UNIVERSITY OF NOTRE DAME

Colleges of Science & Engineering Joint Annual Meeting

2nd Annual COSE-JAM for Graduate Students & Postdoctoral Fellows

Friday – December 7, 2018

Jordan Hall

PROGRAM SCHEDULE

Morning Session (9-12:15pm): 24 podium presentations in Jordan auditoriums (101 & 105)
(continental breakfast/snacks/drinks in Galleria; 10:30-10:45 mid-morning break)

Lunch (12-1:30pm): Jordan Galleria – participants, discussants, moderators, co-authors, etc.

Award Presentation (12:30-12:35pm): 101 Jordan – Presentation of *Edison Innovation Award*

Panel Discussion (12:35-1:20pm): 101 Jordan – Panel Discussion on Careers in STEM

Associate Dean of Research and Graduate Studies – College of Science

Directors of Graduate Studies – Aerospace and Mechanical Engineering, Bioengineering, Biological Sciences, Chemistry and Biochemistry, Integrated Biomedical Sciences, Civil and Environmental Engineering and Earth Sciences

Associate Program Director – Office for Postdoctoral Scholars

Afternoon Session (1:30-4:30pm): 64 poster presentations in Jordan Galleria
(light snacks/soft drinks in Galleria)

Afternoon Social (3:30-6:00pm): Jordan Galleria – opportunities for formal and informal interactions among attendees (snacks/soft drinks/beer/wine)

PANEL DISCUSSANTS (lunchtime at 12:30-1:20pm – 101 Jordan)

Michael Hildreth, Ph.D., is Associate Dean of Research and Graduate Studies in the College of Science. Dr. Hildreth is also a Professor in the Department of Physics.

Prof. Hildreth's primary physics interest is in discovering and understanding the mechanism or mechanisms responsible for Electroweak Symmetry Breaking. Simply put, this would answer questions like: "why is there mass?" Prof. Hildreth is a part of the CMS Experiment at CERN's Large Hadron Collider (LHC) in Geneva, Switzerland, where he and the rest of the Notre Dame High Energy Physics group played key roles in the recent discovery of a Higgs boson. His group is involved in measuring Higgs properties, specifically the coupling of the Higgs boson to top quarks. These measurements are essential in determining if the Higgs we see is really the source of Electroweak Symmetry Breaking and the origin of particle masses, or whether new physics is required. He is also working on searches for new physics beyond the Standard Model of particle physics, specifically looking for new physics in final states involving high energy photons and, separately, high energy tau leptons.

Hildreth is currently leading the CMS group responsible for modeling the interaction of particles with the material of the detector elements. This is essential for understanding the response of the detector to the signals for all of the various physical processes one wishes to study at the collider.

Since 2012, Prof. Hildreth has led a multi-university team that is exploring the programmatic and technical intricacies of knowledge preservation in science. The DAta and Software Preservation for Open Science (DASPOS) team consists of physicists, computer scientists, and digital librarians from Notre Dame, University of Chicago, University of Illinois Urbana-Champagne, University of Nebraska Lincoln, New York University, and the University of Washington. This is a multi-disciplinary effort designed to explore the knowledge preservation needs of various disciplines and to construct a prototype data and software preservation architecture that can be used as a template for knowledge preservation efforts in different fields of science.

Prof. Hildreth is also involved in an accelerator instrumentation project the KEK laboratory in Tsukuba, Japan. He leads a primarily undergraduate group of students who are building laser interferometer systems to monitor the mechanical stability of accelerator components at the 10 nanometer level. The primary goal of this research is to demonstrate that a precision energy spectrometer based on beam position monitors can attain the necessary resolution.

Hildreth is a graduate of Princeton University, and holds a Ph.D. from Stanford University.

Rebecca A. Wingert, Ph.D., is Director of Graduate Studies and the Elizabeth and Michael Gallagher Associate Professor in the Department of Biological Sciences.

The Wingert Lab studies the genetic and molecular mechanisms that control how renal stem cells accomplish kidney formation, impact kidney homeostasis, and facilitate kidney regeneration following organ injury. Understanding these processes has broad implications for identifying the basis of renal birth defects and the responses to tissue damage that lead to kidney disease. Kidney diseases are a growing global healthcare issue: they affect epidemic numbers of children and adults worldwide, and are steadily climbing in incidence. Kidney diseases can be treated with renal replacement through dialysis or organ transplant, but both strategies require life-long medical management and can involve significant complications. Knowledge obtained from studying the basic biology of the renal system can provide a valuable way to discover innovative therapies for kidney disorders.

Dr. Wingert is a graduate of Muhlenberg College, and holds a Ph.D. in Cell and Developmental Biology from Harvard University. She was a postdoctoral fellow at Harvard Medical School and Massachusetts General Hospital.

Brandon L. Ashfeld, Ph.D., is Director of Graduate Studies and Associate Professor in the Department of Chemistry and Biochemistry.

The Ashfeld Lab is focused on the development of new methods to enable unconventional bond formations in the synthesis of complex natural products and designed materials. His main objective is to use new chemical constructs to design and synthesize improved chemotherapies for brain and CNS cancers, and materials that will ultimately lead to the reduction of atmospheric concentrations of anthropogenic CO_2.

Dr. Ashfeld is a graduate of the University of Minnesota-Twin Cities, and holds a Ph.D. in Chemistry from the University of Texas at Austin. He was a NIH/NRSA postdoctoral fellow at Stanford University.

Jeff S. Schorey, Ph.D., is Co-Director of the Integrated Biomedical Sciences Graduate Program and George B. Craig Professor in the Department of Biological Sciences.

The Schorey Lab investigates the pathobiology of mycobacterial diseases. Mycobacterial species have a long history as human and animal pathogens and are the etiological agents of diseases such as tuberculosis and leprosy. Tuberculosis (TB), caused by the bacteria *Mycobacterium tuberculosis,* is a particularly deadly disease accounting for approximately 1.5 million deaths annually and is the leading cause of death due to a single infectious organism. A global threat in recent years has been the significant increase in multi-drug resistant strains of *M. tuberculosis*. Other pathogenic mycobacteria include *M. avium*, a major opportunistic pathogen of AIDS patients in the US, and now increasingly associated with COPD and Cystic Fibrosis patients. His research aims to control mycobacterial infections via a better understanding of *Mycobacterium*-host interactions and develop the next-generation of diagnostic tools, vaccines and antibiotics directed toward eradicating TB and other mycobacterial diseases.

Dr. Schorey holds a Ph.D. from the University of Texas Health Science Center. He was a post-doctoral fellow at Washington University School of Medicine.

Antonio Simonetti, Ph.D., is Director of Graduate Studies and Associate Professor in the Department of Civil and Environmental Engineering and Earth Sciences.

The Simonetti Lab focuses on: developing innovative microanalytical techniques and/or novel methods for the identification of forensic signatures within post-detonation materials and natural nuclear materials for the purpose of accurate and rapid source attribution; characterizing the chemical and isotopic nature of Earth's upper mantle through the investigation of alkaline complexes (carbonatites, alkali silica-undersaturated rocks) worldwide; geochronological investigations of igneous rocks and biogenic materials; long-range tracing of atmospheric pollution; and strontium isotope studies of teeth from burial sites of Archaeological interest.

Dr. Simonetti received a BS and MS from McGill University, and has a Ph.D. from Carleton University. He was an NSERC postdoctoral fellow at ENS Lyon and Max Planck Institute.

Glen L. Niebur, Ph.D., is Director of the Bioengineering Graduate Program and Professor in the Department of Aerospace and Mechanical Engineering.

The Niebur Lab is interested in orthopedics, including bone quality, damage mechanics of trabecular bone, hard-tissue mechanobiology, hard and soft tissue constitutive modeling, computational mechanics of tissues, and genetic factors affecting bone quality. Current projects are investigating the interactions between microdamage formation in bone and the changes in bone porosity and structure that accompany osteoporosis. Osteoporosis results in changes at multiple levels of the hierarchical structure of bone, and these can either compensate for or enhance fracture risk. Medical imaging methods, especially computed tomography (CT) are used to image and quantify bone structures in bone samples and in live animals. A current project is using medical imaging to longitudinally monitor and understand fracture healing. Most recently, work has begun in the area of bone marrow mechanics, effects of aging and disease on bone marrow morphology, and interactions between bone and bone marrow.

Dr. Niebur received a BME and MSME from the University of Minnesota, and holds a Ph.D. from the University of California at Berkeley.

David B. Go, Ph.D., is Director of Graduate Studies and the Rooney Family Associate Professor in the Department of Aerospace and Mechanical Engineering.

The Go Lab examines energy, fluid, and charge transport from millimeter to nanometer scales. They seek to understand the fundamental phenomena, engineer new technology, and solve problems of high importance in order to solve the grand challenges of our world. Applications being studied include thermal energy conversion and management, materials synthesis, and biological/chemical analysis. We approach these topics theoretically, computationally, and experimentally, ranging from basic phenomena to technology development.

Dr. Go is an alum of the University of Notre Dame. He has a MS in Aerospace Engineering from the University of Cincinnati and a Ph.D. in Mechanical Engineering from Purdue University.

Valli Sarveswaran, Ph.D., is the Associate Program Director with the Office for Postdoctoral Scholars at the University of Notre Dame. As the Associate Program Director, Valli is responsible for career counseling, professional development, and social engagement for all scholars appointed through the University of Notre Dame's Office for Postdoctoral Scholars.

He was previously, the Director of McNair Scholars Program at Cleveland State University, Cleveland OH for more than eight years. The McNair Scholars Program is a federally funded program that prepares undergraduate students for graduate schools. Valli has held postdoctoral research positions and administrative positions in various educational institutions in Canada and the United States.

He holds a BS in Chemistry from the University of Jaffna, Sri Lanka, and a Ph.D. in Organomettalic Chemistry from the University of Cambridge, England.

MORNING PODIUM SESSIONS (9am-12:15pm – 101 & 105 Jordan)

Jordan 101 (moderator: Susan Lad)

8:30 – Upload all presentations

9:00 – **Alyssa Oberman**: The Effects of LiCl Treatment on Bone Formation *In Situ*

9:15 – **Daniel Henriques Moreira**: Visual Data Integrity, Accountable Computing, and Privacy Protection Leveraging Computer Vision Techniques

9:30 – **Erin Howe**: Rab11b-Mediated Control of the Cell Surface Proteome Drives Metastatic Adaptation

9:45 – **Ashabari Majumdar**: Development of St. Andre Ion Beam Facility

10:00 – **Martin Fevre**: Dynamics and Control of Underactuated Biped Robots

10:15 – **Emily Nett**: Eyes without a Face: Ontogeny of Orbit Orientation in Primates

10:30 – Break

10:45 – **Ek Adhikari**: Total Yield of Reactive Species Originating from an Atmospheric Pressure Plasma Jet in Real Time

11:00 – **Tyson Lager**: Aberrant Cell Surface Expression of GRP78 in Breast Cancer Cells Marks a Stem-Like Population that has Increased Metastatic Potential *In Vivo*

11:15 – **Yinan Li**: Data Privacy: Differential Privacy in Empirical Risk Minimization Problems

11:30 – **Ramezan Paravitorghabeh**: Tissue Level Regulation of Ca2+ Signaling in Epithelia

11:45 – **Mohsen Darayi**: A Numerical Study on the Wrinkling of Neo-Hookean Elastic Multi-Layers

12:00 – **Susan Lad**: Bone Remodeling in the Macaque (*Macaca fascicularis*) Skeleton: Effects of Loading Frequency and Magnitude

Jordan 105 (moderator: Abigail Weaver)

8:30 – Upload all presentations

9:00 – **David Armitage**: Negative Frequency-Dependent Growth Underlies the Stable Coexistence of Two Cosmopolitan Aquatic Plants

9:15 – **Bradley Ellis**: Recovery of hiPSC *In Vitro* Myocardium Model is Promoted by Adipose Stem Cell Conditioned Medium

9:30 – **Martin Imre**: Exploring Time-Varying Multivariate Volume Data Using Matrix of Isosurface Similarity Maps

9:45 – **Chissa-Louise Rivaldi**: Defining Characteristics and Community Structure of the Gut and Oral Microbial Communities of Long-Tailed Macaques (*Macaca fascicularis*) in Singapore

10:00 – **Charlotte Wood**: Benchmarking Substellar Evolutionary Models using New Age Estimates for HD 4747 B and HD 19467 B

10:15 – **Marwa Asem**: Regulation of Ovarian Tumor:Microenvironment Dynamics by Compressive Stress

10:30 – Break

10:45 – **Joel Brogan**: Tracing the Stories of Images on the Internet

11:00 – **Chinedu Madukoma**: Snapping: A Long Range, Type IV Pili-Dependent, Group Motility of *Pseudomonas aeruginosa*

11:15 – **Sean McGuinness**: Production of 52Fe from Symmetric Complete Fusion-Evaporation Reactions

11:30 – **Andrew Wightman**: Probing Effective Field Theory Models using Associated Top Quark Production in Multiple Lepton Final States at 13 TeV

11:45 – **Bridgette Drummond**: The Zebrafish Renal Progenitor Cell Mutant *oceanside* (*ocn*) Reveals that the Osr1 Transcription Factor Regulates Wnt Signaling to Control Kidney Development

12:00 – **Elizabeth Harper**: Aging Promotes Changes to Peritoneal and Omental Collagen Structure that Contribute to Increased Ovarian Cancer Metastatic Success

AFTERNOON POSTER SESSION (1:30-4:30pm – Jordan Galleria)

Laura Alderfer: Predicting Pre-Eclampsia using Exosomal miRNA

Wendy Alvarez Barrios: Integrative Platform Reveals Subcellular Changes of Single Cells and Exposes a Potential PTEN-Dependent Vulnerability to Mechanical Stress during Metastatic Mechanical Arrest in the Brain Vasculature

Luis Felipe Avila: Elucidating the Interactome of the Lytic Transglycosylase RlpA of *Pseudomonas aeruginosa*

Gozde Basara: Dual Crosslinked Gelatin Methacrylol Hydrogels for Photolithography and 3D Printing

Sarah Bliese: Detection of Degradation Products of Ceftriaxone Using Paper Analytical Devices (PADs)

Luca Boccioli: Simulating the Explosion of a Supernova for a Detailed Nucleosynthesis Study

Shelby Brantley: The Effects of Charge Scaling Ions in the DNA Ion Atmosphere

Sean Breckling: Unified Bayesian Networks for Uncertain Inputs and Partial Model Ensembles

Kurtis Breger: Elucidating the Kinetic Mechanism of Human METTL16

Alejandra Cartagena-Sierra: Oceanographic Variability across the Mid-Pleistocene Transition at the Agulhas Plateau

Alexandra Chirakos: Discovery of Novel Regulatory Pathways of the ESX-1 Secretion System in Pathogenic Mycobacteria

Hannah Corman: Development of Novel Anti-Leishmania Chemotherapeutics: High-Throughput Screening and Investigation of Structure-Activity Relationships of 2,4-diaminoquinazoline Heteroaromatic Scaffolds

Stephen Cortese: Primate Health Responses to Extreme Drought in Northwestern Costa Rica

Hernan Delgado: Effect of Competing Oxidizing Reactions and Transport Limitation on the Faradaic Efficiency in Plasma Electrolysis

Aleksandar Dimkovikj: Examining the Influence of the Nutrient Environment on Antibiotic Susceptibility of *Pseudomonas aeruginosa*

Nima Ehsani: Hydrologic and Biogeophysical Parameter Estimation for Simulating Watershed-Scale Conservation to Reduce Nutrient Losses to Surface Waters using SWAT

Micah Ferrell: Genetic Analysis of ESX-1 Substrates Reveals Complex Secretory Phenotypes in Mycobacteria

Catherine Flanley: *Phlebotomus papatasi* Salivary Gland Gene Diversity in Distinct Ecotopes of Egypt and Jordan

Taylor Gambon: Using Template Models to Identify Exoskeleton User Intent

Benjamin Gombash: Metabarcoding Techniques Provide a New Tool for Assessing Long-Tailed Macaque Diets

Ian Guldner: Microglia Subset Revealed by Single Cell Analyses Promotes Brain Metastasis Outgrowth through Fractalkine Receptor-Dependent Interferon Response

Karlyn Harrod: Data Assimilation on Lumped Parameter Models for Diastolic Heart Failure

Lauren Hensley: Pressure Estimation and Fluid Domain Segmentation using Physics-Based Deep Learning

Francisco Herrera: The Effects of Supported Catalyst on the Plasma in a Packed-Bed Dielectric Barrier Discharge Reactor for Ammonia Synthesis

Atul Kedia: Relativistic Electron Scattering and Big Bang Nucleosynthesis

Kristi Kilgore: Determining Virulence Factors in MAC Infections

Charlotte Kunkler: Stability of RNA•DNA-DNA Triple Helices Depends on Base Triple Composition and Length of the RNA Strand

Liguang Li: Cover Crops Increase Bioavailable Legacy Phosphorus in an Agricultural Watershed

Xue Li: Explicit Solution of Cardiovascular Model Ensembles with Random Field Material Properties on GPUs

Yinan Li: Anapel: Adaptive Noise Augmentation for Privacy-Preserving Empirical Loss Minimization

Yinan Li: Panda: AdaPtive Noisy Data Augmentation for Regularization of Undirected Graphical Models

Daniel Martin: Measuring the Plasma Radius at the Plasma-Liquid Interface in a Pulsed, DC Discharge

Ian McAlister: Using XCone as an Exclusive Jet Clustering Algorithm for Collisions in the Compact Muon Solenoid Detector

Phillip McCown: Structural Analyses of Human MALAT1

Hannah McGarraugh: Selective Photothermal Heating with Near-Infrared Croconaine Rotaxanes

Tierney Miller: Counter Cation-Specific Effects on Transport in Aqueous Hydroxide Solutions

Kelci Mohrman: Tools for Trigger Rate Monitoring at CMS

Kathleen Nicholson: MMAR_2894 is an ESX-1 Associated PE-Protein in *Mycobacterium marinum*

Kevin O'Brien: EMG-Driven Musculoskeletal Simulations Using New Threshold Optimization Technique

Keith O'Connor: Plant Water Fractionation along a Latitudinal Transect of Northern Alaska

Agnieszka Ruszkowska: Structural Studies of Human Methyltransferase-Like Protein 16

Kevin Sanchez: Characterizing Transcriptional Regulation of Virulence in *Mycobacterium marinum*

Jessica Schiltz: Fatigue Performance of Direct Metal Laser Sintered Parts using Reused Metallic Feedstocks

Cassandra Schaffer: New Means of Gold Recovery using Novel Gold Capture Molecules

Samantha Sherman: Implicit Symmetric Tensor Decomposition with Applications in Data Analysis

Madeline Smith: The ChemoPAD: A Paper Analytical Device for Detecting the Presence of Four Chemotherapy Drugs

K. James Soda: DTK-Dengue: A New Agent-Based Model of Dengue Virus Transmission Dynamics

Shannon Speir: Quantifying the Recovery of Nitrogen Removal Capacity via Denitrification Following Stream Dredging and Floodplain Construction in an Agricultural Watershed

Robert Stanley: Determining the Defensive Mechanisms in Green Ash (*Fraxinus pennsylvanica*) Resistant to Emerald Ash Borer (*Agrilus planipennis*)

Casey Stefanski: Loss of APC Mediates Doxorubicin Resistance in Breast Cancer

Shannon Stoffel: Investigations of a Molecular Machine, Cyclodextrin Rotaxane, using NMR Methods

Ceara Talbot: Using a Replicated Watershed Design to Evaluate the Role of Cover Crops in Reducing Nutrient Pollution

Xi Tan: Simulation Study of the Asymmetric Vibrational Excitation in CO_2 Field Emission-Driven Townsend Discharges

Hui Yin Tan: Isolation of Monoclonal Antibodies using Mimotope-Containing Membranes

Audrey Taylor: Biomarker Records of Plio-Pleistocene Paleoclimate from the Southeast African Margin

Matt Trentman: Comparing Biotic Controls on Phosphorus Cycling in Stream Sediments and Floodplains Soils in Agricultural Streams

Vijay Velagala: Reverse-Engineering Unit Operations of Morphogenesis: Factors Modulating Epithelial Spreading Dynamics in *Drosophila*

Qingfei Wang: Single-Cell Profiling Guided Combinatorial Immunotherapy for CDK4/6 Inhibitor Resistant HER2-Positive Breast Cancer

Abigail Weaver: Complex Microbial Communities Relevant to Prosthetic Joint Infections

Annaliese Wieler: Inocolum Dose Dependency of Influenza Infection

Xinyue Zhao: The Impact of Time Delay in a Tumor Model

Junjun Zuo: Plakoglobin as a Potential Marker for a More Aggressive Population in Breast Cancer

ABSTRACTS

(alphabetical by presenter)

Oral Presentation:

Total Yield of Reactive Species Originating from an Atmospheric Pressure Plasma Jet in Real Time

Ek R. Adhikari,[1,2] Vladimir Samara,[2] and Sylwia Ptasinska[1,2]

[1]Department of Physics, University of Notre Dame, Notre Dame, IN 46556, USA

[2]Radiation Laboratory, University of Notre Dame, Notre Dame, IN 46556, USA

The reactive oxygen species of a helium atmospheric pressure plasma jet (APPJ) was measured via *in situ* absorption spectroscopy using an acidified ferrous sulfate solution (Fricke) as a sample. The rate of yield of Fe^{3+} from the Fe^{2+} corresponds to the amount of reactive species reached to or originated in the sample. We observed that the number of reactive species formed in the plasma jet is proportional to the applied pulse voltage and repetition frequency. However, there is a decrease in the yield of Fe^{3+} per pulse for an increase in the frequency. For higher frequencies, there is not enough time between two consecutive pulses to complete all reactions. Whereas, for lower frequencies, this yield is higher due to the longer time period between two consecutive pulses which requires to complete the relatively slow reactions. Further, the flow rate of feed gas and treatment distance, which is the distance between the sample and glass capillary, have a minor effect on the formation of reactive species, but the yield of Fe^{3+} gradually decreases for a treatment distance longer than 20 mm. Moreover, we calculated the yield of Fe^{3+} in a very short time (equivalent to time period used in the experiment) to get more insight of short-lived reactive species and their importance to initiate the biochemical reactions oxidizing Fe^{2+} into Fe^{3+} ions.

