Informing Green Tax Policy through the Laffer Curve

Jenny Fung

On Identifying and Analyzing Significant Nodes in Protein-Protein Interaction Networks

Rohan Khazanchi

Feature Articles

Summaries of Student Work
The logo for the Office of Undergraduate Research, on the front cover of this publication, consists of an “impossible triangle” within a starburst. To some, the triangle evokes the challenge of puzzles to be solved or the eternal research question “How does that work?” To others, the triangle represents the Greek letter ∆, the mathematical symbol for change.

WUURD, the Washington University Undergraduate Research Digest, is published by the Office of Undergraduate Research once a semester each academic year.

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The Office of Undergraduate Research is funded by the College of Arts & Sciences.

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Foreword

Washington University undergraduates are engaged in research at our school as well as at other institutions where they represent us with excellence. The work reported in this volume of the Washington University Undergraduate Research Digest has been carried out by graduating students who were completing senior theses and capstones, as well as younger students who have recently begun their research journeys.

Jenny Fung was motivated to dig deeper into the politics of climate change legislation and tax policies in her class “Environmental and Energy Issues”. In her paper entitled Informing Green Tax Policy through the Laffer Curve, she analyzes the success of the carbon tax instituted in Ireland, employing the Laffer Curve Theory developed during the Reagan years. Her analysis finds that the Laffer Curve could be used to inform decisions related to green tax implementation in the U.S., serving as a bridge between liberals and fiscal conservatives. An opportunity to work in his home town in the Bioinformatics Laboratory at the University of Nebraska, Omaha led Rohan Khazanchi to study the identification of hub and driver nodes in protein-protein interactions (PPIs). Analyzing PPI networks of humans, yeast, rats, and mice, Rohan and his colleagues confirmed their hypotheses that structurally important nodes do in fact correspond to relevant biological information. A Conference Travel Grant from the Office of Undergraduate Research allowed Rohan to present his paper On Identifying and Analyzing Significant Nodes in Protein-Protein Interaction Networks at the International Conference on Data Mining 2013.

In addition to the feature articles contained in this volume, readers are encouraged to explore the Summaries of Student Works which have been gathered from a broad range of disciplines. Each author has been attentively mentored by a member of the faculty and to them we owe a debt of gratitude. We in the Office of Undergraduate Research invite you to enjoy and become inspired by the works herein.

Respectfully,

KRISTIN SOBOTKA

Editor
ABSTRACT

Green policy often falls off the legislative agenda due to a prioritization of concerns more routine and immediate than climate change. A clear understanding that environmental policy can fit into a nation’s political and economic schema and goals may be key to the successful timing of implementation. Green taxes, carbon taxes, or eco taxes are particularly salient and global political discussions have found praise among liberals and fiscal conservative alike. A prominent theory of Reaganomics is the Laffer Curve, which is a mathematical approach to determining optimal tax rates. Through examining secondary sources, I apply the Laffer Curve Theory to Ireland and the United States to evaluate its applicability to inform successful adoption of green tax policy. First, I analyze Ireland in 2010 when the country implemented its now quite successful carbon tax to understand if the economic theory can be an indicator of success. I then attempt to model the viability of an ecotax policy in the U.S. in 2013, using Ireland as a basis of comparison. Applying the Laffer Curve Theory to green tax policy enactment may prove a valuable methodology for implementing green taxes prudently, especially in the U.S. where the American bipartisan party system has proved especially challenging to progressive federal policy in recent years.

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PROFESSOR OF POLITICAL SCIENCE


ACKNOWLEDGEMENTS

Recognizing Professor Bill Lowry and his course “Energy and Environmental Issues,” which allowed me the time to find passion in this matter and write this, my favorite college paper; Professor Robert Holahan who first inspired an interest in environmental politics; Kristin Sobotka and the Office of Undergraduate Research for supporting this work. Thanks to all.
INTRODUCTION

The rapid and exponential global industrialization seen since the industrial revolution has produced latent negative impacts on the environment. We are experiencing, for example, higher frequency and strength extreme weather episodes, a thinning ozone layer, and corrosive acid rain. The causes of these and other events have been attributed in large part to anthropogenic air emissions. Particularly salient are our carbon contributions to the atmosphere, primarily through the burning of fossil fuels for energy, whose heat-trapping effects drive rapid climate change. Today, every government is grappling with its response to climate change, intentionally or unintentionally. Many are changing policy to reduce carbon emissions.

One prominent form of climate change policy seen today is a green tax. Green taxes rely heavily on both the government and market response to determine prices. The concept of green taxes became popular among academics in the 1970s. Since then, they have been implemented by many different governments, such as in Ireland and British Columbia, and have been toyed with in yet others, as the United States. In 1993, President Clinton proposed a BTU tax where all non-renewable fuel sources would be taxed by their heat content and in 2013 the Climate Protection Act proposed a carbon pollution fee that would increase per ton through time. The ecotax, and other climate change policies such as “cap and trade” emissions permits, address the current market failure where societal and environmental costs of emissions are considered externalities. However, such costs ultimately default to tax payers, as is becoming apparent today.

Aside from the altruistic benefit suggested by their name, green taxes in theory may have many additional benefits. According to the double dividend hypothesis, how green taxes leverage taxes may improve economic efficiency in addition to reduce pollution to the environment.1 There is, to say, a light at the end of the tunnel in that although an ecotax proposes a new tax, it is designed to be self-extinguishing because its revenue is applied toward solving finite environmental problems and consumption and emissions practices are expected to improve in response. Additionally, a carbon tax is a revenue building policy thus making it more efficient at environmental protection than a policy relying on outside funding. On the other hand, as an additional consumptive tax, ecotaxes are thought to be regressive as they would impact the poor disproportionately (see Figure 1). Regardless of the argument for or against green taxes, the most salient common concern revolves around their effects on the economy.

In the 1970s, the very theoretical Laffer Curve was made famous to explain tax efficiency in terms of tax rates and revenues.2 The Laffer Curve became a central tenet to Reaganomics and is hailed by “supply-side” economics. When tax rates are plotted versus tax revenue, the curve describes an optimal point before and after which tax revenues are suboptimal (see Figure 2). At a 0% tax rate, the government collects no revenue to provide services and at 100% tax rate, citizens have no income to contribute to the economy. If on the downward slope, or past optimum, it suggests a tax cut-back to reach said point. If on the upward slope, or before optimum, the curve suggests a tax increase to reach the point of optimum revenue. Analyses of various systems certainly support the existence of the Laffer Curve (see Figures 3 and 6).
Figure 1
From “Carbon Taxes: Which Households Gain or Lose?” by Scott and Eakins, published by Ireland’s EPA
It is important to recognize the Laffer Curve model and decisions based off it must be greatly simplified. First, it is difficult to calculate. Our complex economic reality makes it challenging to graph an absolute and system-wide curve. A multitude of outside factors are integrally important to predict response to tax rate shifts: time period, loopholes, illegal and alternative markets are examples. However, since the Laffer theory is mathematically open-ended, there is substantial wiggle room in how it may be plausibly considered and calculated. Some complicated formulas have been established in “On the Analytics of the Dynamic Laffer Curve,” which conclude that high-tax, high-transfer economies, seen as of 2000 in some countries in Northern and Western Europe (e.g. Sweden and Denmark), experience the Laffer effect more strongly and may be at the peak or even beyond.³ Concerns in Europe are reflected by other analysts but are neither strongly supported nor refuted.⁴

Additional qualitative considerations to interpretation of the Laffer Curve must be made. Note the different temporal outlooks of one’s position on the curve. For example, in the short term a tax cut may stimulate economic growth while at that same tax rate the lowered revenues may detract from capital accruement that could be crucial to long-term government implemented programs. Consider too that not all citizen groups will be at the same position on the graph—rather, the position is a
societal average. All limitations considered, the Laffer Curve is still a helpful tool in considering the design and implementation of specific taxes at any point in time: “If the hazards can be managed, dynamic scoring [the general method by which the Laffer effect and other economic summaries are calculated] offers the promise of a more accurate picture of the budgetary consequences of policies and of more fairly reflecting the advantages of policies that enhance economic performance.”

One such type of tax is green tax policy. Examining existing tax systems and determining where they lie on the curve before and after the added ecotax may be a powerful informant of economic success and how to best improve the system. The Laffer Curve and projections from existing systems may also be useful in forecasting if an outside tax system may be conducive to a new green tax. To do this we will look at Ireland and the United States.

IRELAND
In 2010, Ireland implemented the carbon tax system it had seriously proposed in 2008 in response to the global recession and the first Kyoto Protocol deadline for 2012. As framed by government reports, green taxes were employed to broaden the tax base to
**Figure 4a**

**Figure 4b**
help raise revenue and the state’s fallen GDP after the financial crisis; strengthen national funding sources; and reduce carbon emissions across all polluting groups.6

The policy is as so: fuels are taxed according to their emissions of carbon dioxide at the rate of 20 euro/ton of CO₂. In 2013, solid fuels were added to petrol, auto-diesel, oils, and natural gas. The price of the tax is to increase over time as set by the government.

Ireland has historically responded positively to green initiatives. Their policies reflect active attempts to reach Kyoto Protocol emissions goals. Even before the green tax proposal in 2008, greenhouse gas emissions showed a consistent downward trend since the late 1990s to mid-2000s across different polluting sectors: agriculture, transportation, waste, energy, and industry despite consistent population and industry growth during that period and today (see Figure 4). The only polluting category not already improving was the residential sector, which is explained by Ireland’s substantial population growth since per capita energy use efficiency improved. All sectors decreased their emissions compared to Ireland’s 1990 emission levels except for energy, which was only slightly increased.7

Data from the EPA from 2010, when Ireland’s green tax policy went into effect, through 2012 show residential emissions fell 22.4%, with percentages being based off 1990s emissions values. Although other polluting sectors within Ireland, especially industry (~25%), produced marked drops in fuel use following the recession, residential fossil fuel usage actually increased slightly from 2008-2010. The green tax, from the same data, seemed only modestly successful in its emissions reductions amongst industry (a drop of 3-4%) and enormously successful amongst residences (-22.4%). Eamon Ryan, Ireland’s Energy Minister from 2007-2011, told The New York Times that the Irish “are not saints like those Scandinavians—[they are] lapping up fossil fuels, buying bigger cars and homes, very American.”8

Recognizing its positive effects on the environment, we now consider the carbon tax policy’s economic success. Nearly one billion euros ($1.3 billion USD) were raised from 2009 through 2012, providing the Irish government with 25 percent of the 1.6 billion euros in new tax revenue it needed to narrow its budget gap since 2008.9 Using GDP growth rate as a rough measure of economic health and prosperity, Ireland’s GDP growth rate become positive for the first time since the 2008 financial crisis in 2010 (see Figure 5). It continues to maintain positive average growth thus far.10

In just three years, the carbon tax proved to be a successful revenue source, green policy, and economic stimulant. If the Laffer theory were indeed applicable, it would be supposed that Ireland at its 2008 tax rates was on the upward slope and the green tax may have shifted Ireland more toward the point of optimal tax revenue.

A curve calculated for Ireland averaging labor tax revenue growth paths from 1995-2010 concluded movement to the Laffer hill peak was sizeable (see Figure set 6).4 This is consistent with the observed effects of the 2010 carbon tax. This correlation is supportive of the Laffer curve being a valuable and relevant informant to the implementation of carbon taxes.

