Undergraduate Research Symposium May 19, 2017 Mary Gates Hall

Online Proceedings

Poster Session 1

Balcony, Easel 88

11:00 AM to 1:00 PM

Examining Cluster Analysis Validation and Solution Variability Using Real Data

Matthew Robert (Matt) Anderson, Senior, Psychology
Mentor: Brian Flaherty, Psychology

Cluster analysis is a very popular data analysis technique that groups observations by degree of similarity. The goal is to obtain a small number of clusters that summarize important differences among groups of observations. In this case, cluster membership may be an important and useful summary of a scientific topic. Hierarchical cluster analysis produces cluster solutions ranging from 1 to N, meaning that every observation is their own cluster. A key question about the results of cluster analysis is how scientifically valid are they? Are important clusters identified, or does random variation in a single data set drive the reported results? Much of our understanding of how cluster analysis works in data is based upon simulations. Simulation studies create random data to analyze and then examine how an approach performs over many simulated samples. However, real data often do not behave as well as simulated data. In this work, we examined how cluster analysis performed on repeated subsamples from a larger sample of people. We treated the full data set (N=919) as the population. Hierarchical cluster analysis was performed on this full sample and treated as the population model. We then examined how the results are recovered under different subsampling plans. We used a variety of sampling methods such as convenience and random. We varied the number of observations in the subsample, as well as by equal and unequal subsample selection probabilities. This analysis shows how stable the results across a variety of scientifically plausible situations. Implications for the use of cluster analysis in social and behavioral research will be discussed.

Session 1C

Sensory Integration, Learning, and Motor Control in Animal and Human Models

Session Moderator: Horacio de la Iglesia, Biology

MGH 231

12:30 PM to 2:15 PM

* Note: Titles in order of presentation.

Sensory and Memory in Foraging Behavior: A Comparative Analysis in Humans and Rodents

Gusti Lulu (Lulu) Fatima, Senior, Biology (Molecular, Cellular & Developmental)
Levinson Emerging Scholar, UW Honors Program
Mentor: David Gire, Psychology
Mentor: Brian Jackson

Foraging behavior in mammals requires the integration of various sensory cues to allow the subject to navigate through the environment. When the search becomes predictable and repetitive, memory can be used to enhance the sensory cues. To model the dynamic interactions between sensory and memory, we performed a comparative analysis on rats and humans by designing a two-stage task paradigm: search and return. The subjects were trained to search for rewards in a confined space with limited sensory cues. After the end of each trial, they were trained to return to the start position. The rat task was performed in an automated arena that allowed the rats to follow the reward's olfactory cues but prevented visual and hearing cues. Similarly, the human task simulated the paradigm using a computer game that allowed the subjects to search and return in a virtual room with limited visual cues. We predict that sensory cues have a more significant impact on the search strategies compared to the return strategies. If the reward locations are fixated in every trial, we also expect the subjects to increasingly rely on memory for both the search and return strategies. Our research will provide insight on the tracking methods and analysis in studying the roles of sensory and memory in complex foraging behavior.

Poster Session 2

MGH 241, Easel 131

1:00 PM to 2:30 PM

Studying Cellular Aging Using the Replicative Lifespan Assay in Yeast

Yaechan (Sam) Song, Senior, Biochemistry
Sunny Nguyen, Senior, Anthropology: Medical Anth & Global Hlth, Anthropology: Anth of Globalization
Nicolas John (Nick) Tonel, Junior, Biology (Molecular, Cellular & Developmental)
Mentor: Brian Wasko, Department of Pathology

Aging is a process which causes the deterioration of cellular function in organisms. In order to understand the mechanisms of aging and to begin to identify ways to extend healthy life expectancy, research in the Kaeberlein lab uses *Saccharomyces cerevisiae*, a species of yeast. The technique that our lab uses to quantitate lifespan in yeast is known as the replicative lifespan (RLS) assay. When a yeast cell divides, the original "mother" cell and the newly produced "daughter" cell can be differentiated based on size. Daughter cells are microdissected away from mother cells, the cell division is recorded, and this cycle repeats until the mother is no longer able to produce daughters. We have tested the effects on lifespan resulting from the manipulation of thousands of genes and numerous environmental conditions. This data can be analyzed to understand the process of aging in yeast cells. By studying the mechanisms of aging in unicellular yeast cells, we can transfer these findings to identify conserved factors in the aging process that are also present in multicellular organisms. The study of the basic biology of aging in yeast can yield insights into the aging process that may contribute to our understanding of aging in humans and help facilitate the development of therapies aimed at decreasing age-related diseases.