Poster Presentation:

Predicting Pre-Eclampsia using Exosomal miRNA

Laura Alderfer, Zeinab Ramshani, Brian Coe, David Go, Hsueh-Chia Chang, Donny Hanjaya-Putra

Department of Aerospace and Mechanical Engineering, Department of Chemical and Biomolecular Engineering, University of Notre Dame

Pre-eclampsia (PE), a hypertensive disorder that arises during 3-5% of all pregnancies, affects 10 million women globally. PE is annually responsible for 76,000 maternal deaths and 500,000 infant deaths but current diagnoses only occur once symptoms are presented and the only treatment available is delivery of the child. While the symptoms of PE, which include hypertension, thrombocytopenia, renal insufficiency, and cerebral or visual disturbances, are resolved postpartum, PE has long-term health risks for mothers which include cardiovascular disease, metabolic syndromes, and stroke.

microRNAs (miRNAs) are stable in circulation and have the capability to be used as predictive biomarkers of PE. Endothelial colony-forming cells (ECFCs) release exosomes which contain miRNAs and these exosomes can be collected in a maternal plasma sample. Three angiogenesis associated miRNAs, miR-210, miR-574, and miR-1233, have been consistently over-expressed in patients with PE.

By analyzing miRNA concentrations at different stages of gestation in both healthy patients and those with PE, a correlation between these miRNA of interest and the development of PE can be established and used as a predictive tool. Rather than waiting for symptoms of PE to present, miRNA levels in a mother's plasma can be measured to monitor her risk of developing PE. This predictive tool will improve immediate care and could also help to reduce the long-term risks of cardiovascular disease and stroke. By using a microfluidic device which contains a nanomembrane sensor that is specific to the miRNA of interest, the miRNA concentration can rapidly be measured after the exosomes have been isolated and lysed. In preliminary studies, the concentration of miR-210 has been measured to be over a hundredfold greater in patients with PE, as compared to healthy patients, and serves as a potentially promising biomarker.

Poster Presentation:

Integrative Platform Reveals Subcellular Changes of Single Cells and Exposes a Potential PTEN-Dependent Vulnerability to Mechanical Stress during Metastatic Mechanical Arrest in the Brain Vasculature

Wendy V. Alvarez Barrios[1,2,3], Huijie Lu[4], Kyle Cowdrick[2,5], Michelle Galarneau[2,5], Lan Jiang[1,2], Emily Abramczyk[1,2], Melinda Lake[6], Lin Yang[7], Zhuo Zhao[7], Danny Chen[7], David Hoelzle[6], Zhangli Peng[4] and Siyuan Zhang[1,2,3]

[1]Dept. of Biological Sciences, [2]Harper Cancer Research Institute, [3]IBMS Program, [4]Dept. of Aerospace and Mechanical Engineering, [5]Dept. of Chemical and Biomolecular Engineering, [7]Dept. of Computer Science and Engineering, University of Notre Dame, Notre Dame, IN 46656, [6]Dept. of Mechanical and Aerospace Engineering, Ohio State University, Columbus, OH 43210

During metastasis of breast cancer tumor cells dissociate from the primary tumor, disseminate through the vasculature, and colonize secondary organs such as the brain, lungs, liver and bones. Mechanical arrest of circulating tumor cells (CTCs) in capillary beds is an essential step in the metastatic cascade for the successful early colonization of secondary organs. During mechanical arrest, tumor cells are subjected to extreme physical stresses such as shear stress exerted by blood flow, and compression from the constricting capillary on the restricted cell. These mechanical stresses may critically impact metastatic success.

However, the precise physical and intracellular response of the disseminated tumor cells at the time of arrest in the vasculature to the mechanical forces of spatial constraint and shear stress remain largely unknown. Here we present an integrative platform that combines the use of a microfluidic device, computational model, and various imaging modalities to reliably reproduce the mechanical arrest of single cells and quantitatively determine their physical response to precisely controlled mechanical forces of shear stress and spatial constraint. Though this platform we revealed that when CTCs undergo mechanical arrest under shear stress, they experience extensive morphological deformations including, but not limited to: 1) membrane elongation, 2) clumping and fragmentation of the mitochondrial network, and most surprisingly 3) PTEN-dependent altered dynamics of mitochondrial fragments that results in an overall decrease in cell viability.

Our results demonstrate that our integrative platform is a viable model system for the qualitative and quantitative study of physical cell behavior that can expose previously unexplored vulnerabilities of tumor cells. Particularly, our results highlight the direct influence of physical forces on the restricted tumor cell, and suggest the importance of these external cues as dynamic determinants of cellular processes and ultimately of metastatic success. We anticipate our platform to be a starting point for future studies seeking to understand the reciprocal molecular and biophysical interplay imposed by mechanical forces in a dynamic 3-dimensional physical microenvironment, particularly at the stage of mechanical arrest in cancer metastasis.

Oral Presentation:

Negative Frequency-Dependent Growth Underlies the Stable Coexistence of Two Cosmopolitan Aquatic Plants

David Armitage and Stuart Jones

Department of Biological Sciences, University of Notre Dame, Notre Dame, IN 46556

Identifying and quantifying the mechanisms influencing species coexistence remains a major challenge for the study of community ecology. These mechanisms, which stem from species' differential responses to competition and their environments, promote coexistence if they give a species a growth advantage when rare. Yet despite the widespread assumption that co-occurring species stably coexist, there have been few empirical demonstrations in support of this claim. Likewise, coexistence is often assumed to result from interspecific differences in life-history traits, but the relative contributions of these trait differences to coexistence are rarely quantified, particularly across environmental gradients. Using two widely co-occurring and ecologically similar species of freshwater duckweed plants (*Spirodela polyrhiza* and *Lemna minor*), we tested hypotheses that interspecific differences in facultative dormancy behaviors, thermal reaction norms, and density-dependent growth promote coexistence between these species, and that their relative influences on coexistence change as average temperatures and fluctuations around them vary. In competition experiments, we found strong evidence for negative-frequency dependent growth across a range of both static and fluctuating temperatures, suggesting a critical role of fluctuation-independent stabilization in coexistence. This negative frequency-dependence could be explained by our observation that for both species, intraspecific competition was over 1.5 times stronger than interspecific competition, granting each species a low-density growth advantage. Using an empirically parameterized competition model, we found that while coexistence was facilitated by environmental fluctuations, fluctuation-independent stabilization via negative frequency-dependence was crucial for coexistence. Conversely, the temporal storage effect — an important fluctuation-dependent mechanism — was relatively weak in comparison. Contrary to expectations, differences in the species' thermal reaction norms and dormancy behaviors did not significantly promote coexistence in fluctuating environments. Our results highlight how coexistence in two ubiquitous and ostensibly similar aquatic plants is not necessarily a product of their most obvious interspecific differences, and instead results from subtle niche differences causing negative frequency-dependent growth, which acts consistently on both species across environmental gradients.

Oral Presentation:

Regulation of Ovarian Tumor:Microenvironment Dynamics by Compressive Stress

Marwa Asem[1,2 3], Alejandro ClaureDeLaZerda[3], Matthew J. Ravosa[3,4], and M. Sharon Stack[1,2,3,4]

[1]Department of Chemistry and Biochemistry, [2]Integrated Biomedical Sciences Program, [3]Harper Cancer Research Institute, [4]Department of Biological Sciences, University of Notre Dame, Notre Dame, IN

Ovarian cancer (OvCa) is the most fatal gynecologic malignancy and the fifth leading cause of overall cancer death among American women with a low (27%) 5-year survival rate, as 75% of women are diagnosed with disseminated intra-peritoneal (IP) metastasis. OvCa cells detach from the primary tumor and shed into the peritoneal cavity, adhere to the peritoneal mesothelial cell (MC) monolayer, intercalate within this layer, and invade into the submesothelial matrix, where they form secondary lesions.

More than one third of OvCa patients develop ascites that correlates with relapse and poor prognosis. The accumulated ascites can reach volumes up to 5 liters, causing a striking elevation in intraperitoneal pressure (IPP) from normally sub-atmospheric ~5mmHg to as high as 27 mmHg. The pressure created by accumulated ascites alters the force environment in the peritoneal cavity, causing strain and compressive forces on peritoneal structures. Yet, the mechanism through which ascites-induced IPP influences OvCa progression is poorly understood. The aim of this study is to understand how ascites-induced IPP promotes OvCa progression.

To model the compressive force present *in vivo,* due to accumulated tense ascites (~27 mmHg), we evaluated the effects of compressive force on the MC monolayer and OvCa cells using the Flexcell Compression System. Strikingly, compressed MC retracted and formed abundant extracellular extensions. Moreover, compressed OvCa cells also exhibited phenotypic alterations and intense extracellular extensions formation *in vitro* and in an *ex vivo* adhesion assay. These extracellular extensions displayed features of tunneling nanotubes (TNT), which are cell membrane extensions that modulate transfer of organelles between cells under stress. Remarkably, TNT formed under compression display membrane distension indicative of active transport of materials between cells.

This study reveals a novel response of OvCa cells and the tumor microenvironment to mechanical compression, uncovering a new mechanism by which OvCa metastatic success may be regulated.

Poster Presentation:

Elucidating the Interactome of the Lytic Transglycosylase RlpA of *Pseudomonas aeruginosa*

Luis Felipe Avila, Stefania De Benedetti, Matthew Champion, Shahriar Mobashery

Department of Chemistry and Biochemistry, University of Notre Dame, Notre Dame, IN 46556

Pseudomonas aeruginosa is a Gram-negative opportunistic pathogenic bacterium. Many existing antibiotics that treat *P. aeruginosa* infections target the cell wall of the organism. Inhibition of synthesis of the cell by β-lactam antibiotics results in bacterial cell lysis. However, drug-resistant *P. aeruginosa* strains have acquired the genes necessary to allow for the detection of β-lactams, which initiates a signaling pathway that culminates in the production of the AmpC β-lactamase, an antibiotic resistance enzyme, which hydrolytically degrades the β-lactam antibiotics. This pathway utilizes the cell-wall recycling process of the organism in its signaling. Lytic transglycosylases (LTs) are enzymes that facilitate cell-wall recycling by catalyzing the cleavage of peptidoglycan of the cell wall. Rare lipoprotein A (RlpA) is one of the 11 LTs of *P. aeruginosa* and little is known of its interactome, the complex assembly of other proteins that interact with it. In the present report, we have identified the putative binding partners of RlpA, using a pull-down approach, followed by mass spectrometry. We have cloned and purified the recombinant proteins detected in our mass spectrometry assay and have explored their interactions with RlpA using a modified dot-blot assay. Verified binding partners will be studied by surface-plasmon resonance and X-ray crystallography. Elucidating the interactome of the LTs, and specifically RlpA, is important in understanding the bacterial physiology of resistance and in aiding drug-discovery efforts.

Poster Presentation:

Dual Crosslinked Gelatin Methacrylol Hydrogels for Photolithography and 3D Printing

Gozde Basara and Pinar Zorlutuna

Department of Aerospace and Mechanical Engineering, University of Notre Dame

Gelatin methacrylol (GelMA) hydrogels have been used in tissue engineering and regenerative medicine because of its tunable mechanical and rheological properties, biocompatibility and printability. However poor mechanical properties limit its application for modelling some diseases or tissues. In this work, a dual crosslinking method for GelMA was introduced. Firstly, the methacrylate incorporated amine groups of GelMA were photo-crosslinked and the initial shape of the gels were fabricated. Secondly, microbial transglutaminase (mTGase) solution was introduced on the gels to enzymatically crosslink the gels by initiating chemical reaction between glutamine and lysin groups within GelMA hydrogel. The results showed that treating gels with mTGase solution improved the stiffness and rheological properties and did not affect the cell viability. The findings also showed that swelling of the gels were reduced with mTGase treatment and photolithographically patterned shapes were preserved better. This effect was also observed when 3D printed substrates were treated with mTGase.

Keywords: dual crosslinking, photo crosslinking, enzymatic crosslinking, microbial transglutaminase, photolithography, 3D printing

Poster Presentation:

Detection of Degradation Products of Ceftriaxone Using Paper Analytical Devices (PADs)

Sarah Bliese and Marya Lieberman

Department of Chemistry and Biochemistry, University of Notre Dame

Substandard and falsified pharmaceuticals are a world-wide problem, with the largest impact in low-and middle income countries (LMICs). Ceftriaxone is a broad-spectrum injectable antibiotic on the World Health Organization (WHO) Model List of Essential Medicines and is often used for treatment when resistance to other antibiotics has developed. Ceftriaxone can undergo ring opening due to hydrolysis, which reduces its antimicrobial activity. We found that a paper analytical device (PAD) can detect falsified, adulterated, and thermally degraded ceftriaxone injectable formulations. Ceftriaxone and changes associated with the thermal degradation of ceftriaxone caused changes in the colors of several lanes of the PAD. To study the thermal degradation, samples were dissolved in sterile water and stored at room temperature. The formation of degradation products was tracked using both the PAD and high performance liquid chromatography (HPLC); the products were identified by liquid chromatography-mass spectrometry (LC-MS). Four degradation products were identified. Their retention times match those found in base degradation studies. A rise in pH of the solution was also observed, which when compared to the kinetics of degradation suggests that ceftriaxone undergoes auto-catalyzed base hydrolysis at room temperature. Eighty blinded samples (30 falsified, 20 thermally degraded, 10 adulterated, and 20 good quality) were evaluated with the PAD, and all but one sample were correctly classified via a principle component analysis (PCA). Forty dosage forms collected in Western Kenya were also assessed, and the PADs correctly identified three of the four substandard samples. The sample that was missed had an 88% ceftriaxone content, which is just outside the 90-110% range allowed.

Poster Presentation:

Simulating the Explosion of a Supernova for a Detailed Nucleosynthesis Study

Luca Boccioli, Grant J. Mathews

Department of Physics, University of Notre Dame

Most elements in the periodic table are synthesized during the final stages of stellar evolution. More specifically, there are three main sites where heavy elements are produced: Asymptotic Giant Branch Stars, Neutron star mergers, and Supernovae. This last explosive event is the focus of this research.

Computer simulations of supernova explosions have been greatly improving in the last ten years. Due to increasing CPU power, different groups are running one, two, and three-dimensional simulations, which employ very detailed physics. Nonetheless, the mechanism driving the explosion is not fully understood yet; what is well-established is that it is triggered by neutrinos. We use a one-dimensional (1D) simulation that has the advantage of being faster with respect to higher-dimensional models, at the price of treating some of the physics with approximate or parametric theories. However, the lower CPU demand allows to tweak some of the parameters to obtain a successful explosion, which enables to study late-time nucleosynthesis that with higher-dimensional models would be much harder to study.

We are currently validating this 1D simulation, comparing it to other codes which use the same initial conditions. I will present some of the results of this validation. In the future, the outputs of the simulation will be used to study the nucleosynthesis during the explosion.

Poster Presentation:

The Effects of Charge Scaling Ions in the DNA Ion Atmosphere

Shelby Brantley, Steven Corcelli

Department of Chemistry and Biochemistry, University of Notre Dame

Charge scaling is a method of accounting for charge screening that occurs when an ion is present in solution. It is known that DNA must reside in an atmosphere consisting of ions and water to remain structurally stable, but charge screening has never been accounted for during molecular dynamic simulations of DNA systems. In this study, we probe the effects of charge screening of monovalent ions in the DNA ion atmosphere on the structural properties of the DNA strand. We systematically decrease the amount of charge on the monovalent ion to determine structural trends, using +1, +0.9, +0.8, and +0.7 charges. Na^+ and Rb^+ are utilized as the ions of interest due to their respective biological and experimental relevance. The results show that when Na^+ is charge scaled, the ion atmosphere moves closer to the DNA strand. This indicates Na^+ ions experience greater repulsive forces from neighboring ions than attractive forces to the phosphate backbone of the DNA strand. However, for Rb^+, the ion atmosphere moves farther from the DNA as the charge is scaled lower. Interestingly, we see three distinct binding sites in the minor groove when the ion atmosphere is closer to the DNA strand for both ion systems.

Poster Presentation:

Unified Bayesian Networks for Uncertain Inputs and Partial Model Ensembles

Sean Ryan Breckling, Daniele Schiavazzi, Thomas Juliano

Department of Applied and Computational Mathematics and Statistics, University of Notre Dame

We present a prototype system for probabilistic assessment of thermo-structural failure in hypersonic vehicles, based on a unified Bayesian network. A probabilistic characterization of failure in such systems presents significant challenges due to the complex dependence among a large number of uncertain parameters, the availability of an ensemble of models each describing a particular aspect of the underlying physics, and the presence of multiple mission-critical components like thermal protection system (TPS) and control surfaces. We start by considering an idealized model of the Space Shuttle orbiter, where parameters are assigned to the vehicle geometry, the flight trajectory, and TPS material properties. We use a simplified method to compute the heat flux and pressure load histories on the TPS surface and a two-dimensional plane strain characterization of its structural response. Failure is assessed based on thermal stress and maximum temperature in operation. Using a Bayesian network with discrete random variables, we perform inference using brute-force approaches and message passing. We also investigate how the results are affected by observations from pressure and temperature sensors.

