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WASHINGTON UNIVERSITY

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[FEATURE ARTICLES]

The Three Delays Revisited:
Barriers to Maternal and Infant Health in Iganga, Uganda
Victoria Collins

“No Man’s Land”:
Missing Voices in the Anglophone Canon of Russian Literature
Hilah Kohen

Cultivating Community:
Towards a Black Women-Centered Alternative Food Politic
Sally Rifkin

[SUMMARIES OF STUDENT WORK]

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The primary requirement for inclusion in the Digest is that a paper represent research—contribution of new knowledge through data collection and original source analysis. Students need not be seniors, or receiving honors, or have been funded by our office. Work need not be performed here at Washington University. Work need not be prepared alone; in fact, because research involves working with others, we anticipate including much collaborative work in these pages.

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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 Δ , the mathematical symbol for change.



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FOREWORD

Undergraduate students at Washington University in St. Louis engage in research in a wide variety of disciplines and fields of study. Mentored by dedicated faculty, students conduct research that may lead to solutions to many of today's pressing social problems, to new interpretations of the past, and to the creation of new knowledge. In many cases, students' research may even lead to new questions to be studied by future investigators.

Of the students whose work is contained in this volume of the *Washington University Undergraduate Research Digest*, some conducted research in St. Louis while others traveled abroad. They worked over the summer and into the school year. They spent hours in the field, in laboratories, and in libraries, collecting, analyzing, and interpreting data. They have written theses, published papers, and presented findings. Consider the work of the authors of our feature articles:

Victoria Collins explores why current public health initiatives to reduce high maternal and infant mortality in Uganda have failed. Her work asks why delivery rates remain low in professionally staffed health care facilities despite efforts to promote their usage.

Hilah Kohen analyzes how a variety of circumstances of a text's production and distribution prevented contemporary Russian writers from gaining a readership in English in the early twentieth century, even as their nineteenth-century predecessors rapidly gained popularity.

Sally Rifkin examines the motivations, successes, and challenges of two food justice organizations in St. Louis, Missouri, both of which were started and are sustained by Black women, focusing her research on particular ways in which Black women mobilize around food issues, challenging the notion that women's food work is apolitical.

The students who wrote the following feature articles and abstracts could not have conducted their research without dedicated faculty mentors, to whom we owe a debt of gratitude. We also gratefully acknowledge the work of the Peer Review Board in carefully editing our feature articles. Finally, we invite you to enter the world of research at Washington University and become inspired by the works herein.

Respectfully,

A handwritten signature in black ink, reading "Lindsey Paunovich". The script is fluid and cursive, with the first name "Lindsey" written in a larger, more prominent style than the last name "Paunovich".

LINDSEY PAUNOVICH

Editor



THE THREE DELAYS REVISITED: BARRIERS TO MATERNAL AND INFANT HEALTH IN IGANGA, UGANDA

Author:

Victoria Collins

Victoria is a rising senior in the College of Arts & Sciences majoring in Anthropology with a minor in Psychology. In 2017, she received a Student Undergraduate Research Award to study maternal and infant health in Iganga, Uganda, under the guidance of Dr. Shanti Parikh. Victoria aspires to promote equity in health through evidence-based models. She intends to complete her senior honors thesis on adolescent perspectives on tobacco use in the upcoming year.

KEY TERMS

- Maternal Health Outcomes
- Three Delays
- Barriers to Care
- Infant Mortality
- Care-Seeking
- Emergency Medicine
- Primary Health Care

Peer Editors:

Chase Antonacci, a junior majoring in Philosophy-Neuroscience-Psychology

Madison McManus, a junior majoring in Ancient Studies

ABSTRACT

Uganda has the fifth highest fertility rate in the world, with an average of 5.8 children per woman. This high birth rate is paired with maternal and infant mortality rates that remain high despite government efforts. Among pregnant women in Uganda, the majority of deliveries occur outside of a health facility and with no health care professional present, increasing the risk of mortality. The objectives of this project were to examine how women make decisions about where to seek care, what barriers they face in accessing health care, and where gaps in understanding exist between biomedical care providers and the communities they serve.

We conducted 38 semi-structured interviews in the Iganga District with women, men, and a variety of biomedical and traditional care providers. The analysis of these interviews builds on Sreen Thaddeus and Deborah Maine's "Three Delays Model" of maternal mortality. Our findings suggested a disconnect between health care providers and women surrounding the first delay: a delay in the decision to seek care from a health facility. Midwives in government health centers largely attributed these delays to women's inadequate knowledge and recommended further health education for the community. In contrast, the women we spoke to easily articulated the benefits of delivery in a health center, but offered an array of structural barriers that constrained their care-seeking options. The misattribution of these decisions to a lack of knowledge may result in the neglect of more systemic failures that lie at the root of the problem.

FACULTY MENTOR: SHANTI PARIKH, PH.D., ASSOCIATE PROFESSOR OF ANTHROPOLOGY, AFRICAN AND AFRICAN-AMERICAN STUDIES

Professor Parikh's research focuses on the intersection of local transformations; global processes; and structures of inequalities surrounding issues of sexuality, particularly gender, sexual and reproductive health, regulation, courtship and romance, and marriage. Recently, she has begun further research on infidelity and HIV transmission and the social history of sexuality in rural post-colonial Uganda.

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INTRODUCTION

Uganda has the fifth highest fertility rate in the world, with an average of 5.8 children per woman (Uganda Bureau of Statistics [UBOS] 2017). This high birth rate is coupled, unfortunately, with an infant mortality rate of 43 deaths per 1,000 live births, meaning that one in 23 of these children will die during the first year of life (UBOS 2017). The outlook for mothers is similarly bleak. As of 2015, a Ugandan female's lifetime risk of dying from maternal causes was one in 47 (The World Bank). Childbirth itself is the riskiest time: approximately half of these maternal deaths and 30-50% of newborn deaths will occur within one day of delivery (Waiswa *et al.* 2012). Many of the causes of mortality are preventable, so life or death may depend on how quickly the treatment of complications is initiated during this critical window of time (Thaddeus & Maine 1994). For this reason, it is particularly concerning that only 42% of deliveries in Uganda are supervised by health professionals (Waiswa *et al.* 2010).

The country has taken steps to address this problem, but more effective interventions are plainly needed. This research is aimed at identifying why current interventions have failed, and how a new focus has the potential to make a lasting impact in reducing maternal and infant mortality.

RESEARCH QUESTION AND OBJECTIVES

The vast majority of maternal and neonatal deaths worldwide are preventable with timely medical intervention (Thaddeus & Maine 1994; UNICEF 2018). For this reason, Ugandan public health initiatives aggressively promote childbirth in facilities staffed with health care professionals. Despite these efforts, however, rates of delivery in these health facilities remain low.

The purpose of this project was to explore the reasons behind these low rates of usage, specifically examining: (1) How women make decisions about where to seek care during pregnancy and delivery, (2) What barriers women face in accessing biomedical care, (3) Where gaps in understanding might exist between health care providers and the communities they serve. These areas of focus may serve to illuminate topics for further research to inform more effective approaches to maternal and infant health in Uganda.

METHODOLOGY

My research methods consisted of focus groups, community mapping exercises, and semi-structured interviews. I conducted my research in the summer of 2017 in Iganga Municipality and three of its surrounding sub-counties: Nakigo, Ibulanku, and Nawandala. In each sub-county, my research collaborators and I worked with the local village health team (VHT¹) member to identify health care providers and members of the community willing to participate. I conducted a total of four focus groups, three

¹VHTs consist of volunteer community health workers who have basic medical training and serve as links between their communities and local health facilities.

involving five to six women with children in each of the sub-counties, and one group of elderly men and women in the Iganga Municipality. I also conducted 38 semi-structured interviews with local women, men, and a variety of biomedical and alternative health care providers, ranging from drug shop proprietors to traditional birth attendants (TBA). The bulk of my data was collected from interviews and focus groups with local women. In total, 29 women participated, ranging in age from 19 to 75. Two thirds of these participants had not been educated beyond the level of primary school, and 80% cited agriculture as their main source of income. The 15 women who were interviewed individually described a collective total of 62 pregnancies and deliveries. Data gathered on each pregnancy included outcome, complications, delivery location, fees, and post-natal care, among other factors. Questions also explored women's health literacy and reasoning for making care-seeking decisions.

