

27th Annual CNSM Student Research Symposium

April 23, 2021

Live Zoom Event, 1-3 PM

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Schedule of Presenters

1:00 PM – Welcome from Stephen Addison, CNSM Dean

Biology/ENVR Group:

1:10 PM

Student: Kristyn Killian

Faculty: Kari Naylor

Identifying Binding Proteins of FszA and FszB in *Dictyostelium discoideum*

Mitochondrial dynamics play a role in neurodegenerative diseases and mitochondrial related disorders, but the relationship is unclear. In our model system, *Dictyostelium discoideum* used to study mitochondrial dynamics, two proteins (FszA and FszB) have been identified that are important to these dynamics, but we do not understand their function. Our goal is to identify the protein partners of FszA and FszB by pull down assays to gain a better understanding of the roles these proteins play in mitochondrial dynamics and in disease. We have cloned FszA and FszB into pTXFLAG and pDM320 vectors and via electroporation have created FLAG-FszA and FLAG-FszB strains. We have confirmed that FLAG-FszA construct is present in our cells and are working to determine if FLAG-FszA mRNA or protein is expressed. Once expression has been confirmed FLAG tagged FszAs will be immunoprecipitated using an antibody to FLAG. This will ultimately pulldown FszA or FszB (depending on the strain) along with the binding proteins of each. In order to identify the binding partners of each protein the immunoprecipitation samples will be submitted to UAMS for mass spectrometry. Identification of the interacting proteins will allow us to speculate on the different roles FszA and FszB play in mitochondrial dynamics.

1:20 PM

Students: Willow Newman, Chance Garrett

Faculty: Ginny Adams, Reid Adams, Matthew Gifford

The Kings River in northwest Arkansas is host to a diversity of fishes and other aquatic organisms vulnerable to disturbances, including increased temperatures due to climate change. This study aimed to quantify the upper thermal tolerance of 23 species of fishes in the Kings River, spanning six families (Cyprinidae, Catostomidae, Fundulidae, Cottidae, Centrarchidae, Percidae). Critical thermal maximum (CTM) protocol was employed for this experiment using Loss of Equilibrium as the endpoint. We collected fishes, held them in flow-through nets in the river overnight, and tested them within 24 hours on-site in a temperature-controlled circulating water bath. We acclimated fishes and tested them in river water starting at temperatures naturally experienced in the river (25-28°C). A total of 229 individuals were tested ranging from 4 to 16 individuals per species. Species with restricted ranges (endemic to the Ozarks) had an overall lower ($36.3^{\circ}\text{C} + 0.23\text{SE}$) CTM compared to species with more widespread distributions ($37.6^{\circ}\text{C} + 0.13\text{SE}$; t-test $P < 0.001$). Species inhabiting run habitat ($36.5^{\circ}\text{C} + 0.21\text{SE}$) had a significantly lower CTM compared to those inhabiting pools ($37.6^{\circ}\text{C} + 0.14\text{SE}$) and riffles ($37.7 + 0.21\text{SE}$; ANOVA, $P < 0.001$). On average Cottidae (34.9°C) and Cyprinidae (36.8°C) had the lowest CTM, with Centrarchidae (39.0°C) and Fundulidae (40.8°C) tending to have the highest mean value. By understanding the thermal tolerance of fishes, we can better predict how community assemblages may change in the future as climate change continues.