Poster Presentation:

Elucidating the Kinetic Mechanism of Human METTL16

Kurtis Breger, Agnieszka Ruszkowska, Jessica A. Brown

Department of Chemistry and Biochemistry, University of Notre Dame

Over 150 RNA modifications have been discovered, yet only recently have they been studied in depth due to recent technological advancements. N^6-methyladenosine (m^6A) is an abundant RNA modification in messenger RNA (mRNA) and long non-coding RNA (lncRNA) that affects various cellular functions such as mRNA stability. Methyltransferase-like protein 16 (METTL16) is one of two catalytically active m^6A RNA methyltransferases in humans. Two well-known methylation targets of METTL16 are U6 spliceosomal RNA and a hairpin in the 3' untranslated region of MAT2A mRNA. However, METTL16 binds to many other RNAs, including the 3' triple helix of MALAT1. Using *in vitro* methyltransferase assays, we have started to investigate the kinetic mechanism and other fundamental properties of METTL16. Our *in vitro* methyltransferase assays consist of purified recombinant human METTL16 (1-562) in combination with the U6 RNA substrate and *S*-adenosylmethionine (SAM), the methyl donor, to initiate the reaction. Thus far, we have recapitulated the methylation of A43 in U6 RNA and measured an observed rate constant of 0.015 min^{-1}. However, under our assay conditions, the MALAT1 triple helix is not a substrate of METTL16 at position A8290 and other adenosine residues seem unlikely. We are currently optimizing buffer conditions by examining how buffer pH, KCl, $MgCl_2$, and TCEP affect the rate of methylation catalyzed by METTL16. Increasing ionic strength of KCl (0-200 mM) or $MgCl_2$ (0-20 mM) increased the rate of methylation by 7.4- and 4.8-fold, respectively. Our next steps after buffer optimization are to use single-turnover assays, steady-state kinetic assays, and isothermal titration calorimetry to measure kinetic parameters of key steps in the kinetic pathway. Future studies will focus on METTL16 mutants in cancer to determine how these mutations affect the kinetic mechanism of METTL16.

Oral Presentation:

Tracing the Stories of Images on the Internet

Joel Brogan, Daniel Henriques Moreira, Aparna Bharati, Kevin W. Bowyer, Anderson Rocha, Walter J. Scheirer, Patrick J. Flynn

Department of Computer Science and Engineering, University of Notre Dame; DARPA; NIST; The University of Campinas

Everything on the internet these days borrows content from one source or another. People modify images on the web for a myriad of reasons, from political commentary to cyber-bullying. Simultaneously, image cloning, splicing, and compositing techniques have become so advanced in such a short span of time that many classical digital forensic techniques for detecting modifications are no longer fully adequate to analyze forged imagery. In today's "fake news" era, it has never been more vital to keep reality discerned from the counterfeit. Whether the purpose is for art, meme culture, or propaganda, it is important to be able to understand how a modified image came to be. The task of tracing the story of how images are uploaded, re-uploaded, filtered, and modified during their time on the web is called Image Provenance. If we can understand how sets of images are related to one another, or find the original images that a composite was based on, we can begin to gain insight as to how and why the image was modified. This talk highlights our group's efforts to build automatic tools that fetch composited images and trace their origins and modifications on a million to billion-image scale.

Poster Presentation:

Oceanographic Variability across the Mid-Pleistocene Transition at the Agulhas Plateau

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The Agulhas Current, a western boundary current that transports heat and salinity from the Indian into the Atlantic Ocean through the Agulhas Leakage, plays a key role in global ocean circulation and climate. However, efforts to better understand the mechanisms driving changes at the Indian-Atlantic Ocean gateway across major climate transitions, such as the mid-Pleistocene transition (MPT), are limited. The Agulhas Plateau is located at the Agulhas retroflection pathway, an area affected by latitudinal migrations of the subtropical front and provide a strategic location to study the effects of the establishment of high amplitude 100-kyr glacial-interglacial cycles during the MPT. Using sediments recovered at IODP site 1475 on the Agulhas Plateau, we present new records of water temperature ($U^{k'}_{37}$ and TEX_{86}), primary productivity (chlorins and alkenones), and sea surface salinity ($\delta D_{alkenones}$), spanning from 1.2 to 0.3 Ma. Our multiproxy reconstructions highlight glacial-interglacial periodicity, showing more abrupt and higher amplitude cycles after the MPT from which we infer changes in Agulhas Current strength and leakage variability. Following the MPT, offsets between the two water temperature proxies during glacials and interglacials suggest varying contributions of regional water masses at Agulhas Plateau.

Poster Presentation:

Discovery of Novel Regulatory Pathways of the ESX-1 Secretion System in Pathogenic Mycobacteria

Alexandra Chirakos[*1], Matthew Champion[2], Patricia Champion[1]

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Mycobacterium marinum, an opportunistic human pathogen, is an established model organism used to study the virulence of *Mycobacterium tuberculosis* (Mtb), the causative agent of tuberculosis (TB). A main virulence determinant of Mtb is the ESX-1 secretion system, which is highly conserved between these two organisms. The ESX-1 system secretes protein virulence factors (substrates) that are required for bacterial survival within the host. In clinical strains, increased production of ESX-1 substrates directly correlates with increased virulence and transmission. We discovered a novel feedback mechanism that regulates the expression of ESX-1 substrates in response to assembly of the secretion machinery. Importantly, we found that a subset of ESX-1 substrates post-transcriptionally regulate gene expression. We are currently defining the role of secreted substrates in these regulatory pathways, and how they impact virulence and ESX-1 secretion. It is critical that we understand the underlying regulatory mechanisms controlling this key virulence determinant to understand how mycobacteria cause disease.

Poster Presentation:

Development of Novel Anti-Leishmania Chemotherapeutics: High-Throughput Screening and Investigation of Structure-Activity Relationships of 2,4-diaminoquinazoline Heteroaromatic Scaffolds

Hannah Corman[1], Douglas A. Shoue[1], Brianna Norris-Mullins[1], Bruce J. Melancon[2], Mary Ann McDowell[1], Miguel Morales[1]

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The high toxicity associated with the current anti-leishmanial therapies, increase of resistance, and the absence of a vaccine that is safe and effective in humans, demand the identification of new anti-leishmanials. We utilized fluorometric high-throughput screening (HTS) of small molecule libraries followed by combinatorial chemistry to identify new lead scaffolds to address this need. Primary screening of 10,000 compounds from the DIVERset-EXP library (Chembridge), was performed against axenic *L. donovani* amastigotes constitutively expressing the red fluorescent protein mCherry. Active compounds moved on to a secondary screening against intracellular *L. donovani* and *L. major* amastigotes in the human THP-1 macrophage cell line, and finally an *in vivo* murine model of cutaneous leishmaniasis (CL) was used to identify lead scaffolds.

One hundred and sixteen compounds had an effectiveness greater than 90% of the 50μM miltefosine response; 61 exhibited effectiveness equal to that of 50μM miltefosine. Three scaffolds were represented multiple times in the 'hit' compounds from the preliminary screen, one such scaffold was the 2,4-diaminoquinazoline (2,4-DAQ). Active compounds that exhibited EC_{50}s in the less than 10μM range, were selected for secondary screening. Twenty-six (26) of the 2,4-DAQs assessed in secondary screening exhibited EC_{50}s between 1-10μM against axenic *L. donovani* amastigotes with selectivity indices ranging from 1-122. One of two 2,4-DAQ compounds tested in our *in vivo* imaging CL model was as effective as antimony tartrate. Comprehensive analyses of SAR of all active scaffolds is ongoing utilizing medicinal chemistry for enhanced efficacy and selectivity as well as optimal adsorption, distribution, metabolic and excretion (ADME) profiles. Utilization of this robust high-throughput platform allows for identification of novel anti-leishmanial compounds. These compounds are both potent and selective, with efficacy in an *in vivo* CL model. Future studies will test activity of these compounds in a visceral leishmaniasis model.

Poster Presentation:

Primate Health Responses to Extreme Drought in Northwestern Costa Rica

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While the impact of climate change on human health has received much attention, surprisingly little has been documented in regards to climate change and wildlife health. This information can be helpful in predicting and understanding human responses to environmental degradation caused by climate change. Additionally, as we become more certain that climate change is, at least in part, caused by anthropogenic forces, it becomes imperative that we document how it affects all life forms in order to combat these effects. In this study, we investigate health effects of extreme drought on a species of wild Neotropical primate, *Cebus capucinus imitator*, in the Santa Rosa Sector of the Área de Conservación Guanacaste, Costa Rica. Average yearly rainfall from 1979-2015 was 1800mm, but 2015 was a record drought year with only 660mm. We non-invasively collected urine from habituated individuals residing in three long-term study groups and in-field conducted urinalysis using urinary dipsticks. We compared results for samples collected pre-drought (June 2010, n=87) to those collected post-drought (June 2016, n=32). Of the ten health markers investigated, 6 differed between years: the presence of leukocytes and ketones were more common in the 2010 samples, while protein (38% in 2016 vs 20% in 2010), blood (above trace levels; 50% in 2016 vs 9% in 2010), and bilirubin (22% in 2016 vs 0 in 2010) were more common in the 2016 samples. With a mean specific gravity of 1.015 in the 2016 samples (vs 1.022 in 2010), the presence of blood (suggestive of urinary tract infection or reduced kidney function), proteins (indicative of stress), and bilirubin (reflecting potential issues in liver function) are particularly relevant. These results imply that the health of our study animals declined between the pre and post-drought sampling periods.

Oral Presentation:

A Numerical Study on the Wrinkling of Neo-Hookean Elastic Multi-Layers

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In this work, we study the effects of the stiffness ratio and layer spacing of two layers with the same stiffness embedded in an infinite-sized homogeneous matrix under uniaxial compression using a linear stability analysis. Symmetric and antisymmetric wrinkling configurations have been taken into account. The results indicate that symmetric mode precedes the antisymmetric when the layers are close to each other. Increasing the spacing of the layers leads to the emerging of the symmetric and antisymmetric modes. The critical wavelength is mainly determined by the influence of stiffness ratios. When layers are softer than the matrix, both layer spacing and stiffness ratio play an important role in reaching the unstable states. Our computation illustrates the need for a finite element investigation on multilayer models' instabilities where layers are softer and a specific range of layer spacing exists.

Poster Presentation:

Effect of Competing Oxidizing Reactions and Transport Limitation on the Faradaic Efficiency in Plasma Electrolysis

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Plasma electrochemistry consists of an electrolytic cell where the cathode or the anode is replaced by a direct current (DC) plasma. Unlike conventional electrolysis, chemical reactions are initiated by highly reactive species such as the solvated electron (e^-_{aq}), and the hydroxyl (OH) radical, instead of the properties of the solid electrode. Using this configuration, plasmas have been used to process chemicals, create long-lived chemical species, and synthesize nanoparticles in electrolytic cells. Here, a non-thermal, atmospheric argon DC plasma was used as a cathode coupled with a platinum anode in an electrochemical H-cell with aqueous sodium perchlorate or sodium tetraborate as background electrolytes. Two chemical species, ferricyanide or chloroacetate, were used as chemical indicators to study the competitive reactions driven by e^-_{aq} and OH. A simple kinetic and transport model was used to analyze and interpret the data, revealing that the Faradaic efficiency in these systems is mostly limited by species depletion close to the interface.

Poster Presentation:

Examining the Influence of the Nutrient Environment on Antibiotic Susceptibility of *Pseudomonas aeruginosa*

Aleksandar Dimkovikj[*1] and Joshua D. Shrout[1, 2]

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It is known that slow-growing and dormant bacterial cells are generally less susceptible to many antibiotics. However, in addition to growth state, antibiotic susceptibility can also be influenced by the nutrient conditions for actively growing cells. These observations that link nutrient conditions with antibiotic efficacy are poorly understood. For example, the opportunistic pathogenic bacterium *P. aeruginosa* has been shown to exhibit reduced susceptibility to aminoglycoside and ß-lactam antibiotics when grown with increasing concentrations of the divalent ions magnesium (Mg^{2+}) and calcium (Ca^{2+}). This form of resistance has been linked to membrane-based two-component systems which act as efflux pumps for the antibiotic when divalent ions are present. No research has yet been published linking monovalent ions to similar membrane-based systems. In this study, I perform susceptibility testing in order to determine whether potassium (K^+) and sodium (Na^+) alter *P. aeruginosa* susceptibility to the aminoglycoside gentamicin. Preliminary results suggest that cultures grown with minimal media in the presence of excess potassium exhibit lesser susceptibility with increasing gentamicin concentrations that are above the published minimal inhibitory concentration (MIC) for *P. aeruginosa*. This effect is considerably different from that of sodium, which tends to decrease *P. aeruginosa* susceptibility to gentamicin only for concentrations below the MIC. Media containing no sodium (supplied as +/- NaCl) has reduced susceptibility to gentamicin at antibiotic concentrations of 60 μg/mL or greater.

Oral Presentation:

The Zebrafish Renal Progenitor Cell Mutant *oceanside* (*ocn*) *R*eveals that the Osr1 Transcription Factor Regulates Wnt Signaling to Control Kidney Development

Bridgette E. Drummond[1], Brooke E. Chambers[1], Marisa N. Ulrich[1], Paul T. Kroeger[1], Gary F. Gerlach[1], Ignaty Leshchiner[2], Wolfram Goessling[2], Rebecca A. Wingert[1*]

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A challenge in creating innovative regenerative treatments for kidney disorders is our limited genetic knowledge about the development of renal cell types. To identify essential regulators of kidney cell ontogeny, we performed a forward genetic screen in zebrafish using the mutagen N-ethyl-N-nitrosurea (ENU). From the screen we isolated the novel renal stem cell mutant *oceanside* (*ocn),* which exhibited a specific loss of anterior kidney cell types. Whole genome sequencing revealed a nonsense mutation encoding a premature stop codon in the zinc-finger transcription factor *odd skipped related-1* (*osr1*). *ocn* mutant phenotypes are more severe than previously documented *osr1* knockdown studies, and were rescued by provision of *osr1* mRNA. Interestingly, we discovered that while kidney progenitors are initially specified, an apoptosis event occurs in the anterior kidney field that triggers the abrogation of blood filter and proximal tubule precursors in this area. This event occurs concomitantly with an upregulation of hemangioblasts in this region, indicating that *osr1* is requisite to suppress blood and vasculature lineages and to maintain the kidney progenitor pool. Further, we determined that expression of *wnt2ba* in renal progenitors was significantly decreased in *ocn* mutants, suggesting Osr1 regulates canonical Wnt signaling. *wnt2ba* loss of function analysis revealed that this factor is essential for emergence of the podocyte lineage that will comprise the kidney blood filtering apparatus. Taken together, these results show for the first time that *osr1* is necessary for renal progenitor maintenance and that it functions upstream of *wnt2ba* to promote podocyte formation during development. This knowledge can provide crucial insights about congenital kidney diseases and guide the formulation of new therapeutic applications.

Poster Presentation:

Hydrologic and Biogeophysical Parameter Estimation for Simulating Watershed-Scale Conservation to Reduce Nutrient Losses to Surface Waters using SWAT

Nima Ehsani, Jennifer L. Tank, Alan F. Hamlet, Todd V. Royer, Sheila F. Christopher, Ashish Sharma, Kyuhyun Byun, Matt T. Trentman, Shannon L. Speir, Lienne Sethna, Ceara J. Talbot, and Ursula H. Mahl

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The croplands of the Midwestern United States are critically important for the economy and play a vital role in feeding the country and the world. At the same time, agricultural activities are a major source of nutrient pollution to aquatic systems in the form of excess dissolved nitrogen (N), phosphorus (P) and sediments. Along with affecting the local rivers and lakes, the runoff from the agricultural fields in the Midwest has significantly impaired water quality of downstream water bodies such as the Great Lakes, the Mississippi River system, and the Gulf of Mexico. Winter cover crops have been identified as an effective conservation practice for reducing nutrient runoff from fields into adjacent waterways. Cover crops are planted in the fall and are terminated before planting of the cash crop the following spring, keeping the biological cover on what would typically be bare ground, which protects fields from soil and nutrient loss, especially during winter snowmelt and spring storms. Over the past four years, watershed-scale cover crops have been implemented at varying levels of cover crop saturation in the Shatto Ditch Watershed (SDW) and Kirkpatrick Ditch Watershed (KDW) in northern Indiana, and high-frequency water quality data will be used to calibrate high-resolution baseline SWAT models in both SDW and KDW for streamflow and water quality. Using these initial small-scale modeling studies, we will estimate hydrologic and biogeophysical model parameters needed to develop SWAT models at larger spatial scales that can accurately forecast the potential benefits of cover crop implementation in larger river basins, under both historical and projected future climate. We will also test the ability to transfer these model parameters to nearby watersheds (and across scales) by comparing the independent calibrations in SDW and KDW, and also by implementing and calibrating SWAT models in the Paw Paw River watershed in southern Michigan where cover crops are planned for future implementation. The approach presented determines how observed field data can be used to test parameter transfer schemes among watersheds and scales and informs scaling of SWAT results to larger watersheds.

Oral Presentation:

Recovery of hiPSC *In Vitro* Myocardium Model is Promoted by Adipose Stem Cell Conditioned Medium

Bradley W. Ellis, Dmitry O. Traktuev, U. Isik Can, Stephanie Merfeld-Clauss, Keith L. March, and Pinar Zorlutuna

Department of Aerospace and Mechanical Engineering, University of Notre Dame

Introduction: Organ transplantation is a key life-saving therapy for end-stage organ failure. However, this treatment is limited by severe shortage in donor organ supply. In addition, approximately 70% of allografts are rejected due to stringent acceptance criteria, including storage time requirements. Amelioration of ischemia/reperfusion injury can prolong transport times, improving graft preservation, increasing access to organ transplantation. In this study, we developed a human induced pluripotent stem cell (hiPSC) derived *in vitro* myocardium model for transplantation to evaluate the effect of adipose stem cell conditioned medium (ASC-CM) on cardiomyocyte preservation during organ storage.

Methods: Induced cardiomyocytes (iCM) were differentiated from hiPSCs. Protein and mRNA expression of canonical CM markers in iCMs were compared to expression in human left ventricle obtained from the Indiana Donor Network. For the myocardium model, iCMs were exposed to UW cardioplegic solution alone or supplemented with ASC-CM for 2-8 hours. UW then was replaced with basal, standard, or ASC-CM supplemented media. iCM recovery was assessed for 24 hours through beating rate/strength and biochemical analyses.

Results and Discussion: iCMs displayed similarity to human myocardium at protein and mRNA levels. Storage in ASC-CM supplemented UW led to significantly faster and higher recovery of iCMs regardless of UW incubation time. Additionally, ASC-CM added to the recovery media after UW incubation further improve the rate and degree of iCM functional recovery. Furthermore, knockdown of antioxidants in ASC-CM significantly decreased iCM recovery.

Conclusion: This study utilized human iCMs as an *in vitro* model to evaluate the therapeutic effect of ASC-CM on iCM during cold cardioplegia. We observed the addition of ASC-CM to UW as well as to recovery media has the potential to increase organ storage time. Additionally, we observed evidence that this recovery is achieved through mediation of reactive oxygen species pathways. This work provides a critical step towards increasing the number of available transplant organs.

