UNC GREENSBORO

THE 16TH ANNUAL UNCG REGIONAL MATHEMATICS AND STATISTICS CONFERENCE

November 14, 2020

Conference History

The UNCG Regional Mathematics and Statistics Conference (RMSC) started under the name UNCG–RUMC (the University of North Carolina at Greensboro Regional Undergraduate Mathematics Conference). The first conference took place in 2005, and we have run the conference every year since. It started as an interdisciplinary conference that focused on student research in mathematical biology. However, the topics of student conference presentations were always open to all areas of research in the mathematical sciences. Recent conferences included presentations by both graduate and undergraduate students in a wide variety of research areas.

Conference in Numbers

Year	Student presentations	Student attendees	Non-student attendees
2005	12	23	12
2006	12	30	13
2007	15	36	14
2008	11	28	12
2009	20	44	21
2010	26	64	22
2011	48	132	30
2012	56	120	44
2013	57	115	42
2014	65	127	42
2015	49	125	39
2016	67	154	54
2017	57	154	32
2018	46	138	42
2019	44	88	33

Recent Plenary Speakers

Year	Speaker	Affiliation
2015	Narayanaswamy Balakrishnan	McMaster University
2015	Laura Taalman	James Madison University
2016	Dominic Klyve	Central Washington University
2017	Talitha Washington	Howard University
2018	Suzanne Weekes	Worcester Polytechnic Institute
2019	Brian Reich	North Carolina State University

Schedule

08:45–09:00	**Welcoming remarks**
09:00–10:00	**Plenary lecture:** Folashade Agusto, The impact of changing behavior, sentiments, and risk perception on COVID-19 transmission
10:00–10:15	**Break**
10:15–11:15	**Parallel morning sessions M1–M3**
11:15–12:00	**Break**
12:00–13:00	**Professional development seminar:** Igor Erovenko, The art and science of great presentations
13:00–13:15	**Break**
13:15–14:30	**Parallel afternoon sessions A1–A3**
14:30–14:45	**Concluding remarks**

Plenary Lecture

The impact of changing behavior, sentiments, and risk perception on COVID-19 transmission

Folashade Agusto

University of Kansas

COVID-19 is a respiratory disease caused by a recently discovered, novel coronavirus, SARS-COV2. The disease has led to over 21 million cases, with over 1 million deaths, and over 13 million recovered individuals world wide. In the current social and political climate, the risk of COVID-19 infection is driven by people's perception of risk of the infection. A number of factors drive public perception of disease risk, these include peoples beliefs, knowledge, and information about a disease. In this seminar, I will present two different models for COVID-19 looking at peoples' behavior and their sentiments about the disease. One model uses game theory and appropriate payoff functions relating to the perception of risk measured using disease incidence and severity of infection to account for a series of human behaviors. Which leads to a complex interplay between the epidemiological model, that affects success of different strategies, and the game-theoretic behavioral model, which in turn affects the spread of the disease. The second model uses tweets from twitter to account for peoples' sentiments about the disease. It also takes into account negative sentiments driven by misinformation. The results from these models shows that rational behavior of susceptible individuals can lead to a second wave of the pandemic; these multiple waves of the pandemic are possible if the rate of social learning of infected individuals is sufficiently high. To reduce the burden of the disease in the community, it is necessary to ensure positive sentiments and feelings and to incentivize such altruistic behavior by infected individuals as voluntary self-isolation.

Morning Sessions M1–M3

Morning Session M1

10:15–10:30 Usra Shuja, Estimation of population mean of sensitive study variable based on randomized response technique using auxiliary information in the presence of measurement errors under two-phase sampling.

10:30–10:45 Andrea Simkus, Statistical reproducibility as a prediction problem.

10:45–11:00 Norah Alalyani, Nonparametric predictive inference for reproducibility of one-way layout tests.