CONTEXT

The concept of primary health care (PHC) has been the central pillar of the Ugandan health system for nearly four decades (Tashobya & Ogwal 2004). Described as essential health care based in science and made universally accessible, PHC was introduced in the 1978 Declaration of Alma-Ata and included, as one of its eight basic services, maternal and child health care (World Health Organization [WHO]). The fundamental principles of PHC require that these essential services be *available, affordable, accessible, and acceptable* (WHO 1978). Uganda's efforts to implement PHC were "fragmented and uncoordinated" from the beginning due to political instability and poor governance. It is generally recognized that the country has struggled to implement PHC objectives (Tashobya & Ogwal 2004, 1).

The disconnect between vision and implementation of PHC is evident in Uganda's maternal and infant health services, which are supposed to offer free, high-quality care at government health centers. In reality, however, these facilities are often plagued by drug and staffing shortages and are unable to provide free treatment (Ministry of Health 2006). As a result, community members may turn to other practitioners such as traditional healers and traditional birth attendants (TBA²) to fill the gap in access to care. These practitioners often live in the community they serve, typically have no formal training, and are not recognized by the government.

Several attempts have been made to increase rates of health facility-based childbirth. While 92% of women now visit a health facility one or more times during pregnancy³, the rate is much lower for the actual delivery: fewer than half of all infants are born in health facilities (Waiswa *et al.* 2010). Despite decreases over the last few decades, Ugandan maternal and infant mortality rates are still some of the highest globally. The persistence of these poor indicators strongly suggests the need for better interventions in maternal and infant health.

²A traditional birth attendant (TBA) delivers babies and acquires her skills by delivering babies herself or through an apprenticeship to another TBA (Ministry of Health). She may attend to mothers in her home, often with the aid of traditional herbal medicines.

³Ministry of Health guidelines advise four prenatal care visits during pregnancy.

FINDINGS AND ANALYSIS

The realities of maternal and infant mortality are perhaps best summarized by a mother in Nawandala who had experienced more than one complicated pregnancy. Due to the language barrier, I have paraphrased an abbreviated version of her response, taking care to preserve the original meaning of her words:

The greatest danger for us delivering mothers is that most of the health facilities are far away from us and we may die on the way because of the long distances. For example, in the case of a complication or emergency while in Nawandala Health Centre, they refer you to Iganga Hospital, which is relatively far for a dying mother or infant.⁴ And you will have to spend a lot of money on the way. Sometimes, you may not be able to find the money for a taxi or a boda boda⁵.

You will also need to have some money for upkeep. In most cases, if you arrive at the hospital without money to help you be worked on or to buy particular medicines, you may be forced to go back home and sell some item in order to get money for treatment. For example, you may be pregnant, not knowing that you will require a C-section. When you reach the hospital, they may tell you that you are supposed to be operated on, and they will want money for the operation. When you don't have money for the operation, you or the people who accompanied you may be forced to go back and sell some of your property in order to get money for the operation. If it takes them too long to sell the property, you may die (Interview 26, pers. comm. 2017).

THREE DELAYS MODEL

To structure this analysis, I will employ the Three Delays Model, a widely used explanatory framework for maternal mortality that has been also modified by researchers in Tanzania to apply to perinatal deaths (Mbaruku et al. 2009). Research on the primary causes of maternal mortality has shown that “a majority of these deaths could have been prevented with timely medical treatment. Delay, therefore, emerges as the pertinent factor contributing to maternal deaths” (Thaddeus & Maine 1994, 1092). The Three Delays Model identifies three crucial phases during which delays may occur. A Phase I delay is a “delay in deciding to seek care on the part of the individual, the family, or both” (Thaddeus & Maine 1994, 1092). A Phase II delay is a “delay in reaching an adequate health care facility” (Thaddeus & Maine 1994, 1092). Finally, a Phase III delay is a “delay in receiving adequate care at the facility” (Thaddeus & Maine 1994, 1092).

For the purposes of this report, I will define “care” as biomedical treatment by a certified health professional at a government-recognized health center, clinic, or hospital. This is not meant to discount the services that may be provided by other practitioners,

⁴Iganga Hospital is approximately one hour from Nawandala Health Centre III by taxi or boda boda.

⁵Boda bodas are motorcycle taxis that serve as the primary form of transportation in Iganga.

such as traditional healers or TBAs; however, high-quality biomedical care is the standard goal of maternal and infant health initiatives. According to the Three Delays Model, one must focus on “the interval between the onset of an obstetric complication and its outcome,” that is, analyzing the steps taken when a complication arises, to see where delay influences the outcome. (Thaddeus & Maine 1994, 1092).

I would argue that in Iganga, the onset of labor is an obstetric complication in itself. Any delivery may suddenly become complicated, and a normal delivery may go awry when a mother delivers by herself at home or when attended to by a TBA who lacks the equipment or medications to handle routine problems. By the time a serious complication presents, it is often too late. I use the Three Delays Model because the same delays that put women and infants at risk of death, in the most extreme of cases, are also common causes of other adverse outcomes including morbidity and disability in what might otherwise be routine deliveries. For every mother who dies in Uganda, six more survive, but with “chronic and debilitating ill health” (Ministry of Health 2006, 7).

Phase I: Delay in Deciding to Seek Care

The first phase in which care may be delayed begins with the onset of labor or of a complication. An example of a Phase I delay was described to me by one mother who delivered at home by accident. She had intended to deliver at a health facility but when she went into labor, it was a night when her husband was not around and she did not have enough money to go to the hospital (Interview 30, pers. comm. 2017). She believed she did not have time to reach a health facility because her water had broken, which she believed meant imminent delivery (Interview 30, pers. comm. 2017). She delivered by herself at home and sent her older son to fetch a neighbor, who helped her cut the umbilical cord and remove fluid from the baby’s mouth and nose (Interview 30, pers. comm. 2017).

In a document outlining the country’s strategic plan to address maternal and neonatal health from 2007-2015, Uganda’s Ministry of Health explained Phase I delays:

“The first delay occurs within the household/family level and is related to the limited ability of the woman and her close relatives to make a decision to seek care. This is closely linked to the inability to appreciate danger signs of pregnancy, delivery and postpartum due to inadequate knowledge. In addition, some cultural practices restrict women from seeking health care, while poverty at the household level also limits decision making to seek health care” (2006, 19).

This definition emphasizes ignorance (“inadequate knowledge”) as the primary reason women delay in going to health facilities, with cultural factors and poverty seemingly added as afterthoughts. The logical solution to this problem is health education for women about danger signs during pregnancy and the benefits of childbirth in a health facility. My research did not fully support this thesis, however. Although the women I spoke to offered several reasons for giving birth outside of health centers, few of these could be traced to inadequate knowledge. Perhaps attesting to the success of education programs, the women I interviewed described accurately how health facilities could prevent mother-to-child HIV transmission or provide an injection to stop postpartum hemorrhage. They further understood the risks of tetanus from home deliveries, yet

they continued to deliver at home or with a TBA. The reasons women cited included long distances to health facilities, lack of money, and mistreatment or ridicule by health workers. Thus, it was not inadequate knowledge that kept women from health facilities, but rather structural barriers that made the use of those facilities impossible or unreliable.

In contrast, when I asked 12 health care providers about what could be done to reduce maternal and infant mortality rates, additional health education for communities was suggested 35 times. It seems apparent that there is a significant gap in understanding between women, health workers, and Uganda's Ministry of Health about the causes of first delays.