Oral Presentation:

Dynamics and Control of Underactuated Biped Robots

Martin Fevre, James P. Schmiedeler

Department of Aerospace and Mechanical Engineering, University of Notre Dame

In the past few decades, robotics research has sought to engineer versatile walking biped robots that can move efficiently alongside humans in unstructured environments. In the future, applications for such robots may include in-home assistance of the elderly and people with disabilities, parcel delivery, warehouse logistics, military assistance, security, construction, and even space exploration. Moreover, the study of bipedal locomotion has the potential to inform the design of powered prostheses, exoskeletons, and other bio-inspired robotic devices to assist in rehabilitation. Even state-of-the-art applications, however, are incapable of coping with unforeseen perturbations when the magnitude or frequency of the disturbances becomes too high. These practical challenges still limit the ability of efficient biped robots to achieve their envisioned potential in today's society. This oral presentation will showcase the robotics research done in the Locomotion and Biomechanics Lab at the University of Notre Dame that intends to address these limitations by pursuing two complementary objectives. The first objective identifies the main source of instability of biped robots and develops a novel method to enlarge their stable region by using a library of stored dynamic motions. This method was shown to give robots the ability to transition among walking gaits just like humans switch gaits to robustly and efficiently navigate man-made environments and uneven natural terrain. Secondly, this presentation will highlight a novel method for optimizing gaits and mechanical designs for robust and dynamic bipedal locomotion. This novel method identifies the measure of dynamic coupling between the different degrees of freedom of the biped robot and evaluates its relationship to 1) energetic efficiency and 2) robustness to disturbance.

Poster Presentation:

Genetic Analysis of ESX-1 Substrates Reveals Complex Secretory Phenotypes in Mycobacteria

Micah J. Ferrell*[1], Alexandra E. Chirakos[1], Matthew M. Champion[2], Patricia A. Champion[1]

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Mycobacterium tuberculosis (*M. tb*) is a globally significant pathogen killing an estimated 10 million people each year. Virulence of *M. tb* is dependent upon the secretion of virulence factors by the ESX-1 (ESAT-6-system-1) secretion system to thwart phagocytic killing within macrophages. Strains lacking a functional ESX-1 system such as the widely-used *M. bovis* BCG vaccine strain are attenuated. Despite the central role of ESX-1 in mycobacterial disease the specific functions of ESX-1 substrates in secretion and virulence remain undefined. Initial studies of ESX-1 secretion using transposon mutagenesis did not clarify substrate function as disruption of substrate genes largely produced a common secretion-null phenotype. We have generated targeted knockouts of ESX-1 substrate genes in *M. marinum* and characterized their secretory phenotypes. In contrast to the transposon mutagenized strains, clean deletions of substrate genes produced a range of intermediate secretory phenotypes. These results suggest that the common null phenotype previously reported was in part an artifact of the transposon mutagenesis. To further characterize the functional roles of substrates we constructed strains with simultaneous deletions of substrate pairs. Many of these double deletion strains exhibited unique and unexpected secretory phenotypes that differed from the respective single deletion strains. These results suggest the presence of complex functional relationships between individual ESX-1 substrates.

Poster Presentation:

Phlebotomus papatasi Salivary Gland Gene Diversity in Distinct Ecotopes of Egypt and Jordan

Catherine M. Flanley[1], Marcelo Ramalho-Ortigao[2], Iliano V. Coutinho-Abreu[3], Rami Mukbel[4], Hanafi A. Hanafi[4], Shabaan S. El-Hossary[5], Emad El-Din Y. Fawaz[5], David F. Hoel[2],Gwen Stayback[1], Douglas A. Shoue[1], Shaden Kamhawi[3], David W. Severson[1], Akio Mori[1], Mary Ann McDowell[1]

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Phlebotomus papatasi sand flies inject a host of pharmacological salivary proteins to assist with blood feeding and modulate host defenses. These salivary proteins have been studied for their role in cutaneous leishmaniasis disease outcome with different salivary proteins attenuating or exacerbating lesion size. Studies have shown that while co-administered sand fly saliva exacerbates *Leishmania major* infections in naïve mice, animals pre-exposed to saliva are protected, with the infection attenuated via a delayed-type hypersensitivity immune reaction. The immunogenicity of salivary components results in a hostile environment making it difficult for *L. major* to successfully establish an infection in pre-exposed individuals. These studies highlight the potential of the salivary components to be used as a vaccine. One protein in particular, *P. papatasi* salivary protein 15 (PpSP15) has been intensively studied due to its ability to protect mice against *L. major* challenge. The number of antigenic molecules included in vaccines is restricted thus emphasizing the role of population genetics to identify molecules, like PpSP15, that are not experiencing positive selection pressure. Functionally significant proteins conserved across populations and under purifying selection demonstrate great promise as a vaccine component. Three distinct ecotope study sites in Egypt (Aswan) and Jordan (Swaimeh and Malka) were chosen based on their elevation, rainfall, vegetation, differing reservoir species, and the presence or absence of *L. major*. The objective of this work was to analyze the intra- and inter-population diversity of nine of the most abundantly expressed salivary proteins including SP12, SP14, SP28, SP29, SP30, SP32, SP36, SP42, and SP44 and to predict their ability to elicit an immune response.

Poster Presentation:

Using Template Models to Identify Exoskeleton User Intent

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Robotic exoskeletons present the opportunity to restore mobility and independence following musculoskeletal injury. Existing control strategies for these exoskeletons provide varying levels of user intent matching and comfort, ranging from finite state machines that identify discrete gait modes to continuous strategies that amplify user-initiated actions. Many existing control strategies, such as automatic pattern recognition, typically treat the human/exoskeleton system as a black box, with no a priori information about the relationship between signal inputs and the appropriate gait mode output. Such an approach neglects all that is known about the nature of human walking. For example, several very low dimensional "template" models, such as the Dual Spring-Loaded Inverted Pendulum (SLIP) model, reliably exhibit the salient characteristics of human walking and could help to inform the user intent detection problem. Mapping model parameters to current kinematic patterns would provide critical information about the intended COM trajectory in the near future as long as the exoskeleton controller does not mask the user's intent by rigidly following its own desired trajectory. To characterize the human/exoskeleton response to changes in user intent, a human subjects study was completed using the EksoGT exoskeleton in a motion capture arena. Individuals walked naturally in the exoskeleton before being given a command to either speed up, slow down, or make no change to their gait. Preliminary assessment of the motion capture data and the internal log of exoskeleton states suggest that there is a measurable change to the system following an intent change, but that this change is dependent on the exoskeleton assistance settings. For trajectory-free assistance settings that only provide gravity compensation, the intent change is distinguishable through joint kinematics, but not joint torques. The opposite is true of trajectory-based assistance settings. These preliminary findings will guide the mapping of template gaits to the human/exoskeleton gaits.

Poster Presentation:

Metabarcoding Techniques Provide a New Tool for Assessing Long-Tailed Macaque Diets

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Humans and long-tailed macaques have shared the islands of Bali and Singapore for centuries, with humans altering these islands in multiple ways. The human-macaque relationship is complicated. Macaques are garbage/crop raiders and potential reservoirs for disease, but they are also a source of tourism-based income and hold religious significance. Understanding how different human land-use practices impact macaques is valuable for monitoring this complex relationship. One way that macaques interact with their anthropogenic environment is through their diet. Primatologists typically use behavioral observation to describe the diet of primates. Behavioral observations can be time consuming, produce information on relatively few individuals, and may only allow identification to a relatively high taxonomic level. More recently, metabarcoding techniques have been utilized to assess the diet of a many organisms, including primates. Metabarcoding is relatively quick, can survey many individuals, and has the potential to identify diet items more specifically. The long-tailed macaque has not had its diet characterized via metabarcoding, but has a varied diet which includes various plant parts, vertebrates, and invertebrates. There are multiple potential metabarcoding regions to choose from, and most target a specific taxon (i.e. fungi). A benefit of using the 18S region for metabarcoding is the ability to capture DNA from all eukaryotes simultaneously (i.e. plants, arthropods, etc.). The following is an exploration of the diet of the macaques of Bali and Singapore using the 18S metabarcoding method, and a comparison to previous findings from behavioral observations across Southeast Asia. The metabarcoding technique reveals a wider range of plant diet items than previously described, a more detailed examination of arthropod diet items, and the ability to investigate non-diet items that are probably incidentally consumed (i.e. algae). This improved diet characterization can be used to investigate relationships between the diet of macaques and their environment, anthropogenic influences, and parasites.

Poster Presentation:

Microglia Subset Revealed by Single Cell Analyses Promotes Brain Metastasis Outgrowth through Fractalkine Receptor-Dependent Interferon Response

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Breast cancer brain metastasis is an incurable malignancy that results from the colonization and outgrowth of disseminated tumor cells in an immunologically unique brain microenvironment. Possessing highly heterogeneous ontogenies, myeloid cells predominate the brain immune landscape. Microglia, self-sustaining brain-resident myeloid cells, and infiltrating bone marrow-derived myeloid cells (BMDMs) cooperatively regulate brain homeostasis and disease. Yet, their functional roles in regulating brain metastasis outgrowth have not been fully revealed. Here, combining single cell analyses with transgenic mouse models, we elucidated the functional relevance of the myeloid heterogeneity in promoting brain metastasis outgrowth. First, genetic depletion of all myeloid cells significantly reduced brain metastasis incidence, implying a pro-metastatic role for myeloid cells. High-dimensional mass cytometry analysis showed that the brain metastasis myeloid landscape consisted of both microglia and BMDMs. Unexpectedly, inhibiting BMDM infiltration to metastases did not alter brain metastasis incidence or survival, suggesting that microglia are the primary myeloid effectors during brain metastasis. Furthermore, despite transcriptional heterogeneity among metastasis-associated myeloid cells (MAMs) as identified by single cell RNA-seq, all MAMs downregulated myeloid homeostatic genes, particularly Cx3cr1, compared to naïve myeloid cells. Knocking out Cx3cr1 in MAMs resulted in increased brain metastasis incidence and reduced survival. Mechanistically, ablation of Cx3cr1 led to a MAM transcriptome signature enriched in interferon signaling pathways and an upregulation of interferon-induced protein Cxcl10. Significantly, ectopic co-injection of recombinant Cxcl10 with tumor cells increased metastatic outgrowth. Therapeutically, treating mice with minocycline, an antibiotic with anti-neuroinflammatory properties, reduced MAM Cxcl10 expression and brain metastasis incidence, implicating minocycline as a potential anti-brain metastasis therapy. Collectively, our results point toward a potent microglia population that drives brain metastasis through a Cx3cr1-Cxcl10 signaling axis. More broadly, our study identifies a unique myeloid state not yet characterized in other brain pathologies, which may have important implications in brain metastasis treatment.

Oral Presentation:

Aging Promotes Changes to Peritoneal and Omental Collagen Structure that Contribute to Increased Ovarian Cancer Metastatic Success

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Aging is one of the biggest risk factors for the development of ovarian cancer (OvCa), the deadliest cancer of the female reproductive system. Half of OvCa diagnoses are in women over the age of 63, and older OvCa patients have a higher risk of mortality. Despite this, age is understudied in the OvCa field. Using a C57Bl/6 mouse model of aging, young (Y) mice ranging from 3-6 months of age, and aged (A) mice ranging from 20-23 months of age, corresponding to women aged 20-30 years (Y) and 60-67 years (A) were used to study the role aging has on metastasis. Fluorescently tagged C57Bl/6 syngeneic ID8 $p53^{-/-}$ mouse OvCa surface epithelial cells were injected intraperitoneally in Y and A mice and disease progression was evaluated for 5.5 weeks. Organ-specific tumor burden was quantified with ImageJ, revealing increased tumor burden in aged mice compared to their young counterparts. These results were reproduced in the FVB mouse model using syngeneic $PTEN^{shRNA}/KRAS^{G12V}$ modified FVB OvCa oviductal epithelial cells. Second Harmonic Generation Microscopy (SHG) was used to visualize collagen of the peritoneal and omental tissues from Y and A C57Bl/6 mice. Distinct structural differences were shown in omental collagen in the Y vs A cohorts and validated with Scanning Electron Microscopy (SEM). Collagen isolated from the tails of Y and A C57Bl/6 mice was incubated with Matrix Metalloproteinase-1 (MMP1) or OVCAR5 cells, a human cell line expressing MMP14, and imaged using SEM. These images showed a distinct difference in the interaction between MMPs and Y vs A collagen. Invasion assays showed that OVCAR5 cells invade more readily through A collagen than Y. Additionally, Nanoindentation illustrated mechanical differences between Y and A peritoneal samples. In conclusion, aging induces changes in the structure and mechanical strength of peritoneal and omental collagen, which contribute to OvCa metastasis.

Poster Presentation:

Data Assimilation on Lumped Parameter Models for Diastolic Heart Failure

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It is estimated that about one-third of all deaths due to heart failure are caused by diastolic ventricular dysfunction. This pathology affects the ability of the left ventricle to relax during filling. However, it has no effect on indicators such as the systemic blood pressures or cardiac output, which makes this condition difficult to diagnose. In this context, a reliable predictor of diastolic left ventricular dysfunction is secondary pulmonary hypertension, i.e., an abnormal but reversible increase of the pulmonary arterial pressure which can be measured only though invasive right heart catheterization.

In this study, in lieu of an invasive procedure, we leverage the hemodynamic consistency of a differential circulation model to predict the pulmonary arterial pressure in adults from a collection of non-invasive clinical data. This is a numerical exercise involving various aspects of forward and inverse uncertainty analysis. Specifically, we investigate the physiological admissibility of the model under healthy and heart failure conditions as well as the parameter identifiability and sensitivities. This is done in an effort to reduce the dimensionality of the estimation problem. Bayesian parameter estimation is performed on a cohort of 84 patients. We also discuss the use of machine learning classifiers to constrain parameter realizations associated with realistic physiologic response and to detect pulmonary hypertension based on assimilated model parameters.

Oral Presentation:

Visual Data Integrity, Accountable Computing, and Privacy Protection Leveraging Computer Vision Techniques

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People are often confused by the present visual data deluge. On the one hand, manipulated or repurposed pictures are used in a range of deceptions, from selling miraculous weight-loss products, to attacking the reputation of individuals. On the other hand, the integrity of authentic pictures is wrongly questioned due to "the boy who cried wolf" effect: the everyman who has been deceived before tends to automatically negate the integrity of content, especially if it contradicts their beliefs. Additionally, cameras benefit from the ubiquity of their host devices (e.g., mobile phones), allowing the pervasive recording of anybody, raising concerns about privacy protection. In this scenario, at the Computer Vision Research Laboratory (CVRL), we have been dealing with the issues of data integrity, accountable computing, and privacy protection by employing techniques of Computer Vision (CV), the discipline of image and video interpretation. This presentation summarizes three CV applications developed in the last two years at CVRL, to the respective fields of Image Forensics, Biometrics, and Computer Graphics. The first, named Image Provenance Analysis, aims at assessing the integrity of an image through the estimation of the sequence of transformations (e.g., blur, rotation, splicing) that yielded its content. The second, named Human-Inspired Iris Recognition, aims at providing accountable automated iris recognition to the incredulous everyman, by relying on observations of the behavior of humans in the occasion of performing iris verification. The third, named Synthesis of Realistic Facial Videos, aims at data augmentation and at protecting the privacy of subjects eventually captured in videos; the idea is to guarantee anonymity by replacing original identities with multiple artificial individuals. All applications are the result of the work of the present postdoctoral researcher in essential collaboration with graduate students and supervision of four professors. Publications, insights, and discussions of results are presented for each case.

Poster Presentation:

Pressure Estimation and Fluid Domain Segmentation using Physics-Based Deep Learning

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Recent advances in MRI scanner technology and image processing have opened new possibilities to measure time-varying spatial velocity fields in-vivo on patients. Since hemodynamics is governed by the incompressible Navier Stokes equations, their reformulation into a Poisson pressure equation leads, in principle, to the possibility of estimating the relative pressure [1] which is, in many cases, clinically relevant. This, however, requires preliminary segmentation of the region of fluid and the solution of a Poisson equation on a typically large computational grid.

Alternatively, deep convolutional neural networks (DCNN) have garnered much success in image classification and segmentation tasks. Additionally, recent approaches to dense classification and regression have been proposed (e.g., UNet [2]) but they do not take advantage of the underlying physics to improve learning efficiency.

We have adapted the UNet network to the problem of predicting the relative pressure from parametric flow templates. Specifically, we have tested our approach using a Poiseuille flow with parabolic velocity profile defined on an ideal cylindrical domain with parametric diameter. Our preliminary results show how our DCNN is able to accurately reproduce both the spatial pressure distribution and the size of the fluid domain.

[1] Schiavazzi D., Nemes A., Schmitter S. and Coletti F., The Effect of Velocity Filtering in Pressure Estimation, Experiments in Fluids, 58(5):1-21, 2017.

[2] Ronneberger, O. and Fischer, P. and Brox, T., U-net: Convolutional networks for biomedical image segmentation, International Conference on Medical image computing and computer-assisted intervention, 2015.

Poster Presentation:

The Effects of Supported Catalyst on the Plasma in a Packed-Bed Dielectric Barrier Discharge Reactor for Ammonia Synthesis

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The non-equilibrium plasma is a weakly ionized gas, with its electron temperature (~10000 K) much higher than the temperature of other species such as ions, excited molecules and neutrals (~100K). On the other hand, a catalyst is a substance which increases the rate of a chemical reaction. When non-equilibrium, low-temperature plasmas and catalysts interact, they can exhibit synergistic behavior that enhances the chemical activity above what is possible with either process alone. Unlike thermal catalysis, in plasma-assisted catalysis the non-equilibrium state of the plasma produces reactive intermediates, such as excited species, that may play an important role in the catalytic process. There are two primary plasma-surface mechanisms that could produce this synergy: the effect of the plasma on the catalyst and the effect of the catalyst on the plasma state. This work focuses on the latter. We use a laboratory-scale, packed bed, dielectric barrier discharge (DBD) reactor to observe the influence of multiple alumina (Al_2O_3) supported, transition metal ammonia (NH_3) synthesis catalysts on the plasma electrical and optical properties. Through an analysis of variance (ANOVA), we find that while the rates of ammonia synthesis over the materials considered, including Fe/Al_2O_3, Ni/Al_2O_3, and Co/Al_2O_3, are different, the macroscopic properties of the DBD do not show statistical difference. These results support the argument that the observed synergy in our catalysis experiments is not due to catalyst modification of the bulk plasma.

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Oral Presentation:

Rab11b-Mediated Control of the Cell Surface Proteome Drives Metastatic Adaptation

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Breast cancer brain metastases are an urgent clinical problem, accounting for 30% of breast cancer mortality. Tragically, as targeted therapies provide better control of localized and systemic disease, women who respond to initial treatment ultimately develop brain metastases, for which no clinically approved drug shows promising efficacy. Communication with the metastatic microenvironment is critical for metastatic success, but the exact nature of this communication is poorly understood. To dissect the dynamic nature of brain metastatic progression, we performed transcriptome analysis of MDA-231 brain metastases at 7 and 40 days post injection (dpi). We hypothesize that genes up-regulated during the progression from single cells to actively proliferating brain metastases are functionally required for metastatic progression. We utilized a *Drosophila* model to screen 448 RNAi constructs representing 108 up-regulated human genes for a functional role in brain metastasis, and identified Rab11 as an important mediator of brain metastatic outgrowth. Rab11 regulates recycling of surface proteins in the endosomal transport system. We show that Rab11b is strongly up-regulated early in brain metastasis formation, when cells have successfully adapted to the brain microenvironment and initiated metastatic outgrowth. Further, up-regulation of Rab11b is required for brain metastatic outgrowth. Modulation of Rab11b alters retention of proteins on the cell surface, and we find that the surface proteome is altered during brain metastatic outgrowth. Our results suggest an increased reliance on glutamate metabolism during brain metastasis. Finally, we show that inhibiting Rab11b function by preventing prenylation with statin treatment strongly inhibits brain metastasis formation, and increases survival. Taken together, our findings indicate that during adaptation to the brain microenvironment, breast cancer cells transcriptionally up-regulate Rab11b, thereby inducing a significant shift in cellular behavior through recycling-mediated control of the cell surface proteome.