As a notable aside, although the Irish carbon tax seems a success, current public opinion is mixed. No one likes a new tax or tax increase. Gas costs a whopping $8/gallon across Europe. Not to mention, the Irish public transportation system is less than ideal, especially for long-distance commuters. The coalition party that initially
Figure 5
Data from the Central Statistics Office Ireland published on Trading Economics
http://www.tradingeconomics.com/ireland/gdp-growth

Figure 6a
Laffer effect data calculated from 1995-2010 data by Trabandt and Uhlig in “How Do Laffer Curves Differ across Countries”
Figure 3: Labor and capital tax Laffer curves across all countries. The model is calibrated to the average of 1995-2010, see table 2 (gross US debt). Parameters for technology and preferences are set as in table 1 (gross US debt). Shown are steady state (balanced growth path) total tax revenues when labor taxes (upper panel) or capital taxes (lower panel) are varied between 0 and 100 percent. All other taxes and parameters are held constant. Total tax revenues at the average 1995-2010 tax rates are normalized to 100. Stars indicate positions of respective countries on their Laffer curves. Note that the first letter of each country name indicates the peak of their respective Laffer curve.

Figure 6b
Laffer effect data calculated from 1995-2010 data by Trabandt and Uhlig in “How Do Laffer Curves Differ across Countries”

Figure 6c
Laffer effect data calculated from 1995-2010 data by Trabandt and Uhlig in “How Do Laffer Curves Differ across Countries”
Figure 5: Distance to the peak of Laffer curves for average 1995-2010 vs. 2010 calibration. The model is either calibrated to the average of 1995-2010 or to the 2010. See table 2 (US gross debt). Parameters for technology for preferences are set as in table 1 (US gross debt). Horizontal axis shows calibrated tax rates. Vertical axis shows distance to the peak in terms of tax rates. The dashed-dotted line shows the distance to the peak for the US when the initial steady state tax is varied and the model is re-calibrated for each assumed tax rate.

**Figure 6d**

Laffer effect data calculated from 1995-2010 data by Trabandt and Uhlig in “How Do Laffer Curves Differ across Countries”

**Figure 7**

From the U.S. Congressional Budget Office (http://www.cbo.gov/)
implemented the green tax was voted out of office in 2011.8 Lucky for the green tax, it is widely supported by environmentalists and economists alike.

THE UNITED STATES

Given that the apparent success of Ireland’s carbon tax system supported the Laffer methodology of economic analysis, it may be possible to understand if another national economy is a good candidate for green taxes by the same modelling.

The United States is a hotbed of extreme political polarity on environmental issues. The idea of climate change legislation has been proposed and squashed several times: Clinton’s BTU tax in 1993, the Waxman-Markey Climate Bill of 2009, the infant Kerry-Graham-Lieberman climate change bill in 2010. Newly proposed is the 2013 Climate Protection Act, which, among other measures, proposes an initial carbon pollution fee of $20/ton to be increased over time.

The U.S. is similar to Ireland in many ways. The American government and economy were struck hard by the 2008 global recession. The U.S. government budget deficit skyrocketed (see Figure 7) and, though it has fallen substantially, the question of how to close our federal budget gap remains. Therein lies the opportunity for green taxes to be used as a tool, as was done in Ireland in 2010. According to the Trabandt and Uhlig analysis, the U.S. is also on the upward slope and has quite a distance left before the optimal revenue point is reached.4

The same authors calculated that the U.S. can afford to pay the highest interest rate on national debt if only labor taxes are adjusted to service the additional debt burden.4 They use maximum affordable debt interest rate for the nation as an indicator of maximum revenue that can be earned by taxes. The U.S. can afford the highest interest of compared countries if labor taxes are adjusted upward to make up that tax burden. The scope of this work is only to consider labor taxes as a revenue source, but, following Ireland’s example, green taxes would be a viable and savvy alternative.

In a comparison of maximum income tax rates per person, Ireland’s is greater. 2012 rates were 48% in Ireland and 35% in the U.S.11 Keeping our analysis simple and true to the Laffer effect, this difference is further evidence that the U.S. has the likely potential to benefit from increased taxes.

For the United States, public opinion will play a strong role in the consideration of a green tax. According to a recent poll by Gallup, we’re in a period when Americans aren’t complaining much about taxes as a result of the Bush tax cuts in 2003.12 While this opinion is changing steadily as time progresses and taxes and government expenses are increased, a current majority (55%) still say we pay a fair amount of income taxes.13 It could be crucially advantageous for policy makers in favor of green taxes to act now while this opinion is still in majority.

CONCLUSIONS

Arthur Laffer’s tax efficiency theory, though simple, has great power as an economic policy informant when modelled. Here, it was applied retrospectively to Ireland to see if it is indeed applicable and how the green tax system introduced in 2010 affected the country as a green policy and economic recovery tool in light of the Laffer effect. Data
collected since policy implementation that shows reduced greenhouse gas emissions across all polluting sectors, increased average GDP growth, and increased federal revenue, frame the policy as a success. These effects are supported by calculations of Ireland’s Laffer curve. Thus, the Laffer curve as an informing methodology seems plausible. Projected onto the U.S.A., a nation that does not have a green tax system but as a result of the 2008 world recession has suffered economic woes comparable to those in Ireland, the Laffer curve indicates that the present American economy and government are likely to benefit from a green tax system.

However, in the political climate of the United States, it is not that simple. Current politics present a high barrier to a green tax in the U.S., even if economic analyses and successful policy implementations on the world stage provide convincing support for them. Fortunately, there is no singular way to design green taxes. A carbon tax can follow one of two budget procedures: one in which the revenue is considered as an additional source of public finance or one where revenue is earmarked to tax cuts elsewhere in the economy. A popular idea among economists is that carbon taxes may produce negligible impact when they replace a share of payroll or personal income taxes, which are designed as though they are a punishment of “good,” labor, rather than “bad,” pollution. An aforementioned concern is the disparate impact of the tax upon certain groups, especially the poor. As practiced in British Columbia and proposed in the Climate Protection Act of 2013, green tax revenues have the potential to be partially reallocated to tax payers and households, especially to those whose disposable income sits on the downward slope of the Laffer curve.

Perhaps it is most important to note that in interpreting these findings, the goal is not necessarily to be at the top of the curve at all times. Tax policy and economic needs are extremely dependent on the time period. Mixed policy through time of tax breaks, and increases varying with short- and long-term national needs in mind, is a better approach. The Laffer curve serves as an informant to that decision-making process.

Studies to further examine the applicability of the Laffer curve to green tax systems could be done elsewhere such as British Columbia, Canada; Boulder, Colorado; or many Western and Northern European countries. Such study would be especially informative where the governed body is thought to be at or beyond the Laffer hill top, as in Denmark or Sweden (see Figure set 6).

References


9 Id.

10 Central Statistics Office Ireland published on Trading Economics

   http://www.tradingeconomics.com/ireland/gdp-growth

11 “Individual Income Tax Rates Table,” last accessed December 5, 2013,


13 Id.


On Identifying and Analyzing Significant Nodes in Protein-Protein Interaction Networks

Author:
Rohan Khazanchi
Rohan is a sophomore planning to major in Biology with minors in Music and Psychology in the College of Arts & Sciences. His fascination with Bioinformatics stemmed from an interest in the interdisciplinary applications of computer science to biological research, which led him to spend two summers in Dr. Ali's lab. His research there inspired him to continue pursuing research— he spent this summer at the WUSTL Phage Hunters Summer Workshop before returning home to work in a pulmonary research laboratory under Dr. Todd Wyatt at the University of Nebraska Medical Center.

ABSTRACT

Network theory has been used for modeling biological data as well as social networks, transportation logistics, business transcripts, and many other types of data sets. Identifying important features/parts of these networks for a multitude of applications is becoming increasingly significant as the need for big data analysis techniques grows. When analyzing a network of protein-protein interactions (PPIs), identifying nodes of significant importance can direct the user toward biologically relevant network features. In this work, we propose that a node of structural importance in a network model can correspond to a biologically vital or significant property. This relationship between topological and biological importance can be seen in/ between structurally defined nodes, such as hub nodes and driver nodes, within a network and within clusters. This work proposes data mining approaches for identification and examination of relationships between hub and driver nodes within human, yeast, rat, and mouse PPI networks. Relationships with other types of significant nodes, with direct neighbors, and with the rest of the network were analyzed to determine if the model can be characterized biologically by its structural makeup. We performed numerous tests on structure with a data-driven mentality, looking for properties that were potentially significant on a network level and then comparing those properties to biological significance. Our results showed that identifying and cross-referencing different types of topologically significant nodes can exemplify properties such as transcription factor enrichment, lethality, clustering, and Gene Ontology (GO) enrichment. Mining the biological networks, we discovered a key relationship between network properties and how sparse/dense a network is—a property we described as “sparseness”. Overall, structurally important nodes were found to have significant biological relevance.

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Professor Ali's research interests include Bioinformatics, Graph Theory/Modeling, and Algorithms and Wireless Networks. He also serves as the Dean of the College of Information Science and Technology.

ACKNOWLEDGEMENTS

I would like to thank my co-authors and mentors, Dr. Hesham Ali, Dr. Kathryn (Dempsey) Cooper, and Ishwor Thapa and the rest of the UNO Bioinformatics lab for their guidance, instruction, and support. This work was made possible by Grant Number P20 RR16469 from the National Center for Research Resources (NCRR), a component of the National Institutes of Health (NIH) and its contents are the sole responsibility of the authors and do not necessarily represent the official views of NCRR or NIH. Finally, I want to thank Kristin Sobotka and the Office of Undergraduate Research for the opportunity to present and publish this paper.

KEY TERMS
- Protein-Protein Interaction Networks
- Driver Nodes
- Hub Nodes
- Network Enrichment
- Graph Theory
- Clustering

Another version of this work has been published in ICDM Workshops 2013: 343-348.
INTRODUCTION

With biological data becoming increasingly available as technology and methodology for acquisition of new data improve, the need for analysis of this new data has become extremely important. In many circumstances, data is collected and left untouched because of a lack of proper analysis techniques. Utilizing bioinformatics to analyze biological data is not only efficient, but also practical. It provides computational methods that work on massive data sets that would be painstakingly difficult to analyze using other techniques. We use a systems biology approach to model and visualize biological networks that we study as graphs. In our case, we utilize a network model of protein-protein interactions. In this model, proteins are represented as nodes, and an interaction between two proteins is represented as an unweighted edge (see Figure 1). Graphical models make it easier to process data because they can be analyzed with user-friendly tools to identify significant properties of networks that can be further tested via computational techniques. While basic analysis of biological networks reveals important features, sophisticated data mining tools are needed to extract useful knowledge from the networks. In this research, systems biology and bioinformatics are used to identify significant characteristics in given data sets, using a network model, and to further analyze the topological characteristics of these models by linking them to their known biological purposes. The specific graph properties we examine are hub nodes, driver nodes, and clusters. Hub nodes, in this case, are proteins that are highly interconnected with the rest of the network; in graph theoretic terms, they are nodes of high degree. Driver nodes have less extensive previous research than hub nodes due to their recent identification as significant network properties and are defined as nodes whose control is sufficient to fully control the dynamics of a system. These nodes are identified by an algorithm described in the “Proposed Network Model (Methodology)” section that utilizes maximum matching in the network—the maximum set of links that do not share start or end nodes. Finally, clusters are groups of tightly interconnected nodes that we hypothesized share similar functional enrichment.

