic functional groups in nature and in the lab; however, their use in forming carbon-carbon bonds has been limited to some Aldol Condensation reactions like Michael Additions and Knoevenagel Condensations. Consequently, a reaction that could construct an all-carbon substituted tertiary center via a sequential, direct substitution of a dielectrophilic aldehyde would improve the synthetic utility of this functional group.

The initial intent of this research project was to optimize reaction conditions to generate a tertiary, all-alkyl substituted carbon center from an aryl propargyl aldehyde. Based on previous research that the Ashfeld lab had conducted where zinc metal and titanocene dichloride controlled an addition of a carbon-based nucleophile and activated the resulting alkoxide for a second addition, it was hypothesized that using an aryl propargyl aldehyde and propargyl iodides as the carbon-based nucleophiles would yield triynes.

Forming bonds between two carbons in a reaction has traditionally been of critical importance in organic synthesis, and having two of these bonds form at once would have made the proposed reaction rather valuable. Perhaps the best benchmark of this importance has been exhibited by the Royal Swedish Academy of Sciences: the Grignard reaction (1912), the Diels-Alder reaction (1950), the Wittig reaction (1979), Olefin metathesis (2005), and Suzuki Coupling (2010) have been just a few examples of reactions that form carbon-carbon bonds and yielded the Nobel Prize in Chemistry to their discoverers. Needless to say, the prospect of researching a reaction that had the potential to form two carbon-carbon bonds in one flask could have had significant implications in the field of organic chemistry.

Despite the promise, attempts using phenyl-2-propynal and phenyliodoacetylene were not fruitful as the products formed in the trials led to inconclusive results. No triyne or even diyne formation was observed in the attempts, so this aspect of the project was set aside.

The second intent of this research project was to synthesize a collection of propargyl iodides for use in a natural product synthesis of the family of compounds known as clausamines. The propargyl iodides synthesized were 1-(2-iodoethynyl)-4-methoxybenzene, 1-(2-iodoethynyl)-4-trifluoromethylbenzene, 1-chloro-4-(2-iodoethynyl)benzene, [(3-iodo-2-propyn-1-yl)oxy]methyl]benzene, 3-iodo-2-propyn-1-ol, and 3-iodo-2-propyn-1-al.
A number of isomeric triazoles of general structure 1 and 2 were produced by metal catalyzed reaction of azides with alkynes. In this study it was demonstrated that these isomeric triazoles can be distinguished using simple 1-dimensional $^{13}$C NMR spectroscopy. Experimental evidence, as well as calculated GIAO chemical shifts, shows that isomers 1 have a characteristic NMR signal due to the C$_5$ carbon at 120 ppm which appears as a doublet of triplets. The related isomers 2 have a signal at 133 ppm due to the C$_4$ carbon, which appears as a simple doublet. Exceptions of these chemical shifts are found in carbonyl compounds, with resonance effects result in further deshielding. These studies show that simple 1-dimensional $^{13}$C NMR spectroscopy of isomeric triazoles serves as an efficient identification tool. This should eliminate the need for more arduous, expensive, and time intensive identification techniques such as X-Ray crystallography or multi-dimensional NMR spectroscopy.
Determine dose response to chemotherapeutics and identification of ARID3B interacting proteins in epithelial ovarian cancer cells

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The viability of two epithelial ovarian cancer cell lines (OVCA 429 and OVCA 433) was measured in response to two types of chemotherapeutic drugs administered in a range of concentrations. While each cell line generally demonstrated decreased viability as drug concentration increased, there were changes in viability trends between cell lines. Following the dose curve experiments, immunoprecipitations (IPs) were performed using OVCA 429 cells. IP experimentation focused on ARID3B, AT Rich Interactive Binding Domain 3B, a DNA binding protein. Our lab previously demonstrated that ARID3B is overexpressed in ovarian cancer. Through this work, appropriate parameters were determined for effective immunoprecipitation. As a result, an ARID3B antibody was validated for use in IPs, expanding the utility of this antibody which had been previously validated for use in immunofluorescence and western blots. Following isolation of plasma membrane proteins, IP detected the presence of ARID3B, suggesting the presence of ARID3B in the plasma membrane. Then, a co-IP was revealed the presence of E-cadherin within the immunoprecipitated ARID3B proteins of the plasma membrane, suggesting interaction between ARID 3B and E-cadherin. One future direction of this work is to reduce non-specific binding in the IP method in order to improve IP effectiveness.
CdSe quantum dot solar cells can be used to convert solar energy into electrical energy by the
light-induced excitation of an electron in the quantum dots into TiO₂ layer and onto a conductive
cell. As CdSe solar cells grow during synthesis, they change color, energy levels, and band gap
sizes. A rainbow quantum dot solar cell, in which yellow and red CdSe quantum dots are
layered, would theoretically take advantage of the larger band gap and shorter charge injection
time of the yellow, higher energy, CdSe quantum dots while also increasing the range of
wavelengths absorbed with red, lower energy, CdSe quantum dots. To accomplish this layering
of the CdSe quantum dots into the cell, TiO₂ is first coated with mercaptopropionic acid, which
will chemically link the dots to the TiO₂. Then, electrophoretic deposition is used to drive the
dots into the film, controlling the deposition time and voltage potential of each color deposition.
The success of the layering is tested by comparing the absorption spectra of the front and the
back of the solar cell. Finally, the effectiveness of the final product will be determined by
comparing the photocurrent of the rainbow quantum dot solar cell with that of a red solar cell
and a yellow solar cell.
Poster Presentation

*The Synthesis of Amides and Hydrazones via the Use of Organophosphorus Activation*

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Advisor: Brandon Ashfeld, Dept. of Chemistry and Biochemistry

The use of phosphorus to produce reactive intermediates for novel organic transformations are known in the literature, but are not as extensive as those applying harsher methods of substrate activation. In our lab, we are examining the use of chlorophosphites to both activate the carboxylic acid in situ followed by facilitating the decomposition of an azide reagent to give an aza-ylide intermediate. Under the conditions we have found, the aza-ylide can undergo an intramolecular reaction giving a highly efficient route to amides directly from carboxylic acids. This method is chemoselective, tolerating other functional groups present in the carboxylic acid, and is easily purified due to the extrusion of phosphinic acid as a water-soluble by-product. The broad scope of our method allows for synthesis of not only conventional amide products, but lactams and peptide coupling targets as well. We would like to further examine this reaction by designing a catalytic variant in which the phosphorus is recycled with the help of an organic silane. N-acyl hydrazones are useful in organic synthesis as shelf stable alternatives for more traditional imine substrates. As such, we are also researching a novel route to N-acyl hydrazones via the activation of carboxylic acids using phosphorus. This methodology is still under optimization with the reaction conditions and reagents such as stoichiometry, order of addition, nature of the phosphorus reagent, acids, bases and solvents systematically being investigated. A simple and efficient route to substituted hydrazones would be advantageous to those interested in areas such as ligand and catalyst design due to the ease of enantioselective reduction of N-acyl hydrazones to chiral amines.