Oral Presentation:

Exploring Time-Varying Multivariate Volume Data Using Matrix of Isosurface Similarity Maps

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Time-varying multivariate volumetric data sets are typical output from various science and engineering simulations. We present a novel visual representation and interface named the matrix of isosurface similarity maps (MISM) for effective exploration of large time-varying multivariate volumetric data sets. MISM synthesizes three types of similarity maps (i.e., self, temporal, and variable similarity maps) to capture the essential relationships among isosurfaces of different variables and time steps. Additionally, it serves as the main visual mapping and navigation tool for examining the vast number of isosurfaces and exploring the underlying time-varying multivariate data set. We present temporal clustering, variable grouping, and interactive filtering to reduce the huge exploration space of MISM. In conjunction with the isovalue and isosurface views, MISM allows users to identify important isosurfaces or isosurface pairs and compare them over space, time, and value range. More importantly, we introduce path recommendation that suggests, animates, and compares traversal paths for effectively exploring MISM under varied criteria and at different levels-of-detail. A silhouette-based method is applied to render multiple surfaces of interest in a visually succinct manner. We demonstrate the effectiveness of our approach with case studies of several time-varying multivariate data sets and an ensemble data set, and evaluate our work with two domain experts.

Poster Presentation:

Relativistic Electron Scattering and Big Bang Nucleosynthesis

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Big-bang nucleosynthesis (BBN) is a valuable tool to constrain the physics of the early universe. It is the era after the big-bang when the universe first forms nuclei like Helium and Lithium. An assumption for calculating abundances of these from BBN is that the nuclei obey Maxwell-Boltzmann(MB) statistics. Here we show that this assumption is invalid and we find a modified Maxwell-Boltzmann(mMB) for nuclei in BBN.

We first recognize that the nucleic distributions could be obtained by understanding how it interacts with its surrounding particles. A nucleus is surrounded by lot more electron, than all other particles. Then we also recognize that electrons are relativistic and hence obey a relativistic statistic called modified Maxwell-Juttner(mMJ) distribution. Given these we follow two approaches:

Langevin model approach: We use this for Brownian motion of a heavy particle(nuclei) in a bath of light particles(electrons). We then solve for the equilibrium condition with relativistically distributed light particles. Imposing equipartition of energy amongst light and heavy particles we obtain a mMB distribution for nuclei. Altered only by a factor in temperature of the MB distribution of a nuclei.

Monte-Carlo simulation approach: We also simulated the *thermalization* process for nuclei in BBN environments. In the simulation electrons have an mMJ energy distribution, and scatter-off and exchange some energy with a test nucleus. When repeated statistically significant times the test nuclei's energy distribution should reflect its physical BBN distribution. We notice that the distribution is indeed the one obtained in the Langevin model approach, further corroborating our results.

When employed for BBN calculations, this modified nuclear distributions alters the thermonuclear reaction rates. This also alters abundances of light-element from BBN, and worsens the discrepancies between BBN and observed primordial light-element abundances possibly suggesting the need for new physics.

Poster Presentation:

Determining Virulence Factors in MAC Infections

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Mycobacterium avium complex (MAC) infection is a non-tuberculosis mycobacteria (NTM) that causes disseminated disease in immunocompromised hosts; such as HIV-positive patients and patients with preexisting pulmonary disease. In recent years, MAC infection rates have been increasing worldwide. Clinically, there are two types of MAC infection; progressive and stable. In this study, we compared stable and progressive patient isolates to identify genes that could be causing isolated strains to be more progressive. We began this study by comparing genomes from 28 stable patient isolates and 18 progressive patient isolates from Japan to identify genes unique to progressive strains. 609 genes were found to be unique to progressive isolates; 82 of which were significant and 24 which are probable virulence factors. Using the identified genes, we have begun analyzing 75 clinical isolates obtained from the Mayo Clinic to begin evaluating whether these genes can be used to identify patients with progressive MAC and to determine if there is regional specificity.

Poster Presentation:

Stability of RNA•DNA-DNA Triple Helices Depends on Base Triple Composition and Length of the RNA Strand

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Recent studies indicate that long noncoding RNAs interact with genomic DNA to form RNA•DNA-DNA triple helices as a mechanism to control gene expression. However, the base triple composition of pyrimidine motif RNA•DNA-DNA triple helices is not well understood beyond the canonical U•A-T and C•G-C base triples. Using native gel-shift assays, the relative stability of sixteen different base triples, Z•X-Y (where Z = U, A, C, G and X-Y = T-A, A-T, C-G, G-C), at a single position in an RNA•DNA-DNA triple helix were determined by measuring the apparent equilibrium dissociation constant between the RNA and DNA-DNA. As expected, the canonical U•A-T and C•G-C base triples were among the most stable base triples, although 11 non-canonical base triples also allowed for triple helix formation. Only three base triples completely disrupted the triple helix and showed no binding between the RNA and DNA-DNA strands. We further show that the stability of the triple helix decreases as the number of successive non-canonical base triples increases. In addition, the third strand has a minimum length for binding, but increasing the length of the third strand beyond this minimum length does not increase the stability of the triple helix. The relative stability of the same sixteen base triples at a single position in a DNA•DNA-DNA and RNA•RNA-RNA triple helix was also determined. Our results show that the relative stability of base triples is unique for RNA•DNA-DNA, DNA•DNA-DNA, and RNA•RNA-RNA triple helices and that the overall stability is D•D-D > R•D-D >> R•R-R. This study shows that the relative stability of RNA•DNA-DNA base triples is not well represented by either DNA•DNA-DNA or RNA•RNA-RNA triple helices.

Oral Presentation:

Bone Remodeling in the Macaque (*Macaca fascicularis*) Skeleton: Effects of Loading Frequency and Magnitude

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Haversian remodeling is a process by which damaged cortical bone is resorbed and replaced by new bone, resulting in the formation of secondary osteons. Remodeling is incited by the microdamage caused by high strain and/or fatigue loading, but the relative effects of load magnitude and frequency on microdamage accumulation, and thus remodeling, are uncertain. We test whether strain magnitude or strain frequency results in more remodeling activity by measuring secondary osteon population density (OPD), osteon cross-sectional area (On.Ar), and relative osteonal area (%HAV) in adult macaque (*Macaca fascicularis*) mid-level ribs and mid-diaphysis femora, tibiae, and fibulae (n=5 individuals). Ribs experience relatively low strain, but relatively high loading frequency (breathing at a rate of 33 times per minute) in terms of cycles per day. Limb bones have lower daily loading frequency than ribs, but femora and tibiae presumably undergo the greatest load magnitude due to impact loads involving gravitational forces. The fibula experiences a fraction of the total gravitational loads. ANOVAs returned significant differences in OPD (P=0.010) and On.Ar (P<0.001). Post hoc pairwise t-tests revealed significantly lower On.Ar in the rib than in all other bones, possibly because the rib's narrow cortex imposes a constraint on osteon size. OPD was significantly higher in the rib than tibia or femur, and higher in the fibula than femur. The high fibular OPD was surprising given that the femur and tibia are more weight bearing. The high rib OPD implies that remodeling activity is more responsive to loading frequency than strain magnitude.

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Oral Presentation:

Aberrant Cell Surface Expression of GRP78 in Breast Cancer Cells Marks a Stem-Like Population that has Increased Metastatic Potential *In Vivo*

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Reliable approaches to identify and target stem-cell mechanisms that mediate aggressive cancer could have great therapeutic value, based on the growing evidence of embryonic signatures in metastatic cancers. However, how to best identify and target stem-like mechanisms aberrantly utilized by cancer cells has been challenging. We harnessed the power of induced pluripotent stem cells (iPSCs) to identify embryonic mechanisms exploited by cancer. A screen comparing the cell surface proteome of iPSCs and breast cancer cells identified GRP78, a heat shock protein that is normally ER-restricted, but has been shown to be aberrantly expressed on the cell surface of several cancers, where it can act as a signaling molecule by poorly understood mechanisms. Although cell surface GRP78 (sGRP78) has emerged as an attractive chemotherapeutic target, understanding how sGRP78 is functioning in cancer has been complicated by the fact that GRP78 can function to regulate a variety of cellular responses, using a diverse array of reported binding partners, which can vary by cell type. Therefore, without insight into the specific GRP78-dependent mechanisms that are responsible for mediating aggressive cancer, it will be difficult to determine how to best target GRP78. We have discovered that (1) sGRP78 is expressed on iPSCs (but not their somatic parental populations) and plays an important role in reprogramming, (2) sGRP78 promotes cellular functions such as proliferation/survival and migration in both stem cells and breast cancer cells (3) overexpression of GRP78 in breast cancer cells leads to an induction of a previously established $CD24^{-}/CD44^{+}$ 'cancer stem cell' (CSC) population (4) $sGRP78^{+}$ breast cancer cell populations are enriched for genes involved in stemness and appear to be a subset of previously established CSCs (5) $sGRP78^{+}$ breast cancer cell populations show a significantly enhanced ability to seed metastatic organ sites *in vivo* (6) GRP78 interacts with Dermcidin (DCD) at the cell surface of cancer cells and iPSCs, where it is important in regulating stem cell and cancer cell migration. These collective findings suggest that sGRP78 marks a stem-like population in breast cancer cells that has increased metastatic potential *in vivo*, and that sGRP78 and DCD cooperate to regulate key cellular functions important in mediating tumorigenesis. Overall, this work has implications for understanding how cancer cells exploit embryonic-like mechanisms, which could provide novel strategies for chemotherapeutic targeting of aggressive breast cancer cell populations.

Poster Presentation:

Cover Crops Increase Bioavailable Legacy Phosphorus in an Agricultural Watershed

Liguang Li[1,2], Jennifer L. Tank [1,2], Sheila Christopher [1,2], Ursula H. Mahl [2], and Todd V. Royer [3]

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In the agricultural Midwest, decades of farming and associated fertilizer application have resulted in phosphorus (P) accumulation in soils. This legacy P is available to cash crops but also complicates efforts to reduce P runoff from fields to adjacent freshwaters. Presently, the effects of agricultural conservation practices on legacy P in soils are understudied. We examined the effects of the watershed-scale planting of cover crops on soil P in the Shatto Ditch Watershed (Kosciusko Co, IN), where fertilizer P is no longer applied due to high legacy P in soils. Over four years, we sampled soils each fall and spring in nine fields with cover crops (CC) and four fields without cover crops (NoCC). We found that multiple P species, soil P storage capacity, organic matter content (%OM), and several other physiochemical variables (i.e., pH, Manganese, Iron, Aluminum) were all different between CC and NoCC fields. For the P species, Mehlich P in 0-5 cm depth decreased more in CC than in NoCC fields, suggesting that cover crops facilitated bioavailable P uptake in surface soils, while water extractible P (WEP) was relatively stable over the study period with no significant difference between 0-5cm and 5-20cm depths. In contrast, in CC fields, there was a significant difference between depths for Mehlich P, Bray P and Total P, but no difference between depths for NoCC fields, indicating that cover crops can alter the vertical distribution of plant available P. Finally, Mehlich P, Bray P and TP were positively correlated with %OM in CC fields, but not in NoCC fields, suggesting that cover crops can induce biological control on the removal of legacy P. In conclusion, cover crops may increase the use efficiency of bioavailable P in soils, without the added risk of elevated P leaching (via WEP) from fields to waterways.

Poster Presentation:

Explicit Solution of Cardiovascular Model Ensembles with Random Field Material Properties on GPUs

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Non-intrusive approaches in uncertainty quantification typically consider the underlying deterministic solver as a black box, requiring independent solutions at various parameter realizations. This leads to a lack of efficiency, particularly for solution algorithms relying mostly on matrix multiplication, such as explicit time integration of finite element spatial discretizations for the stress analysis of vascular tissue. In such cases, the analyst needs to solve the same dynamic problem under a variety of constitutive models and spatial distributions of vascular wall thickness.

We propose an efficient GPU-based approach to solve these problems efficiently, going beyond the embarrassingly parallel repeated solution of the same model. We focus on the problem of determining the variability of various measures of stress in patient-specific models of the thoracic aorta. We determine the pulsatile variation of pressure and wall shear stress from a stabilized, implicit in time, finite element solution for the fluid, and apply these forces to the wall simulated through a simplified three-d.o.f.s shell model, discussed in the literature in the context of the coupled momentum method [1]. We also adopt a discretization of a Gaussian random field with covariance of the Matern class through the solution of a stochastic partial differential equation on our finite element mesh [2].

Our study will be used to validate previous results from the stress analysis of the thoracic aorta and coronary arteries under uncertainty in the spatial variability of the material properties [3]. We will also discuss our implementation combining MPI and CUDA to perform matrix multiplication during the explicit solution of the equations of motion. Future work will focus on coupling the explicit structural solver with variational multiscale finite element fluid solvers.

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Oral Presentation:

Data Privacy: Differential Privacy in Empirical Risk Minimization Problems

Yinan Li, Fang Liu

Department of Applied and Computational Mathematics and Statistics, University of Notre Dame

With growing privacy concern in the big data era, data privacy has become a hot research topic that quickly adopted by governments and industries. Among the research fronts of data privacy, differential privacy, aiming at protecting individual privacy is being studied intensively and applied in our daily life. Look into your iPhone and locate Settings > Privacy > Analytics > Analytics Data, you could find the information being shared with Apple in entries that begin with "DifferentialPrivacy". One major aim in this research field is to design algorithms that output results of high utility, while preserving privacy. A recently developed line of work focuses on the class of Empirical Risk Minimization (ERM) problems, intuitively including all generalized linear models (GLMs), which provides differentially private (DP) parameter estimations of higher utility than traditional sensitivity-based methods. Although sensitivity-based methods adapt to a wider range of models, for research purpose, ERM models consist of a significant amount of our everyday research. Therefore in this talk I will first give an overview on the existing DPERM methods, their properties and how to implements, then introduce the new variable selective DPERM method, Adaptive Noise Augmentation for Privacy-preserving Empirical Loss Minimization (ANAPEL), we recently developed. For more details on ANAPEL methodology, please stop by the poster session.

Poster Presentation:

Anapel: Adaptive Noise Augmentation for Privacy-Preserving Empirical Loss Minimization

Yinan Li, Fang Liu

Department of Applied and Computational Mathematics and Statistics, University of Notre Dame

We propose Anapel, an Adaptive Noise Augmentation method for Privacy-preserving Empirical Loss Minimization (ERM) problems. With data augmented by specifically designed noises, Anapel iteratively utilizes non-private ERM solvers to achieve a variety of target regularization effects and promote sparsity by both the target regularization and the differentially private (DP) noise term while preserving privacy. The Anapel realized target regularization effects are in nature weighted l_2 regularization, contributing to the strong convexity of the noise perturbed ERM and reducing the additionally required l_2 regularization effect. When strong convexity is guaranteed purely by target regularization effects, Anapel is able to retrieve and recycle or reimburse part of the wasted privacy budget. After obtaining the DP parameter estimation, by implementing the Wishart mechanism to obtain DP Hessian matrix, we derive the private-preserving asymptotic Normalities for likelihood-based ERMs such as the generalized linear models (GLMs). Theoretically, with reduced additionally required l_2 regularization, Anapel decreases the excess risk bound and sample complexity, especially when required strong convexity is purely guaranteed by the target regularization effects. We illustrate in simulations, against existing ERM solvers, the significant effects of mitigating over-regularization, variable selection, wasted privacy budget retrieving and recycling, prediction accuracy and standard deviations of asymptotic Normalities for both $\epsilon -$ and (ϵ, δ) $-$DP cases in GLM settings. And we compare our classification accuracy with existing ERM solvers using the Adult dataset.

Poster Presentation:

Panda: AdaPtive Noisy Data Augmentation for Regularization of Undirected Graphical Models

Yinan Li, Fang Liu

Department of Applied and Computational Mathematics and Statistics, University of Notre Dame

We propose PANDA, an AdaPtive Noise Augmentation technique to regularize estimating and constructing undirected graphical models. PANDA iteratively solves MLEs given noise augmented data in the regression-based framework until convergence to achieve the designed regularization effects. The augmented noises can be designed to achieve various regularization effects on graph estimation, including the bridge, elastic net, adaptive lasso, and SCAD penalization; it can also offer group lasso and fused ridge when some nodes belong to the same group. We establish theoretically that the noise-augmented loss functions and its minimizer converge almost surely to the expected penalized loss function and its minimizer, respectively. We derive the asymptotic distributions for the regularized regression coefficients through PANDA in GLMs, based on which, the inferences for the parameters can be obtained simultaneously with variable selection. Our empirical results suggest the inferences achieve nominal or near-nominal coverage and are far more efficient compared to some existing post-selection procedures. On the algorithm level, PANDA can be easily programmed in any standard software without resorting to complicated optimization techniques. We show the non-inferior performance of PANDA in constructing graphs of different types in simulation studies and also apply PANDA to the autism spectrum disorder data to construct a mixed-node graph.

We also extend the PANDA to jointly learning the structures of multiple graphs. We design and introduce two types of noises to augment the observed data. The first type of noises is to regularize the estimation of each graph while the second type of noises promotes either the structural similarities, referred as the joint group lasso regularization, or numerical similarities, referred as joint fused ridge regularization, among the edges in the same position across multiple graphs.

Oral Presentation:

Snapping: A Long Range, Type IV Pili-Dependent, Group Motility of *Pseudomonas aeruginosa*

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Pseudomonas aeruginosa is a Gram-negative, ubiquitous, opportunistic human pathogen and a member of the ESKAPE family of bacterial pathogens. According to the Center for Disease Control and prevention (CDC), *P. aeruginosa* is among the leading cause of hospital acquired infections such as pneumonia, ventilator associated infections, and surgical site infections. *P. aeruginosa* infection is notable for its presence in cystic fibrosis lung infections, where it grows as a biofilms. To effectively colonize surfaces, *P. aeruginosa* depends on the actions of two appendages: a single polar flagellum and type IV pili (TFP). For *P. aeruginosa*, flagella-mediated swarming motility is typically evaluated in the laboratory using 0.45-0.7% agar while type IV pili (TFP)-mediated twitching is studied using 1.0% agar. Beyond these assay conditions, little is known about the shift from flagella-dependent motility to TFP-dependent on semi-solid surfaces. We recently observed that *P. aeruginosa* develops small clusters of cells as the organism transitions from flagella motility to TFP motility. It is hypothesized that *P. aeruginosa* cluster formation require TFP-TFP interaction and that cooperative retraction of bundled TFP fibers promote rapid small group movements. We investigated *P. aeruginosa* surface-air motility on non-traditional motility assay conditions containing 0.8% agar. We find that these transient clusters exhibit unique motility phenotype where the entire cluster travel across multiple cell length to join another cluster or contract to bridge the gap between cells. We aim to understand the roles of TFP after the initiation of surface colonization by the flagella-mediated swarming.