1:30 PM

Student: James DuBose

Faculty: Tammy Haselkorn

The relationship between the social amoeba *D. discoideum* and its endosymbiotic bacteria, *Paraburkholderia* provides a model system for studying the development of symbiotic relationships. When food bacteria are scarce, *Paraburkholderia* allows *D. discoideum* to carry its own food (termed “farming”) to its next location. Only three *Paraburkholderia* species, *P. agricolaris*, *P. hayleyella*, and *P. bonniea* have been demonstrated to confer farming, however, the ecological relevance of this farming symbiosis is not clear. Each of these farming symbiont species differ in laboratory measurements of their farming ability and costs of infection. In this study, we determined the prevalence and identity of *Paraburkholderia* infection in *D. discoideum* populations sampled across several locations and compared them to collections from 20 years ago. We hypothesized that beneficial symbionts will increase in prevalence in natural populations over time and may affect the amoeba microbiome. Collected soil samples were grown in the lab, amoeba fruiting bodies were collected, and DNA was extracted. PCR was performed using *Paraburkholderia* and *Dictyostelium* specific primers. Using Sanger sequencing, we were able to identify *Paraburkholderia* infection status and identity in our *D. discoideum*

samples. We are currently using 16S rRNA next-gen sequencing to compare the microbiome of *Paraburkholderia*-infected and uninfected amoebas. *P. agricolaris* prevalence in *D. discoideum* increased from 14.9% in 2000 to 26.5% in 2019, suggesting that it is a more ecologically relevant and beneficial symbiont. *P. bonniea* prevalence showed a decrease from 2.6% to 0.79%, suggesting that it is a less beneficial symbiont. *P. hayleyella* had an 8% prevalence in 2000 and no current samples had this symbiont, suggesting that it is more pathogenic. *Paraburkholderia* prevalence was highly variable across the different locations and microhabitats, and this is being further explored. Utilization of this model allows us to tease apart the ecological mechanisms by which symbiotic relationships develop in general.

1:40 PM

Students: Lorrin Hooten, Mackenzie Hoogshagen, Gabe Dubose
Faculty: Tammy Haselkorn

Microorganisms such as bacteria have the ability to form symbiotic relationships within other living organisms. Symbiotic relationships are seen in terrestrial and aquatic environments, and are responsible for the diversification of species and appearance of new life forms. The social amoeba, *Dictyostelium discoideum* has an interesting symbiotic relationship with *Paraburkholderia* bacteria, which provides a useful model for studying symbiosis. Chlamydiae bacteria are also symbionts of *D. discoideum*, and are known pathogens of humans and other animals. While bacterial symbionts have been characterized in *D. discoideum*, the widespread distribution of bacterial symbionts in populations of other social amoeba species is not fully understood. To begin to more fully characterize these host/symbiont relationships, we collected soil samples from different ecological regions in Arkansas, using PCR and DNA sequence analysis we determined the distribution of the symbiont bacteria in natural amoeba populations. The prevalence of *Paraburkholderia* and Chlamydiae bacteria is highest in upland regions, 29.2% and 65.7% respectively. Though there is a much higher infection rate of Chlamydiae bacteria, infecting 45.4% of the total sample, and *Paraburkholderia* infecting 19.3% of the total sample population. Through genetic analysis, we have identified many different species of *Paraburkholderia* and Chlamydiae infecting social amoeba species.

1:50 PM

Students: Hunter Strom, Dylan Romine, Tori Hebert

Faculty: Hal Halvorson

Land use effects on stream invertebrate colonization of leaf litter in the Point Remove watershed, Arkansas

Anthropogenic factors alter land use and land cover, and therefore can affect environmental conditions by decreasing riparian cover and increasing the amount of dissolved nutrients in aquatic ecosystems. Effects of land use and land cover can be seen at trophic levels as low as macroinvertebrates. This study aims to examine the effects of terrestrial land use (i.e., forest vs. agriculture) caused nutrient pollution and light availability on aquatic macroinvertebrate composition and abundance. The study was conducted in eight first-order, headwater streams in the Point Remove watershed in central Arkansas. In each stream, coarse mesh bags (6-mm) containing red maple (*Acer rubrum*) leaf litter were deployed in clear and opaque whirlpak bags to allow for aquatic macroinvertebrate colonization over 3 to 9 weeks. Macroinvertebrates from each leaf bag were collected, identified to the taxonomic level of family, and counted for abundance. Initial results show trends indicating no major difference in taxonomic richness or abundance between forested vs. agricultural sites. However, there are interesting trends in the families present and their pollution tolerance. For example, Physidae, a family of tolerant snail, were only present in agricultural sites. Lepidostomatidae and Limnephilidae, families of more sensitive caddisflies, were only present in forested sites. These community shifts may result in altered ecosystem functions such as leaf decomposition or nutrient cycling within headwater streams.