![Reaction Scheme 1](image1)

*Figure 1: Intramolecular nucleophilic acyl substitution through *in situ* activation of carboxylic acids.*

![Reaction Scheme 2](image2)

*Figure 2: Synthesis of N-acyl hydrazone via carboxylic acid activation.*
Access Functional Star Polymers with Controlled Nanostructures

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Aerospace Engineering  
Ashley Hanlon, Dept. of Chemistry and Biochemistry  
Advisor: Haifeng Gao, Dept. of Chemistry and Biochemistry

My current research focuses on synthesis of star-shaped polymers that have tunable size in nanometer scale and core-shell structure. One fascinating feature in this star polymer is that the core domain can selectively complex with metal ion precursors and confine the formation of nanoparticles within the star interior when reducing agents are added. Since the star structure is critical for the formation of the inorganic nanoparticles and their catalytic properties, we are using a controlled polymerization technique, atom transfer radical polymerization (ATRP) to synthesize star polymers with high molecular weights and uniform structure. These polymers will constitute very stable organic carriers for the nanocatalysts. There are myriad uses for a tunable star with these qualities, from biomedical to fuel cell applications. So far, we have successfully synthesized the most promising candidates for different types of arms and cores. We are currently testing their reactivities and how successfully we can convert these reactants into a star product with the qualities we are looking for. So far, we have successfully synthesized pure crosslinkers of 1,4-DVB and 1,3-DVB. Typical star synthesis uses a mixture of these three cores, but we hope to find that just one or a set combination of two will be more conducive to optimal star qualities. Additionally we are conducting reactions to find the optimal conditions for star synthesis. If it turns out that star synthesis is much better with a pure crosslinker, our findings will reflect this data and other scientists can use it with their own research into nonlinear polymers.
It is no secret that solar energy has incredible potential. It is also no secret that modern attempts at converting the sun’s energy into viable power have not met the threshold of efficiency needed to make solar energy a feasible reality. Widespread research is being conducted on materials that have the potential to boost efficiency. In our corner of the world, at the Radiation Laboratory, we are developing solar cells that use quantum dots to draw even more power from the solar spectrum. The advantage of quantum dots lies in their flexibility. We are able to grow the dots to various sizes, which in turn dictates their color. Quantum dots of certain colors are able to absorb certain wavelengths of light. This means that we have the ability to create dots that absorb the wavelength of our choosing. When suspended in a conducting network, such as TiO2, the excitation of the dots when hit by photons produces an electrical current. Unfortunately, as with many other forms of solar cells, recombination is an issue. To help reduce recombination, we are currently researching ways of creating rainbow quantum dot solar cells. As its name implies, a rainbow cell is a layering of different colored quantum dots in spectral order within a single TiO2 network. So far we have been able to use electrophoretic deposition (EPD) to push the dots through the TiO2 so that we are able to see an absorbance on the back of the cell as well as the front. To then create a multi-color layering of these dot-saturated networks, we have tried changing various EPD settings, creating different recipes of TiO2, and using the linker agent MPA. These attempts have been met with gradual success, as we recently were able to create a crude rainbow cell. We are getting closer everyday and a bona fide rainbow quantum dot solar cell is within reach.
Additions to carbonyl compounds are some of the most fundamental reactions in organic chemistry. In order to accomplish the addition, the carbonyl must first be activated. Phosphorus can be used to activate carboxylic acids for nucleophilic acyl substitutions. Carboxylic acids were reacted with chlorophosphites and azides to generate the corresponding amides. An organic base was used to activate the carboxylic acid to give an activated phosphite ester. Primed for attack, the phosphite ester rearranges via a 1,3-acyl migration to give the desired amide. The azide functions as a masked amine; the attack of the phosphite complex places the newly formed amine in position to attack the carbonyl. The benefits of this synthetic approach allow the carbonyl to be activated in situ, reducing the number of steps toward the target product, and increase the selectivity of the reaction due to the tethered amine. This synthetic approach using phosphorus as an activating agent is predicted to give similar results with phosphoric and sulfonic acids to produce phosphoramides and sulfonamides.
Poster Presentation

_Synthesis and catalysis of location-specific cobalt nanoparticles supported by carbon nanotubes for Fischer-Tropsch Synthesis_

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Yuan Zhu, Yingchun Ye, and Shiran Zhang, Dept. of Chemistry and Biochemistry  
Advisor: Franklin Tao, Dept. of Chemistry and Biochemistry

Gas prices have risen considerably throughout the past years, diminishing reserves and volatile supplies have had resounding effects on the world market. Fischer-Tropsch Synthesis (FTS) is a catalytic process that turns a mixture of gaseous hydrogen (H₂) and Carbon Monoxide (CO), referred to as syngas, into hydrocarbon chains that can be used in fuel production. Syngas can come from a variety of sources, like coal and biomass, both of which are abundant and protected from swings in the market. A variety of metals can be used as catalysts; iron and cobalt are among those most studied. Reaction conditions for the synthesis are around 200°C and 20 bar, conditions too harsh for most spectroscopic techniques and thus difficult to determine proper reaction pathways. This makes it important to correlate the effects of location and surface chemistry on a catalyst’s performance. Carbon nanotube (CNT) supports have become a popular research topic because of their improvement to the activity and selectivity of iron catalysts when placed on the internal wall. The internal wall of a CNT creates a reduced environment that prevents the iron nanoparticles from oxidizing during catalysis. However there is no significant difference between the activity and selectivity of cobalt nanoparticles when placed on the internal or external wall of a CNT, suggesting a different reaction pathway for the various catalysts. The next phase of research is working with the new ambient pressure X-ray photoelectron spectroscopy (AP-XPS) built in the lab of Professor Tao to observe catalysts under reaction conditions.
Poster Presentation

*Non-classical Oxygen Atom Transfer Reactions Involving Oxomolybdenum(VI)bis(catecholate) and Pyridine-N-oxides*