Phase II: Delay in Reaching a Health Facility

The second opportunity for delay occurs after the decision to seek care has been made, as the mother attempts to travel to an adequate health facility. Such issues were frequently noted by women in the community when asked how maternal and infant mortality might be reduced. One participant in Nawandala explained that the majority of maternal deaths are due to the long distances in search of medical care, and offered the example of a blood transfusion (Interview 26, pers. comm. 2017). If you go to Nawandala Health Centre III requiring a transfusion, she explained, they will refer you to Bugono Health Centre IV (Interview 26, pers. comm. 2017). If Bugono cannot handle the case, they will refer you to Iganga Main Hospital, where you may arrive only to find that they do not have blood in stock for a transfusion (Interview 26, pers. comm. 2017). All of these referrals take a lot of time, she said, and in the process, either the mother or child may die (Interview 26, pers. comm. 2017). She requested that Bugono Health Centre IV be upgraded to a main hospital, arguing that if advanced services are brought closer to the community, maternal and infant mortality rates will drop (Interview 26, pers. comm. 2017).

While a few women described textbook examples of Phase II delays in their own childbirth experiences (e.g., waiting for an ambulance to arrive), the majority of references to the second delay occurred when women explained why they chose not to seek treatment from a health facility. Thus, Phase II concerns played into Phase I decisions. It is important to recognize that a decision to seek medical care during labor in Iganga is automatically beset by obstacles. Travel is costly and many women have only indirect access to money through a husband. One does not know how long labor may last. A woman may be incapacitated by contractions and unable to bear the pain of travel by motorcycle or crowded taxi. One solution—to travel before labor begins—could mean being away from home for an indeterminate length of time, which may simply be unfeasible. Thus, it is understandable that many women take the chance of delivering outside a health facility, not out of ignorance but because their choices are constrained by other Phase II obstacles. Of the 25 infants delivered at home or with a TBA, fear of delivering while en route to the health facility was identified as a factor in 16 cases. In stark contrast to these reports from the community, however, the health care providers I interviewed proposed efforts to address the second delay only five times.

Phase III: Delay in Receiving Adequate Care

Finally, Phase III delays refer to impediments to accessing medical care within a health facility. Health centers and hospitals near Iganga often lack even the most essential items, such as gloves, qualified personnel, blood, and lifesaving drugs. As one key informant

explained, health centers are restocked infrequently, and may have medicine for two weeks, only to run out for the following three months. When a patient requires a drug that the health center does not have, she is given a prescription and instructed to buy that medication from a drug shop. Patients are often unable to afford such medicines, and as a result drug stores will sell a patient just half or a quarter of the dose they require (Interview 33, pers. comm. 2017). Government-employed midwives reported long hours, inadequate staffing, and poor compensation in their jobs.

One unexpected cause of delay was related to the personnel in government health facilities. In several of my interviews, both health care providers and women described the problem of health workers abusing patients. Women reported experiencing verbal abuse in particular—being shamed or neglected for not providing their own birth equipment, being denied lifesaving treatment because they delivered with a TBA, and even being slapped by midwives when they took too long to answer a question. One participant recounted the story of her daughter, who had gone to a health facility to give birth, but asked to be referred to a higher facility because her labor was not progressing (Focus group 1, pers. comm. 2017). The health workers refused to give her referral documents, saying that they had already spent a long time suffering with her (Focus group 1, pers. comm. 2017). The refusal to refer may have been due to the fact that the health workers would not receive a delivery fee if they referred the mother. The participant reported that when her daughter finally gave birth, the baby was dead (Focus group 1, pers. comm. 2017). The health workers did not report the death and simply kept quiet and buried the baby (Focus group 1, pers. comm. 2017). This story was not unique; midwives and health workers were frequently described as rude, callous, and harsh by women in Iganga. Five women and two health care providers proposed that more attentive and compassionate care from health workers could reduce maternal and infant mortality.

TBAs appear to treat laboring mothers completely differently. In interviews with 15 women, I asked them how they chose the location where they delivered each of their children. Women who delivered with a TBA often mentioned how caring she was during pregnancy and delivery and cited this as a factor in their decision. The women who delivered at health centers or hospitals recognized the high quality of medical care they received, but the health workers and midwives were never once described as caring or kind. Psychology research has shown that social judgments of individuals and groups are largely determined by two traits: warmth and competence (Fiske et al. 2007). Through my interviews with both health care providers and women in the community, government health workers were consistently described as cold, though it was acknowledged that they usually provided competent care.

One may wonder if abuse that in most cases is verbal should be enough to deter women from delivering in a health facility. After all, aren't a healthy mother and baby worth enduring some coldness or harsh words? For Ugandan women, however, emotional support during labor has special significance.

The importance of warmth was articulated for me by one mother who recalled being mistreated at a health facility while in labor with her second child (Interview 12, pers. comm. 2017). Women deserve care and kindness from midwives, she explained, because during delivery they exist in a space between life and death (Interview 12, pers. comm. 2017). A safe and healthy delivery, a relatively routine experience for women in the Global North, is anything but a guarantee for women in Uganda. With the risk of death

looming over her, it is easy to understand a pregnant woman's desire for compassion and respect. Also notable is research finding that a perception of warmth is more difficult to reestablish than a perception of competence (Cuddy *et al.* 2011). This suggests that an expectant mother would be quicker to regain confidence in a kind TBA who has made a medical error than in a health worker who verbally abused her, even if that health worker provided competent medical care.

Misunderstanding of the factors causing a first delay can also perpetuate Phase III delays in access to appropriate medical care. A traditional birth attendant reported that when her clients go to health centers for post-natal care, they are scolded by midwives for delivering with a TBA, and their infants are sometimes denied immunizations (Interview 12, pers. comm. 2017). The reasons for this treatment emerged from the narratives of the health workers I interviewed, who blamed mothers for delaying before coming to the facility or for delivering with a TBA. Midwives appeared to interpret these behaviors as willful disregard of their advice, overlooking the structures of inequality that might prevent women from accessing recommended care. Such reports from TBAs, midwives, and community members indicate a clear need for better communication between patients and providers.

CONCLUSIONS

One shortcoming of the Three Delays Model is its linearity; it treats each type of delay as an isolated event. Our research, however, produced numerous examples where women declined to seek care—a seeming Phase I delay—because they could anticipate a Phase II or Phase III obstacle (e.g., inability to pay for transportation). This was true of the vast majority of first delays described to us. Rather than failures of mothers to recognize a problem, as the Ministry of Health suggested, they were logical products of past experience. Thus, after the first encounter with long distances, expensive treatment, or inadequate care at a health facility, these Phase II and III factors will become Phase I considerations. Particularly in Uganda, where the average woman has five or six children, the compounding second and third delays encountered in early pregnancies may deter future care-seeking behaviors, magnifying the risk of maternal and infant mortality with each subsequent pregnancy.

Of the seven women who delivered with a TBA, five had previously delivered a child at a health facility or hospital, suggesting it was not lack of knowledge about the benefits of facility-based birth that drove their decisions. Of the eight deliveries that occurred at home, seven were attributed to the inability to reach an adequate health facility. These women cited sudden, intense labor pains, long distances to health facilities, and lack of money for transportation as reasons they delivered outside of a health center. Several women noted the level of compassionate, high-quality care they received from a TBA as a factor in their decision, contrasting it with stories of harassment and neglect by government health workers.

Despite the variety of Phase II and III factors contributing to these decisions, each of the deliveries might simplistically be categorized as examples of the first delay. There is reason, therefore, to revisit findings on neonatal mortality in Uganda that implicate the first delay as the greatest contributor to mortality and prescribe yet more community education as the solution (Waiswa *et al.* 2010). Such a response, however, would be

insufficient because it fails to address the systemic Phase II and III factors at the root of the decision to delay biomedical care.

RECOMMENDATIONS

Based on my analysis of the narratives of women in Iganga and the advice I received from both health care providers and community members, I propose three recommendations for future health care initiatives.

The most fundamental recommendation is to shift the emphasis of maternal and infant mortality interventions from educating women about health to holding the government accountable for addressing more systemic issues. The Ugandan government claims to offer free health care to citizens, but until there is access to affordable transportation and health centers are close to the community and fully stocked with drugs, equipment, and well-compensated staff, this promise will not become a reality. Focusing the bulk of intervention efforts on empowering women to seek health care in a system that constantly thwarts their efforts can actually be counter-productive, as it shifts the responsibility for maternal mortality to the women themselves. Though it may seem counterintuitive, the first delay can perhaps best be addressed by efforts to mitigate delays in Phases II and III.