POSTER SESSION 2

Commons West, Easel 16

1:00 PM to 2:30 PM

Screening of NIH Clinical Compound Library and Characterization of Putative Therapeutics in a *C. elegans* Model of Tauopathy

Kaili Chickering, Senior, Biology (Physiology)
Mentor: Brian Kraemer, Medicine

The accumulation of pathological tau protein in the brain neurons occurs in many neurodegenerative diseases. Alzheimer's disease and related dementia disorders are the most common diseases with pathological tau. In order to identify potential therapeutics for Alzheimer's disease and related disorders, I screened the National Institute of Health's Clinical Compound Library for modifiers of the disease associated phenotype seen in tau transgenic *Caenorhabditis elegans* (*C. elegans*). The compound library consists of drugs with a history of use in humans that we can assess for other potential uses, a process known as drug repurposing. Observing *C. elegans* disease models for specific drug effects may ultimately lead to identifying ways to alter or prevent accumulation of tau aggregates in the brain. Populations of tau-expressing *C. elegans* were cultured on nematode growth media (NGM) in the presence of a single library compound and assessed for modification of disease phenotype at day one of adulthood; roughly 3 days after eggs are placed on the media. I specifically looked for improvement or deterioration of coordination as well as the speed of growth, number of offspring, mortality, and general health and size of the population as compared to control populations without drug. I then evaluated the data and selected the best compounds for further analysis on the basis of each compounds dose responsiveness. Drugs generally have optimal effect at a specific dosage, so by observing a range of concentrations of the drug I can determine the best concentration for study. Once this has been completed, I will analyze the hits more closely and follow up with further experimentation including quantitative analysis of *C. elegans* behavioral response, and tau protein biochemistry. We hope that this work may be able to identify potential therapeutics able to ameliorate symptoms in dementia patients with pathological tau.

POSTER SESSION 2

MGH 241, Easel 130

1:00 PM to 2:30 PM

Characterizing a Temperature Dependent Growth Arrest Phenotype Following V-ATPase Impairment

Katherine Brower, Senior, Microbiology
UW Honors Program
Vesal Mobasher, Senior, Biochemistry
Youji Hong, Senior, Public Health-Global Health, Sociology
Mentor: Brian Wasko, Department of Pathology

Cytosolic pH is sustained by the movement of protons out of the cytosol. The vacuolar ATPase (V-ATPase) is a conserved protein complex that localizes to the membrane of organelles and transfers protons from the cytosol into the organelle lumen. The V-ATPase couples the energy of ATP hydrolysis to transport protons. Proper pH homeostasis is important for many organelles such as endosomes, lysosomes, and secretory vesicles. In *Saccharomyces cerevisiae*, the Pma1 protein localizes to the plasma membrane and pumps protons out of the cell, helping to maintain cellular pH homeostasis. In *Saccharomyces cerevisiae*, we have found that loss of activity of the V-ATPase results in a growth arrest at low temperature. We generated 66 yeast V-ATPase mutant strains that are able to suppress the low temperature induced growth arrest. In complementation tests of these mutants, our results suggest that all of the mutants belong in the same complementation group. We have performed whole genome sequencing on one strain and analysis of the whole genome sequencing data has identified a single putative mutation. We are validating that the identified mutation is causative for the phenotypic sup-

pression, and performing targeted sequencing of the candidate gene in the other suppressor strains.

SESSION 2A

POWER MADE VISIBLE: IMAGE, IDENTITY, NARRATIVE ACTIVISM

Session Moderator: Juliana Villegas, English
MGH 171
3:30 PM to 5:15 PM

* Note: Titles in order of presentation.

Impact of Video Exposure to Fatal Police Violence on Black Males

Havana Jane (Havana) McElvaine, Senior, Sociology
Mary Gates Scholar, UW Honors Program
Mentor: Hedwig Lee, Sociology
Mentor: Ralina Joseph, Communication
Mentor: Brian Sargent, Sociology

Black men are disproportionately represented among the number of people killed through the use of police deadly force each year. With the development of technology and the pervasiveness of social media in every day life, people have the ability to watch and re-watch these deaths on a daily basis. This phenomenon has become particularly prevalent in recent years, sparked by the graphic videos of deadly force used on Eric Garner and Philando Castile. Although there is a significant body of literature on the impact of racism, discrimination, and violence on black male self-perception, group identity and political attitudes, little is understood about the impact of this new form of publicized fatal violence. For this research project, I explore how black men are being exposed to this specific type of fatal violence, and outcomes related specifically to changes in political response, attitudes, and group identity. This process included a series of three open-ended focus groups, each comprised of 7-8 black male undergraduate and graduate students at the University of Washington. From these focus groups I identified 4-5 individuals and conducted semi-structured in-depth interviews to build on themes established in the focus groups. The information from these focus groups and interviews provide a unique insight into changing forms of discrimination and violence black men face, and the implications this violence has for their own political actions and behaviors.