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Redox chemistry is a common theme in current energy research. In classical inner-sphere redox chemistry the changes in oxidation state and bonding are co-localized, usually around a metal center. This co-localization is not, however, required. In so-called non-classical redox reactions, the changes in bonding still occur at the metal center but the oxidation state changes occur on coordinated redox-active ligands. We examined the reaction between oxomolybdenum(VI)bis(3,5-di-tert-butylcatecholate) and various pyridine-N-oxides to form 3,5-di-tert-butyl-1,2-benzoquinone, free pyridine, and molybdenum trioxide. It is proposed that interconversion between free and bound pyridine-N-oxide occurs via an associative mechanism ($\Delta H^{\ddagger} = 7.8 \pm 0.2 \text{ kcal mol}^{-1}$, $\Delta S^{\ddagger} = -19.1 \pm 0.5 \text{ cal mol}^{-1} \text{ K}^{-1}$). Two electrons from 3,5-di-tert-butyl-catecholate are then transferred to the oxidant, breaking the O-N bond on the pyridine-N-oxide. This leads to the formation of a double bond between the molybdenum center and the oxygen, and the release of free pyridine and 3,5-di-tert-butyl-1,2-benzoquinone. In situ NMR spectroscopy with an internal standard indicates that the production of the quinone (2.07±0.12 equiv) and free 4-picoline (2.03±0.09 equiv) is consistent with this proposition. The reaction is also found to be first order in molybdenum via UV-visible spectroscopy and NMR spectroscopy, and independent of the concentration of excess Opy, which indicates that the rate-limiting step involves the pyridine-N-oxide adduct. This is consistent with the large enthalpy of activation and low entropy of activation observed ($\Delta H^{\ddagger} = 27.0 \pm 1.3 \text{ kcal mol}^{-1}$, $\Delta S^{\ddagger} = +0.4 \pm 3.8 \text{ cal mol}^{-1} \text{ K}^{-1}$). The mechanistic data indicate that the key step in the reaction results in formation of a dioxomolybdenum(VI) moiety bonded to two partially oxidized catecholate ligands. The reaction therefore constitutes an example of non-classical oxygen atom transfer.
Cellular and embryonic polarity is crucial for development. Early cellular polarity is achieved in part by mRNAs, which are moved to specific intracellular locations. Vg1 mRNA is localized to the vegetal hemisphere of *Xenopus* oocytes and is anchored along the vegetal cortex by stage IV of oogenesis. Vg1 mRNA, which encodes a protein in the TGF-β family of signaling proteins, contains a 340-nucleotide region called the Vg1 localization element (VLE) within the 3’UTR. The VLE is necessary for localization. *Trans*-acting factors associate with the VLE, creating a ribonucleoprotein (RNP) complex that directs the movement of Vg1 mRNA. Surprisingly, these same protein factors are also involved in localization of other mRNAs to the opposite (animal) hemisphere of the oocyte. We hypothesize that additional factors are present in the RNP complex of Vg1 that specify directionality. In order to identify all protein factors in the RNP complex, we are using RNA affinity tags, or aptamers, to isolate complexes that from *in vivo*. RNA affinity tags are structures that bind with high affinity to a particular ligand, which in these experiments are either streptavidin or tobramycin. Tagged VLE RNA will be microinjected into oocytes, allowing the RNP complex to form on the VLE. Streptavidin or tobramycin will be used to isolate the VLE RNP complex associated with tagged RNA. The RNA-associated proteins will be identified using electrospray mass spectrometry and MALDI mass spectrometry.
Poster Presentation

*Asymmetric Ketone Hydrogenations by Ruthenium Noyori Catalysts: A Computational Study*

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Advisor: Olaf Wiest, Dept. of Chemistry and Biochemistry

The Nobel Prize in Chemistry was awarded to Royoji Noyori in 2001 for his development of transition metal catalysts which featured diamine and diphosphine ligand systems. Today those catalysts are widely used in industrial syntheses because of their high efficiency, economy, and yield. This project computationally examines ruthenium-based Noyori catalysts as applied to asymmetric ketone hydrogenations to form a chiral alcohol. Transition states were optimized by a combination of Gaussian and Jaguar computer programs to generate energy values, bond distances, and frequency calculations. The end goal of this project is to build a force field for predicting these measurements as well as enantiomeric selectivity in novel reactions.
Solar energy has a unique potential in shaping the future of global energy production. Almost all solar panels on the market today are manufactured from silicon. Due to a fixed band gap, silicon is only able to efficiently capture a certain range of the solar spectrum, and is also expensive to purify before it can be used in a high-efficiency cell. In light of these obstacles, there is intensive research being done in the materials sciences to find a replacement technology. Much of recent solar cell research operates at the nano-scale. The unique properties of semiconducting nanostructures allow for devices with tunable band gaps to be fabricated cheaply with the potential to capture a larger portion of the solar spectrum than silicon and other bulk semiconductors. In particular, quantum dot solar cells offer a particularly promising new technology. Semiconductor quantum dots are portions of matter confined in all three dimensions and have the ability to absorb different wavelengths of light depending on their size (and corresponding color) due to a mechanism called the Bohr Effect. The goal of my project was to grow yellow, orange, and red CdSe quantum dots on TiO2 nanoparticles using a deposition method called SILAR (Successive ionic Layer & Adsorption). Using this technique, I was able to tune the size of the quantum dots based on the number of SILAR cycles and thereby produce different colors corresponding to different absorption wavelengths of light. I then converted the resulting powders into a solar “paint”, which I tested on conducting optically transparent electrodes for their external quantum efficiency and current-voltage characteristics.
The synthesis and characterization of high quality CdSe nanosheets (NS) are described. A solution-based approach is used to synthesize the NSs by first mixing precursors with an organic fatty acid and a non-coordinating solvent at low temperatures. Subsequent injection of a cadmium acetate and selenium solution into the reaction vessel induces two-dimensional (2D) NS growth. This leverages advances in the development of high quality colloidal quantum dots (QDs) with those of producing 1D nanowires (NWs) in order to create large-scale synthetic procedures for 2D NSs. Resulting rectangular CdSe NSs are approximately 30 nm in width, 90 nm in length, and 2 nm thick. Intra-sheet width variations are very small, although sheets exhibit both straight and curved edges along their widths. High-resolution transmission electron microscopy (TEM) images reveal that the sheets are crystalline. In addition, quantum confinement effects are observed in the UV-visible absorption spectra of the CdSe NSs. Synthetic approaches used to vary the lateral dimensions of CdSe NSs are reported. This facile synthesis affords more opportunities for further investigations of the optical and electrical properties of 2D nanomaterials. The decoration of CdSe sheets with gold nanoparticles, for use in photochemical hydrogen generation, will be explored in future experiments. Overall, this investigation presents simple synthetic routes to the size control of 2D CdSe NSs that have potential uses in photovoltaics, nanodevices, optoelectronics, functional materials, and solar hydrogen generation.
“Non-classical” redox reactions are a unique type of redox reactions in which changes in bonding occur at the metal center, but oxidations or reductions occur at the redox-active ligands attached to the metal center, rather than at the metal center itself. This spatial separation of electron transfer and the changes in bonding similarly occurs in fuel cell catalysis, suggesting that these non-classical redox reactions may give insights concerning the electron transfers involved in fuel cell systems. One such compound that undergoes non-classical redox reactions is tris(3,5-di-tert-butylcatecholato)molybdenum(VI) ($\text{tBu}_2\text{Cat}_3\text{Mo}$). As a result of its strong Lewis-acidity, $\text{tBu}_2\text{Cat}_3\text{Mo}$ forms a stable seven-coordinate dimer with bridging catecholates, as well as seven-coordinate monomeric species with ligands including pyridine and pyridine-N-oxide. ($\text{tBu}_2\text{Cat}_3\text{Mo}$ reacts with pyridine-N-oxide in this “non-classical” manner to produce one equivalent of oxobis(3,5-di-tert-butylcatecholato)molybdenum(VI) ($\text{tBu}_2\text{Cat}_2\text{MoO}$) and one equivalent of 3,5-di-tert-butylbenzoquinone. The ($\text{tBu}_2\text{Cat}_2\text{MoO}$ species undergoes further oxidation to produce MoO$_3$ and two additional equivalents of 3,5-di-tert-butylbenzoquinone. In a similar reaction, ($\text{tBu}_2\text{Cat}_3\text{Mo}$ is oxidized by molecular oxygen, forming one equivalent of ($\text{tBu}_2\text{Cat}_2\text{MoO}$ and one equivalent of 3,5-di-tertbutylbenzoquinone.
Poster Presentation