2:00 PM

Student: Stephany Crabtree

Faculty: Kari Naylor

Inappropriate use of antibiotics and inadequate wound management has led to the development and spread of antibiotic resistant pathogens which pose a serious threat to public health. This growing public health threat and subsequent increasing need for alternative antimicrobial strategies has led to the re-evaluation of ancient therapeutic remedies from botanical sources and by-products such as honey. Recent studies suggest that honey has the potential to decrease antibiotic resistance. Changes in antibiotic sensitivity and biofilm formation after exposure to honey has yielded a promising avenue for insight on honey's mechanism of action; however, more definitive research is needed. The aim of this study is to evaluate the impact of various honey types on antibiotic susceptibility and virulence factor expression of seven clinically relevant bacteria species. After a 14-day exposure to a honey concentration of 4%, several bacteria species have shown a dramatic increase in their zone of

inhibition for several antibiotic classes while other bacteria species have demonstrated little to no change in zones of inhibition across all four honey types being tested. These trends indicate that honey does increase antibiotic susceptibility for certain bacteria species and yields a promising insight into alternate therapeutic strategies for antibiotic resistant wound infections.

2:10 PM

Students: Grace Davenport, Jennifer Main, George Gavrielides, Calvin Rezac

Faculty: Ginny Adams, Reid Adams

Do Farm Ponds and Small Impoundments Influence Fish Assemblages in the Black River Watershed in Arkansas?

Although many studies have focused on the impacts of large reservoirs on stream fish assemblages, few data have been published on the influences of farm ponds and small impoundments. Impoundments are often negatively correlated with stream fish diversity and may lead to homogenization of fish assemblages due to species introductions and extirpations. This study investigates the relationship between data related to farm ponds and small impoundments with persistence and stability of fish assemblages in the Black River watershed (Strawberry, Eleven Point, Spring, and Fourche rivers). The USGS StreamStats program was used to delineate upstream catchments of each site. Catchments were brought into Google Earth Pro where satellite imagery was used to determine distance of ponds from the stream, area of ponds and impoundments, whether connectivity to the stream was evident, and surrounding land use. We measured 323 farm ponds and small impoundments across 24 sites on the Strawberry River, 234 across 13 sites on the Eleven Point River, and 2,708 across 27 sites on the Spring River. Where historical data existed (57 of 64 sites), stability was positively correlated with mean distance of farm ponds and small impoundments to the stream ($r = 0.35$). Stability was negatively correlated with percent of farm ponds and small impoundments with obvious connection to the stream ($r = -0.39$), percent of ponds classified as impoundments ($r = -0.31$) and percent of farm ponds and small impoundments within 50 m of the stream ($r = -0.30$). Persistence was negatively correlated with percent of farm ponds and small impoundments within 50 m of the stream ($r = -0.30$). Additional analyses on presence of likely stocked species (e.g., bluegill, redear sunfish, largemouth bass, western mosquitofish), and species losses and additions will be discussed.

