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Identifying a Useful Dynamic Range for Perimetry Data Relating to Disease Progression in Glaucoma Patients

Glaucoma is an eye disease associated with ocular hypertension that can lead to severe optic nerve damage and eventual blindness. Current practice for diagnosing glaucoma and monitoring its progression uses standard automated perimetry (SAP) testing. SAP maps a patient's visual field sensitivity by measuring his or her responses to various levels of light intensity while targeting different areas of the eye. However, it is recognized that some levels of light intensity in SAP cause a higher test-retest variability and therefore are less reliable for clinicians. Testing patients over a relevant range of light intensity values would improve efficacy of SAP as a whole and make its output more practical for clinical use. This research focuses on identifying a Useful Dynamic Range (UDR) of decibel light intensities that can reliably determine if a patient's glaucoma is progressing or not.

Research Mentor **Gideon K.D. Zamba**, Associate Professor, Department of Biostatistics, University of Iowa Sabah Munir Wartburg College Journey Penney Willamette University

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Genetic Risk Factors for Preterm Birth

Preterm birth, which affects 5-18% of pregnancies worldwide, occurs when an infant is born before 37 weeks of gestation. Studying the factors associated with preterm birth is important, for it is the leading cause of death in children under five years old. Besides many environmental factors, genetics also dictate the risk of preterm birth. This current research project is based upon the sequenced exomes of 93 pairs and 2 trios of sisters from Denmark who have a history of preterm birth. The goals of this project were to (1) develop gene burden tests to analyze the experimental data against the general population data obtained from the Exome Aggregation Consortium, (2) identify rare variants that may contribute to the risk of preterm birth, and (3) compare the two methods of statistical analysis that we developed. Gene burden tests collapse all variants on the same gene together, and then analyze each gene as a whole by determining the significance of its impact on preterm birth. We developed a count-based method based on the Poisson distribution and a weighted version using the normal distribution. The genes producing the smallest p-values were examined further, which led to the identification of several promising variants to be studied more in future research.

Research Mentor **Patrick J. Breheny**, Associate Professor, Department of Biostatistics, University of Iowa Roger Netherton University of Missouri-Columbia

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Creating County Health Rankings: State of Iowa

For modern civilizations, understanding the overall health of the population is of crucial importance. In an effort to monitor the overall health of the people in the United States, the United States Department of Health and Human Services created the Healthy People program. Using that format, the Iowa Department of Public Health created the Healthy Iowans program. To take this healthy initiative one step further, we have seen the creation of the Healthiest State Initiative for Iowa, with communities ranked according to health status. We participate in health assessment by ranking the 99 counties in Iowa from the most healthy to the least healthy according to a variety of health measures. Due to the rural nature of Iowa, many of these measures have small counts, which lead to highly variable estimates. We use Bayesian spatial smoothing techniques to arrive at reliable estimates of the chosen measures of health. We then combine those measures in a statistical model to provide health status ranks for the 99 counties in Iowa, and we display the ranking on a map of the state. Finally, we create a dynamic interface (Shiny application) by which different health factors can be chosen to base a ranking upon.

Research Mentor **Jacob J. Oleson**, Associate Professor, Department of Biostatistics, University of Iowa

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How Comparable are Clinical Trials Results Reporting on ClinicalTrials.gov versus a High-Impact Neurological Journal

The website ClinicalTrials.gov -- administered by the Food and Drug Administration (FDA) and United States Congress -- is intended to consolidate all information from public/private clinical findings on drugs, biological agents, and medical equipment (for studies under FDA jurisdiction). ClinicalTrials.gov can then be utilized to provide accessible, accurate information to patients, health-care specialists, and the public-at-large. In 2000, the United States Congress mandated all FDA-regulated studies must be registered on ClinicalTrials.gov and the results be posted within 12 months of completion. However, a study done by Jessica E. Becker (2015) revealed discrepancies between published trials' results and corresponding ClincalTrials.gov reports' results; these discrepancies range from total absence of reported results to slight variance in statistical measures. This project will investigate the efficacy, efficiency, and accuracy between clinical trials' peerreviewed publications and the trials' required corresponding ClinicalTrials.gov registration. This project focuses specifically on U.S.-sponsored, published, *interventional* clinical trials from the 2014 edition of Neurology -- compared directly to the articles' cited ClinicalTrials.gov registrations. This particular study is critical to understanding trends in investigators' reporting of results' of clinical trials, particularly in light of the University of Iowa Clinical Trials Center's focus on neurological conditions and concurrent participation with ClinicalTrials.gov.