**Developing Simple Colorimetric Verification Tests for Antibiotics on PADs (Paper Analytical Devices)**

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The counterfeiting of pharmaceuticals in developing countries is becoming more and more prevalent. Receiving counterfeit or under dosed antibiotics can be life-threatening to the patient and encourages the development of antibiotic resistant strains of bacteria. The goal of the PADs (paper analytical device) team is to develop inexpensive, user friendly, colorimetric tests that can help determine the validity of a drug sample outside of a laboratory setting. These tests are designed not only to be qualitative but also semi-quantitative. Isolated hydrophilic lanes or circles are preloaded with chemical reagents that will produce colorimetric results when a drug sample is applied. These can be interpreted visually or by picture message sent to the PADs project computer imaging system. The PADs team hopes to save the lives individuals receiving antibiotics, especially in developing countries, by providing a simple, reliable way to test that the medication being taken is valid.
Although deltahedral Zintl ions were introduced in the late 1890’s and early 1930’s, it was not until the last decade that nine atom germanium clusters have been at the forefront of rapidly developing and exciting new chemistry. These ions were not expected to react with other chemicals, however, Sevov et. al. were the first to design groundbreaking experiments to functionalize them with organic alkynes and halides, resulting in the first organo-Zintl class of compounds. The germanium clusters are readily soluble in ethylenediamine, but in order to have a successful reaction in other solvents (i.e pyridine or MeCN,) an addition of sequestering agent, 18-crown-6 or 2,2,2-crypt, was required. Feng Li of the Sevov group gathered inspiration from the preparation of Grignard reagents, where the THF soluble halide compound combines with the insoluble magnesium metal to form a strong nucleophile, RMgX. Sevov and Li showed that a tri- and tetra-functionalized germanium cluster were possible without the need for sequestering agents. Building off of these unprecedented results, attempts are currently being made towards the functionalization of K4Ge9 clusters with various organic functional groups in the solvents toluene, THF and acetonitrile in the absence of sequestering agents. Results have shown both intact clusters as well as mono-, di-, and tri-functionalized clusters after reacting with organic alkynes and halides.
Cancer is a complex disease that involves many changes in the genomic and proteomic profile of the cell. In healthy cells, the nuclear pore complex plays an important role in regulation of gene expression by selectively transporting transcription factors and mRNAs through the nuclear envelope. However, specific nuclear pore proteins have been found to be up-regulated in cancer cells and have been implicated in increased nucleocytoplasmic transport and cell metabolism. An early RT-PCR study we performed showed the nucleoporin p62 C-terminal-like protein (Nup62CL) transcript to be one of the most highly over-expressed: in colorectal cancer cell lines, Nup62CL transcript levels are on average nearly 30 times as high as in normal colon lines. However, preliminary data showed that RNA interference of this single nucleoporin did not significantly decrease cancer cell viability compared to normal cell viability, and studies have not yet found evidence for the existence of Nup62CL at the protein level. We are uncertain whether this is due to the transcript not being translated at all, or whether levels in non-carcinogenic and/or cell lines from outside of the colon are lower than those found in our colorectal cancer lines. The sequence of the predicted Nup62CL peptide suggests that it could mimic Nucleoporin Nup62, making it potentially detrimental to regulated nucleocytoplasmic transport. In order to test for the presence of a translational Nup62CL product, we have attempted several experimental techniques, including western blot and immunofluorescence, with inconclusive results. To test whether these results derive from a non-specific antibody, we will employ a mass spectrometric approach. We will use Multiple Reaction Monitoring (MRM), a novel technique that involves targeting and quantifying a highly specific peptide through a series of mass analyzers. We hope that the combination of these techniques will reveal translational evidence for the over-expressed Nup62CL transcript.
Many people talk on cell phones these days, but few people stop to think about how these wireless devices actually affect their bodies. A cell phone, regardless whether it is in use or not, releases radio frequency-modulated electromagnetic fields (RF-EMFs), which increase the brain’s glucose metabolism causing spikes in brain activity specifically in the orbito-frontal cortex and temporal pole of their brain. Glucose is used by the brain to harvest energy necessary for functioning. The orbito-frontal cortex is a region in the front of the brain and has been proposed to be involved in decision making and sensory integration, specifically hearing, through a rostral and caudal fiber pathway. Fiber pathways convey neural signals throughout the areas of the brain. The pathway between the temporal lobe and orbito-frontal cortex could provide a link through which these RF-EMFs travel. Researchers have hypothesized that neural tissue may be harmed from exposure to this radiation, which is also emitted from many household items, such as hair dryers and microwaves. Avoiding RF-EMFs entirely would be a difficult task, and the good news is that there may be some benefits associated with the increased glucose metabolism they produce. Some studies suggest that cell phone RF-EMFs may actually be helpful in lowering the risk of Alzheimer’s due to the increased amount of glucose heightened brain activity. There continues to be controversy in the scientific community surrounding this topic, and the interactions of these devices with the human brain, specifically the orbito-frontal cortex and the temporal lobe, have yet to be fully evaluated. Since cell phones have rapidly become one of the most common accessories for the average person to have, questions about the long-term effects of use will continue to surface. A comprehensive investigation of the research literature for Professor Brinkmann as our Chemistry project provided interesting health related information for consideration.
Colorectal adenocarcinoma is usually treated as a single disease. However, malignancies arising from the ascending colon (right side or right colon cancer (RCC)) versus the descending colon (left side or LCC) have statistically different incidences in cancer and cancer-related deaths. In addition, it has recently been shown that many genes are differentially expressed in RCC versus LCC. Unfortunately, many of the cell lines commonly used in colorectal cancer research derive from unreported sites in the colon. To aid in the identification of cell line origins, we are developing a diagnostic panel of genes to predict right versus left origins of cell lines. Our panel of genes, HOXB13, CTGF, CRIP1, SST, CYR61, REG1A, HOXB6, PRAC, PI3, and ANPEP have previously been shown to be significantly differentially expressed in primary right versus primary left tumor samples. We will use RTPCR to test the expression levels of our diagnostic genes on cell lines of known origin and then use our diagnostic panel to examine cell lines of unknown origin. With our diagnostic panel of genes, we will be able to determine if the additional cell lines are associated with ascending or descending colons.
Niemann-Pick Type C disease (NPC) is a lethal, autosomal recessive disorder whose hallmark symptoms include an accumulation of unesterified cholesterol and other lipids in the late endosomal and lysosomal (LE/Ly) cellular compartments, eventually causing progressive neurodegeneration and death. The disease occurs in approximately 1 in 150,000 births. Although the age of onset may vary in those affected, NPC is universally fatal. In this study, we researched the effects of various drugs, the majority of which modify the epigenetic control of gene expression, in lowering the otherwise harmful elevated intracellular cholesterol levels in NPC cells. It is believed that through increasing the transcription and translation of semi-functional proteins responsible for cholesterol and lipid transport, the symptoms of NPC can be alleviated. Many of the drugs we analyzed are already FDA-approved for other conditions. Our studies utilized a technique developed by Maxfield et al., which allowed us to make quantitative comparisons of the efficacy of these drugs in lowering cholesterol levels. By measuring the amount of unesterified cholesterol in perinuclear LE/Ly compartments, and comparing it to the total area of the cell, such analysis is possible. Of the drugs analyzed, several were found to significantly lower the relative amount of unesterified cholesterol found in the LE/Ly compartments, indicating that, in the future, they may potentially be useful in treating NPC.
ABSTRACTS – PHYSICS
The effect of X-ray induced radiation on DNA and poly-L-arginine