2:20 PM

Student: Ashlyn Estes

Faculty: Erin Wiley

Effects of late season defoliation and winter flooding on pin oak saplings

Flooding and defoliation are common disturbances in forests which can reduce rates of tree growth and survival, but the impacts of these disturbances at the end of the growing season and over winter are not well studied. Both flooding and defoliation can reduce carbohydrate storage, and so late season defoliation and over-winter floods could affect early spring leaf flush, which is essential in ensuring tree survival for the next growing season. In order to test how these disturbances impact carbohydrate storage and the amount and timing of leaf flush, we subjected pin oak (*Quercus palustris* Münchh) saplings to four treatments: defoliated/flooded, defoliated/control, non-defoliated/flooded, and non-defoliated/control. For the defoliation treatments, all leaves were removed in late-August. For the flood treatment, saplings were flooded with water to 6cm above the soil surface outside in late-December to simulate a stagnant, late winter flood. After six weeks, saplings were moved into a growth chamber with the same flooding treatment but with warmer conditions to simulate an early spring flood. Control saplings received the same temperature treatment without the flooding. Prior to the winter flood treatment, defoliated saplings had significantly less stem and root starch concentrations than non-defoliated saplings, but surprisingly had higher root sugar concentrations. Flooding did not affect the timing of leaf flush, but defoliation tended to delay leaf flush. We also discuss how flooding and defoliation affected the amount of leaf growth.

2:30 PM

Students: Dylan Romine, Hunter Strom, Tori Hebert

Faculty: Halvor Halvorson

Land Use and Light Effects on Leaf Litter Decomposition in the Point Remove Watershed, Arkansas

As forested land declines and agricultural land is established, adjacent streams experience loss of riparian zones and increased runoff containing sediment, pesticides, and nutrient input from agricultural activity. This may be impactful on stream ecosystem functions such as leaf decomposition. We investigated the effect of land use on decomposition rates of red maple (*Acer rubrum*) leaf litter in 4 agricultural and 4 forested first order, headwater streams of the Point Remove watershed. Leaf litter was placed in 6mm coarse mesh bags and deployed in either light or dark treatment bags to decompose for 1, 3, or 9 weeks during winter-spring of 2021. Initial data suggests that after 3 weeks of decomposition, mass loss was greatest under light treatment within forested sites (29% average mass loss) as compared to other treatments

(25-26% mass loss). This may indicate less efficient carbon cycling in agricultural sites when compared to forested sites, potentially suggesting difference in ecosystem function related to land use or light availability.

2:40 PM

Students: Natalie Burklow, Zach Degon

Faculty: Arijit Mukherjee

Abiotic factors, such as salt stress, heat and drought stress, and nutrient deficiency, are a major concern for crop productivity. For instance, most of our food crops, such as rice and maize display severe yield losses (50-80%) under moderate to extreme salinity. Problems associated with soil salinity are anticipated to worsen because of climate change. For improving crop performance under saline conditions, we need to implement sustainable agricultural strategies. One option is to take advantage of beneficial plant-microbe associations. Plants can form associations with different beneficial microbes including, arbuscular mycorrhiza, rhizobia bacteria, plant growth-promoting bacteria (PGPB). Several studies have suggested that PGPB improve plant growth via multiple mechanisms, including biological nitrogen fixation, hormone synthesis, protection against biotic and abiotic stresses, etc. *Azospirillum brasilense* is one of the most studied PGPB for the mitigation of salinity stress in different crops such as maize and wheat. However, not much is known about the molecular mechanisms by which *A. brasilense* mitigates salt stress. Recently, we optimized an experimental system where rice growth was improved in *A. brasilense*-inoculated plants compared to the uninoculated plants when these were grown under high salt concentration (200 mM NaCl). Currently, we are investigating the expression pattern of a salt-sensitive reporter gene (OsCam1) in rice plants inoculated with or without *A. brasilense* and grown under high salt concentration. In the future, we will perform an RNA-seq experiment to identify the transcriptomic responses in rice plants during *A. brasilense*-mediated salt stress tolerance. Overall, the results from this project will provide important insights into salt stress mitigation in rice by *A. brasilense*.