11:00–11:15 Fatimah Alghamdi, Nonparametric predictive inference for reproducibility of estimation based on randomised response data.

Morning Session M2

10:15–10:30 Erin Cronce, Using topology to analyze Antarctic firn samples.

10:30–10:45 Shalmali Bandyopadhyay, Bifurcation results for elliptic problems with subcritical nonlinearity on the boundary.

10:45–11:00 Ananta Acharya, Sigma shaped bifurcation curves.

11:00–11:15 Amila Muthunayake, Modeling the effects of trait-mediated dispersal on coexistence of mutualists.

Morning Session M3

10:15–10:30 Romesh Ruwan T Liyana Arachchige, Karhunen Loeve expansion for axially symmetric Gaussian processes on the sphere.

10:30–10:45 Sarangan Balasubramaniam, Kriging process through minimizing the mean-squared prediction error.

10:45–11:00 Wonkyung Jang, Word embeddings and their relations to distributional semantics in educational linguistics research.

11:00–11:15 Sage Sigler and Spencer Stingley, Fuzzy group shrinkage and selection with application to integrative omics data analysis.

Afternoon Sessions A1–A3

Afternoon Session A1

13:15–13:30 Hanna Noelle Griesbach, Isomorphic polynomials: When is a polynomial isomorphic to an even polynomial?

13:30–13:45 Tommy Meek and Justin Clifton, Avoiding blue edges in 3-uniform hyperpaths.

13:45–14:00 Anuraag Bukkuri, Coevolution, red queen dynamics, Zahavi handicap, and double binds: From ecology to cancer.

14:00–14:15 Kalani Thalagoda, Bianchi modular forms.

14:15–14:30 Hammed Olawale Fatoyinbo, Influence of sodium inward current on dynamical behaviour of modified Morris–Lecar model.

Afternoon Session A2

13:15–13:30 Gabriel Ackall, Mohammed Elmzoudi, Richard Yuan, An exploration into the detection of COVID-19 from chest X-Ray scans using the xRGM-NET convolutional neural network.

13:30–13:45 Elizabeth Duncan, Influence of protein eos and environmental signals on T cell differentiation.

13:45–14:00 Hannah Scanlon, Minimizing the economic impact of COVID-19.

14:00–14:15 Emily Guo, Baptism of fire: Modeling the effects of prescribed fire on tick-borne disease.

14:15–14:30 Alex Fulk, How does variable diffusion affect the spread of Lyme disease in Kansas.

Afternoon Session A3

13:15–13:30 Maxwell Lovig and Sumaita Rahman, A mixture binary RRT model with a unified measure of privacy and efficiency.

13:30–13:45 Jazmin T. Jones, R simulations of a unified-mixed effects model.

13:45–14:00 Badr Aloraini, Variance estimation using randomized response technique.

14:00–14:15 Pujita Sapra, A mixture binary optional RRT model with a unified measure of privacy and efficiency.

14:15–14:30 Luke Vilaseca, A permutation based mixed effect model in rare variants association study.

Presentations

Sigma shaped bifurcation curves

Ananta Acharya[1], Juan Quiroa, Nalin Fonseka

[1]*UNC Greensboro*

We study positive solutions of steady state reaction diffusion equation in a bounded domain where a positive parameter influences the equation as well as the boundary condition. We show that there exist multiple positive solutions for certain range of the parameter such that we get a sigma shaped bifurcation diagram. We prove our results using the method of sub-super solutions.