Background & Previous Work

In 1999, Barabási and Albert introduced their cornerstone paper on scale-free networks, revealing that networks can be used to reflect evolutionary history, social disparities, and much more.\cite{Barabasi1999} For the first time, networks were thrust into the scientific spotlight and further network research began. They called for a better description of complex systems, and this description could only be created by classifying significant properties of networks. This work was followed in 2001 by Jeong et al., who specifically examined hub nodes (nodes with larger number of connections than other nodes) in protein-protein interaction networks (PPINs).\cite{Jeong2001} They introduced the centrality-lethality rule, which played a major factor in our lethality studies by explaining why the essentiality of nodes is significantly higher in nodes of high degree (hub nodes). Also determined in this work was the importance of topological position of individual proteins. This finding helped identify evolutionary robustness in yeast against mutations.

In 2003, Pržulj et al. expanded studies of node properties and PPIN analysis tools to include degree, clustering, shortest paths, connectivity, and function.\cite{Przulj2003} This paper
displayed the vast amount of information that can be generated through analyses of networks by defining many rising concepts of significance in network theory. Later, in 2006, He and Zhang found empirical evidence confirming the centrality-lethality rule without using the high-degree of hubs as their only justification. By scientifically testing and proving the rule using yeast data and without using solely structural properties as validation, they provided a strong foundation for future research to use this rule as fact. The results of this paper created an explanation of why essential interactions and their proteins are essential and did so without needing to invoke network architecture. [2] and [4] were both reasserted by Zotenko et al. in 2008, who once again confirmed the centrality-lethality rule. However, in new analysis of network connectivity and controllability, [5] proved through experiments that essential hubs are no more important than nonessential hubs to keep a network connected. In other words, hubs are not necessarily the key pieces that keep and control a network. This opened the door for examining driver nodes as perhaps equally significant, if not more significant. However, Song and Singh did prove that hubs tend to have a higher lethality than non-hubs (a fact which we also assert in lethality tests on the hubs of the yeast PPIN; see Results).

**Figure 1**

An overview of the overall approach—first networks are created using known protein-protein interaction databases, then hubs, clusters, and drivers are identified. The method used to identify driver nodes is contained as pseudocode shown on page 21.
One issue with the centrality-essentiality rule, for many years, was defining a formal threshold/identifying a definite parameter for the hub node. Vallabhajosyula et al. determined that the method to isolate hubs is setting an *ad hoc* degree scale that determines topological and functional significance[7]. They defined hubs in three different manners and across all three asserted the significance of hubs in multiple fashions, finding that their approach was able to yield consistent results with previous studies. Their results suggest that this *ad hoc* approach can properly identify hub nodes in a PPIN, as we did in our study.

In 2011, Liu et al. introduced the concept of driver node identification, expanding structural concepts from simply topology and functionality to network controllability[8]. Driver nodes are a bit more complex than hubs—[8] helped clarify a previously foggy definition. The established definition of driver nodes is that they are proteins that must be controlled to maintain controllability over the entire network. They outlined the beginning stages of defining driver nodes and their significance and discussed how to identify nodes that were needed to control a network. They also established why control theory and network theory, when intermixed, proved very helpful in the identification of significant network properties, such as drivers. This paper is one of the cornerstones of driver node research.

More recent experiments in applications of network theory have further studied clusters, lethality, betweenness centrality, closeness, and other structures in various network types (social, physical, biological, technical, etc.)[9],[10],[11].etc. However, despite the biological significance of the driver node remains relatively unknown. Thus, our goal is to extensively probe the role of driver nodes within networks while continuing to analyze hubs in new ways.

**PROPOSED NETWORK MODEL/METHODOLOGY**

Multiple tools were utilized to improve the functionality of our data and perform the various tests we planned via computational methods; the general approach used is described visually in *Figure 1*. The first step of this entire project was the visualization of our biological networks. Each network was downloaded from BioGrid’s May 25th, 2013 organism release (3.2.101). Each node in our network models represents a single protein in the biological data set, while each edge represents an unweighted, undirected interaction between two proteins. Each network was visualized using Cytoscape[12], and we confirmed their scale-free qualities, similar to those described in [1].

The significant nodes we wanted to study were hub nodes and driver nodes: hubs to verify that our models were consistent with previous findings, and drivers to further understand their role in the PPIN. The R statistical computing language along with the igraph package in R[13] were used to perform much of our initial identification and analysis tests. Hub nodes are calculated by an *ad hoc* selection of nodes of the highest degrees within a network, as outlined by [7]. Calculation of driver nodes primarily involves employing maximum matching and bipartite graph theory to identify nodes that must be controlled to control the entire network’s dynamics. Using the R and igraph packages, an algorithm based on the process identified in [8] was developed and implemented to identify driver nodes in our networks.
PSEUDO CODE OF DRIVER NODES ALGORITHM

Load igraph library

g <- Graph read in as input

b <- Edgelist version of g

d <- Unique edgelist from b (removes duplicates)

f <- Create vector with values from 1 to length of b

FOR a number i between 1 and the length of b
    x equals d if it equals b at position i
    f at position i equals x

FOR a number i between 1 and the length of f if the remainder of i/2 is 0,
    f at position i equals itself plus the length of d

g1 <- Bipartite graph of f

m <- Maximum bipartite matching of g1

k <- Create vector with values from 1 to length of f

p <- Perform difference on vectors k and m

p <- Subtract the length of d from p value in previous line

result <- Select all nodes from original unique edgelist that are represented by p

OUTPUT result
To perform the rest of our computational tests, we ran multiple scripts written in Perl and Python on a UNIX platform via the University of Nebraska’s Morph-G, Sapling, and Rapids servers. All Gene Ontology (GO) Enrichment graphs and analyses were generated via the PANTHER online database/analysis tool (http://www.pantherdb.org/) under default parameters.[14],[15]

RESULTS

The various computational tests we performed on the driver and hub nodes yielded some interesting results. Regarding the concentration of driver nodes within networks, we found a relationship between network size and the number of driver nodes that exist in that network. As shown in Table 1, more driver nodes exist within more spread out, sparse networks, like that of *Rattus norvegicus*. However, in tightly-packed, dense networks like that of *Saccharomyces cerevisiae*, there exist a lower percentage of driver nodes. It is known that PPI databases are fraught with false positives and further, in larger model organisms, the known set of PPIs is not complete. We speculate that as these datasets continue to mature, they will become less sparse, and as such, their number of driver nodes will increase accordingly to reflect the controllability of the more dense networks. We calculated sparseness as $1-(2e)/[n(n-1)]$ where $n =$ number of nodes and $e =$ number of edges.

By accessing databases of lethal proteins and transcription factors in yeast, we were also able to test the driver and hub nodes of *Saccharomyces cerevisiae* for their essentiality within the network and to see if they had transcription factor (TF) functionality; we hypothesized driver nodes could be regulators of the network, which TFs are, since they are required for controllability. Hubs tended to not be transcription factors, but exhibited more lethal properties. Drivers, on the other hand, were about the same percentage lethal as the overall network, but did have a tendency to serve the purpose of being a transcription factor. *Table 2* shows these results.

<table>
<thead>
<tr>
<th>Organism</th>
<th>Total Nodes</th>
<th>Total Edges</th>
<th>Network Sparseness</th>
<th>Driver Nodes (Percentage of Network)</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>H. sapiens</em></td>
<td>17,349</td>
<td>131,098</td>
<td>99.91288%</td>
<td>10,410 (60.003%)</td>
</tr>
<tr>
<td><em>M. musculus</em></td>
<td>7,329</td>
<td>14,639</td>
<td>99.94549%</td>
<td>5,005 (68.290%)</td>
</tr>
<tr>
<td><em>R. norvegicus</em></td>
<td>2,366</td>
<td>3,217</td>
<td>99.88502%</td>
<td>1,735 (73.331%)</td>
</tr>
<tr>
<td><em>S. cerevisiae</em></td>
<td>6,344</td>
<td>216,877</td>
<td>98.92208%</td>
<td>1,714 (27.018%)</td>
</tr>
</tbody>
</table>

*Table 1*

The relationship between network sparseness (number of edges in relation to number of nodes) and number of driver nodes.

COLUMN 1: Species name for PPIN

COLUMN 2: Number of nodes in the network (Nodes = Proteins)

COLUMN 3: Number of edges in the network (Edges = Interactions between two proteins)

COLUMN 4: 100% - Network density, or how many edges are missing from the complete network.

COLUMN 5: The number of driver nodes found in the network (Percentage of driver nodes in the network).
Next, we analyzed the neighbors of these nodes by utilizing first-degree neighbors of hubs in each network. Initial analysis after isolating the neighbors from the rest of the network showed yet another relationship with network sparseness. In more sparse networks (M. musculus, R. norvegicus), the first-degree neighbors of hub nodes represented an extremely large percentage of the network’s driver nodes, while in more dense networks (H. sapiens, S. cerevisiae), the first-degree neighbors represented about the same percentage of driver nodes as the rest of the network.

The sparser networks had more hubs than the dense networks, but the first degree-neighbors of these hubs still represented a smaller percentage of the network, a result likely explainable by the more spread out nature of sparser networks. These results are shown in Table 3.

| Table II | The lethality and transcription factor enrichment of significant nodes in yeast. |
|-----------------------------------------------|
| COLUMN 1: Node type within yeast PPIN |
| COLUMN 2: Number of proteins identified within subnetwork. |
| COLUMN 3: Number of proteins found within list of known lethal proteins. |
| COLUMN 4: Ratio of % of lethal drivers/hubs to % of lethal non-drivers/non-hubs |
| COLUMN 5: Number of proteins found within list of known transcription factors. |
| COLUMN 6: Ratio of % of transcription factor drivers/hubs to % of transcription factor non-drivers/non-hubs |

| Organism | Total First-Degree Neighbors of Hubs (Percentage of Network) | Hubs (Total Hubs) | Driver Nodes (Percentage of Neighbors) |
|-----------------------------------------------|
| H. sapiens | 11033 (63.59%) | 6 (6) | 6714 (60.85%) |
| M. musculus | 2121 (28.94%) | 12 (12) | 1847 (87.08%) |
| R. norvegicus | 1201 (50.76%) | 7 (7) | 1088 (90.59%) |
| S. cerevisiae | 4488 (70.74%) | 6 (6) | 1193 (26.58%) |

| Table III | First-degree neighbors of hub nodes and their properties within each of the network and the driver nodes of each network. |

Newly created networks of only first-degree neighbors of hubs were then used for clustering. We isolated the highly-scored clusters within each network using the MCODE plugin via Cytoscape [12] and found that significant clusters existed among the first-degree neighbors of hubs in the larger networks (H. sapiens, S. cerevisiae). Within these clusters, there were a higher percentage of driver nodes than in the entire
network, including the clusters (Table 4). They also had a GO enrichment [15] with an extremely small p-value (very high enrichment) for translation—which is only minimally enriched in both overall networks (Figure 2). The clusters also had GO enrichment for multiple types of metabolic processes—but each of those traits was also enriched in the overall network just as heavily.

**Figure 2**
Graphs of the Gene Ontology enrichment from the Panther database of the human (top graphs) and yeast (bottom graphs) sub-graphs. Note that the DNA translation enrichment (purple in human cluster—top right, green in yeast cluster—bottom right) is extremely prominent in the clusters, but hardly visible in the overall network graphs. [15]
Finally, we analyzed the connectivity between hub nodes in each network. We wanted to see how hubs interacted with each other, so after determining the hub nodes, we used R to isolate the shortest paths between each hub node. The results are shown in the graph below (Figure 3). Each “jump” represents one node between each hub—so if two hubs are one “jump” apart, then they are directly connected.