There is also a clear need to rebuild community trust in the health system. I recommend that concerted efforts be made to reduce the rates of abuse and neglect that patients experience at the hands of government health workers. According to my interviews with local women, health workers accused of abuse are sometimes transferred to other facilities, but this merely relocates the problem. Further research is indicated to identify effective methods of addressing such issues, perhaps looking to TBAs for guidance in compassionate care delivery. In addition, research may explore ways to involve TBAs in the government health system, leveraging their skills to rebuild trust and link mothers and infants to advanced care. Eliminating neglect and abuse by health workers is an inexpensive intervention that could substantially reduce delays in the decision to seek care.

Finally, it appears that many of the problems outlined above are exacerbated by misunderstandings between health care providers and patients. In Iganga, knowledge about maternal and infant health flows in one direction: from providers and policymakers to individuals. Scholars such as Paulo Freire argue for the importance of dialogue, writing that “to substitute monologue, slogans, and communiqués for dialogue is to attempt to liberate the oppressed with the instruments of domestication” (Freire 1970/1993, 47 in Bruzas 2018). To promote a mutual exchange of knowledge, I suggest that maternal and infant health initiatives incorporate the opportunity for an open forum in which biomedical health workers, traditional health care providers, and patients can discuss their experiences, ask questions, and voice their concerns. While open communication will not solve all problems, infinitely more progress can be made toward our mutual goal if health care providers and patients join together. In that way, they may address the real problems and enable Iganga to at last make progress on maternal and infant mortality.

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“NO MAN’S LAND”: MISSING VOICES IN THE ANGLOPHONE CANON OF RUSSIAN LITERATURE

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KEY TERMS

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ABSTRACT

The canon of Russian literature that is widely read in English today only began to form in the first three decades of the twentieth century. This article asks why renowned Russian writers contemporary to that period such as Zinaida Gippius (1869-1945) and Maxim Gorky (1868-1936) were excluded from that canon, which instead promoted older, exclusively male writers like Lev Tolstoy (1828-1910) and Fyodor Dostoevsky (1821-1881). I take Gippius's writing, particularly her 1916 story “No Man's Land,” as a central case study. I argue that the contrast between Gippius's very loud literary work and her nearly silent reception in English indicates that she was excluded from the Anglophone canon of Russian literature not because of the nature or quality of her writing but for social and political reasons that prevented her work from being read in the first place. This article describes one such historical factor: since the Great War, English-speaking readers have largely associated Russian culture with an archaic past dating to the nineteenth century or earlier while defining twentieth-century and contemporary Russia in almost exclusively political terms. Recent Russian literature, which falls between these two Russias, tends to find favor with Anglophone audiences only if they can easily read it as a form of political opposition to the current Russian government. The same standard of interest tends not to apply to nineteenth-century works. Analyzing this somewhat arbitrary factor in literary canon formation provides a first step toward greater exposure in the English-speaking world for Gippius and other underrecognized Russophone writers of the twentieth and twenty-first centuries.

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I. BORN IN TRANSLATION; LOST IN TRANSLATION

Scholars have increasingly called attention to the way translation takes part in the creation and not only in the transfer of literature. A work can be called “bilingual” or “born translated” when it purports to take place in a language other than the one in which it is written, when it appears in translation before it appears in its supposedly original tongue, when its author writes it with subsequent translations in mind, or when she writes and translates in tandem such that the two processes become indistinguishable.[i] The process of self-translation, Jan Hokenson and Marcella Munson have noted, is not new, but major studies of multiple forms of multilingualism, such as Rebecca Walkowitz’s *Born Translated*, have singled out Anglophone literature of the present day. Nonetheless, a story written in Russian a century ago by Zinaida Nikolaevna Gippius (1869-1945) exemplifies how translated birth can bring with it a special, and as yet understudied, kind of afterlife.

“No Man’s Land” was composed in Russian for publication in an English-language anthology entitled *The Soul of Russia*, a literary, political, and philanthropic project directed by the British historian Winifred Stephens whose proceeds were to benefit internally displaced Russian citizens during the First World War.[ii] The Russian version of the story not only went unpublished; its manuscript appears to have been lost.[iii] Gippius, a prominent intellectual impresario and writer of poetry, fiction, drama, memoir, biography, and philosophy, fled St. Petersburg for Paris after the Bolshevik Revolution of 1917. She and her husband, the fellow literary polymath Dmitry Merezhkovsky, found themselves in better material circumstances than many of their colleagues because they already owned property outside Russia, but exile nonetheless took its toll on their collections of books and papers. “No Man’s Land” therefore exists only in a translation produced by Susette M. Taylor, who, though rarely mentioned in written records since her death in 1920, was a noted translator and polyglot in her time as well as one of the first female Fellows of the Royal Geographical Society.[iv] These curious material circumstances lend “No Man’s Land” both a certain prestige and a certain precarity: written by an author considered canonical in the Russophone world but nowhere else, translated by a scholar whose barrier-breaking accomplishments were last mentioned in her own obituary, and published in its second language in an impressively well-resourced but nearly forgotten anthology, “No Man’s Land” remains unrecognized precisely because its creation and distribution were thoroughly intertwined with histories of translation and exile. It did not enter the sphere of world literature despite the international slate of literary figures that prepared it for its translated birth. Studying translation as creation primarily through the cross-linguistic ventures of writers like J.M. Coetzee or Samuel Beckett who write to meet an existing international demand thus risks papering over a less hopeful underside of the phenomenon. When authors and editors issue texts in translation to create a demand for writers who are not yet known, and the demand they imagine does not materialize, the text, left without a foothold in any language, can fall into unwarranted obscurity.

This article is about how certain circumstances of a text’s production and distribution such as birth in translation and contemporaneity itself, traits that scholars tend to find either unrelated to the literary merit of a text or a kind of literary advantage, prevented

contemporary Russian writers from gaining a readership in English in the early twentieth century even as their nineteenth-century predecessors rapidly gained popularity. That time period saw a wave of what scholars have come to call “Russian fever,” a widespread obsession throughout the English-speaking world with nineteenth-century Russian literature and the Russian arts. Thanks to a small group of translators like Constance Garnett, Louise and Aylmer Maude, and S.S. Kotliansky, British readers and writers devoured works by Lev Tolstoy, Fyodor Dostoevsky, Anton Chekhov, and Ivan Turgenev for the first time, and that group of writers solidified into an Anglophone canon of Russian literature that continues to shape reading habits and university syllabi today.[v]

It is curious that each of those four writers was dead by the time “Russian fever” reached its peak in the 1910s while writers of Gippius’s generation, those who saw a canon of nineteenth-century writers form with their own eyes, were excluded from that same canon. Gippius and her contemporaries were not kept out of the English language for a lack of connections; on the contrary, Russian-language scholarship has demonstrated that extensive networks facilitated an unprecedented level of communication between major British and Russian literary figures in the early twentieth century.[vi] The factors that did restrict the Anglophone canon of Russian literature to the nineteenth century were many; therefore, the central purpose of this article is not to explain why “No Man’s Land” never gained recognition in the English language but rather to use the literary potentials of the text itself to demonstrate the arbitrary nature of its absence from Anglophone literary canon. I close my analysis by arguing that a new conception of “Russia” among English speakers emerged in the early twentieth century that has since prevented contemporary Russian literature from gaining prominence in the Anglophone world.

I will begin by establishing a lack of correlation between the nature of Gippius’s texts and their muted Anglophone reception. In the case of “No Man’s Land” in particular, it is clear that Gippius’s writing did not get a fair hearing in English in part because its politically abrasive and literarily groundbreaking contents were met with a reception so muted as to be virtually nonexistent. The bulk of this article is an exercise in the contrast between the controversy a reading of “No Man’s Land” creates and the story’s reception, whose utter lack of controversy can only signal a lack of reading.