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Radiation is known to cause damage to biological macromolecules within cells. It can chemically alter and therefore disrupt the function of proteins and DNA. Deleterious mutations or structural damage of these molecules may ultimately lead to dysfunctional or dead cells. X-ray photoelectron spectroscopy (XPS) and atomic force microscopy (AFM) are both effective ways to investigate and collect quantitative and qualitative data on chemical conditions of realistic biological samples. The combination of poly-L-arginine with DNA allows for a stable bilayer build up resulting from the favorable positive to negative ion interactions of the separate molecules. This also provides a physiological environment by combining DNA with a polypeptide as is found in cells. Bilayer films of poly-L-arginine and DNA as well as films of only poly-L-arginine were prepared on silicon substrates cleaned with Piranha solution (3:7 mixture of H2O2 and H2SO4). AFM was used to image the samples to investigate the uniformity of the surfaces. The samples were then placed under prolonged exposure to radiation, and XPS was used to quantify the chemical changes over time. Irradiating and quantifying the chemical or structural alterations of these molecules leads to a more comprehensive understanding of the effect of radiation damage in realistic biological conditions. The AFM and XPS results of changes to poly-L-arginine and bilayers of poly-L-arginine with DNA are discussed in this presentation.
DNA damage from high-energy radiation occurs in two ways. One is the direct impact of the radiation with DNA, and the others are reactions that occur with secondary electrons. These electrons are produced by the ionizing radiation interacting with the cell. Our aim is to further understand the damage that the secondary electrons cause to DNA.

In order to carry out our studies, we needed to acquire and construct the necessary equipment. We began by receiving an old mass spectrometer that we proceeded to completely dismantle. We acquired this for two reasons: the mass spectrometer’s housing size was appropriate for our power supplies, and we wanted to save some of the parts from the mass spectrometer for future use. In addition, we obtained and cleaned out a vacuum chamber. To this chamber, we will attach an electron gun (1eV to 2000eV energy range), rotational and vertical manipulators, vacuum pumps, and a mass spectrometer. Once the construction is completed, we will test our equipment by irradiating DNA molecules.

As atmospheric pressure plasma jets (APPJs) become more promising in anticancer treatment and research, there is increasing interest in exploring their unique properties and unraveling the mystery that plasma remains to be today. The APPJ is regulated by a variety of parameters including gas concentration and flow rate, voltage, and frequency; alternations in the parameters affect the jet length, stability, and composition of the emitted plasma jet. There is hope that the free radicals and ions produced by APPJs can potentially induce cell apoptosis through means of induced cell signaling and remain a potential treatment for cancer [1]. To ensure the most effective APPJ is used to treat a cell, the free radicals produced must match those needed to force apoptosis. The species (the composition of ions and radicals) of specific APPJ types and configurations can be discovered through the process of optical emission spectrometry. Changing the parameters of the waveform, frequency, and voltage applied as well as gas type and flow rate alternates the plasma species. Data concludes that careful selection of APPJ parameters may allow for induced apoptosis in selected cells. The purpose of this experiment is to show the procedure for characterizing a specific APPJ species as well as understanding the changes to species when certain parameters are varied.

“Atmospheric-Pressure Plasma Jet Induces Apoptosis Involving Mitochondria via Generation of Free Radicals”. Ed by Hak Jun Ahn, Kang Il Kim, Geunyoung Kim, Eunpyo Moon, Sang Sik Yang, Jong-Soo Lee
The objective of this experiment is to determine the most effective means of cleaning surfaces such as silicon, gold. The method used to clean the surfaces is a low-atmosphere plasma system. A glass tube is filled with gas; depending on which gas is used, the pressure is set between 100 mTorr and 3 Torr. There are electrodes at either end of the glass tube, with the sample between them. Once sufficient voltage is applied (between 200 and 1000 volts, 30 kHz AC or DC), the gas is ionized, the discharge is ignited, and then plasma is formed. As the plasma interacts with the sample, it destroys organic molecules, producing smaller fragments, which are then pumped out of the low pressure system. To check the cleanliness of the surface, a “water droplet” test is performed. This is done by first dropping 10 \( \mu \)L of purified water on the sample, then measuring the water’s contact angle. The cleaner the sample, the wider the water droplet will spread.

Variables considered include different gases (Ar, N\(_2\), O\(_2\), He, air), different pressures (100 mTorr – 800 Torr(atmospheric)), and different exposure times (1 – 30 minutes). In addition, an oxygen/UV method is also examined, where oxygen radicals are formed in plasma discharge.
Non-thermal atmospheric pressure plasma is a specialized type of plasma that is used in this study to induce death in cancer cells. Radiation has been used in many forms to combat cancerous cells, but plasma offers a highly selective treatment that has limited effects on surrounding cells.

The experimental phase of this study will test the application of such an atmospheric pressure plasma jet (APPI) to SCC-25 oral cancer cells to determine if it is possible to induce apoptosis or necrosis. Different sources will be used on the cells to find a configuration that kills cancer cells but has no effect on normal cells. The sources have been developed based on the dielectric barrier discharge between two external electrodes surrounding a dielectric tube; such a configuration has been shown to induce breaks in DNA strands [2,3]. Each configuration will be characterized using an optical emission spectrophotometer and iCCD camera to determine the optimal conditions for inducing cell death. The cells will be incubated after irradiation with plasma, and cell death is determined using microscopy imaging to identify antibody interaction within the cells.