![Graph of the tests on hub interconnectivity. Yeast hubs had much higher degrees than the mouse and rat hubs due to the larger size of the yeast network—this is why yeast has more total occurrences.](image)

**Table IV**
Analysis of highly-scored clusters within larger networks and their GO enrichment in translation

<table>
<thead>
<tr>
<th>Organism</th>
<th>Total Nodes in Cluster</th>
<th>Score</th>
<th>Driver Nodes (Percentage of Cluster)</th>
<th>Hub Nodes</th>
<th>Translation Enrichment p-value</th>
<th>Percent of Nodes Enriched</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>H. sapiens</em></td>
<td>79</td>
<td>31.608</td>
<td>57 (72.15%)</td>
<td>3</td>
<td>1.15E-66</td>
<td>69.74%</td>
</tr>
<tr>
<td><em>S. cerevisiae</em></td>
<td>58</td>
<td>25.966</td>
<td>27 (46.55%)</td>
<td>1</td>
<td>1.04E-46</td>
<td>87.76%</td>
</tr>
</tbody>
</table>

**DISCUSSION/CONCLUSIONS**

The results of the tests we performed held multiple significant meanings. The described relationship between network size properties (edge-node ratios, shown in Table 1) and number of driver nodes can be justified by the fact that, as our results showed, networks that are sparser will be less interconnected, and thus, will need more
driver nodes in order to maintain control over the entire network. Networks like the yeast PPIN are extremely well interconnected and are controllable using fewer nodes than large networks with less connectivity, like the human PPIN.

After analyzing our initial topological results, we returned to our original goal of identifying driver node significance and corresponding biological properties. As has been previously defined, we found that hubs were strongly lethal in the yeast network and had a significantly larger lethality ratio in comparison to the driver nodes, which were about as lethal as the rest of the network. This was expected; hubs are extremely important to the survival of a network—they serve as central communication points across the entire network due to their high connectivity. This “centrality-lethality” rule has been described in landmark papers since 2001, including [2], [4], [5], and [6]. Additionally, we discovered that driver nodes actually were more often transcription factors (8%) than to hub nodes (0%), non-hubs (5%), and non-drivers (5%).

Topologically, first-degree neighbors of hubs displayed an inverse correlation to network sparseness than the correlation that driver nodes showed. There are far more first-degree neighbors of hubs in networks that were more densely interconnected and had more drivers. This relationship certainly makes sense because the networks with higher connectivity were more likely to have hubs of a substantially higher degree, causing the increased number of nodes interacting with the hubs. An interesting topological finding was that in the sparser networks (M. musculus, R. norvegicus), despite having a smaller number of first-degree neighbors, an extremely large percentage of driver nodes were represented as first-degree neighbors. In other words, driver nodes are very frequently connected directly to hub nodes. This is in concordance with the network control theory that in order to control a network, one must not simply control the hubs, but control the nodes interacting with the hubs. In attempting to isolate highly-scored clusters of the first-degree neighbors of hub nodes, we found another topological correlation to biological properties. In both of the larger networks (H. sapiens & S. cerevisiae), the highest scored cluster had an extremely strong GO enrichment for DNA translation—which was unusual considering that translation is very slightly enriched in the rest of the network. This result could definitely be analyzed through further testing of clusters within these networks and within other large PPINs.

Our hub connectivity study also yielded some interesting results. In the cases of the yeast and mouse PINs, it is very apparent that the hub nodes are considered assortative, meaning they tend to connect to other hubs. None of the hubs were more than 3 jumps away from each other, showing that these hubs have close interaction with each other. However, a large majority of the hubs did not interact directly with each other—most hubs were 2 or 3 jumps apart. This was explained by Maslov and Sneppen, who stated that connectivity is not likely between two high-degree nodes, but more likely between a node of high degree and a node of low degree. In the case of the rat PIN, the hub nodes seem to be more disassortative—meaning they were not directly connected, reaffirming the assertions of [16]. These results could once again relate to the concept of network sparseness, except on a smaller scale with only hub nodes. These ideas of how hubs are mixed can be further seen in network theory.

So, why are these results significant? The importance of these tests can be found when we return to discussing our initial goal. Each test we performed yielded a result
that showed a correspondence of the topological properties of our PPIs and biologically significant information. Our driver nodes algorithm successfully identified drivers that corresponded to properties we believe drivers should represent in a protein network. All in all, identifying significant nodes and analyzing their relationships can help identify points of importance within PPI networks, and biologically investigating these points of importance in further experiments/computational analyses has a strong potential to yield valuable results.

References


Stereotype threat often manifests during situations in which a stereotype holds that members of one group will perform poorly on a given task. There is evidence showing that making salient group achievements can actually alleviate the stereotype threat. Specifically, experimenters showed that female participants who read about female achievement in the form of biographical sketches performed significantly better on a difficult mathematics test than women in the control condition (in which the stereotype was made salient, but no alleviation techniques were put in place). This study put forth initial evidence that alleviation of stereotype threat could occur, through salience of group achievements.

The present study was stimulated by the work of McIntyre et al. However, we go beyond the previous research in a variety of ways: first, we will be including a condition in which subjects are not exposed to stereotype threat, allowing for interesting analyses both about the effects of stereotype threat and group achievement salience, independently. Second, we include mood and standard trait motivation inventories to make room for interesting dispositional differences between subjects that may contribute to effects.

The intent of both of these studies is to provide further evidence for a practical, relatively novel alleviation of stereotype threat. Additionally, the hope is to have realistic implications on education policy and reform as group achievement-salience can be easily achieved through curricular reform.
Anhedonia, or the loss of experienced pleasure, is a cardinal symptom of Major Depressive Disorder (MDD). Traditionally, anhedonia is measured and explained as a unitary construct however, a more specific characterization of the symptom would provide a greater understanding of the heterogeneous nature of MDD. This research investigates two potentially differentiable mechanistic processes within anhedonia. We examine if the loss of experienced pleasure is explained by impairment in an individual’s consummatory processes (how much one likes a reward) and/or by impairments in their motivational processes, (how much one is willing to expend effort to gain reward). Participants completed three different tasks that measured different aspects of reward responsivity and completed questionnaires that measured depressive symptoms, hedonic capacity, and motivation. The first task was the Probabilistic Incentive Learning Task (PILT), which uses an asymmetric reward schedule to produce a response bias towards a more frequently, rewarded stimulus. Response bias on this task measures to what extent a person modifies behavior to obtain reward. The second task was the Progressive Ratio Task (PRT) where participants had to expend more and more effort over time to obtain additional reward. How long a participant is willing to engage in this task indicates willingness to expend effort to gain a reward. In the final task, the Emotional Picture Rating Task (EPRT), participants rate their emotional response to affective pictures. EPRT ratings indicate the extent to which positive/pleasurable pictures induce positive affective responses. Relationships between behavior on the three tasks as well as between behavior and individual differences were tested. Hierarchical regressions indicated a relationship between EPRT ratings and the questionnaire measures of hedonic capacity, but not motivation whereas PILT and PRT behavior related to motivation but not hedonic capacity. The results suggest that anhedonia can be characterized into component parts of consumption and motivation.
The human vagina is host to many bacterial communities through a finely-equilibrated, mutualistic relationship. The vagina provides nutrients to the bacteria, which in turn help rid the vaginal ecosystem of harmful, non-indigenous species. When the microbiome is disturbed, bacterial vaginosis (BV) often results. Affecting 1 in 3 women in the US, bacterial vaginosis is prevalent, but vaguely characterized. In the clinical setting, women who exhibit vaginal inflammation, fishy malodor upon application of potassium hydroxide, vaginal epithelial cells surrounded by bacteria in wet mount microscopy, or abnormal discharge are diagnosed with bacterial vaginosis. Due to the broad diagnostic features of BV, it has proven difficult to characterize the etiology of the disease. The focus of this research is to identify cellular phenotypes of the vagina that correlate with the presence of BV in order to facilitate the clinical identification of the disease.

Increased epithelial cell exfoliation has long been associated with BV, but this relationship has not been quantified. Our lab has previously studied the epithelial shedding of a clinical sample of women with and without BV and found significantly more exfoliated vaginal epithelial cells in affected individuals. Through a blind study of 222 women with either BV (Nugent score 7-10), intermediate BV (Nugent score 4-6) or no BV (Nugent score 0-3), we seek to correlate the number of exfoliated epithelial cells to the presence and severity of BV in these women. By characterizing the BV phenotype at the cellular level, our lab hopes to shed light on the disease’s complex etiology and to improve our ability to diagnose and ultimately treat BV.
The discovery of human prion diseases including kuru and Creutzfeldt-Jakob disease has obliged us to reconsider existing explanations of infectious agents and examine new ways of addressing emergent epidemics in contemporary society. Medical anthropology examines cultural, environmental, and political-economic factors as constituents of disease and is useful to investigate prion diseases. To expand upon the biomedical literature that tends to explain prion diseases in terms of biological factors, we can draw from the contributions of anthropologists who researched afflicted populations like the Fore of New Guinea in an attempt to retrospectively understand the way in which cultural belief affects patterns of human interaction. These aspects of prion disease lend themselves to anthropological investigation, as we study the impact of other epidemics on individuals, families, and communities. Applying these broad cultural analyses to the practice of transnational epidemiological research raises ethical questions for the medical and social science community.
Human Achilles tendons locate in the low legs behind the calf muscles. They are responsible for connecting calf muscles to calcaneus bones and are crucial to many everyday activities such as walking and jumping. However, Achilles tendon injuries are extremely common among athletes due to sudden stretches and contraction of the tendon, and their recoveries after surgeries are not ideal. In order to prevent such injuries and improve recoveries, a more comprehensive understanding of Achilles tendon’s structure and mechanical property is required.

Previous research on Achilles tendon has mainly focused on its tensile and material properties. However, their results cannot fully explain the commonality of Achilles tendon injuries. Consequently, an explanation from other properties of Achilles tendon is suggested. Our research focuses on the torsional properties of Achilles tendon, which is the behavior of the tendon when it is twisted and under torsional force. We hypothesize that natural torsion in human Achilles tendon provides additional mechanical benefits such as elasticity and energy storage, which facilitates Achilles tendon to sustain high \textit{vivo} stress.