2:50 PM

Students: Devyn Ruiz, John Cook

Faculty: Arijit Mukherjee

Major crops such as rice and maize can benefit from associations with different plant growth-promoting bacteria (PGPB). Studies have shown that these PGPB (e.g., *Azospirillum*, *Herbaspirillum*, *Burkholderia*) promote plant growth primarily via nitrogen fixation and phytohormone secretion. However, our current understanding of the underlying molecular mechanisms involved in these associations is limited. For instance, very little is known about the associations between plants and the symbiotic *Burkholderia* species, *B. unamae*, at a

molecular level. Earlier, we set up an experimental system where PGPB such as *Azospirillum brasilense* and *Herbaspirillum seropedicae* could colonize rice roots and promote plant growth. In this study, we used the same experimental system and show that *B. unamae* can promote growth and colonize the roots of rice plants. Next, using RNA sequencing, we identified the transcriptomic responses in rice roots, 1-day post-inoculation. We identified 1128 differentially expressed genes (DEGs) in rice roots. Several of these DEGs are involved in defense response, flavonoid synthesis, hormone signaling, and nitrate transport. Our findings will be an excellent resource for future studies investigating the genetic pathways controlling this plant-microbe association.

3:00 PM

Student: Chance Garrett

Faculty: Ginny Adams, Reid Adams

Intermittent streams and fishes that inhabit them have been largely understudied. Recent literature has suggested intermittent streams are more biologically important than previously thought, and the ecology of fishes living in them should be further investigated. Current research shows intermittent reaches of aquatic networks host either a unique community distinct from the perennial community or a subset of the larger perennial community. Most of the research exploring fish community changes in response to stream drying has been conducted in arid ecosystems and less is known of community dynamics in intermittent spring-fed headwaters of the Southeast. This study explores fish community responses to summer drying in two tributaries of the Kings River having differing levels of connectivity to perennial reaches. Community samples were collected from Rockhouse Creek and Keels Creek during time periods of connected surface flow (December 2019 and May-June 2020) and intermittency (August 2019, August 2020, and October 2020). These streams had continuous flowing water from November 2019 until June 2020 allowing for immigration of fishes from the Kings River. Beginning in June 2020 water began to retreat upstream with the loss of riffles followed by loss of pools beginning in July 2020. The source population of the Kings River host approximately 36 species. Community samples in Rockhouse Creek detected 11 species in August 2019, 21 in December 2019, 12 in May – June 2020, and 18 in August 2020. Community samples in Keels Creek detected 22 species in August 2019, 28 in December 2019, 21 in May – June 2020, and 23 in August 2020. These data are important as current climate projections predict perennial systems will shift toward intermittent flows while also facing increases in anthropogenic water use and land alterations.

Chemistry, Mathematics, Physics Group

1:10 PM

Student: Will Ward

Faculty: William Slaton

This project describes how to program an Android phone to take atmospheric data during a high altitude flight and capture photographs using the phone's high quality camera. Rather than using Android Studio, however, we are using an application called Phonk. Phonk is considerably simpler and more accessible to someone who has a basic foundation in programming but is not fluent in Javascript. Using Phonk, we are able to access pre-programmed methods which allow us to interface with the phone's sensors and write programs that turn on multiple sensors at once while storing the data into files saved in the phone's memory. While the phone is limited in its capabilities, it is a simple, compact measuring device that can be attached to a payload in order to measure atmospheric data and compare it to theoretical models.

1:20 PM

Student: Grace Zimmerman

Faculty: Debra Burris, *Jessica Friz, *Nathan Perreau

*Aerospace Engineer, NASA Langley Research Center

Generic Robotic Guidance, Navigation, and Control Classes for the OSAM Architecture Simulation System (OASiS)