Faculty mentor: Ratnasingham Shivaji

An exploration into the detection of COVID-19 from chest X-Ray scans using the xRGM-NET convolutional neural network

Gabriel Ackall[1], **Mohammed Elmzoudi**[1], **Richard Yuan**[1]

[1]*UNC Wilmington Summer Ventures*

COVID-19 has spread rapidly across the world since late 2019, causing businesses, schools, and government operations to shut down. The most common method of detecting COVID-19 is the RT-PCR swab test, which suffers from a high false-negative rate and a very slow turnaround of results, often up to two weeks. To complement swab tests, specialists can manually review X-ray images of the lungs to detect the presence of COVID-19 with up to 95% accuracy. Furthermore, neural network algorithms greatly accelerate this review process, analyzing hundreds of X-rays in seconds. Using the Cohen COVID-19 X-ray Database and the NIH ChestX-Ray8 Database, we trained and constructed the xRGM-NET convolutional neural network (CNN) to detect COVID-19 in X-ray scans of the lungs. To further aid medical professionals in the manual review of X-rays, we implemented the CNN activation mapping technique Score-Cam, which superimposes a heat map over an X-ray to illustrate which areas in the scan are most influential over the ultimate diagnosis. xRGM-NET achieved an overall classification accuracy of 97% with a sensitivity of 94% and specificity of 97%. Lightweight models like xRGM-NET serve to improve the efficiency and accuracy of COVID-19 detection in developing countries or rural areas.

Faculty mentor: Cuixian Chen

Nonparametric predictive inference for reproducibility of one-way layout tests

Norah Alalyani[1]

[1]*Durham University*

The reproducibility of research findings is of main interest in many disciplines. Recently, much attention has been paid to the reproducibility of statistical hypothesis tests. Reproducibility addresses the question: If a statistical test was repeated, under the same circumstances, would it lead to the same conclusion with regard to rejection or non-rejection of the null hypothesis? The probability that the test conclusion for the repeated test would be the same as the original test is called reproducibility probability (RP). We investigate the reproducibility of statistical hypothesis tests using nonparametric predictive inference (NPI). The NPI approach is a frequentist statistics framework based on few modelling assumptions, that considers future observations that are exchangeable with the data observations. NPI has a predictive nature which makes it suitable for studying reproducibility of a test. NPI for reproducibility probability (NPI-RP) will be presented for three tests, namely for the Wilcoxon Mann Whitney test for comparing two independent groups, NPI-RP for the Kruskal Wallis test for more than two groups which is used to test the null hypothesis that the location parameters are equal against the alternative hypothesis that at least one of them is different, and NPI-RP for the Jonckheere-Terpstra test where we test the null hypothesis that the location parameters are equal against the alternative hypothesis that the populations location parameters are ordered in some way. The NPI reproducibility is quite poor, in particular if the test statistic is close to the threshold value between rejecting and not rejecting the null hypothesis.

Faculty mentors: Frank Coolen and Tahani Coolen-Maturi

Nonparametric predictive inference for reproducibility of estimation based on randomised response data

Fatimah Alghamdi[1]

[1]*Durham University*

Randomised response techniques (RRT) can be used when data on possibly sensitive information are being collected using a survey. RRT methods are often applied when the goal is to estimate a population characteristic e.g. a mean. The nonparametric predictive inference (NPI) approach is a frequentist statistics framework, which is based on only few modelling assumptions. Due to its explicitly predictive nature, NPI is suitable for inference on the reproducibility of statistical methods applied to real data. The main idea is that a future repeat of the experiment is considered, leading to a probabilistic prediction of the future data, and the resulting future value of

the estimate for the characteristic of interest is compared with the actual estimate based on the real data. According to this contribution, some consequences of the reproducibility are presented, and the findings are discussed of applying of several RRT in various cases, The study proves that many factors are affecting the reproducibility level, and other measurements are used to explore this method and to learn from it.

Faculty mentors: Frank Coolen and Tahani Coolen-Maturi

Variance estimation using randomized response technique

Badr Aloraini[1]

[1]*UNC Greensboro*

When conducting surveys, it is sometimes difficult to make a direct observation on the variable of interest. This is more so in the case where the research involves a topic that is a taboo in nature. In surveys on such topics, some of the respondents might give false responses. To offer a solution to this, a Randomized Response Technique (RRT) was developed by Warner (1965). The technique allows respondents to provide a response while maintaining their privacy. The problem of mean and variance estimation is a topic that has been explored very well by researchers, although less so the problem of variance estimation. This is particularly the case in the context of RRT models. We propose some variance estimators for sensitive variables using auxiliary information. We examine the performance of the proposed estimators through a simulation study and through a numerical example.