To explore the torsional properties of Achilles tendons, specific clamps have to be built to fix Achilles tendons on to the test machine. Our work has mainly been focused on design and manufacture of the clamp. After the clamps were finished, pig’s extensor tendons were dissected and used as a pilot test for human Achilles tendons. Stress, strain and torque were measured under different angles of torsion of pig’s extensor tendons. Future work will focus on getting more data from pig’s extensor tendon, testing on human Achilles tendon and establishing a computational model to explain the behavior of human Achilles tendon under torsional force.
Sniper localization and its applied algorithms can be broken down into two distinct subcategories. One is estimation; that is, determining the approximate location of the sniper. Two is detection; that is, determining if the detected signal is sniper fire or random noise. Each of the problems relies heavily on the acoustic signals generated from the muzzle blast (MB) as well as the shock wave (SW) of the gunshot in order to evaluate and estimate the measurement. In this project we use MATLAB to generate sample measurements for the time difference of arrival of the MB signal model and use statistical methods (maximum likelihood and least squares) to estimate the sniper’s position. From there we are able to determine the signal-to-noise ratio (SNR) for the signal model, as well as determine the Cramer-Rao bound, the lower bound of the sniper position error. In addition to estimating position we used the Neyman-Pearson Lemma to detect whether the measurements of the signal model were sniper fire or random noise. Further exploration of this topic will include multiple and moving-source signal models.
The objectives of this study were to examine the association between intimate partner violence (IPV) and eating disorder among emerging adults and to determine whether the association was moderated by gender. Participants were 311,261 U.S. college students aged 18-25 years old who completed the American College Health Association’s National College Health Assessment II, which included questions regarding past 12-month self-reported emotional, physical, and sexual IPV and eating disorder diagnosis (anorexia nervosa or bulimia nervosa) by a health professional. Data were analyzed using chi-squared tests and logistic regression. Due to high correlations between IPV types, IPV was operationalized as a three category variable: experienced all three forms of IPV (emotional, physical, and sexual), experienced one or two forms of IPV, and no IPV. The prevalence of eating disorders was significantly greater among those reporting all three types of IPV (9.15%) compared with those reporting 1 or 2 types of IPV (3.17%), who in turn had a higher prevalence of eating disorders than college students who did not report IPV (omnibus p<.0001). There was a statistically significant interaction between male gender and IPV (p<.0001). Although IPV was significantly positively associated with eating disorders among both men and women, the association was much stronger in men than in women, especially in those who reported experiencing all three forms of IPV (among men: OR=4.21, 95% CI: 3.51-5.04 for 1-2 IPV types and OR=27.31, 95% CI: 20.31-36.72 for all types; among women: OR=2.07, 95% CI: 1.91-2.24 for 1-2 IPV types and OR=4.68, 95% CI: 3.77-5.82 for all types) compared with individuals who reported no IPV. Additional research to identify the mechanisms by which IPV and ED are related is needed to inform interventions, particularly among men.
An infant’s ability to fight infection is largely due to immune factors transferred to the child through its mother’s breast milk. One such factor is secretory IgA, which serves as a first line defense by entrapping pathogens within a mucus layer to prevent them from entering the intestinal tract. Understanding the cause for differential levels of maternal sIgA in populations can thus help to identify population’s whose infants are at greater risk of infection. Analysis of the differences in levels of sIgA can also help in understanding the relationship between environmental exposure levels, breast milk sIgA concentrations, and infant immunology. Previous studies have shown comparable sIgA concentrations between well-nourished and malnourished populations. Additionally, sIgA has a wide range of concentrations within individual groups with only a slight trend toward lower levels in poorer populations. The reasons behind this range and these differences have not been adequately studied. To measure sIgA concentrations among the sample populations we used an affinity binding plate with highly purified human sIgA. The wells were filled with milk samples and standards diluted with a phosphate buffered solution. SlgA antibody-enzyme conjugate was then added to the diluted samples and the tubes were incubated before the samples were added to the wells of the microtitre plate. After the plate was washed, tetramethylbenzidine was added followed by a stop solution. Finally the sIgA concentration of each sample was determined based on optical density. The results of the analysis showed that milk sIgA concentration was correlated with maternal and infant infection. SlgA concentration is higher in populations with increased rates of pathogen exposure. This shows that maternal immune status influences the levels of sIgA and thus helps confirm immunological protection to infants at risk of exposure.
Long non-coding RNAs (lncRNAs) are important in biological regulation and cellular homeostasis. Recently it has been shown that dysregulation of lncRNAs can lead to disease including tumorigenesis. In fact, several lncRNAs are crucial elements of cancer growth. The overarching goal is to identify new biomarkers in lung cancer as well as understand the mechanism of action of lncRNAs as a means to better understand lung cancer disease pathology.

Recently, the lab has identified lncRNAs as potential important candidates in lung cancer. To determine this list of novel lncRNAs in lung cancer publically available transcriptome sequencing data (RNA-Seq) was used to find previously undocumented lncRNAs. One of the top candidates with high expression in lung cancer is Lung Cancer Associated Transcript 45 (LCAT45). LCAT45 was PCR-amplified to obtain the full length to confirm the RNA-Seq data and for use in future functional studies. Cellular proliferation was decreased when LCAT45 was transiently knocked down with siRNA oligonucleotides. The next step in further elucidating the function of LCAT45 was to confirm an association with LCAT45 expression and ubiquitination processes. To do so, the proteasome was inhibited with the drug MG132 to monitor the effect of altered LCAT45 expression and the level of ubiquitinated proteins in the cell. Preliminary results show that with knockdown of LCAT45 there was a global decrease in ubiquitinated proteins indicating the importance of LCAT45 in the ubiquitin process. Analyzing publically available sequencing data across seven cancers reveals that LCAT45 is also significantly expressed in breast cancer tumors. Future directions will include further verifying the function of LCAT45 in breast cancer cell lines by repeating cellular proliferation assays and monitoring ubiquitination. This study is the first to identify the expression of LCAT45 in lung and breast cancer and the beginning of understanding a potentially important oncogene.
Toward a Better Understanding of...

GUATEMALA:
Weaving and Social Responsibility

Madeleine Docherty

Mentors: Robin Verhage-Abrams and Kedron Thomas

This research project was conducted in summer 2013 and consisted of spending two months in Guatemala studying Guatemalan textiles and socially responsible fashion. I visited Museo Ixchel, Guatemala’s premier weaving museum, and met with one of the museum’s associate researchers. I also apprenticed with a local weaver in San Juan La Laguna and learned the basics of the ancient process of Guatemalan weaving, a process that is still widely practiced today. Additionally, I worked with the production team of an organization called Mercado Global that partners with rural Guatemalan women to connect them with international markets and help them break the cycle of poverty. Through my research I have not only obtained inspiration for future fashion but, more importantly, I have obtained a more complete understanding of how to run and manage a socially responsible fashion business, a business I plan to pursue in the future.
In this project, sniper localization using a network of acoustic sensors was studied. Sensors can be worn by soldiers or placed on military vehicles to create a mobile sensor that detects gunshots. In urban settings, sensors can be placed in various locations along streets in order to detect gunfire and alert authorities. For this project, to determine the source of a shot, the time difference of arrival (TDOA) of the muzzle blast of the shot was measured. Then the maximum likelihood (ML) method was used to determine the most probable location of the shooter. A simulation model was developed in MATLAB to implement this muzzle blast model and generate results from the maximum likelihood method. Statistical analysis including the Cramér-Rao Bound (CRB) and the mean square error (MSE) was used to validate the accuracy of the results. The effects of changing sensor locations, the number of sensors, and noise levels were studied with the MATLAB simulation. The concept of detection was also studied and applied to the simulation. Results concluded that increasing the number of sensors and decreasing the noise level all led to more accurate results.
Music is an abstract collection of sounds organized in an aesthetically appealing manner. When listening to music, the artists’ intentions are less important and emotion is induced by interpretation of personal experience which varies from person to person. In other words, people have their own unique experiences when listening to music which provide almost no insight into the artists’ intentions. When a visual component is added, such as a music video, the artists’ intentions become clearer and the interpretations of individual listeners are more closely aligned with both the artists’ intentions and the interpretations of others.

In this project we look at the overlapping effects that film has on music. One specific example we will be using is *Interstella 5555: The 5tory of the 5ecret 5tar 5ystem* a House Musical film produced by the electronic group Daft Punk. This 2001 film was created in conjunction with the album *Discovery* and its storyline is divided into 14 segments that reflect the varying composition styles of each individual song on the album. The film constantly connects the animation to the emotions induced by the music. We feel that it correlates well with neurocinematic ideals and we show how the wide range of music interpretations are narrowed by the addition of a visual component.
Primary Ciliary Dyskinesia (PCD) encompasses any genetic disorder in which the cilia within the body function abnormally. Cilia move mucus and dirt out of the lungs, move cerebrospinal fluid in the brain, and more. When they do not function properly a variety of health problems can result. Observation of cultured cells from individuals with PCD has allowed clinicians to identify characteristics such as slower beat frequency, but we hypothesize that a more detailed analysis of cilia movement may better differentiate cilia abnormalities and lead to more effective treatment. Within this context, my objective is to discover whether or not Particle Image Velocimetry (PIV) can be applied to high-speed video recordings of beating cilia, in order to quantify the motion of cilia on clusters of cultured cells.

Digital PIV is a method of analyzing movement between images by splitting images into sections and matching image pixel intensity in each section with surrounding sections to create velocity vectors. The intensity on the edges of the cilia differs from that of the surroundings and the lengths of the cilia. For this research, videos of cilia beating obtained through high-speed video microscopy provided the movement analyzed with PIV. After modification, PIVlab 1.32, a MATLAB program, provided the velocity data.

PIV was successful in assigning quantitative values to the motion of cilia in a sequence of images. The velocity data shows a repeating waveform indicating that some form of periodicity is being captured by the analysis. However, it appears that more insight can be gained. The magnitude and periodicity of these values will be analyzed to determine the viability of the results from PIV. Other statistical techniques will be applied, and the data for wild type cilia will be compared to that of mutant cilia.
Development of various types of neurons in the retina requires precisely regulated gene expression, mediated by the coordinated actions of retinal-specific transcription factors and general epigenetic regulators. My research focuses on the epigenetic mechanisms that regulate retinal development in order to better understand how misregulation of gene expression leads to retinal disease. One type of general epigenetic regulator, histone methyltransferases, catalyzes the methylation of specific lysine residues on histone tails. MLL1 is one such methyltransferase, and catalyzes Histone H3 Lysine 4 methylation, which is associated with gene activation. MLL1 has been implicated in adult brain stem cell-mediated neurogenesis, tumorigenesis, and cell cycle regulation, but its function in the retina remains unknown. To determine whether MLL1 is necessary for retinal development and function, we conditionally knocked out Mll1 (CKO) function in retinal progenitor cells, and characterized the retinal phenotype using morphological and electrophysiological assays. Histological analysis showed that the normal three neuronal cell layers formed in the retinas of CKO mice, but that the thickness of each layer was reduced, particularly the inner nuclear layer, which drives visual signal processing. Consistent with this, electroretinograms of Mll1 CKO mice revealed defects in the ability of the retina to convert light stimuli into neuronal signals, resulting in a loss of vision. Gene expression studies of Mll1 CKO retinas revealed a significant loss of horizontal cells, which are an inner nuclear cell type critical for modulating photoreceptor signals, as well as a modest loss of amacrine, bipolar and ganglion cells. Thus, MLL1 appears essential for the development of retinal neuronal cell types that allow for proper visual processing, particularly in specifying horizontal cells, amacrine cells, bipolar cells and ganglion cells.
Toward a Better Understanding of…

Switzerland Right to Die

Vanessa Gravenor

Mentors: Rebecca Lester and Monika Weiss

The Right to Die has been a movement in Switzerland throughout the 20th and 21st century. However, as more and more countries elect to have laws that would grant patients assistance in death, the subject has become more and more controversial. I examined documents in the UN archive in Geneva, talked to select professionals in Switzerland, and examined the landscape of Switzerland as a site that offers a quick and painless death. The project didn't strive to form a moral judgment on the practice, but instead, analyzed the economic system where altruism is performed within the restraints of capitalism and the topography where human bodies cluster and then disappear. Throughout the course of research, I collected pamphlets, newspaper clippings, and articles. I reassembled them upon return to University and photographed them in the lighting studio.
Many musicians require an entire band’s involvement in order to effectively improve. Another fast way musicians can improve is by learning how to play or transcribe songs. This project is aimed at making it possible for a musician to play with a band and transcribe songs faster, thereby expediting improvement. The main goal is to take a prerecorded audio track — consisting of multiple instruments playing together — and separate it into several “stem” tracks of only one instrument each. The main attempt at this goal used non-negative matrix factorization, which factors a recording’s soundwaves (stored as a matrix of numbers) to split it up into single-instrument tracks. This attempt was ultimately fruitless. However, another technique, which involved finding peaks in the amplitudes of dominant pitches in recordings and isolating them, proved to be more robust. While this technique has its fair share of shortcomings, it can separate different sounds and store them on separate tracks. Perhaps by adding functionality to this method, we may be able to create an algorithm that separates a recording into separate tracks accurately and can identify the instruments in this recording.
The C-terminal Linker of FtsZ Acts as an Intrinsically Disordered Peptide during Cell Division in *Bacillus subtilis*

Steven Grigsby

Mentor: Petra Levin

The bacterial tubulin homologue FtsZ polymerizes *in vitro* in a GTP-dependent manner to form long, single stranded filaments. In cells, these filaments assemble into loose bundles at the future division site to form the contractile Z ring, which serves as the scaffold for the rest of the division machinery. FtsZ consists of three primary structural domains: the N-terminal globular core that contains the GTP binding site, a variable and flexible C-terminal linker (CTL), and a conserved region at the C-terminus required for interaction with modulatory proteins known as the grappling hook peptide (GHP). Recently, we have shown that the CTL behaves as a flexible intrinsically disordered peptide (IDP) and is required for proper FtsZ assembly *in vitro* and function *in vivo*.