On-Orbit Servicing, Assembly, and Manufacturing (OSAM) will play a critical role in the development and maintenance of large orbital structures that will allow humanity to study and explore the universe further than ever before, including the In-Space Assembled Telescope (iSAT) and the Lunar Gateway. The OSAM Architecture Simulation System (OASiS) will serve as a modular, high-fidelity simulation environment in which to prototype and evaluate these OSAM technologies and concepts. During my internship at NASA Langley Research Center (LaRC), I worked in the Simulation Development and Analysis Branch to develop generic robotic classes for the OASiS project. I researched and developed generic guidance, navigation, and control (GNC) classes that will serve as a foundation for simulating future specific robotic systems, making the creation of unique robotic system models much easier and faster. I programmed within the Langley Standard Real Time Simulation in C++ (LaSRS++), an object-oriented, high-fidelity simulation framework, to create my generic GNC classes. I then tested and validated my generic GNC classes against a pre-existing robotic system in LaSRS++, the Lightweight Surface Manipulation System (LSMS), to ensure the overall functionality of the classes.

1:30 PM

Student: Audrey Ferrari

Faculty: James Fetterly

The world is filled with problems begging to be solved, which leads to many companies, groups, and individuals all seeking to enhance their problem solving skills. Creativity goes hand in hand with problem solving skills, and thus it stands that an increase in mathematical creativity will be advantageous to solving mathematical problems. Divergent thinking and problem posing have been associated with creativity in mathematics. Furthermore, it has been noted that one of the most efficient and effective ways to foster creativity is to be exposed to creativity. This study is designed to explore the possible effects of mathematical creativity as seen in problem posing and divergent thinking within the classroom. The sample population of students came from a single teacher who had multiple sections of Algebra I from an all boys high school. Using problem posing and divergent thinking as treatments, this study seeks to determine which one will enhance mathematical creativity. One section of students was exposed to divergent thinking treatments while the other section was exposed to problem posing treatments. These treatments were presented to the students by the same university professor. Each group received six 55 minute treatment sessions, one per week over a six week span. To determine effectiveness of the two treatments on mathematical creativity pre- and post-evaluations were given to determine significant differences between the treatment groups.

1:40 PM

Student: Briana Budnick

Faculty: Scott Austin

Using the UCA observatory equipped with the Meade LX200R telescope, ST9-XE camera, Sloan filter set, MaxIM DL and Muniwin 2.1 software, differential photometry was performed on the T-Tauri type star system XZ Tauri (XZ Tau). T-Tauri type stars are pre-main-sequence variable stars that are believed to have a large role in planetary formation and migration. By studying the variability in the XZ Tau system, stellar activity can be observed and further studied using other methods to improve our understanding of planetary formation and stellar activity in this young, active star. Simultaneously, this can be applied to other targets in a larger set of data, eventually streamlining the results and our understanding of stellar activity.

1:50 PM

Student: Brittany Krug

Faculty: Greg Naumiec

Malaria is a disease that disproportionately affects several third world countries. It is a life-threatening illness that is transmitted by mosquitoes that act as vesicles for parasites. The parasites cause a febrile illness in those that are not immune. Children under five are most susceptible to the disease which can lead to multi-organ failure and death. The disease is preventable and curable, but according to the world health organization, countries disproportionately affected cannot afford these preventative care measures or have developed resistance to treatments. Therefore it would be advantageous to develop a new treatment for malaria that focuses on cost effectiveness and something that is new to combat resistance to current treatments. A favorable drug might feature an antibiotic component as well as salicylamide. The antibiotic would combat the disease similar to the antibiotics used to treat now like Doxycycline. The salicylamide component would be beneficial because it could act as an analgesic as well as prevent coagulation and clotting commonly caused by malaria. In the following experiments, reactions and compounds were created in order to achieve a compound with a phenol ring which would make up one half.

2:00 PM

Student: Kayla Richardson

Faculty: Lisa Skultety, Todd Abel

This research project explores College Algebra (C.A.) students' experiences in mathematics and their impact on academic-related decisions. Last fall (2020), C.A. students were given a survey focusing on their personal history in math, their comfortability in doing math tasks, the role math may or may not have played in their school/future career choices, as well as their definition of what makes a "math person." Given the results of this survey, my goal is to help educators better understand what students are coming into the mathematics classroom with. Specifically, this will be accomplished by looking at how C.A. students described their previous math experiences, whether or not these descriptions affected their self-efficacy and post-secondary decision making, and by giving a new definition to what it means to be a "math person" according to C.A. students.