Faculty mentor: Sat Gupta

Karhunen Loeve expansion for axially symmetric Gaussian processes on the sphere

Romesh Ruwan T Liyana Arachchige[1]

[1]*UNC Greensboro*

In this study, we focus on axially symmetric Gaussian processes on the sphere. First, we demonstrate how the Galerkin method, two-dimensional discrete wavelet transformations, and Mercer's theorem can be used to approximate any valid parametric non-stationary covariance functions accurately. Second, we develop an algorithm to generate axially symmetric random processes (global data) on the sphere using Karhunen Loeve (K-L) expansion. Mean squared convergence study for finitely truncated K-L expansion is performed to verify the validity of the approximation. An expression for theoretical L-2 error bounds is obtained for such approximations.

Faculty mentor: Haimeng Zhang

Kriging process through minimizing the mean-squared prediction error

Sarangan Balasubramaniam[1]

[1]*UNC Greensboro*

Kriging is the prediction method that is widely used in spatial statistics. It refers to making inferences on unobserved values of the random process. In this work, we discussed how the kriging works on an axially symmetric random process on the sphere. It is carried out through minimizing the mean-squared prediction error over an unknown weight (λ_i) for the measured value at the ith location subject to $\sum_{i=1}^{n} \lambda_i = 1$. Our proposed kriging approach is demonstrated through simulation studies.

Faculty mentor: Haimeng Zhang

Bifurcation results for elliptic problems with subcritical nonlinearity on the boundary

Shalmali Bandyopadhyay[1], Briceyda Delgado, Nsoki Mavinga, Rosa Pardo

[1]*UNC Greensboro*

We consider an Elliptic equation coupled with a nonlinear boundary condition on a bounded domain. We discuss the existence of positive solutions with respect to a bifurcation parameter when the nonlinearity is superlinear and subcritical. We will show that positive solutions bifurcate from infinity when the bifurcation parameter is zero using degree theory.

Faculty mentor: Maya Chhetri

Coevolution, red queen dynamics, Zahavi handicap, and double binds: From ecology to cancer

Anuraag Bukkuri[1] and Noemi Andor

[1]*University of South Florida (Moffitt Cancer Center)*

The evolutionary dynamics among predators and prey are complex and multifaceted, including several aspects of coevolution, sexual selection, and double binds. In this paper, we create a basic model of predator prey dynamics, starting with the case of one predator and one prey. We examine the emergence of coevolution between the predator and prey, capture red queen dynamics by changing the evolvabilities of the species, and explore the tug-of-war between natural and sexual selection through the Zahavi handicap hypothesis. By changing the predator's niche breadth and maximal capture probability, we then consider the cases of two preys and one predator, and two preys and two predators, considering mechanisms of speciation and convergent evolution of species through sexual selection.

Faculty mentor: Joel Brown

Using topology to analyze Antarctic firn samples

Erin Cronce[1]

[1] *College of William & Mary*

Firn refers to partially compacted snow whose micro-CT scans researchers can use to determine past climate patterns and atmospheric activity. However, one of the main challenges in the field is to distinguish the ice from the interconnected pore space in the scan. We implemented tools from Topological Data Analysis, a novel area in applied mathematics, in our study of several hundred cross-sectional two-dimensional scans of an Antarctic firn column. In this talk, we will discuss the use of topological methods such as thresholding and persistent homology in interpreting firn scans of different resolutions. These topological methods have proven effective in studying scans and extracting distinct components to represent the complete firn sample, focusing on preserving the image's most persistent features. Climate scientists can in turn apply these topological techniques in order to obtain a clearer representation of firn samples and thus more accurately interpret climate records.