To gain insight into the role the CTL in FtsZ assembly, I am testing the structural parameters that define a functional CTL. Using computational predictions, six CTL variants were generated in the context of native FtsZ: CTLV2, CTLV4, CTLV7, CTLV8, CTLV9, and CTLV10. By changing the order and patterning of charged residues in the IDP sequence, these variants undertake either a more extended conformation or a non-globular conformation with hairpin-like structures. I am using immunofluorescence microscopy, growth curves, and plating assays to characterize the impact of these variants on FtsZ ring formation *in vivo* and light scattering and GTPase assays and electron microscopy to characterize the impact of these variants on FtsZ polymerization *in vitro*. The data collected so far suggests that the CTL can tolerate a range of conformations, but linkers that are much more flexible or much more rigid than wild type have significant defects *in vivo*. 
Toward a Better Understanding of...

**Autophagy Induction Promotes Uropathogenic *Escherichia coli* to Persist in the Urinary Tract**

*Amanda Harris*

*Mentor: Indira Mysorekar*

Uropathogenic *E. coli* (UPEC), the major cause of urinary tract infections, establish quiescent intracellular bacterial reservoirs (QIRs). These latent reservoirs, which persist indefinitely, are refractory to antibiotic therapies and can induce recurrence. Autophagy is a cellular degradation process that can eliminate intracellular pathogens by delivering them to lysosomes for destruction. We have shown that deficiency of an important autophagy protein, ATG16L1, leads to a dramatic reduction of QIR formation and defects in the recycling of intracellular membranes of urothelial cells. We further show that this phenotype is urothelium intrinsic and not governed by the immune system. It is recapitulated in mice deficient for another key autophagy protein, ATG7, suggesting that UPEC depend on a functional, canonical autophagy program to be engulfed within autophagosomes and persist. Induction of autophagy in a human bladder cell line increased UPEC intracellular bacterial load. In contrast, knockdown of ATG16L1 reduced the number of intracellular UPEC. Together, our data suggest that UPEC co-opts the autophagy pathway to promote persistence.
Elucidation of the Role of $\sigma^X$-Partner Protein ComW in the Competence Pathway of Streptococcus pneumoniae

Gregory Harrison

Mentor: Donald Morrison, University of Illinois at Chicago

Streptococcus pneumoniae naturally supports the molecular machinery that allows for genetic transformation. Competence is regulated through quorum sensing by the bacterial pheromone competence-stimulating peptide (CSP). The CSP pathway induces expression of several genes, including comW, of unknown function, and comX, which encodes the alternative sigma factor $\sigma^X$ required for competence. In a comW knockout strain ($\Delta$comW), transformation efficiency compared to wild type (WT) is approximately zero: $\sim$1 in 1000. There is some evidence that ComW may act to protect or stabilize ComX. In order to identify potential mechanisms by which ComW functions as a pro-sigma factor, spontaneous mutants were generated in the □comW strain, and mutants that had restored competence in the absence of ComW were enriched through three rounds of transformation with antibiotic resistance markers. After enrichment, it was found that 60% of the recovered mutants transformed at 1-40% of the WT transformation efficiency, indicating that these strains may carry $\Delta$comW suppressor mutations. The best performing mutants were sequenced, and the sequence data indicated that strains with the greatest transformation frequency carried point mutations in one or more of the following genes: GeneA, tmk, aliA, and an uncharacterized putative CAAX protease. Further analysis of these potential suppressor mutations may point to a mechanism by which ComW acts to facilitate genetic transformation.
Since the national controversy over the Oakland School Board resolution in 1996, Ebonics has largely been absent from the conversation about elementary education. Often misunderstood to be a mandate for Ebonics (a term coined and described by Dr. Robert L. Williams otherwise known as African-American Vernacular English) to be taught in the classroom, the Board actually acknowledged that Ebonics-speaking students deserve more affirming Standard English education. The national achievement gap and relatively high special education rates for black students, however, have hardly diminished over the last 18 years. Furthermore, a renewed dialogue concerning Ebonics suggests that reexamining the issues is as relevant as it has ever been. This project investigates the current role of Ebonics in education as it relates to linguistics, politics, and African-American culture. Broadly, political precedence and experts in the field of education openly encourage comprehensive bidialectal education policies (recognizing the legitimacy of more than one dialect while teaching Standard English) that have been previously proven effective. In sharp contrast, the ubiquitous stigma against the dialect continues to undermine the achievement of Ebonics-speaking students, despite the essential role elementary education plays in an individual’s future opportunities. Public education continues to systematically undererve Ebonics-speaking students in this country. This failure has implications for African-American education, socio-economic development, and culture; change is not only an ethical imperative, but also a political necessity in a nation still struggling to guarantee civil rights for all citizens. Evidence for the role of language in culture is not controversial, but few school districts have implemented solutions, which include teacher education, differentiated strategies, and affirming cultural competency to combat prejudice.
Robotic bin picking is a process where a robot acquires a part from a bin, orients it properly and places it in a different place. In the field of robotics, this has traditionally been a challenging problem. Parts can overlap with each other, objects need to be recognized in 3D space and the whole process needs to be fast and accurate. Bin picking has enormous implications in industries where sorting parts to feed a robot is mostly done by people. Here, we have tried to use a single Kinect sensor as a 3D imaging system and use the data to control and operate a robotic arm. The Kinect sensor is able to record an image along with the depth value of every pixel. By fixing the position of the Kinect and calibrating the robot, it is possible to create a transformation matrix which allows us to transform the Kinect coordinates to the robot coordinates. Using the transformation matrix, we then use the image recorded by the Kinect to create a 3-D model of the given environment. The 3D model can subsequently be used for pattern matching of a 3D object and to develop an efficient path for the robot to take. Using our system, we have been able to accurately control the robot by interacting with it through the Kinect data. We have also been able to create a basic 3D model.
Toward a Better Understanding of...

**Merger Hydrodynamics in the Luminous Galaxy Cluster RXJ1347.5-1145**

*Christina Kreisch*

*Mentor: Marie Machacek*

Studying the distribution of large-scale structure in the universe offers a tool to constrain the dark energy equation of state. In galaxy cluster mergers, cluster gas deviates from hydrostatic equilibrium. It is imperative that we understand the cluster's merging history when measuring its mass so that we do not incorrectly use calculations that assume hydrostatic equilibrium. We present deep (186 ks) *Chandra* X-ray observations of baryonic gas hydrodynamics in the merging galaxy cluster RXJ1347.5-1145, a cool-core cluster at a redshift of 0.451. We find that the X-ray brightness distribution reveals cold fronts to the west, south, and east of the primary cluster's cD galaxy. Cold fronts are characterized by gas that is low in temperature, entropy, and pressure. The cold fronts form a spiral that is characteristic of gas sloshing induced by a merger in the plane of the sky. We identify 2 edges in the X-ray surface brightness, forming a Mach cone. The maximum Sunyaev-Zel’dovich decrement and high temperatures lie on the western edge, indicating it is a shock front. We model the density across the eastern shock feature, and use the Rankine-Hugoniot conditions to determine the Mach number and velocity of the shock. The Mach cone and excess X-ray emission associated with the subcluster gas are displaced to the south of the subcluster’s central cD galaxy, suggesting that the subcluster gas has been stripped. The elongated, nonhomogenous entropy contours and low temperature over the subcluster suggest core shredding upon impact as gas is pushed in a tail-like structure to the southwest. We measure the X-ray luminosity of the subcluster gas, and use scaling relations to place a lower bound on the subcluster’s total mass.
Children of mothers with a history of major depressive disorder (MDD) are three times more likely to have depression than children of non-depressed mothers, suggesting maternal MDD is a major risk factor for depression. Additionally, mothers with a history of MDD tend to show a bias towards over-reporting their child’s behavioral problems relative to their child’s self report, a bias not found in non-depressed mothers/children. However, it is unclear whether the mother’s history of depressive symptoms is what causes this bias or if other factors such as current depressive symptoms/hedonic capacity are responsible for the differences in reporting.

A sample of mothers and 7-11-year-old children were drawn from the St. Louis community (25 healthy mothers; 14 mothers with MDD). Mother and child filled out a series of questionnaires about the child measuring depressive symptoms and hedonic capacity. The mothers also filled out questionnaires about themselves, such as Beck’s Depression Inventory and the Snaith-Hamilton Pleasure Scale.

A repeated-measures ANOVA and post-hoc regression analyses were conducted in order to test effects of reporter (mother- vs. child-report), depression risk (maternal history of depression or not), maternal depressive symptoms, and maternal hedonic capacity on ratings of child depressive symptoms. There was a significant main effect of both mothers’ current depressive symptoms and hedonic capacity, and an interaction of reporter with mother’s current depressive symptoms (trend).

The results of this study demonstrate that mother’s current depressive symptomology positively and hedonic capacity negatively predicts the child’s depressive symptoms reported by both the mother and child (showing a stronger relationship between BDI scores and parent report than child report). Importantly, discrepancies in reports of child symptomology related to the mother’s current depressive symptoms rather than her history of psychopathology.
Prenatal malnutrition and anemia, risk factors for several negative health outcomes like infectious disease, premature birth, and low birth weight, are extremely common and preventable issues faced by poor expecting mothers in India. This study draws from a month of clinical shadowing and health counselling within the OB/GYN wards of Niloufer Hospital for Women and Children in Hyderabad, a government hospital that serves the urban poor. This study examines how social and clinical attitudes of government medical providers towards poor mothers determine their understanding and treatment of prenatal and postpartum malnutrition. Nation-states have historically staked agendas of “progress” upon the bodies and behaviors of mothers. The construction of poor south Indian mothers as “backward” operates within a development discourse that may have a negative impact on patient attitudes and compliance. I suggest avenues of future empirical research that prioritize the lived experiences of lower-class women and provide alternative discourses to those endorsed by government medical institutions in Hyderabad.
The Hypothetical Presidency: The Social and Political Reflections of The West Wing on the Presidencies of Clinton and Bush

Evan Linden

The West Wing was a staple of late 1990s and early 2000s television programming. While it was certainly an entertaining program, it was a multiple season case study of the American government, dissecting the Presidencies of both Clinton and Bush. The show aired at a time filled with political tumult (domestically and internationally), national tragedy and technological improvements. From the show’s conception in 1999 to its end in 2006, it existed on a parallel timeline to the events going on in actual American politics and popular culture while serving as a third party narration for many of these events.