Historically, galaxies have been classified by their shapes and physical properties into two main groups: ellipticals and spirals. Stars, on the other hand, have been classified according to their color, luminosity, and spectral curves. In this experiment, we attempted to classify galaxies using the methods of star classification—that is we analyzed the spectral curves and band intensities of both types of galaxies, attempting to notice trends among the data. In particular, using spectral curves provided by Sloan Digital Sky Survey, we calculated the ratio of flux at 9000Å to that at 4000Å for each galaxy. Furthermore, we calculated the color (u-r) of each galaxy by subtracting the band magnitude values. We found that, in general, we could classify galaxies to some degree of certainty using only these calculations. In particular, using the color classification, we found that we could correctly classify 94% of our sampled galaxies. We think our results could be used to help astronomers classify galaxies that are too small or too far away to be seen with high resolution.
Poster Presentation

*An Optical Atomic Clock in Neutral Silver*

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The standard for measuring time and frequency has been based for over forty years on the ground-state hyperfine splitting of atomic cesium (Cs). The accuracy of Cs atomic clocks has increased over the decades from $1/10^{10}$ for the first thermal beam system to better than $1/10^{15}$ for the newest systems that employ laser-cooled atomic fountains. The microwave transition at 9 192 631 770 Hz serves as the clock oscillator. Commercial beam-based Cs clocks have an accuracy of $1/10^{12}$ giving picosecond-timing resolution in one second. The world’s best time standards are few and use an atomic fountain to reach an accuracy of $1/10^{15}$ when averaged over one day. Unfortunately, the long averaging time makes it difficult to take advantage of this accuracy in real-time. A clock based on an optical transition with an oscillation frequency near $10^{15}$ Hz could achieve femtosecond-timing resolution in one second, making it possible to improve upon various real-time applications such as the Global Positioning System (GPS), distance ranging, and broad-band communications, as well as fundamental investigations such as mapping gravity, testing general relativity, and measuring the time variation of fundamental constants. It has been demonstrated time and again that advances in clock stability and accuracy lead to important tests of fundamental physics. The neutral silver atom (Ag) has a number of unique features that differentiate it from other clock candidates. One of the most compelling reasons to investigate Ag is that there is a clear path toward the realization of a two photon optical clock, which takes advantage of the relative simplicity that might be achieved by directly exciting the clock transition with simple atomic-beam geometry, making it possible to achieve a number of point-of-use scientific goals such as those requiring space-based clocks.
Analyzing Potential Tracking Algorithms for the Track Trigger Upgrade to the Silicon Tracker of the Compact Muon Solenoid

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The research performed revolves around creating tracking algorithms for the proposed ten-year upgrade to the silicon tracker for the Compact Muon Solenoid (CMS), one of two main detectors for the Large Hadron Collider (LHC) at CERN in Geneva, Switzerland. The ten-year upgrade corresponds to the Super LHC (SLHC) era when the interaction rate of the LHC is expected to increase by an order of magnitude. The sheer number of interactions will make it impossible to use the current trigger system to select interesting events due to the overwhelming backgrounds. The proposed upgrade to the silicon tracker for CMS will use high-speed electronics to trace particle trajectories so that they can be used immediately in a trigger system. The additional information will be combined with other sub-detectors in CMS to distinguish interesting events from background, enabling the good events to be read-out by the detector. The algorithms would be implemented directly into the Level-1 trigger, i.e. the first trigger in a two-trigger system, to be used in real time. One algorithm we created has proven very effective. This algorithm attempts to match hits in the layers of the detector to pre-recognized patterns of particle trajectories. Our group worked on two main tasks. First, we determined the efficiency of the tracking algorithm for different particle species and different background conditions. After each test run, the data was analyzed, and corrections to the algorithm were made to improve its accuracy and efficiency. Second, we updated the algorithm to be compatible with the latest version of the CMS track trigger simulation software, which is constantly evolving. This version of the software will be used for the technical design studies for the tracker upgrade. Having a viable version of out algorithm in the latest software version will allow us to contribute to the design studies.
Above iron on the chart of nuclides, approximately half of the nuclei are created via the r-process, or rapid neutron-capture process. The appropriate environments for such r-process nucleosynthesis require a very high neutron flux. This condition is most often seen in astrophysical phenomena such as supernovae or neutron star mergers. As it is difficult to directly take measurements from such events, research has been focused on computer simulations of the r-process under various astrophysical conditions. It is proposed that one of the key nuclear physics factors influencing the r-process is the beta decay rate of the nuclei involved. To test this, simulations were done to evaluate both the abundances of the relevant nuclei as well as the percent change in abundances due to changing the beta decay rates. The simulations we have run involved a neutron star merger environment, which is primarily a cold r-process, and a supernova environment, which is primarily a hot r-process. Beta decay rates were raised and lowered individually by factors of two and ten in separate runs. We found a correlation between the time-integrated abundance of the varied nucleus and the resulting percent change in the final r-process pattern. However, this correlation is not strong, and suggests that beta-decay rates can influence the final abundances by more than one mechanism. The final goal of the project is to better understand the conditions under which the hot and cold r-processes can take place and the contributions that they make to the observed solar abundances.
Poster Presentation

*Move over Superman! Nuclear Physics Tackles Krypton With Neff*

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This work introduces effective boson numbers (Neff) into the Interacting Boson Model (IBM1) to predict two neutron separation energies for neutron-rich zirconium, strontium, and krypton isotopes. Using a simple Hamiltonian, we determine the functional forms of binding energy and excitation energies as a function of boson number for a given choice of IBM parameters. The energy of the first excited 2+ level is used to fix the effective boson number for a given nucleus, that effective boson number is used to calculate the separation energy. This method accounts for complex interactions among valence nucleons around magic nuclei and successfully predicts the phase transitional signature in separation energies around A=100 for 92-108Zr, 90-104Sr, 86-96Kr, and 100-110Mo. These isotopes are interesting because they are examples of quantum phase transitions, that is the nuclear ground state changes from spherical to deformed very quickly with added neutrons. Understanding shape transitions in neutron rich nuclei such as these is necessary to model astrophysical processes like nucleosynthesis in supernovae.
Our research in the Nuclear Science Lab relies on the technique of accelerator mass spectrometry (AMS). In AMS, samples of interest are sent through the particle accelerator, which then leads to a high-energy analyzing magnet. In the magnet, the particles from the sample are bent differently depending on their masses and charges. By properly calibrating the magnet, we can purify the beam, meaning we will only be left with particles of our desired charge-to-mass ratio. Separating the desired particles from the rest of the beam is no easy task. The whole beam is often orders of magnitude more intense than the desired particles alone. Our research is concerned with the building and testing of a Bragg detector. The detector will be able to measure stopping power of incoming particles, which will give us a better mass resolution of the incoming beam. The design of our detector is based on a detector built by Rehm and Wolfs at Argonne National Lab. Like the Argonne detector, our detector will be used in conjunction with a position sensitive parallel plate avalanche counter (PPAC). We have not yet finished construction of the detector, so we do not have any experimental results, but we are on schedule to finish the detector and begin testing it before the end of the semester. Together, the system will be able to resolve individual medium/heavy isotopes up to the mass 100 atomic units.
Atmospheric Corrections and Periodic Variations at Project GRAND