II. A LOUD STORY

“No Man’s Land” delivers an engaging parable that overlaps political provocation with substantial innovations in literary technique. Gippius and Taylor, who knowingly produced the story for a British audience, could even anticipate the difficulties contemporary Russian writers faced in the English language in the mid-1910s and use them to the story’s advantage.[vii] As contemporary Russia emerged in Britain as a political ally above all else, British readers could easily overlook Russian literature that claimed to be disengaged from its country’s political role. In the opening to “No Man’s Land,” Gippius and Taylor not only undermine this expectation; they establish an unreliable narrator capable of turning the tables on a reader who expects concrete political claims from the story. That narrator complains:

To-day it is very difficult to write stories. People ask for them and ask for them, but are never satisfied. If you think out something like

fact, like something contemporary and authentic, then they say: “Why ever invent something that resembles reality, when one can have reality itself?” This is quite true. And if you write something which is fictitious, again it doesn’t do. “What sort of author is this, who, while worlds are shaking, invents imaginary happenings?[viii]

The narrator of “No Man’s Land” ostensibly turns to his reader as a confidante; he complains not about “you” but about “people.”[ix] However, a reader of an anthology as deeply embedded in current events as *The Soul of Russia* would typically be one of those “people”—someone who has come to a text seeking both a story and earth-shaking political truths suitable for earth-shaking times. The narrator immediately places such a reader in a position of discomfort both by asking her to rethink her assumptions about the story’s purpose and by teasingly trusting that she does not actually hold them herself. The narrator proceeds not to insist upon telling a story anyway, proving the political reader wrong, but to acquiesce to that reader’s concerns, at least rhetorically:

The only thing to do is to imagine nothing, but just to sit down and lazily call to mind some old fairy tales, to tell them to oneself, without effort, and without troubling as to whether they bear upon what is real or not, or even if there be anything in them at all.

The narrator’s resigned tone, it turns out, houses the setup for precisely the kind of fantastic story whose rejection he anticipated. In the end, his acquiescence is only a vehicle for a quiet insistence that, war or no war, stories persist. In these two paragraphs, Gippius and Taylor preempt a criticism that Gippius had already attempted to dismantle in Russian: war must subsume art.[x]

In the second paragraph, the narrator takes his defensive tactics one step further: he uses that criticism to establish the unreliability of the narrative he proceeds to relay. His story is not unreliable in the way critics have come to expect from works like Vladimir Nabokov’s *Pale Fire* or Henry James’s *The Turn of the Screw*, however. This narrator confesses his story to be a fairy tale; he claims no pretense to truth-telling. What his readers cannot trust is his narrative about the relationships between his tale and real life. The narrator claims that the story he will tell may be empty of the real, that he has made no effort to imbue it with significance. In the following paragraphs, he also dissuades his reader from speculating about the real-world source of the tale: it may come from “some book or other,” he says; maybe from “the old almshouse woman who sometimes came to our house on Sundays;” maybe from his young friend Boris, who died of diphtheria; maybe from all of them; maybe from none.[xi] The story’s hidden source provides the narrator with a façade of detached impartiality. Nonetheless, the story is about a war and about the no man’s land that separates the warring sides, and it is part of an anthology about the Great War, whose signature geographical feature quickly became the no man’s land between enemy trenches. It is very difficult to read “No Man’s Land” without reading for an allegory with much to say about the world outside it.

Writing such a story for translation into English provided Gippius with an opportunity to open complicated questions about the merits of war and peace with which she could not have engaged in Russian. As Ben Hellman has described, an early

wave of overwhelming support for the war in Russian public discourse led Gippius to argue publicly for the necessity of the conflict and limit her doubts about it to private spaces like the pages of *Siniia kniga* (*The Blue Book*), the diary she kept at the time.[xii] Once she did begin publicly expressing her pacifism in poems like “Bez opravdan’ia” (“Without Justification,” 1915), those opinions also demanded an unwavering, polemical stance as the war increasingly drew ire from both revolutionary politicians and Russian citizens at large. In English, however, Gippius’s readers would be entirely unfamiliar with her previous statements on the war and unable to put pressure on her to express a particular opinion about it. Gippius seems to have taken advantage of that situation to write a story that never reveals its narrator’s political motivations, leaving its readers to search for them in vain and question both war and pacifism in the process.

The narrator tells a story about two kings. The kings rule two indistinguishable kingdoms that are perpetually at war. When the kings’ descendants finally decide to strike up a peace agreement, they decide to build two high walls stretching across their entire continent, turning the middle half of that landmass, formerly a battleground, into a no man’s land. As peace reigns in both kingdoms, the kings’ subjects find themselves unoccupied and mysteriously begin losing their mental and physical strength. Children who exhibit a higher level of intelligence begin to disappear. The two kings meet on an island off the coast of the No Man’s Land to discuss this dilemma and are shocked to see a blue light flashing from the supposedly abandoned space between the walls. Soon after, the walls collapse outward, crushing their guards, and a flock of enormous birds carrying tall blue people floods into both kingdoms. The blue people declare that their ancestors, bored by life on the other side of the wall, fled to the No Man’s Land and formed a society in which every member is a king and no king goes to war with any other. “No Man’s Land” ends as the new kings colonize the entire world and begin to rule it as they please.

The story weaves a tangle of questions. First, who wins in its moral calculus? The two young kings make peace, but apparently at the cost of the well-being of their peoples. The blue people seek permanent peace, but they colonize their peaceful neighbors. The No Man’s Land is a massive graveyard, but it gives birth to new people with new ideas. Second, is the tale’s position even didactic? The pacifism of its original kings could exist for its own sake or for the sake of permanent division. The pacifism of its blue kings could also exist for its own sake, or it could exist for the sake of unrelenting colonialism. (Only the story’s ableism seems undoubtedly sincere.) Third, what relations connect the elements of the tale to the world as Gippius and Taylor knew it? If the No Man’s Land of “No Man’s Land” is the no man’s land of the Great War, then the two kingdoms find real-world equivalents in the Allied Powers and the Central Powers, but the blue kings are much more difficult to place, as are the two walls and the two kingdoms’ degeneration. In an anthology whose moral stance is set in a pro-Russian, pro-British, pro-alliance, and pro-war direction, such a story not only aims pointed questions at the writings that surround it—it forces its reader to grapple with a piece of literature that, though only eight pages long, puts those questions through a kaleidoscope of ambiguous plot devices in a way that a political opinion piece could not. All that the story justifies concretely is its initial insistence on the ability of art to shock readers out of compliance with the political pressures of war.

“No Man’s Land” is unique not only for its ability to free Gippius to confront her qualms about both militarism and pacifism but for its departure from Russian literature of

the half century that preceded it. British readers of Gippius's time were accustomed to the short stories of Chekhov and Tolstoy, which confronted concrete moral and social issues with emotional stances ranging from empathetic creativity to unforgiving moralism but never with fantasy, unreliable narrators, and moral ambiguity. Other contemporary writers of short fiction like Gorky, Teffi, Leonid Andreev, Aleksandr Kuprin, and Ivan Bunin tended to follow a similar, traditionally realist path. Even the stories of Nikolai Gogol rarely display narrators as self-conscious or allegories as bewildering as those that appear in "No Man's Land," and even that exemplar of self-conscious narrators, Dostoevsky's man from the underground, is himself a relatively transparent polemic against the imposed rationalism of a very real nineteenth-century Petersburg life. Gippius's combination of unreal worlds, untraceable allegory, and unreliable narration represents a major narrative innovation in the field of Russian fiction, and English-speaking readers had exclusive access to it.