SESSION 2S

MODULATION OF CELL BEHAVIOR AND ITS COMPONENTS

Session Moderator: Valerie Daggett, Bioengineering
JHN 175
3:30 PM to 5:15 PM

* Note: Titles in order of presentation.

Measuring the Replicative Lifespan of Yeast

Blaise John (Blaise) Pascual, Senior, Microbiology
Hieu Nguyen, Senior, Microbiology
Diego Molina Ochoa, Junior, Biology (Physiology)
UW Honors Program
Mentor: Matt Kaeberlein, Pathology
Mentor: Brian Wasko, Department of Pathology

The biological basis behind aging in eukaryotic species is defined by a wide range of factors, from diet to environmental conditions and metabolic predisposition. The genetic factors associated with aging are of particular interest because they are highly conserved among all eukaryotes. Determining longevity genes that are broadly conserved among eukaryotic species is a critical step in understanding aging, and is one of the primary goals of this project. The Kaeberlein lab has analyzed the replicative lifespan (RLS) of more than 4700 single-gene deletion mutants of *Saccharomyces cerevisiae*, a eukaryotic model organism. RLS experiments measure the number of daughter cells produced by a mother cell prior to senescence, and is thought to provide a model of aging in mitotically active cells. Mother and daughter cells are visibly differentiated under a light microscope and physically separated using a fiber-optic needle. The number of daughter cells dissected are quantitated and recorded. The total number of cell divisions are then summed for statistical analysis. The result of the investigation yielded 238 gene deletion mutants that exhibited a statistically significant lifespan extension. Longevity genes were found to be clustered within specific parts of an organism's biology. Ribosomal genes and genes related to metabolic responses to nutrients were particularly significant. One particularly significant gene is the LOS1 gene, which functions as a tRNA exporter from the nucleus. Deletion of the LOS1 gene resulted in a dramatic enhancement of yeast RLS, opening the possibilities of lifespan research regarding the subcellular localization of tRNA. Also significant was the discovery that a majority of the longevity genes were concentrated among highly evolutionarily conserved parts of the genome. Ultimately, the success of the yeast RLS project in identifying novel longevity genes and establishing a database of conserved longevity genes in eukaryotes points to the efficacy of such methodology.

POSTER SESSION 3

Commons East, Easel 55

2:30 PM to 4:00 PM

NVIDIA Deep Neural Networks for Game Hints

Benjamin Paul (Ben) Robaidek, Senior, Electrical Engineering, Mathematics
Devin Leigh (Devin) Stoen, Senior, Electrical Engineering
Haonan Wang, Senior, Electrical Engineering
Mentor: Brian Nelson, Electrical Engineering
Mentor: Catherine Feng

Many mainstream video games involve difficult game levels and challenges such as boss-battles and puzzles, leading some gamers to become frustrated as they struggle to advance to the next game level. In some cases, this frustration may lead gamers to give up on playing the game entirely. Although walkthroughs for video games are available online to help gamers when they get stuck, the gamers need to manually locate where they are in the game to obtain appropriate hints. Not only can manually looking for hints be inconvenient and time consuming, but it can also expose gamers to spoilers. We hypothesize that we can improve the gaming experience by providing gamers with a system that can automatically determine their current location in a game and serve up a link to a walkthrough video that demonstrates how to proceed. The goal is to queue up a video from the spot where gamers are stuck without the gamer having to know the level, scene, and time in the walkthrough for the hint. Our proposal is to use Deep Neural Networks (DNN) to learn the association of location and appearance pattern in the game(s) in order to locate the current game level. We will use recorded game play to train a DNN classifier for the games INSIDE and Portal, and evaluate the performance of the classifiers with gamers. Our goal is to design a system for NVIDIA Shield^{TM} that provides gamers with help when needed. We hope by providing gamers with such a system, we improve the overall gaming experience and fewer players will give up on a game.