Faculty mentors: Yu-Min Chung, Sarah Day, Kaitlin Keegan

Influence of protein eos and environmental signals on T cell differentiation

Elizabeth Duncan[1]

[1] *Virginia Tech*

Immune responses are the bodily mechanisms used to counter foreign invaders that pose a potential threat to our health. T cells and their sub-lineages, such as T helper cells or T central memory cells, play a critical role in adaptive immune responses by actively destroying infected cells in addition to signaling other cell types in the immune response. We use differential expression analysis to analyze the effects of the polarizing concentrations of the protein Eos on the regulation of a T cell sub-lineage, T helper 1 cells. Additionally, we develop a system of nonlinear ordinary differential equations that describes the relationships between Eos and other commonly associated genes and proteins. Our results show that high concentrations of Eos positively regulate T helper cell genes such as Prdm1 and Ifng. Conversely, selective deletion of Eos results in decreased expression of T helper 1 cells' associated factors. With this information, we position ourselves to better understand the complexities of immune responses. This insight may allow us to predict and intervene in such behaviors to control our bodies' responses to pathogens that cause diseases and conditions.

Faculty mentor: Lauren Childs

Influence of sodium inward current on dynamical behaviour of modified Morris–Lecar model

Hammed Olawale Fatoyinbo[1], Afeez Abidemi, Sishu Shankar Muni

[1] *Massey University*

In this work we consider a modified Morris-Lecar model by incorporating the sodium inward current. We investigate in detail the influence of sodium current conductance and potassium current conductance on the dynamical behaviour of the modified model. Variation of sodium current conductance changes the dynamics qualitatively. We perform a numerical bifurcation analysis of the model with sodium and potassium current conductances as bifurcation parameters. The bifurcation of solutions varying sodium current conductance produces complex bifurcation structure that is not present in the existing results of original Morris-Lecar model.

Faculty mentors: Richard Brown, David Simpson, Bruce van Brunt

How does variable diffusion affect the spread of Lyme disease in Kansas

Alex Fulk[1]

[1] *University of Kansas*

Lyme disease (LD) is one of the most prevalent tick-borne diseases around the world today and the geographic range of the vectors that transmit this disease is expanding. Ixodes scapularis, also known as the black-legged tick, is a possible vector for LD and it has spread further south and west in the United States and the population has been expanding as far north as Canada. The increased tick prevalence has been largely caused by migratory birds and rising global temperatures that have made environments that were previously off limits to these ticks now habitable. This larger and still growing population has led to increased competition for hosts and thus varied diffusion as ticks search farther and wider for blood meals. To incorporate this heterogeneity, I will provide a spatial model that incorporates variable diffusion. In epidemiology, diffusion is treated as the random motion of vectors, which is usually taken to be constant in all directions. Hence, variable diffusion is motion, but it's not necessarily random or uniform. Therefore, the goal of this project is to create a space heterogeneous model of the spread of LD in Kansas and use it to numerically predict disease incidence and endemicity at various locations.

Faculty mentor: Folashade Agusto

Isomorphic polynomials: When is a polynomial isomorphic to an even polynomial?

Hanna Noelle Griesbach[1]

[1] *Elon University*

We learn in single-variable calculus how important polynomials are. They allow us to analyze parts of functions, while only needing basic arithmetic properties to construct. We can express the roots of polynomials radically up to degree 4, but not necessarily for degree 5 and beyond. The benefit to solving a polynomial radically is that there is no error from loss of precision. Galois Theory is motivated by whether a polynomial can be solved radically or if its roots can only be approximated. For certain polynomials, like even polynomials, there are efficient ways to check the solvability. Our research explored when a polynomial can be transformed into an even polynomial, called isomorphic, for easier root computation. We looked at differences between symmetries of even and non-even polynomials, which are responsible for moving the roots around the function. Looking at how the symmetries moved and grouped the roots showed that even polynomials possess a symmetry that moves the roots to their reflections. Our research concluded that a non-even polynomial is isomorphic to an even polynomial if and only if it contains a symmetry that does not equal the reflection or the identity but when composed with itself two times yields the identity.