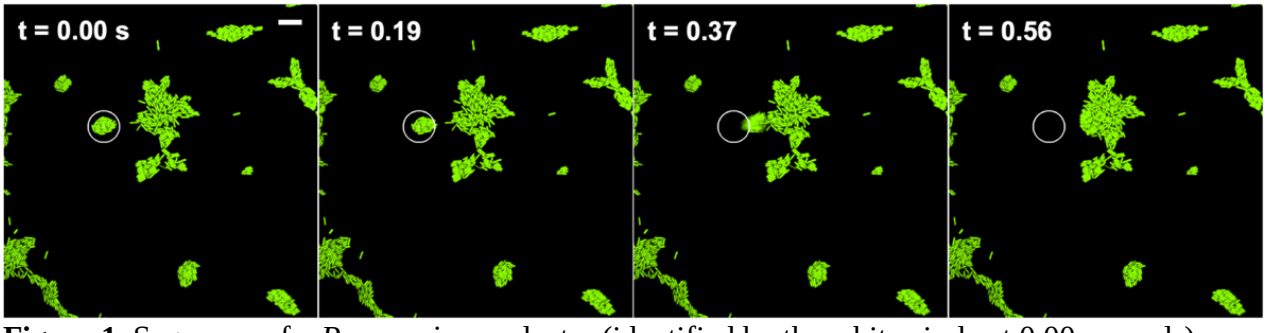

Figure 1. Sequence of a *P. aeruginosa* cluster (identified by the white circle at 0.00 seconds) snapping event over 0.56 seconds. The scale bar represents 10 μm.

Oral Presentation:

Development of St. Andre Ion Beam Facility

Ashabari Majumdar, Graham Peaslee

Department of Physics, University of Notre Dame

A refurbished 3MV tandem Van de Graaff accelerator along with a modified AlphaTross® ion source have been installed as part of a new Ion Beam Analysis Facility in the Nuclear Science Laboratory at the University of Notre Dame. This facility can perform a variety of ion beam analysis techniques, including: particle induced gamma-ray emission (PIGE), particle induced X-ray emission (PIXE) and Rutherford back scattering (RBS). These analyses can be performed on solid targets in vacuum chambers, but at the St. Andre facility the capability to perform PIGE and PIXE *ex vacuo* has also been developed. Initial tests with standards will be presented together with preliminary results from screenings for harmful chemicals in consumer products such as fast food wrappers, carpets, clothing and cosmetics. The ability to run lots of solid samples in air, allows this to become a rapid screening method for environmental contaminants. Another major goal is to provide hands-on training opportunities for graduate and undergraduate students.

The new ion source can produce stable currents (several microamps) of hydrogen and helium ions. The accelerator can produce beams of these particles up to 3 MeV and 9 MeV, respectively, and they can be directed to three beamlines (0°, 45° and 90°) currently, with the provision of adding a fourth one (135°) in the future. An overview of the new facility will be presented, as well as the routine operating procedures developed, and sample applications from a wide variety of disciplines. Future experiments including the routine analysis of aerosols by PIGE and PIXE and multivariate elemental analysis to determine sources of airborne contaminants will be outlined as well.

Poster Presentation:

Measuring the Plasma Radius at the Plasma-Liquid Interface in a Pulsed, DC Discharge

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The study of plasma-liquid interactions is an emerging field with multifarious applications, including medicine (wound healing, sterilization), environmental remediation (water purification, fracking fluid treatment), and material synthesis. These applications are driven by chemical species created in the plasma or at the plasma-liquid interface, such as hydroxyl radicals (OH), hydrogen peroxide (H_2O_2), and solvated electrons (e_{aq}^-). Solvated electrons are free electrons in a polar solution, loosely confined in a sphere of polar charge, notable for their speed of reaction (ns). In our previous work, we detected e_{aq}^-, using absorption spectroscopy, as they are injected steadily into a solution by a gas discharge. To measure extremely small optical densities ($\sim 10^{-5}$), the plasma current was pulsed at high and low values, at a carrier frequency of 20 kHz. Essential to the analysis of the absorption data is the value of the current density at the liquid interface, which can be determined based on the current and plasma radius. However, while the high, low, and average currents are easy to measure, only the average radius of the plasma beam under pulsing conditions can be captured by a conventional camera. This averaging poses a problem because the uncertainty of the plasma-liquid contact area and the current density manifest themselves as significant bias uncertainties in the data analysis. In this work, we used a high-speed camera with a recording speed of 20,000 fps and a 10 μs exposure time to accurately measure the dynamically changing plasma radius. The camera is triggered as the plasma switches between the high and low current states, and with a suitable delay, the states are captured separately. The image processing of the averaged images reveals the plasma radius and reduces the uncertainty in the calculation of key solvated electron parameters (such as the penetration depth) from the absorbance data.

Poster Presentation:

Using XCone as an Exclusive Jet Clustering Algorithm for Collisions in the Compact Muon Solenoid Detector

Ian McAlister, Kevin Lannon

Department of Physics, University of Notre Dame; CMS Experiment

During each particle collision in the LHC, the quarks making up the protons are what will actually collide. Color confinement within QCD, the theory that describes quarks, doesn't allow for free quarks to exist in isolation. When these quarks attempt to fly off in all directions after a collision they undergo a process called hadronization, where the quarks will create other particles to avoid being isolated. This results in a shower of hadronic particles referred to as a jet. Reconstructing particle tracks in the detector into their original jets is among the most important tasks to recreate the original particle the jets came from. There are several jet reconstruction algorithms in use by members of the LHC at the moment, which fall under two categories, either exclusive or inclusive. In an inclusive algorithm, particles are categorized into jets until every particle is part of a jet with some minimum distance R between jets. In an exclusive algorithm the number of jets is predetermined, and particles are clustered until the number of jets is obtained. In general, inclusive jets are better at analyzing substructure of jets, while exclusive jets are more accurate for the properties of the jet as a whole. This work is based on using a relatively new exclusive clustering algorithm known as XCone. XCone addresses a flaw in conventional jet algorithms, where jets are separated into a resolved regime, and a boosted regime, where the jets overlap heavily. XCone is able to transition smoothly between these two regimes, resulting in an overall more accurate clustering of particles into jets.

Poster Presentation:

Structural Analyses of Human MALAT1

Phillip J. McCown[1], Matthew C. Wang[1], Luc Jaeger[2], Jessica A. Brown[1]

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[2]Department of Chemistry and Biochemistry, University of California – Santa Barbara

Human metastasis-associated lung adenocarcinoma transcript 1 (MALAT1) is an abundant, nuclear-localized long noncoding RNA (lncRNA) that has significant roles in cancer. While the interacting partners and evolutionary sequence conservation of MALAT1 have been examined, much of the MALAT1 structure is unknown. Here, using independent datasets that probed RNA structures *in vitro* and in cultured human cells, we propose a secondary structural model for the 8425-nucleotide isoform of human MALAT1. We have been able to predict that at least 45% of MALAT1 has structural features, resulting in the prediction of 203 helical structures and 5 pseudoknots. Of these helices, we predict the formation of 6 three-way junctions, 4 four-way junctions, 1 five-way junction, and 3 complex multi-way junctions. Conservation and covariation analyses identified structural features of human MALAT1 that are present in homologous MALAT1 lncRNAs, suggesting that these conserved structures play important functional roles. Of note are two large regions of MALAT1 whose sequences and structures appear in MALAT1 homologs from human to turtle and alligator, suggesting that these regions may be useful in finding homologous MALAT1 sequences and structures. Mapping of protein binding sites onto the MALAT1 structure show that our predicted structural model conforms to these interactions, while the mapping of microRNA binding sites suggests that several regions of MALAT1 may undergo dynamic structural rearrangements. We anticipate that additional data mining, such as RNA modifications, single nucleotide polymorphisms, and somatic cancer-associated mutations, will reveal additional structure-function relationships that contribute to the function of MALAT1 in cells.

Keywords: lncRNA, miRNA, m^6A

Poster Presentation:

Selective Photothermal Heating with Near-Infrared Croconaine Rotaxanes

Hannah H. McGarraugh, Wenqi Liu, Braden Matthews, and Bradley D. Smith

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There is increasing interest in developing methods of generating heat in nanoscale environments. The most common approach uses the photothermal effect, namely the absorption of laser light by molecules or particles that convert this energy into heat. An area of interest for light absorption is the near-infrared (NIR) window, due to the minimal background signal, sharp probe signals, and increased depth penetration in *in vivo* applications. There are very few dyes that absorb strongly in the NIR region and of these dye families, croconaines remain a relatively unexplored group. We have previously shown that croconaines can be converted to rotaxane structures which exhibit sharp absorption bands, even under conditions that aggregate the molecules. Here, we will show previously reported croconaine dye **C1** and its newly extended counterpart **C2** as well as their relative rotaxanes **1** and **2**. These rotaxanes have distinct and non-overlapping absorbance bands at 830 nm and 980 nm, which lend themselves to the potential for multiplex heating, wherein multiple different croconaines with distinct absorbance wavelengths can be irradiated selectively. This can be utilized for various applications of photothermolysis including photothermal cancer therapy (PPT), photoacoustic imaging (PAI), drug delivery, tissue repair, photothermal reactions, and polymer welding.

Oral Presentation:

Production of ^{52}Fe from Symmetric Complete Fusion-Evaporation Reactions

Sean McGuinness[1], Samuel Ferran[2], John Wilkinson[1], Michael Skulski[1], Tyler Anderson[1], C. Shaun Loveless[2], Samuel Henderson[1], Adam Clark[1], Drew Blankstein[1], Austin Nelson[1], Craig Reingold[1], Suzi Lapi[2], Graham Peaslee[1]

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A promising method for the production and extraction of ^{52}Fe utilizing near-symmetric, heavy-ion fusion-evaporation reactions is presented. A ^{28}Si beam was used to bombard a ^{27}Al target, producing primarily ^{52}Fe through the reaction $^{28}Si + {}^{27}Al \rightarrow {}^{52}Fe + p + 2n$. After irradiation, the aluminum target was dissolved, and the ^{52}Fe was separated from the aluminum matrix and other reaction products through the use of a cationic-exchange column. With a starting aliquot of 4.10 μCi, it was possible to recover 56% with high specific activity. The production yields for this reaction were measured and compared to PACE calculations to demonstrate the potential for dedicated cyclotron production of ^{52}Fe by this method.

Poster Presentation:

Counter Cation-Specific Effects on Transport in Aqueous Hydroxide Solutions

Tierney Miller, Steven Corcelli

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The role of counter cations (Li^+ and Na^+) in aqueous hydroxide solutions is analyzed to support and provide atomistic detail to analogous experimental analyses of KOH, LiOH, and NaOH solutions at varying concentrations. Computational analysis was completed via *ab initio* molecular dynamics simulations in the CP2K open source molecular dynamics package. The presence of counter cations in hydroxide solutions impacts both vibrational spectra and hydroxide mobility in a counter-intuitive manner. Our AIMD simulations lend support to the experimental data that Li^+ holds its solvation shell more strongly, thereby decreasing hydroxide mobility, while simultaneously increasing proton delocalization around the hydroxide oxygen which leads to varying intensities seen in the experimental spectra.

Poster Presentation:

Tools for Trigger Rate Monitoring at CMS

Kelci Mohrman, Kevin Lannon

Department of Physics, University of Notre Dame

Stretching 27 kilometers in circumference as it straddles the Switzerland-France border near Geneva, Switzerland, the Large Hadron Collider (LHC) is the largest and most powerful particle accelerator in the world. Two counterrotating beams of particles are guided around the ring by superconducting electromagnets until they are made to collide within the four main particle detectors at the LHC. Studying the Standard Model and searching for physics beyond the Standard Model, the Compact Muon Solenoid (CMS) detector is one of the two general-purpose particle detectors at the LHC. One of the major challenges for the CMS experiment is the task of reducing event rate from roughly 40 MHz down to a more manageable 1 kHz while keeping as many interesting physics events as possible. This is accomplished through the use of a Level-1 (L1) hardware based trigger as well as a software based High-Level-Trigger (HLT). Monitoring and understanding the output rates of the L1 and HLT triggers is of key importance for determining the overall performance of the trigger system and is intimately tied to what type of data is being recorded for physics analyses. This presentation will discuss the CMS trigger system and some of the tools used to monitor the L1 and HLT trigger rates.

Oral Presentation:

Eyes without a Face: Ontogeny of Orbit Orientation in Primates

Emily M. Nett[1] & Matthew J. Ravosa[1-4]

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Orbit orientation in primates is postulated to result from adaptive factors related to activity pattern and influences of biological scaling (allometry) on orbit position. Although differences in circumorbital form between the two primate suborders (Anthropoidea and Strepsirrhini) have been linked to interspecific disparities in levels of orbital convergence (the degree to which the orbits are forward facing) and orbital frontation (the degree of orbit verticality), there is considerable overlap in convergence between suborders. Unfortunately, putative links between convergence and frontation across primates, and consequent arguments about anthropoid origins, are likely to be influenced by allometry, the size range of the respective samples, and adaptive influences on relative brain size and activity patterns. Indeed, such a multifarious system is less suitable to interspecific treatment across higher-level clades. Arguably, a developmental perspective is one way to evaluate transformations from one character state to another, especially as they pertain to allometric effects on phenotypic variation.

We characterized the development of orbital convergence and orbital frontation in 13 anthropoid and strepsirrhine species. Correlation and regression analyses were used to test hypotheses regarding the structural and adaptive bases of variation in orbital orientation. Growth trajectories were analyzed intraspecifically and interspecifically. While orbital frontation decreased postnatally in all primates due to the negative scaling of brain size, taxonomic differences in the relative amount of frontation were related to corresponding developmental transpositions in relative brain size that varied within, and especially, between suborders. Intraspecific increases in orbital convergence were restricted to strepsirrhines, whereas anthropoids exhibit elevated levels of convergence that varied little during growth. Such comparisons increase our understanding of morphological variation in the circumorbital region that impact characterizations of primate evolution.

Poster Presentation:

MMAR_2894 is an ESX-1 Associated PE-Protein in *Mycobacterium marinum*

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Mycobacterium marinum is an infectious agent of poikilothermic fish and an opportunistic human pathogen which can serve as a laboratory model for *Mycobacterium tuberculosis*. Both of these pathogens rely upon the ESX-1 (ESAT-6 System 1) secretion system for virulence in their respective hosts. This secretion system serves to transport virulence factors from the bacterial cell to the extracellular environment within infected host cells. The ESX-1 secretion system serves to facilitate phagosomal escape using these secreted virulence factors which lyse the phagosomal membrane. We have extensively characterized the secreted proteome using targeted and non-targeted mass spectrometry techniques to identify pathways and genes responsible for virulence. Recently, we identified a PE family protein, MMAR_2894, as a potential substrate of the ESX-1 secretion system in *M. marinum*. Here, we show that MMAR_2894 is a secreted substrate of ESX-1 which is essential for both secretion of EsxA, a known ESX-1 substrate, and lytic ability in a red blood cell lysis model. However, we found that MMAR_2894 is not required for virulence *in vivo* in a RAW264.7 cell infection model. Our findings uncouple the secretion of EsxA from virulence for the first time.

Oral Presentation:

The Effects of LiCl Treatment on Bone Formation *In Situ*

Alyssa Oberman, Glen Niebur

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Osteoporosis is a disease often characterized by an overall loss in bone density, predominantly in trabecular bone, which ultimately increases fracture risk, and poses the potential for more serious repercussions as the disease progresses. Thus it is important to identify potential targets for drug development. The canonical WNT pathway is integral in bone formation by activating transcription factors that control ECM production and could provide an ideal targeting location. Lithium chloride (LiCl) has been implicated in increased bone mass during *in vivo* studies through the activation of the WNT pathway. However, in vitro studies evaluating the effect of LiCl usage on osteoblast progenitors, mesenchymal stem cells (MSCs), have been inconclusive regarding osteogenic potential. We chose to look at an *in situ* bone marrow model to evaluate the effects of LiCl on the bone marrow niche as a whole and to eliminate any potential off-target effects that may also play into the increased bone formation in many *in vivo* studies. Porcine vertebral bone explants were cultured in a bioreactor for 28 days during which time explants were exposed to normal or drug-treated (5mM or 12mM LiCl) media, and static or loaded conditions. Bone explants were imaged with a μCT scanner before and after culture to measure changes in bone volume. Additionally, media was supplemented with 0.5 mM Alizarin Red and Xylenol Orange for 24 hours on day 6 and day 27 respectively for dynamic histomorphometry. Computational models of the bone explants were used to determine the shear stress experienced during loading. An *in vitro* study was performed using MSCs to test the effects of LiCl on differentiation potential. Neither loading nor LiCl treatment increased overall bone formation over the course of the experiment, which is contrary to previous studies performed by our group using the same culture method. We speculate that this is a result of the method through which we moderated media intake. Similarly, *in vitro* results suggested that LiCl might not be acting via the cells in the marrow and further investigation is required to fully understand the implications of LiCl on bone formation.

Poster Presentation:

EMG-Driven Musculoskeletal Simulations Using New Threshold Optimization Technique

Kevin O'Brien[1], Timothy Faw[3], Lise Worthen-Chaudhari[2], Michael McNally[4], Daniel Richie[4], D. Michele Basso[4], and James Schmiedeler[1]

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[2]Department of Physical Medicine & Rehabilitation, [3]Neuroscience Graduate Program, [4]School of Health & Rehabilitation Sciences, The Ohio State University

Musculoskeletal models provide unique insight into the different roles of muscles across a range of activities and walking strategies. With a significant degree of muscle redundancy and complex muscular structure, individual muscle forces cannot be directly calculated from inverse kinematics and kinetics. EMG-driven musculoskeletal simulations are extremely useful in analyzing neural activation in locomotion, particularly in uncommon gaits or populations. For individuals with neurological disorders, for whom these simulations would be uniquely insightful, performing the tasks to normalize EMG signals are particularly difficult. This paper demonstrates an alternative methodology to utilizing the temporal characteristics of experimental EMG in musculoskeletal simulations by considering the signal relative to the resting EMG threshold. To determine the efficacy of such a method, musculoskeletal simulations are run on healthy individuals and different simulation methods are compared. The results of both EMG-driven simulations and computed muscle control (CMC) simulations (no EMG consideration) are analyzed relative to the proposed threshold optimization technique. Joint moments from the simulations are compared to experimentally derived joint moments to confirm the validity of each simulation technique. The proposed threshold optimization technique does a better job of tracking the experimental EMG than the CMC simulations for most muscles, and at least as well for the remainder. Additionally, it tracks experimental EMG as well as the EMG-driven simulations for multiple muscles. Finally, for muscles for which no EMG is used in the simulations, the threshold optimization technique generally influences the muscles in the same way that the EMG-driven simulation does. This study shows that the threshold optimization technique is capable of improving on musculoskeletal simulations, and represent an alternative in gaits where direct EMG tracking cannot be performed.

Poster Presentation:

PLANT WATER FRACTIONATION ALONG A LATITUDINAL TRANSECT OF NORTHERN ALASKA

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Stable water isotopes (δ^2H and $\delta^{18}O$) are commonly used as modern environmental tracers and are also valuable tools for paleoenvironmental reconstructions. The δ^2H values from terrestrial leaf wax compounds preserved in sediments and soils are an increasingly used proxy for paleoenvironmental reconstructions from high latitudes. However, these records are reliant on modern calibration and advanced understanding of water isotope fractionation from high latitude systems and vegetation, which may vary from lower latitude systems [1-3]. Tundra and boreal forest ecosystems have different environmental and ecophysiological controls on isotope fractionation than lower latitude systems, such as continuous sunlight, limited growing season, and the presence of permafrost [2,4].

Plant and soil samples were collected along an 800 km Alaskan transect from the boreal forest of Fairbanks to the tundra of Deadhorse. Xylem and leaf water δ^2H values were compared to leaf wax *n*-alkanes δ^2H values to constrain fractionations associated with soil evaporation and leaf evapotranspiration across multiple species and plant morphologies. Environmental water isotopes were used to determine the local evaporation line and compared to existing environmental isotope data available for Alaska in order to examine water sources of vegetation from across the boreal forest to tundra transition. Using a wide variety of vegetation across a large spatial range, we aim to constrain the environmental and ecophysiological controls on water isotope fractionation that are important to consider for future paleoenvironmental reconstructions of the high latitudes.