POSTER SESSION 3

Commons East, Easel 56

2:30 PM to 4:00 PM

Synthesis of Flexible Anodic Aluminum Oxide Membranes

Lilia Fernanda (Lilia) Rodriguez Ley, Senior, Mat Sci & Engr: Nanosci & Moleculr Engr
Mentor: Bruce Hinds, Mater. Sci. & Engr.
Mentor: Brian Goodall, Materials Science and Engineering

Anodized aluminum oxide (AAO) with macroscopically-aligned, hexagonally-packed nanopores is an attractive substrate both for making nanomaterial templates and forming membranes. AAO has a tunable pore diameter, a well-defined pore structure, and is easily scalable. However, it is brittle which makes it difficult to work with and limits its applications. Here we present a method for synthesizing AAO nanoporous membranes that are flexible. We perform a two-step anodizing process using 99.999% pure aluminum foil in Oxalic acid. We make flexible AAO by patterning aluminum seams in a triangular grid to relieve stress. Additionally, fittings and a patterned gasket protect the aluminum strips from the anodizing solution. With flexible AAO, further research can be carried out on pharmaceutical separation applications and biochemical filtration. For this project I wrote up a protocol for my laboratory to make AAO on site for use in future research projects.

POSTER SESSION 4

MGH 241, Easel 154

4:00 PM to 6:00 PM

Identifying Cellular Mechanisms of Aging in *Saccharomyces cerevisiae* Using Replicative Lifespan Analysis

Priya Anita Uppal, Senior, Biology (General), International Studies
UW Honors Program
Katherine Ann (Katie) Grayden, Sophomore, Pre-Major (Arts & Sciences)
Mentor: Mitchell Lee, Pathology
Mentor: Brian Wasko, Department of Pathology
Mentor: Matt Kaeberlein, Pathology

Aging is characterized by time-dependent deterioration of cellular functions and increased risk for disease and death. The onset of age-related diseases including cancer, Alzheimer's, and other neurological disorders decrease the healthspan of humans. Healthspan is defined as the period of life without infirmity. My research focuses on understanding the basic biology of aging and determinants of healthspan within the emerging interdisciplinary field of geroscience. I use the model system Saccharomyces cerevisiae, a unicellular fungus, to study aging at the cellular level. To analyze cellular aging, I focus on replicative lifespan (RLS), which quantifies the number of daughter cells produced by individual mother cells before they reach replicative senescence and cease to divide. Our replicative lifespan team is composed of a group of undergraduate, graduate, and post-doctoral scientists at the University of Washington who use light microscopy and manual micromanipulation to quantify the RLS of hundreds of yeast mother cells each week. There are four important steps to analyze RLS in yeast: assay setup, incubation to outgrow cells, dissection of daughter cells from mother cells, and quantification of the number of daughter cells produced prior to replicative senescence. Using the replicative lifespan assay, I investigate genetic, environmental, and phar-

macological treatments to determine their impact on cellular aging. Research produced by our RLS dissection team has led to a better understanding of evolutionarily-conserved factors that modulate aging, as well as potential treatments for certain human mitochondrial diseases.

POSTER SESSION 4

Balcony, Easel 106

4:00 PM to 6:00 PM

The Design and Implementation of a Novel Method to Examine Pediatric Weight Management in Families

Shreya Singh, Senior, Biology (Physiology)
Mentor: Maya Rowland
Mentor: Brian Saelens, Pediatrics

Nearly 1 in 3 children in the U.S are already overweight or obese. Pediatric obesity represents a major health crisis with many psychological and physiological consequences. The American Medical Association states that obese and overweight children should receive moderate-to-high intensity behavioral interventions. Currently, it is estimated that about 17% of children age 2-19 in the U.S. are considered obese. The SHIFT study focuses on examining the short and long term efficacy of peer-versus professionally delivered FBT (family based training) on child weight outcomes and is a model that has been developed with studies done in the past. Previous studies like COMPASS and FOCUS tested the treatment model that SHIFT utilizes and EPICH/PPP were designed to pilot test the treatment model with peers. After conducting those studies, modifications were made to create a model for the SHIFT study. The treatment consists of a 5 month period in which 20 family sessions are conducted that are oriented toward helping them learn and implement behavioral skills for eating and physical activity change. The weight criterion for children is a BMI that is 20 to 100% above the median BMI and they should have at least one overweight parent (BMI$>$25) because these children are at a greater risk of maintain obesity into adulthood. The sessions include diet, physical activity, and behavior change that are discussed through parent only/child only groups as well as individual family meetings. Families come in every week and then are separated into child/parent groups in which we discuss prevention strategies for obesity and promote a healthy lifestyle and the children learn about ways to include physical activity in their daily lives. SHIFT works as a new model for FBT delivery that decreases costs and increases intervention availability while maintaining the treatment efficacy by using non-professional interventionists to deliver FBT.