Research Mentor Eric D. Foster, Clinical Assistant Professor, Department of Biostatistics, University of Iowa Chandler Pendleton University of Arkansas-Fort Smith Fabiola Rivera-Rodríguez University of Puerto Rico at Cayey Brenton Washington Kean University

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Tornadoes: Trend in Extreme Weather Events in the US Heartland

Tornadoes are a destructive natural force that can damage property and crops as well create public health hazards. Scientists are still unsure exactly how and why tornadoes form, so it is an active area of very important research. Although it is possible for a tornado to occur anywhere, a section of the United States known as Tornado Alley sees a very high frequency of tornadic activity. A subset of four states inside Tornado Alley was selected and the tornadic activity from 1990 to 2016 was observed to determine whether an increase in the frequency of tornadoes has occurred. In addition, models were created that assessed the relationship between tornado frequency and certain environmental factors.

Research Mentor Mary Kathryn Cowles, Professor, Department of Statistics and Actuarial Sciences, University of Iowa Holly Diop University of Hawaii at Hilo Erica Lleras University of Puerto Rico at Cayey Miguel Quime Los Angeles Mission College Eldon Sorensen Pacific Lutheran University

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Effect of Chronic Graft-versus-Host Disease on Survival in Bone Marrow Transplant Patients

Cancer patients who receive a bone marrow transplant are susceptible to developing Graft-versus-Host Disease (GvHD); a medical condition where the donor cells attack the host body. GvHD can be classified into two categories: acute and chronic GvHD. Acute GvHD develops within 100 days of the transplant whereas chronic GvHD develops after approximately 100 days. Data were collected from 128 cancer patients who received allogeneic bone marrow transplants at the University of Iowa Hospitals and Clinics and were followed prospectively. The objective of our study was to assess and compare the impact of chronic GvHD on overall survival in patients treated with and without antihuman T-lymphocyte immune globulin (ATG). Survival analysis methods were employed in a statistical analysis of the data. In particular, we used Cox regression to model and test for significant survival effects of GvHD and ATG. The applications of our models provide estimates of the degree to which chronic GvHD impacts survival in patients who received allogeneic transplants.

Research Mentor Brian J. Smith, Associate Professor, Department of Biostatistics, University of Iowa Jordan Baker Northwestern College (IA) Serenity Budd Vassar College Carissa Comnick Carleton College

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The Effect of Inter-health Care Facility Patient Sharing Network on Clostridium difficile Infection Rates

According to the CDC, Clostridium difficile (C. diff) caused almost half a million infections in the U.S. in 2011, and out of those infected, 29,000 died within 30 days of initial diagnosis. This bacterium is listed as an "Urgent Threat" not only due to its prevalence, but also its antibiotic resistance. Healthcare workers can spread the bacteria or contaminate surfaces through contact, and without meticulous cleaning,

C. diff can keep a surface contaminated for months. People can become infected if they touch contaminated surfaces and then touch their mouth, nose, or eyes. Since C. diff is a healthcare-associated infection, patient sharing among hospitals may serve as a means for the dissemination of C. diff. Our research focuses on understanding the connectivity patterns via patient sharing between hospitals and how those patterns affect C. diff incidence rates. We used network visualization techniques and employed a more formal linear network autocorrelation model with a spatial component to estimate the network effect on C. diff infection incidence.

Research Mentor **Daniel K. Sewell**, Assistant Professor, Department of Biostatistics, University of Iowa Joseph Boyle University of North Carolina at Chapel Hill Michelle Orozco University of California, San Diego Joshua Tomiyama University of Hawaii

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Modeling Complex Epidemics with Environmental Reservoirs: Studying Cholera Transmission on the Island of Hispaniola with Bayesian Epidemic Models

The 2010-2013 cholera outbreak on the island of Hispaniola provides a rich opportunity to study cholera transmission. The bacterium governing transmission, *vibrio cholerae*, is often spread through contaminated water sources, disproportionately affecting nations lacking public health infrastructure, particularly Haiti. The work at hand seeks to model and map this cholera outbreak as a function of geographic proximity, rainfall, and elevation. Publicly available cholera case data is drawn from the Pan-American Health Organization. Following the logic of compartmental epidemic models, the population is considered to fall into one of the Susceptible, Exposed, Infectious, or Removed categories for analysis. Approximate Bayesian Computation methods are employed, simulating epidemics from prior parameters that iteratively tune towards concordance with observed case counts. The ABSEIR epidemic modeling package in R is used to implement models, and inference is drawn regarding transmission parameters and their respective public health interpretations.

Research Mentor Grant D. Brown, Assistant Professor, Department of Biostatistics, University of Iowa Monica Ahrens, Graduate Student Mentor, Department of Biostatistics, University of Iowa