It is important to explore The West Wing as a cultural text because it was the first show of its kind directly reenacting the Presidency in a predominantly accurate manner. It was revealing of the time period that occurred when it aired as well as presenting creator Aaron Sorkin’s liberal fantasy of what America could potentially look like under slightly different circumstances, decisions and most importantly, a different leader. His construction of the character, President Josiah Bartlet is indicative of the qualities, background and leadership style Sorkin deemed most crucial for a leader of America. It appears the show was successful because viewers enjoyed having a parallel political universe where American triumphs were magnified and consequences of failures were minimized.

In this work, I explore the “false reality” Sorkin created and debate whether or not this ideal image of the country was beneficial or harmful in that time. I also discuss the parallels between the Presidencies of Clinton/Bush and Bartlet as well as their significance in this period of time.
When Does Empathy Matter?
How to Best Evoke Empathetic Responses in Public Service Announcements (PSAs)

Michael Bogatto Lory

Mentor: Fritz Breithaupt, Indiana University

Public service announcements (PSAs) are formal informational advertisements whose main goal is to prevent or encourage certain actions. From a marketing standpoint, PSAs face a dilemma in that they can be ineffective at conveying their message through either flat emotions, or by overindulging the audience with fear and emotion appeals. We reason that the most effective PSAs are somewhere in the middle and evoke empathy.

This pilot study seeks to determine boundaries for empathy and discover the most effective way to get the audience to empathize with the PSA and comply with the stated objective. We gathered data through surveying 200 individuals; each received 3 PSAs (discouraging of texting and driving, discouraging bullying, and encouraging aiding environmental causes) to test their level of empathy with the people in the message and their consequent attunement to the message. Identifiable victims and perpetrators created 7 unique scenarios within each PSA tested: statistical information, victim with a positive outlook, victim with a negative outlook, 3rd person on behalf of the victim, perpetrator repenting, perpetrator self-focusing, and 3rd person on behalf of the perpetrator. By randomly assigning 21 unique PSAs, this test will uncover which style of advertisement is most effective at evoking empathy in a PSA setting.

The goal is to be able to use the information to not only apply this type of advertisement to PSAs that have victims and perpetrators, but to all forms of PSAs, and possibly various forms of commercial advertisements as well. Since empathy and marketing have a close niche to one another, this study creates a layout going forward for marketers to know how and why certain emotion-appeals work and others fall flat.
We as humans draw upon physical experience to enrich communication through the use of metaphor. In general, as formulated by Lakoff and Johnson, metaphor arises from the use of language from one more concrete & physical domain to enhance understanding of a concept from another more abstract domain. While many metaphors are culture-specific, such as TIME AS RESOURCE and ARGUMENT AS WAR, some have more universal groundings in physiological experiences of space and emotion. Metaphors concerning UP-DOWN, IN-OUT, and NEAR-FAR dualities are more stable across cultures because they are rooted in basic embodied experiences of space; however, they contain variation in how these physical experiences are mapped onto abstract concepts. For example, English conceptualizes the past as being behind us while Aymaran conceptualizes it as in front of us. Metaphors plausible to have stronger universal grounding are those that involve emotion and temperature such as WARMTH AS AFFECTION and COLD AS FEAR because the presence of these emotions and specific physiological reactions are known to correlate. For this reason, in this research I examine the stability of conceptual metaphors of emotion across a set of diverse languages, namely Finnish, Russian, Tibetan, Mandarin, Hawaiian, Dyirbal, Tok Pisin, Standard Arabic, Swahili, Yu’pik, and Ayacucho Quechua.
Macrophage dysfunction in obesity and diabetes may predispose individuals to the
development of diabetic complications, such as infection and impaired healing after
tissue damage. Excess saturated fatty acids, such as palmitate, are present in patients
with metabolic disease and may contribute to the pathogenesis of diabetes and its
sequelae. However, the exact mechanism behind the imbalance in lipid uptake and
lipid metabolism is unclear. Here, we identify the nuclear membrane receptor, PPARγ,
as a potential mediator of the lipotoxic environment that leads to macrophage
dysfunction. The activation of PPARγ in normal individuals during infection or injury
leads to resolution of inflammation, but induces persistent inflammation in individuals
with metabolic disease. Using a PPARγ deficient mouse model, we found that the
PPARγ deficient mice with an excess lipid environment had less expression of PPARγ
and associated genes, and were partially rescued from cell death. Our results suggests
PPARγ knockdown as a candidate for therapeutic use in the future for patients with
metabolic disease.
Electrocardiograms (ECGs) are commonly used to analyze heart rhythms and electrophysiology in mouse models of cardiovascular disease. Currently, several techniques are employed for recording in vivo ECGs, including anesthesia-aided ECGs, implantable telemetric devices, and surface paw recordings in restrained mice. However, these methods suffer from important drawbacks. Only surface paw ECGs allow for non-invasive recording in unanesthetized animals, but these recordings often suffer from increased noise (including motion and breathing artifacts) and sympathetic effects on heart rate. Thus, we aimed to develop a novel device for recording mouse ECGs. A custom mouse ECG suit (mECGs) was fitted with recording electrodes, which contact the ventral torso. The performance of the current design was tested relative to a surface paw recording device, the ecgTUNNEL (emka Technologies). Four mice underwent recordings using both methods and signal-to-noise ratio (SNR) was calculated for each recording. The mECGs outperformed the ecgTUNNEL in 3 of the 4 mice tested, with SNR being higher for the suit in those three mice. Relative to the ecgTUNNEL, we identified a trend of increased SNR (average SNR for the suit was 1.16-fold greater, p = 0.101), significantly less baseline drift, and fewer motion artifacts. Currently, our mECGs method offers recordings equivalent to the ecgTUNNEL, with a trend toward outperformance of the tunnel. With ongoing design modifications including the use of 3D printing, we expect the mECGs to surpass the ecgTUNNEL. Additionally, the suit has the potential to collect ECGs without interrupting normal behavior or sympathetic tone of the mouse. Future plans include combining the suit with wireless data transmission to allow the mice more freedom of motion. Our mouse ECG suit will greatly improve the collection of ECGs for the investigation of mouse models of cardiac rhythm disorders.
This project is a critical analysis of Philip Roth’s novella, *Goodbye Columbus*. The Jewish-American community furiously criticized Roth’s novella for negatively portraying the new upwardly mobile Jewish-American community, going as far as to call Roth an Anti-Semite. In order to understand what Roth was truly trying to accomplish in writing *Goodbye Columbus*, I read personal interviews with Roth and books written about his work, but my main source was the text itself. The novella portrays the complex demographic and cultural shifts within the Jewish population, and Roth demonstrates how the development of a Jewish-American identity is both painful and comically paradoxical because Jewish traditions often intersect with the American ideals of upward mobility.

Roth represents the divided identities of Jewish-American through the consumption of food; he uses food as an index and signifier of the degree to which different groups within the Jewish community are assimilated. Differences in food practices illuminate the huge gap between the new, upwardly mobile Jewish-American community and the old traditional community. Roth questions whether a combined Jewish-American identity, one that fully retains the American and the Jewish, is possible. Although there is no concrete resolution to the Jewish-American identity crisis in *Goodbye Columbus*, Roth accomplishes the important task of heightening awareness about the growing gap between the traditional urban Jews and the assimilated suburban Jews of America.
Since the advent of combinatorial antiretroviral therapy (ART), the lives of HIV-positive patients have been significantly prolonged and improved. However, despite the success of ART, drug-free remission has not yet been achieved. HIV can still be recovered from resting T cells of HIV-suppressed patients, and the virus almost inevitably rebounds if ART treatment is stopped or interrupted. Research into histone deacetylase inhibitors (HDACIs) focuses on using epigenetics to force latently infected cells to express the HIV provirus integrated into their genome, whereupon they can be identified, targeted, and eradicated. HDACIs have shown efficacy in activating expression of HIV in cell cultures, and positive results from clinical studies with vorinostat (SAHA) provide proof of principle. However, potential toxicity in any epigenetic therapeutic remains a problem and the use of non-specific modulators of gene expression (all current HDACIs) results in adverse side effects. We are involved in a project focusing on the development of HDACIs that have a high specificity for individual HDAC isoforms as one component for treatment and eradication of HIV infection. Using computational models for virtual screening, several compounds were identified as plausible candidates for isoform-specific inhibition of HDACs and subsequently synthesized. I performed a study of these compounds in J-LAT 10.6 cells (Jurkat cells virally infected with an HIV/GFP construct) as an in vitro model to be compared to the computational model. The screen consisted of an overnight triplicate trial at 0.1, 1, 10, and 100 μM concentrations, toxicity assays at those concentrations, and a dose-response curve about the concentration of greatest effect to determine the EC50. The effect of an HDACI was reported by the amount of HIV-GFP transcribed, determined by flow cytometry. Of the original candidates, nine proved potent inhibitors of HDACs.
Toward a Better Understanding of…

Collecting Comfort: Exploring Disney’s Mickey Mouse and the Firefighter Lapel Pin

Madison Perry

Mentor: Heidi Kolk

This project offers an analysis of an object, the Mickey Mouse and the Firefighter lapel pin, produced by Disney. The pin belongs to a category of kitsch and collecting culture from the aftermath of the September 11th attacks. After September 11th, 2001, Americans sought comfort and security from a variety of sources. One of these sources of comfort was found in consumerism. Americans were encouraged to buy, and to do so was increasingly viewed as an act of patriotism. One of the central questions that this project addresses is whether collecting culture is a legitimate form of therapy, patriotism, and participation in consumer culture. I seek to understand the implications of purchasing and collecting such an item as the pin, and offer a few forecasted implications that these acts may have on American culture.
Detection of P-aminophenylphosphate through an Alkaline Phosphatase-Linked Immunosorbent Assay Made with a Self-Assembled Monolayer on Nanoporous Gold and Flat Gold as the Solid Surfaces