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Oral Presentation:

Tissue Level Regulation of Ca^{2+} Signaling in Epithelia

Ramezan Paravitorghabeh, Dharsan Soundarrajan, Jeremiah Zartman

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Cells detect a broad range of extracellular stimuli that serve as input signals into a biochemical regulatory network. This network acts as a classifier for determining cellular responses. Second messengers such as calcium ions (Ca^{2+}) are important intermediary central integrators within this signaling network. However, the emergent properties of calcium signaling dynamics at the scale of tissues and organs is largely undefined. Here, we have developed and validated a multiscale computational model of calcium signaling in a network of epithelial cells that are connected by gap junctions. Experimental data of calcium signaling generated utilizing a genetic model organ of limb development, the *Drosophila* wing imaginal disc, reveals complex stochastic and highly regulated spatiotemporal Ca^{2+} dynamics. We built a geometrically accurate computational model for intercellular Ca^{2+} signaling that recapitulates the observed diverse set of spatiotemporal patterns. The multi-scale computational model recapitulates the main classes of experimentally observed Ca^{2+} signaling dynamics: single cell Ca^{2+} spikes, localized intercellular transient bursts, intercellular waves and fluttering effect. We show that a wide range of intercellular communication patterns is a consequence of differential regulation of Ca^{2+} toolkit components in the presence of a Hopf bifurcation. This provides evidence that stochastic intercellular signaling dynamics are tightly regulated at the tissue level.

Oral Presentation:

Defining Characteristics and Community Structure of the Gut and Oral Microbial Communities of Long-Tailed Macaques (*Macaca fascicularis*) in Singapore

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Host-associated microbial communities influence a range of important biological functions, including host development, metabolism, and immune defenses. Several factors govern the assemblage of different microbial communities, such as host traits, environment, diet, and interactions with eukaryotic gut parasites – a relationship that is understudied. It has been hypothesized that parasite infections can have profound influences on prokaryotic richness and diversity through the action of different ecological mechanisms (e.g. top-down processes as mediated through host immune responses and bottom-up processes governed by competition and resource flux through the gut). Here we characterize the oral and gut microbial communities of long-tailed macaques in the highly anthropogenic environment of Singapore using 16S rDNA Illumina amplicon sequencing, focusing on the prokaryotic variation found within and between sampling sites. Our data reveal that oral microbial communities exhibit greater taxa richness and stability across sampling sites and are dominated by taxa belonging to the phylum Firmicutes, while taxa dominating gut communities are as likely to be dominated by the phylum Bacteroidetes. We pinpoint family-level taxa driving these shifts in structure and composition by linear discriminant analyses, which reveals over 50 prokaryotic families distinguishing the oral and gut communities. We then incorporate host parasite microscopy data to examine interactions between eukaryotic and prokaryotic communities, using multivariate linear models to identify specific microbial taxa associated with overall protozoan abundance and presence, helminth presence, and presence of the gut parasite *Blastocystis*. Delineating potential ecological interactions between prokaryotic microbiota and eukaryotic parasites presents a path forward for understanding how prokaryotic community structure may serve to block or enhance the invasion of the gut by more pathogenic organisms, which has important implications for coinfection dynamics and human health.

Poster Presentation:

Structural Studies of Human Methyltransferase-Like Protein 16

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N^6-methyladenosine (m^{6}A) is an abundant modification in messenger RNA and noncoding RNAs that affects RNA metabolism. Methyltransferase-like protein 16 (METTL16) is a recently confirmed m^{6}A RNA methyltransferase that methylates U6 spliceosomal RNA and the MAT2A mRNA encoding *S*-adenosylmethionine (SAM) synthase as well as interacts with the 3′-terminal RNA triple helix of MALAT1 (metastasis-associated lung adenocarcinoma transcript 1).

In this study, we present two X-ray crystal structures of the N-terminal methyltransferase domain (residues 1-291) of human METTL16 (METTL16_291): an apo form at 1.9 Å resolution and a post-catalytic complex with *S*-adenosylhomocysteine (SAH) at 2.1 Å resolution. The structure reveals a highly conserved Rossmann fold characteristic of Class I *S*-adenosylmethionine (SAM)-dependent methyltransferases and a large, positively charged groove that is an RNA-binding site. Our ongoing structural studies, which also include cryo-electron microscopy (cryo-EM), are focused on determination of molecular structure of full length METTL16 alone and in complex with the MALAT1 triple helix. To make METTL16 suitable for cryo-EM, we have designed a fusion protein containing the C-terminal domain of METTL16 (residues 292-562) and the oligomerizing domain of pyrroline-5-carboxylate reductase (METTL16_292-562_MtP5CR). The METTL16_292-562_MtP5CR is expected to form decamers (molecular weight ~0.4 MDa), which would satisfy size requirements for cryo-EM. Here, we present our preliminary results of negatively stained electron micrographs of METTL16_292-562_MtP5CR, an early first step toward achieving our long-term goal.

Poster Presentation:

Characterizing Transcriptional Regulation of Virulence in *Mycobacterium marinum*

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Pathogenic mycobacteria, including *Mycobacterium tuberculosis* use the ESX-1 (ESAT-6-system-1) secretion system to promote bacterial survival in the host. ESX-1 secretion directly impacts transmission and disease severity of *M. tuberculosis*. The mechanisms regulating ESX-1 secretion are not well understood. Using *Mycobacterium marinum,* a non-tuberculous mycobacterial species that is an established model for understanding ESX-1 secretion in *M. tuberculosis*, we have uncovered a new fundamental mechanism regulating ESX-1 secretion. Genetic disruption of the ESX-1 system causes a reduction in the levels of secreted substrates inside of the cell via an unknown mechanism. We hypothesized that the bacterial cell can sense the presence of the ESX-1 secretion system and regulate the levels of substrate gene expression accordingly. To this end, we used genetic, biochemical, and proteomic methods to determine that the loss of the ESX-1 apparatus in the bacterial membrane led to the reduced transcription of the genes encoding the WhiB6 transcription factor and the ESX-1 secreted substrates. We sought to identify the mechanism linking gene expression to the ESX-1 secretion system. We discovered a new DNA binding protein, EspM, that interacts with the *whiB6* promoter in an ESX-1 dependent manner in vitro. We found that the C-terminal domain of the protein is sufficient to bind the *whiB6* promoter region. We propose a new model for regulating the ESX-1 system, which may provide new targets for therapeutics against Tuberculosis.

Poster Presentation:

Fatigue Performance of Direct Metal Laser Sintered Parts using Reused Metallic Feedstocks

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Material cost remains a primary obstacle for powder-bed additive manufacturing (AM) to competitively produce large volumes of parts. Material consumption for powder-bed AM processes such as selective laser melting (SLM), is inefficient and especially costly for expensive metallic feedstocks, since unfused powder is discarded after a build. Powder reuse is a simple and direct management strategy to achieve cost savings and involves returning unused powder from a previous build to the supply cylinder. However, the practice of repeated cycling of a percentage of non-virgin feedstock has raised concerns about the resultant part properties. Previous efforts to validate feedstock recycling have examined the static properties of reused AM metals, but no studies to date have assessed fatigue behavior with respect to powder reuse. Fatigue testing is critical for industrial applications to characterize material behavior in response to low-magnitude, cyclic stress. Three metallic feedstocks, two ferrous alloys, 316L and 17-4PH stainless steel (SS) in addition to Ti-6V-4Al (Ti64) were cycled through thermal and atmospheric conditions representative of industrial SLM machines. Fatigue specimens were sintered with powder classified as virgin or eighth reuse using a standard set of machine parameters. All samples were tested in rotating beam fatigue testing, using the stair-case method, minimizing the number of specimens required to determine the average fatigue limit. No statistically significant difference was calculated for the fatigue limit of 316L, 17-4PH, Ti64 with respect to reuse. Density measurements confirmed the lack of reuse-dependent behavior for the stainless steels, and Ti64 showed a statistically significant improvement in bulk density at reuse eight. Results suggest that for the reuse timetable evaluated, accelerated life testing of metallic parts built from reused feedstocks did not compromise fatigue performance. This would suggest that powder reuse can continue to be a viable solution for improved powder-bed AM economics.

Keywords: powder reuse, fatigue, staircase method, additive manufacturing, selective laser melting, mechanical properties, stainless steel, titanium

Poster Presentation:

New Means of Gold Recovery using Novel Gold Capture Molecules

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Current industrial gold recovery methods are effective but also have various drawbacks such as the use of highly toxic cyanide reagents. The development of a safer and more environmentally friendly method of recovery would therefore be desirable, and to that end, alternative approaches have been examined. One such alternative is the conversion of the gold ore to chloroauric or bromoauric acid, $HAuX_4$. These compounds, however, have some drawbacks that make recovery of the purified ore difficult. This presentation describes a new set of capture molecules which can bind the gold guests strongly and co-precipitate them out of solution. The formation of complexes between these capture molecules and the gold ions relies on supramolecular interactions such as cofacial aromatic stacking and hydrogen bonding. Several capture molecules were examined including both macrocyclic and simpler acyclic systems. Additionally, x-ray crystal structures obtained for these complexes show some unique binding characteristics like the unusual way that the proton provides extra stabilization in the crystal lattice. These new capture molecules may have applications in gold recovery as well as other areas like drug delivery.

Poster Presentation:

Implicit Symmetric Tensor Decomposition with Applications in Data Analysis (*)

Samantha Sherman, Department of Applied and Computational Mathematics and Statistics, University of Notre Dame; Tammy Kolda, Sandia National Laboratories.

There has lately been interest in tensor decompositions of symmetric tensors that correspond to higher-order moments. These represent mixture models and have applications is signal separation and data analysis. Given a set of p observations of length n, the dth order moment is formed as follows. For each observation, form its d-way outer product, and then sum the d-way outer products for all p observations. Forming this explicitly requires pnd operations. Instead, we show that the moment tensor can be decomposed using only the original n×p observation matrix and with far less operations. Numerical results confirm our analyses: the implicit method produces the same results as the explicit method and is significantly faster.

(*) Sponsored by the NSF Math Sciences Graduate Intern (MSGI) Program.

Poster Presentation:

The ChemoPAD: A Paper Analytical Device for Detecting the Presence of Four Chemotherapy Drugs

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A paper analytical device was developed and validated to visually detect methotrexate, doxorubicin, cisplatin, and oxaliplatin at concentrations commonly found in injectable dosage forms. By testing residual solution after patient treatment, the chemoPAD can be employed to monitor drug quality without restricting the patients' access to medication. The chemoPAD is produced by wax printing on Ahlstrom paper to create separate reaction areas and depositing small amounts of chemicals to create color changes in response to different active pharmaceutical ingredients (API). This creates a unique "color-bar code" to identify each medication. Internal validation studies show that the chemoPAD has excellent sensitivity and specificity for differentiating between samples of 100 % and 0 % API, which is the distinction relevant to the majority of reported falsified chemotherapy cases. The platinum containing drugs, cisplatin and oxaliplatin, can be detected semi-quantitatively. The cards can be read either visually by comparison to a standard image or by using computer image analysis. Dosage forms were collected from the Ethiopian Healthcare system and analyzed with the chemoPAD followed by high performance liquid chromatography (HPLC). A substandard sample was discovered and reported to the Ethiopian Regulatory Agency.

Poster Presentation:

DTK-Dengue: A New Agent-Based Model of Dengue Virus Transmission Dynamics

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Dengue is a mosquito-borne viral disease that exerts a growing impact on global health and presents a formidable challenge for health officials, in part because many factors related to its transmission are difficult to observe and measure (e.g., levels of population immunity). Agent-based models (ABMs) can explicitly represent these factors and can be calibrated to empirical data to provide insights about the dynamics of both observed and unobserved variables. Disease Transmission Kernel-Dengue (DTK-Dengue) is an ABM for dengue virus (DENV) transmission that extends the Institute for Disease Modeling's Epidemiological Modeling Disease Transmission Kernel (EMOD-DTK). DTK-Dengue includes three major modifications to EMOD-DTK: 1) it incorporates the influence of climatic variables on *Aedes aegypti* mosquito population dynamics, 2) it modifies adult vector activity to reflect *Ae. aegypti* behavior, and 3) it explicitly includes all four DENV serotypes, including their effects on human immunity and rates of symptomatic disease. Although ABMs such as DTK-Dengue can represent a variety of observed and unobserved variables, little is known about the relative contributions of different data types from routine surveillance systems for calibrating such models. We calibrated DTK-Dengue with four complementary datasets from San Juan, Puerto Rico in 2007: the monthly incidence, the monthly number of cases by serotype, the age distribution of cases, and mosquito trap data for two municipalities. We ran five calibrations, each incorporating one possible combination of datasets into the model likelihood. We evaluated the fit of the model to all data types, regardless of whether they were used in the calibration, and assessed how the inclusion of data types influenced model outputs not explicitly included in the calibration. These results provide insight into the relative importance of different types of commonly collected data for calibrating ABMs of DENV transmission and how the inclusion of these types influences model predictions.

Poster Presentation:

Quantifying the Recovery of Nitrogen Removal Capacity via Denitrification Following Stream Dredging and Floodplain Construction in an Agricultural Watershed

Shannon L. Speir, Jennifer L. Tank, Ursula H. Mahl

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Widespread algal blooms and the formation of hypoxic zones are fueled by anthropogenic nutrient loading into aquatic ecosystems. In agricultural streams, floodplain restoration via the two-stage ditch can be implemented to improve water quality. Constructed floodplains slow water velocities, reduce turbidity, and expand bioreactive surface area for microbial processing of excess nutrients. For nitrate-N removal, floodplains can enhance microbial denitrification, thereby reducing N loading to sensitive areas downstream. In the Shatto Ditch (Kosciusko County, IN), 0.5 miles of two-stage was constructed in 2007 at the base of the watershed. In 2017 and 2018, an additional 2.3 and 1.7 miles were constructed, respectively, in naturalized reaches that had no direct ditch management for >10 years. We quantified the recovery of denitrification over time following stream dredging and floodplain construction in these three stream reaches using experimental sediment incubations. Dissolved di-nitrogen gas (N_2) measurements were made using membrane inlet mass spectrometry (MIMS). Prior to construction in summer 2017, we documented measurable sediment denitrification in all reaches (mean = 0.22 µg N g DM^{-1} h^{-1}). At both three weeks and seven months following the 2017 construction, there was no measurable denitrification on floodplain soils in the newly constructed two-stage ditch. In contrast, for stream sediments, denitrification had recovered as early as three weeks post-dredging (0.15 µg N DM^{-1} h^{-1}), but rates remained low relative to the 11 year old two-stage reach (0.57 µg N g DM^{-1} h^{-1}). Our research suggests that stream sediments may recover from disturbance on the order of weeks, likely due to microbial colonization from upstream reaches. However, floodplains, which experience intermittent connection to stream channels during flooding, can take longer to recover. This time lag in ecosystem function post construction is important to consider when evaluating N load reductions that may occur via restoration efforts.

Poster Presentation:

Determining the Defensive Mechanisms in Green Ash (*Fraxinus pennsylvanica*) Resistant to Emerald Ash Borer (*Agrilus planipennis*)

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Emerald ash borer (EAB, *Agrilus planipennis*), an accidentally introduced Asian beetle, poses an acute threat to the native Fraxinus species in North America. Mass mortality in green ash (*F. pennsylvanica*) and white ash (*F. americana*) affects broad swaths of the landscape, from forests and farmland to urban streets. Although urban foresters and communities spend upwards of a billion dollars a year fighting this spread, American ashes are being functionally removed from the landscape. However, a few green ash (<1%) termed "lingering" have been noted to survive for years after all other local green ash have died. Some of these trees have been collected and their defensive responses confirmed (killing some EAB larvae or slowing their growth) in clonally replicated studies. Because these trees appear to use different methods of resistance, these multiple traits can be 'stacked' or pyramided in a selective breeding program to produce trees with greater long-term resistance to EAB.

We are undertaking a multi-faceted, interdisciplinary approach to examine the functional basis for resistance to EAB in lingering green ash. We employ transcriptomics, proteomics and metabolomics to examine differences in gene expression, proteins and secondary metabolites in susceptible green ash vs lingering green ash. This analysis is applied to 200 progeny from lingering x lingering and susceptible x susceptible crosses in twelve different families. As this stands, we have identified a number of ash metabolites that differ significantly between susceptible and resistant trees. We will examine the proteome and transcriptome to see if these changes correspond to protein and transcript differences in a network. Once we identify mechanisms and indicators of resistance, we will have 1. A higher throughput test for breeding lingering trees, and 2. A method to collect more trees from the wild. This will strengthen our goal of producing an ash with enough resistance that EAB becomes a pest instead of a deadly plague.

Poster Presentation:

Loss of APC Mediates Doxorubicin Resistance in Breast Cancer Cells

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Resistance to chemotherapy is one of the leading causes of breast cancer related deaths. Understanding the molecular basis for chemoresistance is essential for the advancement of novel therapeutic approaches to ultimately improve patient outcomes. The *Adenomatous Polyposis Coli* (*APC*) tumor suppressor is either mutated or hypermethylated in up to 70% of sporadic breast cancer; however, little is known about how loss of APC contributes to chemoresistance. Using the $Apc^{Min/+}$ mouse crossed to the Polyoma middle T antigen (PyMT) transgenic model, we demonstrated that APC loss decreased cisplatin and doxorubicin-induced apoptosis. We previously showed that loss of APC in MMTV-PyMT;$Apc^{Min/+}$ cells induced STAT3-activation resulting in an enhanced tumor initiating cell (TIC) population and increased multidrug resistance protein 1 (MDR1) expression. Therefore, we hypothesized that APC loss increased MDR1 activity and decreased doxorubicin-mediated DNA damage, ultimately preventing cell death. Using calcein incorporation, we first demonstrated that APC loss increased MDR1 activity which was normalized to WT control levels by the MDR1 inhibitor, Valspodar. We next showed that MDR1 inhibition in MMTV-PyMT;$Apc^{Min/+}$ cells could restore doxorubicin-mediated apoptosis to that of MMTV-PyMT;$Apc^{+/+}$ treated cells. Due to STAT3 inducing MDR1 activity and TIC population, MDR1 inhibition in MMTV-PyMT;$Apc^{Min/+}$ cells was also shown to reduce the TIC population. In addition, we are investigating the effect of APC loss on DNA damage repair pathways. Preliminary studies have shown decreased γH2AX in MMTV-PyMT;$Apc^{Min/+}$ cells treated with doxorubicin, suggesting a decrease of DNA damage. Downstream signaling of γH2AX, measured by phosphorylation of ATM and ATR, also demonstrated decreased DNA damage. Future studies will investigate whether MDR1 inhibition in combination with doxorubicin will reduce tumor burden *in vivo*. Taken together, APC loss mediates doxorubicin resistance via enhanced MDR1 activity and altered DNA damage repair pathways demonstrating the potential use of combination therapy to overcome resistance to chemotherapy.

Poster Presentation:

Investigations of a Molecular Machine, Cyclodextrin Rotaxane, using NMR Methods

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Supramolecular chemists are working on the rational design of molecular machines; it is necessary for the design process to create an assay that detects functional outputs. NMR relaxation is an underutilized tool to study functional components in molecular machines. A rotaxane system where the rotational function could be turn "ON" and "OFF" by chemical additives was used. [1]Rotaxane is in the "OFF" position and [3]rotaxane is in the "ON" position; comparison of the two allows for the detection of properties related to rotation.[1] The NMR relaxation studies were able to point to differences due to the rotation of the cyclodextrin ring in [3]rotaxane. This methodology will allow chemists to test for rotational motion and allow them to validate the function of the molecular machine synthesized.