Faculty mentor: Chad Awtrey

Baptism of fire: Modeling the effects of prescribed fire on tick-borne disease

Emily Guo[1]

[1] *Washington University in St. Louis*

Climate change has expanded the northern borders of tick habitats and increased winter tick activity, increasing the prevalence of tick-borne diseases and thus the importance of finding a practical and cost-efficient way of managing tick populations. Prescribed burns, a common and necessary form of land management in many different environments, are appealing due to their time and cost efficiency along with their ability to be applied across large amounts of land. This study developed a compartmental model for ticks carrying Lyme disease to see how they are affected by the intensity of prescribed burns and the duration between fires. Sensitivity analysis was conducted to determine what parameters had the largest effect on R0. The parameters with the largest influence are the tick death rate, the carrying capacity, the larvae development rate, and the transmission possibilities for both ticks and mice. Intensity appears to have a larger impact on tick population reduction than the frequency of burns. Burning at high intensity is preferable to burning at low intensity whenever possible, although high intensity burns may be unrealistic due to environmental factors. Annual burns resulted in the most significant reduction of infectious nymphs, which are the primary carriers of Lyme disease.

Faculty mentor: Folashade Agusto

Word embeddings and their relations to distributional semantics in educational linguistics research

Wonkyung Jang[1]

[1] *UNC Chapel Hill*

The purpose of this study is to depict the underlying topics and the topic evolution in the 30-year history of educational linguistics research literature. Automated textual data mining and machine learning algorithms were used to examine the full text of the entire publication history of all 308 articles published in major education, linguistics, psychology, and anthropology journals over the past three decades (i.e., 1990–2020). First, Latent Dirichlet Allocation (LDA), a three-level hierarchical Bayesian model, was used. This is a topic categorization algorithm in which each element in the collection is modeled as a finite mixture over an underlying set of subjects. In turn, each subject is modeled as an infinite mixture over an underlying set of subject probabilities. In the context of the text modeling, the topic probabilities offered an explicit representations of the documents (Aggarwal & Zhai, 2012). Second, the semantic concepts were developed using Social Network Analysis' (SNA) community detection algorithm. Network structures provide an intuitive and flexible representational system that captures interdependence among entities and helps model interconnection patterns: underlying every semantic network is a graph, composed of a collection of nodes and a set of edges connecting pairs of nodes (Yang & Gonzalez-Bailon, 2017).

R simulations of a unified-mixed effects model

Jazmin T. Jones[1]

[1] *Clark Atlanta University*

This research focuses on R simulations based on the article, "A Unified Mixed-Effects Model for Rare-Variant Association in Sequencing Studies" (Sun, Zheng, and Hsu 2013). The Mixed Effect Score Test (MiST) is a test to determine the association between a set of SNPS/genes and continuous or binary outcomes by including variant characteristic information and using (weighted) score statistics. Like other gene or region based tests, MiST evaluates the effects of multiple genetic variants in a gene or

region by increasing power when multiple variants in the group are associated with a given disease or trait. This analysis compares many commonly used tests for rare variant associations, the Burden Test and the Sequence Kernel Association Test. We examined whether the MiST is more sensitive to type I error inflation. Our approach provides in-depth insight into the general testing framework of the MiST package. We used simulations under a wide range of scenarios to determine if error distributions will affect type I error. In particular, we consider three different distributions for our simulations; normal distribution, t distribution, and gamma distribution. For each distribution, we compared type I error rates at varying significance levels.