III. A SILENT RECEPTION

However, if any of those readers took advantage of that access and read "No Man's Land," they read it so quietly that I could discover no practical way to find traces of their readings. I began my search for the reception of "No Man's Land" with familiar sources of printed scholarship: books written and compiled by the prominent Gippius scholar Temira Pachmuss, collections of research on Gippius published by the Institute for World Literature in Moscow, books on Russian or women's writings in the First World War, and Gippius's volume in the reception-centered *Pro et contra* series.[xiii] When I could find no mention of "No Man's Land," I turned to scholarly databases: Project MUSE, JSTOR, a variety of EBSCO databases, the MLA International Bibliography, CyberLeninka, and Zhurnal'nyi zal.[xiv] I searched at first for texts that contained the terms Zinaida and Gippius (or Hippus, as her name was sometimes spelled) as well as the phrase "No Man's Land." I also tried various possible Russian titles (*neitral'naia polosa*, *neitral'naia zona*, *nicheinaia polosa*, *nich'ia zemlia*) in hopes of stumbling across a record of the original Russian manuscript. These searches returned zero hits. Searches for Cyrillic and Latin spellings of Gippius's name had identical results, and searching for "Soul of Russia" or the terms Susette and Taylor instead of the title of the story were similarly discouraging. I soon decided to cast a wider net by turning to search engines and searchable databases with a much broader scope. I selected Google, Google Scholar, Google Books, Yandex, Natsional'nyi korpus russkogo iazyka (The National Corpus of the Russian Language), HathiTrust, and the Internet Archive both for the number of texts they contain and because they allow users to search the full texts of their contents rather than metadata alone. I modified my terms for these broader searches based on the scope and nature of each database. For example, because HathiTrust tends to give only the page numbers of search hits, I first searched for books in which "Gippius" or "Hippus" and "no man's land" were on nearby pages and then searched for "Gilbert" and "Gubar" to see whether the phrase "no man's land" in fact referred to Sandra Gilbert and Susan Gubar's three-volume book series, which it nearly always did. In extremely large search engines like Google and Yandex, I often restricted my searches to the years 1915-1940 so that I could read each result. In no case did I find a record of "No Man's Land," let alone its reception, other than *The Soul of Russia* itself. Finally, I searched the British Newspaper Archive, the

Historical American Newspapers database, and the *Times* Digital Archive, where I found advertisements for and reviews of *The Soul of Russia* but no mention of Gippius's story.

I find it unlikely that no reader has happened across *The Soul of Russia* and turned to page 159 within the past century, especially given that at least 167 copies of the anthology remain in circulation in libraries alone according to WorldCat.org. I also cannot claim that no record of the reception of "No Man's Land" exists at all. However, I can think of no way of searching for it short of combing at random through the private archives of London's wealthier 1916 residents. This is an unusual finding for a short work written by a major Russian author, even a contemporary one, in the early twentieth century.[xv] When the story in question is as provocative as "No Man's Land," such a result suggests that the work did not gain a wider readership because, due to the historical circumstances surrounding the text, not enough readers accessed the story for even one of them to voice an opinion about it in a prominent public forum. "No Man's Land" would not necessarily have found favor with an early twentieth-century British audience; on the contrary, its divergence from the Russian literature to which that audience was accustomed and from the other pieces in *The Soul of Russia* would likely have drawn confusion and criticism. Silence, however, would be an unlikely response to such a text. The remainder of this article illuminates one of the many reasons for that silence.

IV. THE TWO RUSSIAS

What I call the 'two Russias' split targeted contemporary Russian literature as a class by its internal logic alone. Even Maxim Gorky, whose sudden rise to fame ensured that his work would be translated into English with or without the help of his own social maneuverings, fell victim to it simply by virtue of being a contemporary writer. I propose that this split took place around the year 1910: with Tolstoy's death in that year, Chekhov's in 1904, the Anglo-Russian Entente in 1907, and the beginning of the Great War in 1914, the meaning of the word "Russia" (but not *Rossiya*) began to change as the Russian state gained political significance in the predominantly Anglophone countries that fought alongside it. When that word or the phrase "the Russians" appear in texts written after the first decade of the twentieth century, they tend to refer not to a historically continuous nation-state but, after a fashion, either to an archaic nation or to a neoteric state. In the former case, "Russia" is a land of traditional folk art and soulful, occasionally primitive literature. Its temporal home is the nineteenth century and earlier. Its foremost representatives are "the Russians" as Virginia Woolf, D.H. Lawrence, and other literary figures meant the phrase: authors of realist or philosophical prose in the line of Tolstoy, Dostoevsky, and Chekhov. [xvi] A biographical note preceding S.S. Koteliansky's translation of Lev Shestov's book *All Things Are Possible* even notes that "Shestov is one of the living Russians," as though "the Russians" are an old breed whose members have gradually been dying off.[xvii] Russian culture, then, increasingly appeared in English as a phenomenon of the past. The new, present "Russia" was a military ally and a budding revolutionary government. It was the state that appeared in newspaper headlines like "Russia's Struggle" (1915), "Russia and the War" (1917), and "The Allies and Russia" (1920).[xviii] Decades later, this political and military Russia continued to appear, albeit as an enemy, in "Russia Quits World Health Agency" (1949), "No military base in Cuba, says Russia" (1970), and "Trump aide told Australian diplomat Russia had dirt on Clinton" (2017).[xix] The essential

characteristic of this split is not the separation of the political from the cultural. Studies at the intersection of semiotics and international marketing have described that kind of multiplication in national images for a few decades, and their findings are hardly limited to Russia.[xx] What is remarkable about the English-language usage of “Russia” in the twentieth and twenty-first centuries is the temporal split between the political Russia and the cultural one.[xxi] In a literary context, scholars continue to use “the Russians” to refer to Tolstoy and Dostoevsky but not to the political leaders who censored and imprisoned them (and almost never to more recent writers).[xxii] Meanwhile, present-day artistic figures appear in political commentary as the opponents of “*Putin’s Russia*” and not as Russia’s representatives.[xxiii] As this bifurcation in Anglophone representations of Russia began to emerge in the early twentieth century, its formation coincided with and deeply affected the development of the English-language canon of Russian literature.

The history of Zinaida Gippius’s reception in English illustrates how the separation of the two Russias, by denying the very possibility of contemporary Russian literature, first began to limit most English-language readership of Russian literature to the nineteenth century. Specifically, as translators, editors, and readers deemed Gippius and her writings irrelevant to the workings of the post-revolutionary Soviet state, they slowed the circulation of her work rather than finding other sources of interest in it. Even before the Revolution, Winifred Stephens, the editor of *The Soul of Russia*, placed “No Man’s Land” in a section of the anthology entitled “War in General” even though its title pointed clearly to another section, “The Present War.” Stephens appears to reserve the latter section for pieces whose stance on the political issues of the day was immediately clear; a piece called “Face to Face with War” by Olga Metchnikoff, for instance, portrays the citizens of (immediately pre-Revolutionary) Russia as united and ready for sacrifice in the face of a brutal German enemy.[xxiv] *The Soul of Russia* itself soon fell prey to a similar bias: a single year after its publication, its descriptions of a durable Russian-British alliance became obsolete as the new Bolshevik government condemned both the alliance and the imperialism of its predecessor’s ally. Although the Bolshevik Revolution did not actually reduce the value of the anthology’s artistic and literary pieces, the fact that readership of *The Soul of Russia* has since largely been limited to a scholarly audience hints that British readers felt the entire book to be a kind of outdated historical artifact.[xxv]

This theory of a ‘two Russias’ split both explains contemporary Russian literature’s exclusion from Anglophone canon and responds to an emerging question in the study of Russian-British relations about the source of Anglophone interest in Russian cultural products. Rebecca Beasley and Philip Ross Bullock, two leading scholars in that field, observe that “[British] interest in more recent developments in the Russian arts seems to have been almost entirely restricted to dance.”[xxvi] Even post-revolutionary futurist art from Russia, they note, seemed not to attract attention in London. Stephens’s introduction to *The Soul of Russia* carries a hint as to the cause of this disparity: the anthology, she wrote, “describes a circle, so to speak, in the tendency to revive the archaic exhibited by [Dmitry Semyonovich] Stelletsy’s pictures.”[xxvii] Stelletsy’s paintings joined art by Lev Bakst and Natalia Goncharova in the anthology; all three artists were best known outside Russia for producing the sets of the Ballets Russes. The Ballets Russes, I suggest, were by far the most successful form of contemporary Russian art in early twentieth-century Britain not because they centered on dance—after all, their musical

scores and sets also struck a chord with British viewers—but because they could be read as a primitivist expression of the Russian soul. Even the Ballets Russes succeeded only because they fit into the mold of one of the two Russias.