2:10 PM

Student: Maddie Haga

Faculty: Lori Isom

Sequence-specific binding of proteins to their DNA targets involves a complex spectrum of processes that often induce DNA conformational variation in the bound complex. To expand our previous results describing cationic side chain density's relationship to DNA helical bending, we now consider the potential role of aliphatic protein side chains in helical deformation. Selected protein/DNA crystal structures from the PDB were analyzed to detect and classify patterns of aliphatic side chain density in complexes containing unbent, concave, or convex helical curvature. Specific structural criteria were applied to an initial pool of 300 structures, producing a preliminary set of 36 protein/DNA complexes, which were subsequently analyzed using Chimera. For each structure, the preliminary helical bend type was assigned and the arrangement of aliphatic and cationic side chains within close proximity of the DNA (10.0Å and 5.0 Å respectively) were screened independently for patterns. Upon analysis, several preliminary patterns were found to correlate with concave helical bending. Specifically, structures classified as containing a concave bend (contain DNA that bends toward the bound protein) demonstrated a high fraction (0.78) of a pattern we termed aliphatic cupping, in which aliphatic side chains cluster around distinct cationic side chains (0.67) interacting with the bent DNA backbone. A relatively high number of the concave complexes also contained another pattern we describe as an extended aliphatic canopy (0.44) above the protein/DNA interface. Together, these aliphatic patterns could serve to isolate and thereby strengthen the interactions between DNA backbone and the intervening cationic side chains in bend DNA complexes. Interestingly, complexes containing unbent DNA show less aliphatic cupping (0.36 vs 0.78) and canopy (0.04 vs 0.44) formation and more uniform cationic side chain distribution (0.84 vs 0.33). Together these findings suggest a potentially important role for aliphatic side chains in protein-DNA complexes involving helical curvature.

2:20 PM

Student: Kedran Young

Faculty: Yeil Kwon

In a binomial model, the sample proportion $\hat{p} = x/n$, where x stands for the number of successes out of n trials with the dichotomous outcomes (success/failure), is considered one of the best estimators for p (a true success probability). The sample proportion has many desirable properties such as unbiasedness, minimum variance, and convergence to true probability p when the sample size n goes to infinity. However, when we estimate p for infrequent events, the sample proportion might not be the best since the sample proportion is the optimized estimator under the parameter space $0 < p < 1$. In particular, the sample proportion

tends to be inaccurate with a small sample. If we focus on a parameter space appropriately restricted for infrequent events, we may find an improved estimator for p .

In this research, an alternative estimation method for p is proposed under the parameter space restriction for infrequent events. The proposed estimator may be regarded as a generalized form of the Laplace estimator for p . By estimating the additional parameters, the proposed estimator can be expected to achieve a meaningful improvement. The simulation study reveals that the proposed estimator is expected to have a smaller mean squared error (MSE) than the sample proportion, especially for the small sample. Furthermore, the proposed estimator is applied to Major League Baseball (MLB) data to predict the home run rate, demonstrating the proposed estimator's performance in estimating small values of p .

2:30 PM

Student: Nathaniel Gregg

Faculty: Yinlin Dong

The numerical solution of differential equations is essential for modeling the behavior of many real world systems. Finite difference schemes for solving such equations can distort the relevant qualities of solutions so that they are no longer physically meaningful. The study of the qualitative behavior of finite difference schemes can be expanded beyond their order of accuracy. By using Fourier series expansions we can measure the dissipative and dispersive tendency of the errors that the schemes introduce at different distance scales. By tuning a set of parameters describing a family of finite difference schemes, we can find finite difference schemes that are spectral-like --- i.e. the solution is well resolved at most distance scales.