Faculty mentor: Jianping Sun

A mixture binary RRT model with a unified measure of privacy and efficiency

Maxwell Lovig[1], **Sumaita Rahman**[2], Pujita Sapra, Sadia Khalil

[1]*University of Louisiana at Lafayette*, [2]*UNC Greensboro*

In this study, we introduce a mixture binary Randomized Response Technique (RRT) model by combining the elements of the Greenberg Unrelated Question model and the Warner Indirect Question model. We also account for untruthful responding in the proposed model. A unified measure of model efficiency and respondent privacy is also presented. Finally, we present a simulation study to validate the theoretical findings.

Faculty mentor: Sat Gupta

Avoiding blue edges in 3-uniform hyperpaths

Tommy Meek[1] and **Justin Clifton**[1]

[1]*Western Carolina University*

We examine a stochastic process defined on hypergraphs where each vertex begins colored red. Each vertex will switch to blue at a time given by some probability distribution. Our aim is to determine when all vertices in a given subhypergraph have switched to blue. Specifically, we are examining 3-uniform loose hyperpaths and are concerned with when all the vertices in a single hyperedge switch to blue.

Faculty mentors: Andrew Penland and Josh Hiller

Modeling the effects of trait-mediated dispersal on coexistence of mutualists

Amila Muthunayake[1], J.T. Cronin, J. Goddard II

[1]*UNC Greensboro*

We analyse positive solutions (u, v) to the steady state reaction diffusion system:

$$\begin{cases} -\Delta u = \lambda u(1-u);\ \Omega \\ -\Delta v = \lambda r v(1-v);\ \Omega \\ \frac{\partial u}{\partial \eta} + \sqrt{\lambda} g(v) u = 0;\ \partial\Omega \\ \frac{\partial v}{\partial \eta} + \sqrt{\lambda} h(u) v = 0;\ \partial\Omega \end{cases}$$

where $\lambda > 0$, $r > 0$ are parameters and $g, h \in C^1([0,\infty),(0,\infty))$ are decreasing functions. This system models the steady states of two species living in a habitat where the interaction is limited to the boundary. Here, λ is directly proportional to the size of the habitat and we will study the ranges of λ where coexistence and nonexistence occurs. Namely, we will consider three cases: (a) $E_1(1, g(0)) = E_1(r, h(0))$, (b) $E_1(1, g(0)) > E_1(r, h(0))$, (c) $E_1(1, g(0)) < E_1(r, h(0))$. Here $E_1(r, K)$ denotes the principal eigenvalue of: $-\Delta z = rEz;\ \Omega,\ \frac{\partial z}{\partial \eta} + K\sqrt{E} z = 0;\ \partial\Omega$.

Faculty mentor: Ratnasingham Shivaji

A mixture binary optional RRT model with a unified measure of privacy and efficiency

Pujita Sapra[1], Sumaita Rahman, Maxwell Lovig, Sadia Khalil

[1]*UNC Greensboro*

In this study, we introduce an optional version of the mixture binary Randomized Response Technique (RRT) model. The proposed model is a mixture of the Warner and Greenberg models. The model accounts for untruthful responding. The model is evaluated in the light of a unified measure of model efficiency and respondent privacy. The simulation results show that even a small amount of untruthfulness can cause significant harm to the parameter estimates. The simulation results also show that an optional model is better than the corresponding non optional model.

Faculty mentor: Sat Gupta

Minimizing the economic impact of COVID-19

Hannah Scanlon[1] and Jesse Adamski

[1]*Wake Forest University*

While the potential of stay at home orders to control the spread of SARS-CoV-2 is well documented, there is an ongoing debate on the negative economic repercussions of lockdowns. Since both opening up too early and maintaining a lockdown for too long will hurt the economy, we are interested in analyzing how a government implemented stay at home order can be best structured to minimize the economic toll. We formulate a compartmental ordinary differential equation infectious disease

model. This model tracks the number of cases that are estimated to require healthcare in an ICU throughout the pandemic. We couple this ODE system with a cost functional that appropriately scales and combines the costs of labor loss and ICU patient health care. We use both numerical simulations and optimal control methods to find parameters to a stay at home order which minimize economic cost.