Mythili Ramachandran

Nanoporous Gold (NPG) was used to immobilize a self-assembled monolayer (SAM) containing triethylene glycol and galactose on a wire through the formation of thiol bonds. This SAM allowed for binding of the lectin-enzyme complex, peanut arachis hypogaea-alkaline phosphatase respectively, to the NPG wire. Alkaline phosphatase catalyzes the reaction of P-aminophenylphosphate (PAPP) to P-aminophenyl (PAP), which was then measured using square wave voltammetry. This assay allows for the important application of using PAP as an early diagnostic indicator for Down syndrome in fetuses and as a model for more electrochemical assays.
Anhedonia, the inability to experience pleasure, is a key component of depression that has been examined via different experimental modalities in animal and human studies. The Progressive Ratio Task (PRT), a task requiring repeated action to obtain a small reward, is commonly used to assess anhedonia in animals, but has not been widely utilized in humans. Understanding how PRT behavior relates to anhedonia/depression in human populations would help to assess how motivation varies within healthy and clinical populations and provide an important link between human and animal literatures. In the current study a large young adult sample completed a version of the PRT along with questionnaires assessing depression and anhedonia. During the PRT, participants pressed a spacebar an increasing number of times to earn a reward. The first reward required twenty presses, the second required 40 presses, and so on. Participants were informed that they could play the game for as long as they wanted, up to 15 minutes. Data were analyzed only from participants who quit the task prior to 15 minutes, to hone in on individual differences without the ceiling effect. Task performance variables included time spent on task, median reaction time, and the amount of time it took to decide to quit. Participants reporting a history of depression spent less time on the task, and took more time to decide to quit the task. Anhedonic depression symptomology negatively correlated with time spent on the task. These results show that participants with history of depression and relatively elevated anhedonic depressive symptoms are less motivated to expend effort for rewards, and may have difficulty weighing the pros and cons of continuing the task. These findings provide an important link between human and animal literatures, supporting this task’s ability to assess motivation/anhedonia across species.
Neutron stars, along with other compact matter, are some of the most stable structures in the universe. Their stability can be disrupted, however, by radial oscillations, which may cause them to collapse into black holes. John Bardeen, in his *Catalogue of Methods*, detailed two methods by which we can determine the stability of compact stars for a given equation of state: direct calculation of the oscillation frequency or a qualitative examination of a mass-radius plot. These two methods were believed to agree until Glendenning et al. proposed the existence of a white dwarf with a strange quark core. We observed that Glendenning’s white dwarf showed disagreement between Bardeen’s methods. With this motivation, we examined the stability of a similar family of stars: hybrid neutron stars, which contain a quark matter core surrounded by a nuclear matter envelope. The equations of state for such stars exhibit either a kink or discontinuity. By reproducing the calculations of these methods, we observed that Bardeen’s methods do not agree for these stars as well. We are currently determining the cause of this discrepancy.
Major Depressive Disorder (MDD) is an extremely debilitating disorder with respect to physical, psychological, and emotional functioning. However, impairment in people with MDD may vary drastically based on the cluster of symptoms that people exhibit and the severity of those symptoms. The present study examines the relationship between the two gateway symptoms for diagnosis of MDD, anhedonia and depressed mood, and emotional reactivity within a large non-clinical sample. To this end, participants (N=105) were asked to complete an Emotional Picture Rating Task (EPRT). The EPRT required participants to rate the valence and arousal level of their emotional response to 100 pictures (40 negative, 20 neutral, and 40 positive pictures) from the International Affective Picture System. In addition, participants completed self-report questionnaires used to assess levels of hedonic capacity, general affect, and depressive symptomology. We found that elevated levels of anhedonia (i.e. decreased hedonic capacity) predicted blunted emotional reactivity to both positive and negative pictures, while elevated depressive symptoms predicted potentiated negative emotional reactivity to negative pictures. These findings are consistent with current literature that suggests that MDD affects emotional processing, but suggests that different symptoms affect emotional processing in different ways. These findings could suggest that treatment of MDD should be approached at a symptomatic level rather than at a generalized level.
This study tests a novel training paradigm for individuals with anomic aphasia. The study has a multiple baseline design, with 3 lists of counterbalanced words to be learned within 3 distinct conditions. The study presents the results of a single participant in a case study format. The participant had two baseline probes of the trained words, trained 4 times a week for three weeks, and then had a one week follow-up test. During training, the participant attempted to learn each list of words in either a no variability, talker variability, or referent token variability condition. The no variability condition was used as a control. The talker variability and referent token variability conditions were designed as phonologically oriented training and semantically oriented training, respectively. In the variability conditions, the talkers were varied across trials or the referent tokens (pictures) depicting the target item varied across trials. The results preliminarily suggest that the participant learned best in the no variability condition. The possibility that consistent input may be better for recovery in severe anomia is discussed, along with limitations of the current study and avenues for future research.
A novel method has been developed to determine a distribution of binding distances in the HIV Tat/TAR initiation complex. To obtain a better biophysical understanding of this protein-RNA complex, a spin-labeled nitroxide residue was synthesized which was then inserted into a Tat peptide mimic using novel flexizyme methodology. With the insertion of a second spin label in the TAR RNA, a distribution of possible distances was found using Double-Electron-Electron-Resonance, done previously using SDSL cys spin labels. However, given the flexibility of the SDSL label, the use of a nitroxide bond residue gives a more accurate distance distribution. Precise distances of binding modes allow for more accurate computational modeling (using the AMOEBA force field) and development of future anti-HIV therapeutics. This method can also be applied to various other protein systems for studies in molecular recognition.
Email has become one of the most important forms of communication. In 2013, there were about 180 billion emails sent per day worldwide and 65% of the emails sent were spam emails. Links in spam emails may lead to users to websites with malware or phishing schemes. Therefore, an effective spam filtering technology is a significant contribution to the sustainability of the cyberspace and to our society. Machine learning, a branch of artificial intelligence in which a system can generalize from experience, is a viable option for spam detection. A machine learning system could be trained to distinguish spam emails from non-spam emails by learning from past data to determine similarities or significant features in emails. After learning, this system is able to classify future emails as spam or non-spam. The goal of this project is to analyze popular methods in machine learning to discover which techniques work best in email spam detection.
Despite rapidly growing interest in harnessing energy from various unconventional renewable sources in recent decades, coal, along with other conventional fossil sources of energy, remains significant in global energy generation. With the goal of reducing pollutants and boasting energy production efficiency of coal-based processes, in this project, I sought to advance coal-based combustion technology development, which was focused particularly on 1) spray technology for Coal-Water Slurry Fuel (CWSF), 2) coal-biomass co-firing experimentation under oxy-fuel conditions, and the design of associated equipment. In addition, a literature survey of previous studies on a novel coal-biomass slurry fuel was conducted to examine its feasibility. Preliminary experimental results were obtained for the coal-biomass co-firing studies. Though the CWSF project is still largely in progress, I have been able to amass, design and manufacture the required experimental equipment, and am ready to move on to the next step – the characterization of CWSF flame in “Junior”, a cylindrical, horizontally-fired 30 kWth combustor with a 14 cm x 78 cm combustion section, followed by a 37 cm x 120 cm burnout section. Subbituminous Powder River Basin (PRB) coal was used in these studies.
Globalization has had an extreme, negative effect on the world’s food security – the equal availability, access, and use of nutritious foods. People are dependent on a few multi-national corporations to provide cheap, low quality food that is harmful to human health and the environment. To combat this problem, a local food movement is emerging. Farmers’ markets provide local, fresh, sustainable food that supports local businesses, the community, human health, and the environment. In Melbourne, the farmers’ market scene is prominent and in the midst of rapid growth as its popularity increases. In this study I examined how Melbourne’s farmers’ markets influence food security and how the markets can be improved to do so.

I observed four different farmers’ markets to analyze the community, market atmosphere, and to observe the food supply and management. Additionally, I volunteered at a few farmers’ markets to understand how they are run. I interviewed a total of 14 people, including stallholders, consumers, market managers, and an executive officer of a farmers’ market association. I surveyed 56 community members to gather data about their commitment to farmers’ markets, demographics, and impact of the markets on their food supply.

I discovered that farmers’ markets need to improve in location, frequency, and awareness. The ideal market scene contains a collection of small, neighborhood markets scattered across the city that are easy to access. Additionally, to provide for the best food security, the markets need to be more available so that consumers become reliant on the markets rather than the corporations. Finally, education is key to expanding the customer base. As more people realize how the benefits of farmers’ markets far outweigh the costs, the local food movement will grow to provide for better food security.
Toward a Better Understanding of...

**Design and Optimization of Lysine Deacetylase Inhibitors using Various In Vitro and Computational Approaches**

*Richard Brewster Wickersham III*

*Mentor: Garland R. Marshall*

Acetylation is one of the most prominent post-translational modifications in biochemistry, affecting over 1,500 proteins in the cell and playing a major role in epigenetics and gene expression through regulated histone acetylation. Lysine deacetylase (KDAC) is one of two enzymes which control this dynamic acetylation, which is correlated with a number of diseases including HIV latency and parasitic infection. Thus, inhibition of KDAC is a powerful potential therapeutic target. However, there are 11 Zn-based isoforms of human KDAC (and other isoforms in other organisms), and current KDAC inhibitors (KDACi) lack specificity for the different isoforms, a characteristic necessary for mitigating side effects and targeting only non-human KDACs. Here we describe a methodology for developing isoform-specific KDACis, using human KDAC8, *Schistisoma mansoni* KDAC (smKDAC), and *Plasmodium falciparum* KDAC (pfKDAC) as test cases. Using a variety of virtual screening methodologies, multiple sets of known and potential KDACis were screened for activity against various KDAC isoforms for specificity. Compounds which were predicted to have high binding affinities in general or specifically for one or more isoforms were then tested *in vitro* against various isoforms. These data were then used to create computational models of KDAC8 and smKDAC in relation to the other isoforms. These models will allow us to identify chemical features that increase binding affinity for individual isoforms, providing powerful information for the synthesis of inhibitors specific for only that isoform. It remains inconclusive whether the specificity gap between the target isoform and the other isoforms can be broadened enough to be therapeutically relevant, but these models provide the necessary information required for future development.
We seek to understand how the physics of morphogenesis modulates environmental effects on development. Here we ask how salinity affects the sensitivity of sand dollar (*Dendraster excentricus*) embryos to inducers of exogastrulation, a defect in which the archenteron evaginates rather than invaginates. Salinity variation is common in near-shore marine environments and has a clear physical effect: swelling or shrinking cells. We hypothesized that if the apical extracellular matrix resists cell swelling, the pressure inside the embryo will rise, promoting archenteron evagination. However, if the blastocoel matrix resists embryo expansion, the pressure will drop, promoting invagination. If neither the blastocoel nor apical matrix resists embryo expansion, the internal pressure will not change, so salinity should not affect sensitivity to exogastrulation. Exogastrulation can be induced by many treatments. We used low calcium (10% of normal) artificial seawater as an inducer because it is non-toxic. We compared its effects in normal (32 ppt) and low (25 ppt) salinity, a range that *Dendraster* embryos can experience in nature. Low salinity alone did not cause exogastrulation, and low salinity did not reduce exogastrulation frequency when in a low calcium environment. The similarity of blastocoel to cell volume ratio among treatments, combined with gross similarity in blastula shapes, suggests that the internal pressure did not change greatly. While further quantitative analysis is necessary, this is inconsistent with predictions for the hypothesis that the blastocoel matrix resists embryo expansion. We cannot rule out the hypothesis that salinity increased the frequency of exogastrulation, but we tentatively suggest that any increase is not due to internal pressure changes.
The Effect of Relationship Satisfaction on One’s Reaction to Relevant Pictorial Stimuli

Xueer Sherry Yu

Mentor: Sara Estle

Previous research and everyday experiences have suggested that pictures have a strong effect on viewers’ moods. Nitschke et al. demonstrated that this effect is innate to human beings by showing the effects in infants, and Pinhas et al. and Babin and Burns have found the effect salient across situations. However, few studies have looked at how participants with different dispositions respond to the same stimuli, a question this research attempts to investigate. Participants were first instructed to fill out a survey measuring their relationship satisfaction, and then they were randomly assigned to view twenty pictures of natural scenes or positive relationships, before being instructed to complete a mood scale. The results suggested an interaction between participants’ relationship satisfaction and the kind of stimuli they see. Findings may help corporations design marketing strategies, and have implications for interpersonal communication, advocacy and social interactions.
The logo for the Office of Undergraduate Research, on the front cover of this publication, consists of an “impossible triangle” within a starburst. To some, the triangle evokes the challenge of puzzles to be solved or the eternal research question “How does that work?” To others, the triangle represents the Greek letter ∆, the mathematical symbol for change.

WUURD, the Washington University Undergraduate Research Digest, is published by the Office of Undergraduate Research once a semester each academic year.

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The Office of Undergraduate Research is funded by the College of Arts & Sciences.

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