I have turned to the writings of Zinaida Gippius and to “No Man’s Land” in particular because they seem to insist that they need not fit that mold. Gippius’s writings are unabashedly contemporary, not in the sense that they fit what scholars now call contemporary literature but in the sense that they are written in and about their present moment even when, as in “No Man’s Land,” they do not explicitly describe a present world. They are also unabashedly artistic, introducing their viewers to worlds and characters who, like the blue kings of the land between the walls, are often difficult to conceive. Gippius’s narrators tend to be very stubborn about handling contemporary political and social issues through a cryptic narrative medium, and even if that medium occasionally makes Gippius’s works difficult to translate, it also makes them stand out from the writings of her predecessors. Beginning in the 1960s, Gippius’s life, philosophy, and writing finally began to achieve recognition among English-speaking scholars of her generation of Russian writers thanks to the research and translations of Temira Pachmuss. More recently, Olga Matich and Jenifer Presto have brought her works to the attention of Russianists more broadly. This article aims to expand that attention beyond the realm of Russian Studies: the works of Zinaida Gippius merit the attention of a broad audience both within and outside the academy.

NOTES

[i] Rebecca L. Walkowitz, *Born Translated: The Contemporary Novel in an Age of World Literature, Literature Now* (New York: Columbia University Press, 2015).

Jan Walsh Hokenson and Marcella Munson, *The Bilingual Text: History and Theory of Literary Self-Translation* (New York: Routledge, 2014).

[ii] Winifred Stephens, ed., *The Soul of Russia* (London Macmillan, 1916).

[iii] I searched for a Russian version of “No Man’s Land” in the 15-volume edition of Zinaida Gippius’s collected works (*Russkaia kniga*, 2001–2012) and on the Internet as well as in the Russian State Archive of Literature and the Arts (Moscow), in the archives of the Institute of Russian Literature (St. Petersburg), and in the catalog of the Gippius papers at the University of Illinois. I found no mentions of or excerpts from the story. I also searched for the archives of the four individuals through whom “No Man’s Land” entered the English language: Maria Tsetlina, Daniel Gorodetsky, Susette M. Taylor, and Winifred Stephens. While both Tsetlina and Taylor left books and artworks to institutions they valued, none left an accessible archive of documents.

“Temira Pachmuss and Vladimir Zlobin Collection, 1901–1996” (University of Illinois), Record Series Number 15/20/21, University of Illinois Archives, accessed December 29, 2017, <https://archives.library.illinois.edu/uasfa/1520021.pdf>.

[iv] “Ms. Susette M. Taylor,” *The Geographical Journal* 57, no. 3 (1921): 238.

Karen Attar, *Directory of Rare Book and Special Collections in the UK and Republic of Ireland* (Facet Publishing, 2016), 338.

“Education,” in Janet Horowitz Murray and Myra Stark, *The Englishwoman’s Review of Social and Industrial Questions: 1886* (Routledge, 2016).

- [v] Rebecca Beasley and Philip Ross Bullock, eds., *Russia in Britain, 1880-1940: From Melodrama to Modernism* (Oxford University Press, 2013).
- [vi] Olga Kaznina, *Russkie v Anglii. Russkaia emigratsiia v kontekste rusko-angliiskikh literaturnykh svyazei v pervoi polovine XX veka* (Moscow: Nasledie, 1997).
- [vii] Because Gippius's Russian manuscript is unavailable to me, I prefer to think of "No Man's Land" as a collaborative effort. The text that survives was not Gippius's creation alone, and excluding Susette Taylor's role in its composition would misrepresent the source of my analysis.
- [viii] Stephens, *The Soul of Russia*, 159.
- [ix] My choice to describe the narrator of the story using masculine pronouns is based primarily on Gippius's tendency to write both fiction and poetry from a male character's point of view, but my guess could nonetheless be entirely incorrect. In Taylor's rendition of Gippius's story, the narrator uses a single verb that would, in Russian, reveal its speaker's gender ("may have heard"), but it is possible that such a verb did not appear in Gippius's manuscript. It is also possible that the verb reveals a female narrator.
- [x] See, for example, "Togda i opiat'" in Zinaida N. Gippius, *Poslednie stikhi (The Last Verses)*, reprint of *Poslednie stikhi, 1914-1918*. St. Petersburg: 1918. (Letchworth, Herts.: Prideaux Press, 1974). Gippius engages in an internal argument about the merits of wartime art in "Tishe" in the same collection.
- [xi] Stephens, *The Soul of Russia*, 159.
- [xii] Ben Hellman, *Poets of Hope and Despair: The Russian Symbolists in War and Revolution (1914-1918)* (Helsinki: Institute for Russian and East European Studies, 1995), 139-217.
- [xiii] Zinaida N. Gippius, *Intellect and Ideas in Action: Selected Correspondence of Zinaida Hippus*, ed. Temira Pachmuss (München: W. Fink, 1972).
- Zinaida N. Gippius, *Stranitsy iz proshlogo: Iz perepiski Zinaidy Gippius*, ed. Temira Pachmuss (Frankfurt am Main ; New York: Peter Lang GmbH, Internationaler Verlag der Wissenschaften, 2003).
- Z. N. Gippius, N. V. Koroleva, and Institut mirovoi literatury imeni A.M. Gor'kogo, eds., *Zinaida Nikolaevna Gippius: Novye Materialy, Issledovaniia* (Moscow: IMLI RAN, 2002).
- Hellman, *Poets of Hope and Despair*.
- Margaret R. Higonnet, ed., *Lines of Fire: Women Writers of World War I* (New York: Plume, 1999).
- Temira Pachmuss, *Zinaida Hippus: An Intellectual Profile*, 1st edition (Carbondale: Southern Illinois University Press, 1971).
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- Aleksander N. Nikoliukin, ed., *Z.N. Gippius: pro et contra: lichnost' i tvorchestvo Zinaidy Gippius v otsenke sovremennikov i issledovatelei: antologiya* (Russkii khristianskii humanitarnyi institut, 2008).
- [xiv] All searches described in this paragraph were conducted between January 2015 and December 2017.
- [xv] A similar set of searches for *The Green Ring*, one of the other works by Gippius published in English, quickly yields results in both secondary and primary sources. The same goes for randomly selected short stories by Chekhov that were translated in the same period by Constance Garnett. I also searched for Alexander Kuprin's "Captain Ribnikov," published as part of a collection in 1916 in a translation by S.S. Kotliansky and John Middleton Murry, because it

is lesser-known work written by a lesser-known author than Chekhov. That story earned specific reviews and commentary in British newspapers that appear in the British Newspaper Archive although it did not appear as the title story of its collection.

For Chekhov, see e.g. Anton Pavlovich Chekhov, *The Darling, and Other Stories*, trans. Constance Black Garnett (New York, Macmillan, 1921).

Aleksandr Ivanovich Kuprin, *The River of Life, and Other Stories*, trans. Samuel Solomonovich Koteliansky and John Middleton Murry (Boston: J.W. Luce, 1916).

[xvi] See, for example:

D.H. Lawrence, "Forward," in *All Things Are Possible*, by Leo Shestov (New York: R.M. McBride & Co., 1920), 7–12.

Virginia Woolf, "Modern Fiction," in *The Common Reader: First Series* (New York: Harcourt Brace Jovanovich, 1925), 146–54.

Virginia Woolf, "The Russian Point of View," in *The Common Reader: First Series* (New York: Harcourt Brace Jovanovich, 1925), 173–82.

[xvii] Leo Shestov, *All Things Are Possible*, trans. S.S. Koteliansky (New York: R.M. McBride & Co., 1920), 5.

[xviii] "Russia's Struggle," *Wells Journal*, October 15, 1915, British Newspaper Archive.

"Russia and the War," *Evening Despatch*, May 5, 1917, British Newspaper Archive.

"The Allies and Russia," *Sheffield Daily Telegraph*, February 25, 1920, British Newspaper Archive.

[xix] "Russia Quits World Health Agency," *The Nottingham Journal*, February 17, 1949, British Newspaper Archive.

"No Military Base in Cuba, Says Russia," *Birmingham Daily Post*, October 14, 1970, British Newspaper Archive.

Sabrina Siddiqui, "Trump Aide Told Australian Diplomat Russia Had Dirt on Clinton – Report," *The Guardian*, December 31, 2017, sec. US news, <http://www.theguardian.com/us-news/2017/dec/30/donald-trump-russia-inquiry-george-papadopoulos-australian-diplomat>.