Faculty mentors: Chris Jones and John Gemmer

Estimation of population mean of sensitive study variable based on randomized response technique using auxiliary information in the presence of measurement errors under two-phase sampling

Usra Shuja[1]

[1]*Lahore College for Women University*

In this research, the main focus is to develop more generalized randomized response technique (RRT) mean estimators for sensitive study variable using one and two non-sensitive auxiliary variables dealing with simple random sampling and stratified random sampling under the situation when measurement error occurs on study variable in two phase sampling. Efficiency comparisons with the ordinary mean estimator are carried out both theoretically and numerically. A simulation study is presented to evaluate the performance of the proposed estimators.

Faculty mentor: Sadia Khalil

Fuzzy group shrinkage and selection with application to integrative omics data analysis

Sage Sigler[1] and **Spencer Stingley**[2]

[1]*Clark Atlanta University*, [2]*UNC Greensboro*

Multivariate regression models have become a popular method in jointly analyzing the linear relationship between p predictors and q response variables from the same n subjects. In this paper, we have developed a multivariate regression model with the group kth largest norm penalization for integrative omics data analysis. Our method is designed to have the data adaptive grouping functionality among both covariates and predictors. It deals with the data's high-dimensionality by simultaneously running both variable and predictor selection. Numerical studies including both simulation studies and application to TCGA data have demonstrated the advantage of this method.

Faculty mentor: Xiaoli Gao

Statistical reproducibility as a prediction problem

Andrea Simkus[1]

[1]*Durham University*

Hypothesis testing is one of the main statistical methods used in practical applications. The decision on whether or not to reject the null hypothesis is reached. The reproducibility of this decision is of particular importance to the process of scientific research. This work focuses on developing a methodology to determine the statistical reproducibility of this decision by considering reproducibility as a prediction problem. Statistical reproducibility provides inference on the probability that the same decision would be reached if the test were repeated. This presentation introduces a nonparametric predictive inference (NPI) methodology to assess reproducibility. The method is illustrated on an example using Student's t-test. The reproducibility for the t-test was developed on the basis of a pre-existing real life scenario of a preclinical experiment, which involves multiple pairwise comparisons of test groups, where different groups are given a different concentration of a drug. The aim of the experiment is to decide the concentration of the drug, which is most effective.

Faculty mentors: Frank Coolen and Tahani Coolen-Maturi

Bianchi modular forms

Kalani Thalagoda[1]

[1]*UNC Greensboro*

Modular forms are complex analytic objects that play an important role in number theory. In the classical case, modular forms are holomorphic functions on the hyperbolic plane that satisfy symmetry with respect to the special linear group. There are many ways to generalize these. One such generalization gives rise to Bianchi Modular form. Bianchi modular forms are defined over imaginary quadratic fields. There are some similarities between this case and the classical case. However, we face new obstacles. In this talk, I will give a brief introduction to the classical case and talk about how to generalize some concepts in the classical case to our case. Using examples, I will demonstrate some similarities and differences between these two cases.

Faculty mentor: Dan Yasaki

A permutation based mixed effect model in rare variants association study

Luke Vilaseca[1]

[1]*UNC Greensboro*

In the past decade, rare variant association study has become popular in the scientific field to identify disease associated rare genetic variants. A lot of statistical methods have been developed since then, including the method of mixed effect score test (MiST) proposed by Sun et. al.,

2013. Though MiST is a more robust method comparing with other existing methods, it has the limitation of potential type I error inflation under some circumstances. Hence, the aim of my research and presentation is to improve MiST so that it can control type I error well. Particularly, we will use permutation based method to improve MiST and use simulations under various scenarios to examine the performance of this improvement in terms of type I error rate.

Faculty mentor: Jianping Sun