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GRAND consists of 64 proportional wire chamber detector stations located near the University of Notre Dame and has been used to detect muons since 1995. First, single-track muon data of GRAND are corrected for atmospheric effects using NOAA weather data to better understand the effects of pressure and temperature (mean muon creation height) on flux. This analysis yields a pressure correction coefficient ($\beta_p$) of -0.83 and for temperature, a creation height correction coefficient ($\beta_h$) of -0.71. Second, with these corrections a long-term time series from July 2007 to January 2008 was analyzed to investigate the time dependence of the daily mean variation in cosmic ray flux over the course of a season. For this data set, signal-processing techniques were used to identify the evolution of periodic trends, particularly at one and two cycles per day, indicating significant variations.
Discovery of a Wolf-Rayet Star from Detection of its Photometric Variability

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Using observations acquired with the 11-inch telescope at the Jordan Hall observatory, we report the discovery of a new Wolf-Rayet star, WR 142b. Subsequent observations with the 9-m Hobby-Eberly Telescope (HET) in Texas and the 8.4-m Large Binocular Telescope (LBT) in Arizona confirmed the discovery and enabled us to study some of the star’s key properties.

Universally considered to be progenitors of core-collapse supernovae and possibly even gamma-ray bursts, Wolf-Rayet stars (WRs) are among the most exotic stars known to exist. They are highly evolved, luminous descendants of the most massive main-sequence stars and possess exceptionally strong winds that eject the star’s outer layers. WRs emit copiously in ultraviolet wavelengths due to their high surface temperatures, ionizing the ejected material. The resulting emission spectra generally contain some mix of Doppler-broadened He, C, N, and O, all of various ionization states. At most, the WR phase lasts only for several hundred-thousand years—quite short in astronomical terms—and culminates with a core-collapse supernova. WRs are very rare, and for every 100 million stars in the Milky Way, only one on average is a WR.

WR 142b first caught our attention by displaying irregular, short-term variations in its brightness. At the time, it was not known to be a noteworthy star, but spectra obtained with the 11-inch telescope revealed a number of emission lines commonly found in WRs, including He I, He II, and N IV. A follow-up spectrum obtained with the HET confirmed these lines and uncovered many more, showing WR 142b to be a nitrogen-rich WR of spectral class WN6. While WRs frequently harbor massive companion stars, an LBT spectrum of WR 142b in blue and near-ultraviolet wavelengths shows no evidence of a second body in the system.

Extinction from interstellar dust dims WR 142b by ~8.1 magnitudes in optical wavelengths, explaining why the true nature of such an intrinsically bright star has eluded recognition until now. Were it not for the extinction, WR 142b might be visible to the naked eye.

WR 142b is an unusual WR in that its apparent brightness routinely changes over the course of just several hours with no apparent periodicity. It is relatively uncommon for a WR to vary appreciably over such a short time span. The current data does not pinpoint the mechanism of this variability, but it does disfavor several possibilities, such as rotational modulation and binarity.

The discovery paper has been submitted to The Astronomical Journal.
Radiative $W$ production at hadron colliders is an important testing ground for the Standard Model. The DØ detector at Fermilab in Batavia, IL provides data regarding these kinds of processes from Run II of the Tevatron accelerator, which began in March 2001. A crucial part of this analysis is to determine the rate of $qq \rightarrow W^\pm + \gamma\gamma$ event production at the Tevatron since this experimental data is a good way to check the accuracy of the Standard Model and a good test to see if the Standard Model needs to be revised or not. The substance of this analysis involves measuring the transverse energy distributions of the particles in this event. However, these distributions can be skewed by background events that may presumably appear similar to the events that are trying to be measured and analyzed. Thus, cuts must be applied to the data set in order to eliminate the undesired noise in the signal. We will present preliminary results on our search for the $W^\pm\gamma\gamma$ process using a significant fraction of the Run II Tevatron data set.
The research performed revolves around creating tracking algorithms for the proposed ten-year upgrade to the silicon tracker for the Compact Muon Solenoid (CMS), one of two main detectors for the Large Hadron Collider (LHC) at CERN in Geneva, Switzerland. The ten-year upgrade corresponds to the Super LHC (SLHC) era when the interaction rate of the LHC is expected to increase by an order of magnitude. The sheer number of interactions will make it impossible to use the current trigger system to select interesting events due to the overwhelming backgrounds. The proposed upgrade to the silicon tracker for CMS will use high-speed electronics to trace particle trajectories so that they can be used immediately in a trigger system. The additional information will be combined with other sub-detectors in CMS to distinguish interesting events from background, enabling the good events to be read-out by the detector. The algorithms would be implemented directly into the Level-1 trigger, i.e. the first trigger in a two-trigger system, to be used in real time. One algorithm we created has proven very effective. This algorithm attempts to match hits in the layers of the detector to pre-recognized patterns of particle trajectories. Different parameters were tuned to reduce the number of fake tracks while retaining a high level of track finding efficiency. This corresponds to tuning the occupancy of hits in a given bin corresponding to a given pattern. We simulated events with environments equivalent to SLHC luminosities, looking at computer generated stable particles over various ranges of transverse momentum and the various tracks they produce. The future of this project will look to incorporating this code into detector hardware.
In the search for the Higgs particle from proton-proton collisions, the primary challenge is to separate meaningful signal of the particle desired from the background noise of many particles produced. To this end, it is useful to examine common processes identified with the background so that they can be recognized and eliminated. We are looking at one such process, the \( pp \rightarrow Wc \), in which a W boson and charm quark are produced. Specifically, we are attempting to analyze processes in which the c hadronizes to a D0 meson that decays to one kaon and one pion of opposite charge. In order to recognize this process, we must reconstruct pairs consistent with the kaon and pion masses, with opposite charge, and with a total 4-vector invariant mass consistent with the understood mass of the D0. This presents a challenge because there are a myriad of oppositely charged pairs of particles that can be produced in similar interactions. We therefore use a specific series of data cuts to attempt to reduce this background from the D0 signal. To make such cuts, we analyze simulated data to see what restrictions can be applied that will reduce background significantly more than they will reduce signal. These would then be applied to real data from the CMS experiment at the LHC to attempt to find a recognizable D0 signal.
One of the most important reactions in the late stages of the evolution of stars is the 12C+12C fusion reaction. Limited by the detection technique and the available beam intensity, all the current experimental studies on this important reaction are restricted at energies higher than the Gamow window, the energy region of astrophysical interest. Currently, our understanding of the reaction rate of 12C+12C relies on the extrapolation of the cross section measured at higher energies. However, there are many resonances existing in the 12C+12C system. The extrapolation is not reliable because the potential resonances within the Gamow window may lead to a much higher reaction rate than we are thinking now. To improve the detection efficiency and selectivity, a solenoid spectrometer is being developed at Notre Dame to detect the charged particles produced by the 12C+12C reaction. The efficiency of the solenoid spectrometer is very high. It is about a factor of 30 times higher than the detectors used in the past 12C+12C experiments. Results of these measurements will be presented along with future plans for further improvements of the detection efficiency and selectivity.
Poster Presentation