References:

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Poster Presentation:

Using a Replicated Watershed Design to Evaluate the Role of Cover Crops in Reducing Nutrient Pollution

Ceara J. Talbot, Jennifer L. Tank, Matt T. Trentman, Shannon L. Speir, Ursula H. Mahl

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Agriculture is a major source of non-point nutrient pollution to aquatic ecosystems, particularly in the Midwest where fields are bare during winter and early spring, enhancing nutrient runoff during storms and snowmelt. The planting of winter cover crops can mitigate soil nutrient loss through storage in plant tissues during the fallow period. To quantify the water quality benefits of watershed-scale cover crops, we conduct year round sampling at multiple stream sites and subsurface tile drain outlets in two Indiana watersheds: Shatto Ditch (SDW; Kosciusko County; 5 yrs) and Kirkpatrick Ditch (KDW, Jasper County; 3 yrs). In summer 2018, we expanded this work to three small sub-basins of the Paw Paw River Watershed (PPRW; Berrien Co, MI). We coordinated cover crop planting on 51% of croppable acres in one agricultural sub-basin and have two control sub-basins (agricultural with no cover crops vs. forested). Here, we present preliminary data comparing streamflow and surface water nutrients in PPRW to previous data from SDW and KDW, and explore how differences in nutrient yields among watersheds may influence the efficacy of cover cropping. Preliminary data from PPRW during the growing season (July-October 2018) suggests that the two agricultural sub-basins have similar nutrient yields (export per unit area). Mean daily nutrient yields for the two agricultural sub-basins in PPRW (6 g NO_3^--N/ha/day and 125 mg P/ha/day) were higher than yields in KDW (2 g NO_3^--N/ha/day and 27 mg P/ha/day). Compared to SDW, PPRW sub-basins had lower NO_3^--N yields, but similar to SRP yields (25 g NO_3^--N/ha/day and 84 mg P/ha/day). The addition of two control sub-basins in PPRW will help us build on previous work in SDW and KDW, and partition drivers that control nutrient export with and without cover crops.

Poster Presentation:

Simulation Study of the Asymmetric Vibrational Excitation in CO_2 Field Emission-Driven Townsend Discharges

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The reforming of carbon dioxide (CO_2) into useful chemicals such as synthesis gas is challenging due to the stability of the C-O bond in the molecule. Historically, catalytic systems have been used, but one promising emerging approach is to inject energy into the molecule via a gas discharge or plasma in order to promote CO_2 dissociation. If this is done in a way where the plasma action synergistically combines with the catalyst, then it may be possible to achieve greater energy efficiencies and selectivity than previously achievable. In this work, we consider the rational design of a plasma catalysis system for the splitting of CO_2. We show that CO_2 molecules that are vibrationally excited in the asymmetric stretch have a higher dissociation probability on nickel catalysts than those in the symmetric stretch. We then demonstrate that field emission-driven microdischarges (also called microplasmas) can selectively excite the asymmetric stretch mode relative to the symmetric stretch mode. These results show that field emission-driven microdischarges could form the basis for intentionally coupling the plasma state with a catalyst for improving the performance of CO_2 reforming.

Poster Presentation:

Isolation of Monoclonal Antibodies using Mimotope-Containing Membranes

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Convenient antibody isolation is vital for determining therapeutic monoclonal antibody (mAb) concentrations and assessing post-dosage mAb levels in human serum. Conventional methods, such as enzyme-linked immunosorbent assays and liquid chromatography/mass spectrometry (LC-MS), are time-consuming and costly. This work employs porous nylon membranes functionalized with a Her2 mimotope peptide, KGSGSGSQLGPYELWELSH (K19), for rapid and selective capture of Herceptin, a mAb used for breast cancer treatment. LC-MS confirms the high purity of Herceptin recovered using K19-modified membranes. For membranes loaded with 10-120 μg/ml of Herceptin in 1:3 diluted serum, the intrinsic tryptophan fluorescence of the eluted mAb increases linearly with the loading concentration. Thus, K19-modified membranes should enable Herceptin analysis without labeling or secondary antibodies. Mimotope-containing membranes mounted in spin columns allow mAb quantitation in minutes, and such analyses may aid physicians in assessing the need for additional doses of expensive therapeutic mAbs.

Poster Presentation:

Biomarker Records of Plio-Pleistocene Paleoclimate from the Southeast African Margin

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The climate of the Limpopo River catchment, located in southeastern Africa, is sensitive to hydrographic changes in the nearby Agulhas Current (AC) and atmospheric circulation variability driven by large-scale, global climate dynamics. Despite the potential significance of climate's role in regional hominin evolution, records of Plio-Pleistocene terrestrial climate in southeastern Africa have been limited by a prior lack of drill cores. Here we examine the molecular and isotopic composition of marine and terrestrial biomarkers recovered from deep-sea sediments near the Limpopo River drainage (IODP Site U1478) to provide a continuous record of terrestrial climate in southeastern Africa and its relation to global climate and the AC. Our compound-specific hydrogen isotope (δ^2H_{wax}) record of hydroclimate variability and corresponding haptophyte algae ($U^{k'}_{37}$) and marine archaea (TEX_{86}) lipid-based temperature records span from 4.3 to 1.75 ma, encompassing the mid-Pliocene warm period, the Plio-Pleistocene transition, and some developments in early hominin evolution. Our biomarker records document a transition to wetter conditions between 4.3 and 4 Ma that persist into the late Pliocene, followed by increasing aridity at 3 Ma and a shift to higher amplitude variability in hydroclimate that characterizes the latest Pliocene and early Pleistocene. We discuss the connections between Plio-Pleistocene climate change in the Limpopo River catchment and both continental ice sheet and Indian Ocean variability and explore the potential implications of our climate records for the interpretation of early hominin evolutionary transitions in East Africa.

Poster Presentation:

Comparing Biotic Controls on Phosphorus Cycling in Stream Sediments and Floodplains Soils in Agricultural Streams

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Maximizing nutrient removal from agricultural streams is one mechanism for alleviating eutrophication in downstream water bodies, such as Western Lake Erie and the Gulf of Mexico. In the agricultural Midwest, the construction of inset floodplains in formerly-channelized streams and ditches can increase nutrient removal, yet the impact of floodplains on phosphorus (P) dynamics is understudied compared to nitrogen. Similarly, within channels, stream sediments can either retain or release P, depending on local conditions. The duration of floodplain inundation and the balance between sediment deposition and scouring varies seasonally with stream flow, which can ultimately influence the balance between P export and retention. We examined the role of seasonal biotic processes influencing P pools and fluxes on floodplains and in adjacent stream sediments in three agricultural streams in northern Indiana. We predicted that biotic P assimilation, assessed via microbial respiration (R) and extracellular enzyme activity (alkaline phosphatase activity, APA), would be driven primarily by P and organic matter (OM) availability. Pools of biologically available P varied significantly among some seasons and sites for both stream sediments and floodplain soils. Soil R was significantly different among streams, and seasons, and was positively correlated with soil OM content, linking microbial P assimilation with carbon availability. Stream sediment respiration only varied among streams and was not correlated with any predicted drivers. Floodplain soil APA varied among streams, but not among seasons, while, stream sediment APA varied only among seasons. Contrasting APA dynamics were likely a result of hydrologic differences; there was consistent flow over stream sediments, while floodplains were exposed to a variable inundation regime among sites. Overall, we found strong evidence for biotic P assimilation in both sediments and floodplain soils; however, the ability to remove water column P differs with hydrologic variability as well as soil/sediment physicochemical characteristics.

Poster Presentation:

Reverse-Engineering Unit Operations of Morphogenesis: Factors Modulating Epithelial Spreading Dynamics in *Drosophila*

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Epithelia play important roles in shaping tissues and organs during development process and protects inner tissues. Epithelial spreading is a common and fundamental mode of tissue rearrangement that occurs throughout many stages of development and wound healing. Epithelial spreading involves the coordinated migration of cells and often involves the replacement of other cell populations. However, the biophysical regulation of cellular properties such as cell stiffness and cellular activities such as cell growth and death during epithelial spreading remain poorly understood. Here, we have systematically investigated the dynamics of epithelial spreading during *Drosophila* head involution, which occurs in late embryogenesis to internalize part of the ectoderm. Head involution serves as a prototype of developmentally controlled tissue spreading that is amenable to genetic perturbations, and *in vivo* live imaging. However, little is known about what determines the rate of epithelial spreading in relationship to earlier developmental processes. In initial experiments, we have found that ectopic cell proliferation significantly slows epithelial spreading, and epithelial spreading is accompanied by upregulation of intermittent intercellular calcium transients. An improved understanding of how to regulate epithelial spreading can facilitate new methods to accelerate wound healing and define important design criteria for synthetic morphogenesis.

Poster Presentation:

Single-Cell Profiling Guided Combinatorial Immunotherapy for CDK4/6 Inhibitor Resistant HER2-Positive Breast Cancer

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Targeted cancer therapy has pioneered the concept of precision medicine by integrating genetic profiling of each patient's tumor biopsy with rationally-designed targeted therapy. Trastuzumab (Herceptin™), a humanized monoclonal antibody targeting the extracellular domain of human epidermal growth factor receptor-2(HER2), is one of the most successful examples of targeted therapies for HER2-positive breast cancer. However, drug resistance remains daunting challenges. The recent development of cyclin dependent kinase(CDK) 4/6 small molecule inhibitors has provided patients with relapsed trastuzumab resistant tumors a new hope. New combinatorial regimen of CDK4/6 inhibitors plus trastuzumab is currently under active clinical investigations. Cancer is a consistently evolving multicellular ecosystem, and the selection pressure imposed by drug treatment will inevitably lead to acquired resistance. In this study, we seek to prospectively model the in vivo response to CDK4/6 inhibitor plus trastuzumab using transgenic Her2/Neu mouse model in parallel with the current clinical trial scenario. Strikingly, after initial response, acquired resistance to the anti-Her2/Neu antibody plus CDK4/6 inhibitor Palbociclib (Ab+Pal) combination treatment emerged quickly. By leveraging high-throughput single cell RNA-seq analyses of the evolving tumors over the course of treatments, including treatment naive, sensitive/residual and resistant/progressive tumors, we revealed although Ab+Pal treatment enhanced antigen processing and presentation and interferon signaling on tumor cells, a distinct immature myeloid immunosuppressive cells(IMCs) infiltrated in the resistant tumor microenvironment. Guided by single cell gene set enrichment analysis based drug screening, we identified and evaluated a combinatorial immunotherapy regimen. We found that combinatorial immunotherapy with receptor tyrosine kinase inhibitor Cabozantinib and immune checkpoint blockades overcome Ab+Pal resistance by inhibiting IMCs and enhancing anti-tumor immunity. More importantly, our rationally designed sequential combinatorial regimens enabled durable response and sustained controlling of the emergence of acquired resistance, thus significantly improved outcomes of rapidly evolving CDK4/6 inhibitor resistant Her2/Neu positive breast cancers. Our findings implicate that single-cell RNA sequencing guided combinatorial immunotherapy as a strategy to mitigate the emergence of resistance and to achieve maximal benefit merits clinical translation.

Poster Presentation:

Complex Microbial Communities Relevant to Prosthetic Joint Infections

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Prosthetic joint infections (PJIs) are challenging to treat therapeutically because infectious agents often are resistant to antibiotics and capable growth in surface-attached biofilms. These infections can be debilitating to deadly. Though infection rates are low, ca. 1-2%, joint replacement surgeries are becoming more and more common and number of infections are anticipated to rise. A challenge in studying PJI is absence of consensus with respect to identification of microbial species comprising PJI ecology. This study examines PJI populations from seven patients using combined culturing and whole genome shotgun sequencing (WGSS) to establish population profiles and compare WGSS and culture for detection and identification of the PJI microbiome. WGSS detected strains when culture did not, notably dormant, culture-resistant, and rare microbes. PJI profiles were assembled using combined results from the CosmosID algorithm, to detect microorganisms present in the PJI and discriminate contaminants, with a culturing strategy. Variability between and among PJIs showed that most of the infections were, in fact, distinct and unique. Comparative analysis of the cultured PJI populations with the WGSS microbiome populations revealed PJIs to form clusters related, but separate, to skin and gut microbiomes. Fungi and protists were detected by WGSS, but the role of fungi is just beginning to be understood and for protists it is unknown. It is yet to be understood how novel and strain specific microbial interactions impact patient outcomes in PJIs. The role of polymicrobial infections, including viruses and protists with bacteria and fungi must be addressed to develop more effective treatments.

Poster Presentation:

Inocolum Dose Dependency of Influenza Infection

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Problems arise when studying influenza infections due to the ephemeral nature of the virus and sudden onset after exposure. Unlike long-term or chronic diseases such as tuberculosis and HIV, influenza patients only experience symptoms for a few days, so the virus must be detected within hours of initial exposure to record data accurately. Also, the amount of pathogen that the patient was exposed to cannot be known when the disease is acquired naturally. Influenza challenge studies have been performed since 1946 to test various prophylaxis and treatment methods as well as to study epidemiological trends. In these studies, volunteers are purposefully inoculated with a known amount and type of influenza virus in a controlled setting. The control groups of these studies mimic natural infection but allow researchers to collect information than would be impossible in a natural setting. This meta-analysis will use data from the control groups of methodically reviewed literature in to determine patterns for how different conditions surrounding inoculations affect the severity of the disease. This information could suggest an efficient way to control the spread of influenza.

Oral Presentation:

Probing Effective Field Theory Models using Associated Top Quark Production in Multiple Lepton Final States at 13 TeV

Andrew Wightman, University of Notre Dame, Mike Hildreth, University of Notre Dame, Reza Goldouzian, University of Notre Dame, Kevin Lannon, University of Notre Dame, Anthony Lefeld, The Ohio State University, Kelci Mohrman, University of Notre Dame, Goeffrey Smith, University of Notre Dame, Brian Winer, The Ohio State University

There are many motivations to search for new particles or interactions at the LHC: The existence of dark matter and dark energy, the asymmetry between matter and antimatter, and most solutions to the hierarchy problem imply that the full list of nature's constituents has not yet been discovered. However, there is no guarantee that new particles exist in the mass range directly accessible at the LHC. To extend the discovery reach of the LHC, it is therefore prudent to consider not only direct searches for new particles, but also through indirect means. One flexible framework for undertaking such indirect probes is that of effective field theory (EFT). We extend the standard model (SM) lagrangian by adding terms with mass dimension higher than four. Each term is constructed from products of only SM fields and must respect the symmetries and conservation laws observed in nature. The LHC provides a unique opportunity to study in detail the production of heavy particles such as the top quark, in addition to the H, W and Z electroweak bosons. EFT provides a powerful framework in which to extract evidence of new physics or to set constraints on the degree to which it might be present in the data. We attempt to set limits on dimension six EFT operators by considering their impact on the production of one or more top quarks in association with one or more W, Z, or H bosons. We consider final states in which multiple bosons decay leptonically, involving either: a same-sign dilepton pair, three leptons, or four leptons.

Oral Presentation:

Benchmarking Substellar Evolutionary Models using New Age Estimates for HD 4747 B and HD 19467 B

Charlotte Wood, Peter Garnavich

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Constraining substellar evolutionary models (SSEMs) is particularly difficult due to degeneracies between the masses, ages, and luminosities of brown dwarfs. In cases where a brown dwarf is a companion to a star, as in HD 4747 and HD 19467, the mass of the brown dwarf can be determined by orbital dynamics and properties such as age can be more accurately measured by studying the star instead. As a result, the mass, age, and luminosity of the brown dwarf can be determined independently, making it an ideal object to benchmark SSEMs. Using the Center for High Angular Resolution Astronomy Array, we measured the angular diameters of the host stars HD 4747 A and HD 19467 A. After fitting their parameters to the Dartmouth Stellar Evolution Database, MESA Isochrones and Stellar Tracks, and Yonsei-Yale isochronal models, we adopt age estimates of 11.41 +4.37/-4.27 Gyr for HD 4747 A and 10.66±0.51 Gyr for HD 19467 A. Assuming the brown dwarf companions HD 4747 B and HD 19467 B have the same ages as their host stars, we show that many of the SSEMs under-predict luminosities by ~1 dex for HD 4747 B and ~0.5 dex for HD 19467 B. The discrepancies in luminosity correspond to over-predictions of the masses by ~15% for HD 4747 B and ~33% for HD 19467 B. We also show that SSEMs including cloud physics reduce the discrepancies to ~0.6 dex for the luminosity and ~8% for the mass of HD 4747 B, an L/T transition object that is cool enough to form clouds. One possible explanation for the remaining discrepancies is missing physics in the models, such as the inclusion of metallicity effects.

Poster Presentation:

The Impact of Time Delay in a Tumor Model

Xinyue Zhao, Bei Hu

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We consider a moving boundary tumor growth model with a time delay in cell proliferation and study how time delay affects the stability and the size of the tumor. The model consists of a coupled system of an elliptic equation, a parabolic equation and an ordinary differential equation to describe the cells' location under the presence of time delay, with the tumor boundary as a moving boundary. A parameter μ in the model is proportional to the "aggressiveness" of the tumor. It is proved that there exists a unique classical radially symmetric stationary solution (σ_*, p_*, R_*) which is stable for any $\mu > 0$ with respect to all radially symmetric perturbations [S. Xu, Q. Zhou, and M. Bai, Qualitative analysis of a time-delayed free boundary problem for tumor growth under the action of external inhibitors]. However, under non-radially symmetric perturbations, we prove that there exists a number μ_*, such that if $\mu < \mu_*$ then the stationary solution (σ_*, p_*, R_*) is linearly stable; whereas if $\mu > \mu_*$ then the stationary solution is unstable. It is actually unrealistic to expect the problem to be stable for large tumor aggressiveness parameter, therefore our result is more reasonable. Furthermore, it is also proved by the authors that adding the time delay in the model would result in a larger tumor, and if the tumor aggressiveness parameter is larger, then the time delay would have a greater impact on the size of the tumor.

Poster Presentation:

Plakoglobin as a Potential Marker for a More Aggressive Population in Breast Cancer

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Similarities have been found in gene expression and transcriptional signatures in stem cells and cancer cells. Mechanisms specifically used by stem cells can be exploited by these cancer cells to obtain stem-like properties, i.e. generating other clonal types of cancer cells within the tumor. These cells, as a result, have been shown to often be more tumorigenic and aggressive. To strategically identify these potential therapeutically relevant embryonic-like targets on cancer cells, we performed mass spectrometry of the cell surface proteome to identify surface molecules shared by induced pluripotent stem cells (iPSCs) and breast cancer cells that could be potential targets to pursue mechanistic studies. Plakoglobin emerged as a candidate of interest in this screen. Plakoglobin is best known as a cell-cell adhesion protein but has been reported to have special roles in cancer cell aggressiveness and stem cell maintenance. Our qRT-PCR results show that plakoglobin expression is upregulated in iPSCs and breast cancer cells, compared to somatic cells. Within the breast cancer cell line MCF7, the expression level of plakoglobin is elevated in an established cancer stem cell subpopulation compared to total MCF7. Plakoglobin-overexpressing breast cancer clonal lines are also more stem-like compared to wild type cells as judged by a gene stemness profile. Bioinformatic analyses suggest that higher levels of plakoglobin is relevant to more severe tumor progression in patients. Further studies will explore how high level of plakoglobin correlates with the stem-like population in cancer and the mechanisms it uses to drive aggressiveness of cancer cells.