*Which Household Pollutant is most harmful to Aquatic Life: The Effect of Various Pollutants on the Survival Rate of Daphnia*

Darius Balsara  
Northern Indiana Regional Science and Engineering Fair Winner  
Schmucker Middle School

Water pollution is a major problem in the twenty first century. This is due to increase in factories and industries all over the world. Another contributing factor is the rapid increase in population that taxes the natural resources. Some of the most common household products that we use unwittingly contribute to water pollution. Bleach, detergent, and weed killers are routinely used. These products very easily find their way in the waterways, affecting aquatic life. In my experiments, I used the water flea, Daphnia magna a known sensitive bio-indicator. The Daphnia were exposed to different concentrations (0%, 1%, 0.1%, and 0.01%) of bleach, detergent, and weed killer and the rates of their heartbeats per minute were recorded. My data demonstrated that when the pollutants were present at 1% concentration, no heartbeats were detected, indicating no survival. However, at 0.01% concentration of bleach the heartbeats of the Daphnia were most depressed compared to 0.01% detergent or weed killer. This indicates that bleach is the most harmful pollutant. It was also observed that the higher concentrations of the chemicals decreased the survival of Daphnia compared to lower chemical concentrations.
Poster Presentation

The Effect of Tin and Radiation on the Death of Simulated Cancer Cells

Dinuka Cooray
Northern Indiana Regional Science and Engineering Fair Winner
Saint Anthony De Padua School

For this science fair, I wanted to find an efficient, inexpensive way to cure cancer. By placing tin metal among Saccharomyces cerevisae (yeast) and irradiating the variables, I wanted to know whether this "cancer treatment" would work and destroy the simulated cancer cells. My variables were: yeast with tin, yeast with tin and irradiated, yeast alone irradiated, and yeast neither irradiated nor with tin (control). To do my experiment I made all of the variables and irradiated the variables that needed radiation for five minutes in an electron accelerator. After diluting each of the variables two times to have three dilutions, I spread the dilutions on the agar plates using sterile beads. The variables were placed in an incubator for 48 hours. I observed and recorded number of yeast colonies on the plates. I repeated my experiment five times. In the end I found out that my hypothesis was half correct. The plates with the tin had the least colonies and was most effective. Next was the plates with tin and radiation. Afterwards was the plates with just radiation, and finally my control was last with the most colonies, least effective.
Due to the increasing volume of CO2 being emitted into the atmosphere, scientists predict the ocean pH to drop from its current level of 8.1 to 7.8 by the end of this century. The shells and skeletons of marine calcifiers are made primarily of calcium carbonate. Polymorphs of calcium carbonate have different solubility rates, suggesting calcifiers may be affected differently based on which polymorph they consist of. It is hypothesized that seawater temperature, pH and seashell type are all factors that influence decalcification. This study used a 2x3x3 factorial design (18 groups) to study the change in mass of three seashell types (ark, mixed, mussel) exposed to seawater of two pH levels (8.1 and 7.5) and three temperatures (3CF, 20C, 33C) over a 3-week time period. Shells comprised primarily of low-magnesium calcite (Ark Shells) were the least affected by pH or temperature. Groups containing Mussel Shells consistently lost more mass than those with Mixed or Ark shells, averaging an overall loss in mass of 1.7559% compared to a 0.3448% loss by the Mixed Shells, and a gain of 0.0044% by the Ark Shells. A Main Effect of Shell Type was observed, indicating the sensitivity Mussel Shells have to pH and temperature. Interactions were found between all factors. The group “Mussel Shells x 3C x 7.5pH” experienced the largest average loss in mass of all 18 groups at 2.1846%. Since Mussel Shells are sensitive to ocean acidification, nations that depend heavily on them for food and income may be greatly affected.
Bugging Around With Magnets: An Analysis of Strength of a Horseshoe Magnet on the Velocity of a Magnet

Joshua Leady
Northern Indiana Regional Science and Engineering Fair Winner
Christ The King School

The purpose of the experiment is to see if the velocity of a Hexbug has a correlation with the magnetism of a horseshoe magnet and to find out how the Hexbug is affected by the magnet if it is. I predicted that the closer the magnet is to the Nano, the lower the velocity of the Nano will be. I built a racetrack to control the route of the Hexbug and then timed it to calculate its velocity. After repeating the experiment with more Hexbugs, I found in my data that the magnet increased the velocity of the Hexbug as it became further and further away. Shockingly, after being over 15 mm from the glass surface of the track, the velocity began to decrease. Overall, I found that at the beginning of the timing of the Hexbugs, the results matched with my predictions, but at the end of the racing, the velocity was not as anticipated. I believe this to be the result of either a lowering battery or that the magnet centered the Hexbug so that it would not slow down due to bumping into walls.
Due to all of the concerns over fossil fuels, scientists are placing their focus on Green Energy options. Since solar power was new to me, I did some pretests to learn more about my panel and to determine how to set up my experiment. I tested light bulbs, angles of incidence, color filters and light blockers. I decided due to the overcast days to use a 100w light bulb, use an angle of 00, no color filter, and 12 layers of aluminum foil covered in electrical tape to make my shading pieces. My experiment was to incrementally shade portions of the solar panel (independent variable) and measure energy output (dependent variable). My hypothesis was: If I shade a portion (percentage) of a solar cell, the cell will produce less energy than just the amount (percentage) shaded. I marked my lamp placement (control), I attached the solar panel to a block of wood and centered the center of the light bulb with the center of the solar panel and marked its placement (control). I connected the 6V panel and 6V LED light bulb to a voltmeter then repeated with an amp meter. In between each of my 10 trials I used a light eliminator box to cover the panel and allow the meter to read close to zero (control). My hypothesis was correct. For example, I covered 20% of the panel and there was a 26% loss in volts and a 25% loss in wattage. Placement of solar panels is important, a tree or fence could cause you to lose valuable power.
The World Wide Web allows people to pass information through e-mails quickly and to many people through forwarding. One forward that we have received at our home refers to a linguistics study that says you can easily read paragraphs where the letters in the words are scrambled, as long as the first and the last letters of those words remain in their original places. My project looks at whether or not this is true. Because some critics of this study point out that the scrambled paragraph used was possibly too easy, I decided to structure my experiment with three levels of difficulty for scrambling the paragraphs: Easy, Medium, and Hard. I developed specific criteria for how to scramble the paragraphs in each difficulty level. I tested 100 subjects, each reading three paragraphs. I tested 50 people on the original paragraphs and 50 different people on the scrambled paragraphs. I used this large sample size to ensure a strong average for the two tests. I timed each person on their particular set of paragraphs and found the average reading times for the regular and scrambled paragraphs. My hypothesis was that it would take longer on average to read the three scrambled paragraphs because the words would look unfamiliar to the reader. This hypothesis was supported by my results. On average, it takes longer to read the scrambled paragraphs.
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