[xx] Nicolas G. Papadopoulos and Louise Heslop, *Product-Country Images: Impact and Role in International Marketing* (Psychology Press, 1993).

[xxi] I most frequently use the words "politics" and "political" in this article in the second sense given by the *Oxford English Dictionary*: I refer to the state and to the people officially charged with running it. Those words effectively convey the conglomerate of government and military actors that many Anglophone commentators labeled as representatives of Russia after the nineteenth century. When I use "politics" in a broader sense, I say so explicitly or use a compound term such as "politics of gender."

"Politics, n." *OED Online* (Oxford University Press, n.d.), <http://www.oed.com/view/Entry/237575>.

[xxii] Studies in the field of British Russophilia exemplify this trend:

Neil Cornwell, *James Joyce and the Russians* (Basingstoke: Macmillan, 1992).

Roberta Rubenstein, *Virginia Woolf and the Russian Point of View* (New York: Palgrave Macmillan, 2009).

Joanna Woods, Katerina: *The Russian World of Katherine Mansfield* (Auckland: Penguin, 2001).

George J. Zytaruk, *D. H. Lawrence's Response to Russian Literature* (The Hague: Mouton, 1971).

[xxiii] Emphasis added. Perhaps the best example in recent months can be found in commentary published in English-language news sources on the criminal allegations leveled against the theater director Kirill Serebrennikov. Unlike coverage of the same events in independent Russian-language sources like *Meduza* and *Novaya gazeta*, pieces selected for publication in American and British sources often explicitly identify Putin but not his opponents with ownership or representation of Russia. Compare the following:

Oleg Kashin, "Opinion: Portrait of the Artist in Putin's Russia," *The New York Times*, September 14, 2017, sec. Opinion, <https://www.nytimes.com/2017/09/14/opinion/artist-putin-russia-serebrennikov.html>.

Pavel Merzlikin, "Advokat Ekateriny Voronovoi otvechaet na voprosy, vznikshie posle pis'ma eyo podsashchitnoi o dele 'Sed'moi studii.' 'Suda nad Katei prosto ne dolzhno byt,'" *Meduza*, December 1, 2017, <https://meduza.io/feature/2017/12/01/advokat-ekateriny-voronovoy-otvechaet-na-voprosy-voznikshie-posle-pisma-ee-podzaschitnoy-o-dele-sedmoy-studii>.

Sasha Sulim, "'Posmotrite na menia, na moyom litse net sledov prestupleniia.' Figuranty dela 'Sed'moi studii' ostalis' pod arestom," *Meduza*, December 14, 2017, <https://meduza.io/feature/2017/12/04/posmotrite-na-menya-na-moem-litse-net-sledov-prestupleniya>.

[xxiv] Stephens, *The Soul of Russia*, 174-176.

[xxv] The anthology is discussed briefly in 1954 in Dorothy Brewster's early and highly valuable contribution to the study of British Russophilia, but I could find very few references to it in earlier documents, including those dating to the era of "Russian fever" itself, beyond newspaper advertisements. Dorothy Brewster, *East-West Passage: A Study in Literary Relationships* (London: Allen & Unwin, 1954), 170-172.

[xxvi] Rebecca Beasley and Philip Ross Bullock, "Introduction: The Illusion of Transparency," *Translation and Literature* 20, no. 3 (November 2011): 283-300, 295.

[xxvii] Stephens, *The Soul of Russia*, vi.

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"Russia Quits World Health Agency." *The Nottingham Journal*. February 17, 1949. British Newspaper Archive.

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CULTIVATING COMMUNITY: TOWARDS A BLACK WOMEN-CENTERED ALTERNATIVE FOOD POLITIC

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KEY TERMS

- Alternative Food
- Soul Food
- Mothering
- Community Organizing
- Black Feminist Anthropology

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Derrick Ogola, a junior majoring in Philosophy-Neuroscience-Psychology

ABSTRACT

Black women are often on the frontline of the battle for food justice in their communities. This research examines the motivations, successes, and challenges of two food justice organizations in St. Louis, Missouri, both of which were started and are sustained by Black women. A central thread through this project is naturalization—how linking identity with inequality "naturalizes" social difference and limits the potential for radical reimaginings of equality and food justice. It seeks to "denaturalize" the process of gentrification and the assumptions that food injustice can be solved on the individual level, that food work is women's work, that alternative food is for white people, and that parenting is apolitical. Operating with the understanding that lasting change originates within a community, not from outside, this project reveals how Black women have taken on leadership roles in food sovereignty projects in their own communities. It examines the organizing principles that guide these women, including the politics of parenting, women-centered organizing, and free spaces. It also discusses the potential for collaboration between people of different identities and organizations while maintaining the vital importance of Black women. By revealing the historical roots of alternative food in Black communities, this research makes the case for a food justice movement built around survival strategies particular to Black communities. This project argues for a movement that centers the legacies of Black alternative foodways and Black women-centered community organizing as the building blocks for food justice and food sovereignty.

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INTRODUCTION

On a surprisingly mild July day in 2017, I sat outside the basement entrance to Greater St. Mark Family Church in North St. Louis County, Missouri. Next to me were the grandchildren of Reverend Abby Harris, a dedicated church member and community organizer, and Lisa Smith, a founding member of United People Market. The market is an organic food co-op dreamed up by Abby. Each Saturday, a truckload of fresh produce was brought over by staff from City Greens Market, another St. Louis food co-op started by women in 2008. United People was still in its early stages and we were working to find community members to purchase market memberships so we could afford to continue selling affordable organic produce to a community of low-income, mostly Black residents. Attendance at the market had been sparse that day, but an event at the church that had drawn lots of attendees began to let out as we enjoyed the breeze outside. Lisa caught the attention of one man on his way to his car, telling him from a distance about the “fresh, local, organic” produce we were selling inside. The man surveyed us with an impressed expression. “Y’all black?” he asked. Lisa laughed, gesturing to the herself and Abby’s grandchildren and said, “yeah, look at us!”

The man clearly saw that everyone sitting outside the market (except for me) was Black. But he wasn’t asking the question for clarity. He was simply surprised that an organic food market could be conceived of and run by people that looked like him. United People Market is an example of a market that works towards a goal of *food sovereignty*, or gaining “power for managing and regaining ownership of the food system” (Alkon and Agyeman 2011, paraphrased by Kato 2013). Community food initiatives like United People Market are often the projects of well-meaning white people (Alkon and Agyeman 2011, Kato 2013). To have a food co-op in a community of color run by women of color is unusual and even radical. This moment is representative of the intersection of race, food, and gender that fueled my interest in food work led by Black women in their own communities.

Throughout this paper, I make use of various terminology to describe the current movements towards the access and consumption of healthy, fresh, organic, natural, slow, and/or locally-grown food. I employ the term “alternative food” as an umbrella term to encompass the sentiment that the solutions to the problems of the industrial food system lie in some “alternative” form of food production, procurement, preservation, preparation, and/or consumption. I also use the language of “food justice” and “food sovereignty” separate from that of “alternative food,” which encompass the understanding that the utopic alternative food scene needs intervention when it does not engage with issues of race, class, and gender. They envision a world in which “communities [exercise] their right to grow, sell, and eat [food that is] fresh, nutritious, affordable, culturally appropriate, and grown locally with care for the well-being of the land workers, and animals” (Just Food 2010, cited in Alkon and Agyeman 2011). I imagine food sovereignty as a necessary antecedent to just food systems. However, organizations often fail to address the importance of community agency in developing food solutions, instead identifying access as the primary inhibitor to food justice. Yuki Kato (2013) found that when community members at a New Orleans CSA box program were presented with “foreign” food items, such as microgreens or arugula in their boxes,

they took it as a sign that the CSA was out of touch with the community's needs. The residents, therefore, often had food access without food sovereignty. Finally, I use the language of "community food" to draw a link between the theory of alternative food and food justice and the praxis of community engagement with food issues.

The focus of my research is food justice organizations because of the particular way food issues galvanize communities; as a few of my interviewees pointed out, "we all have to eat" (Smith 2017, Harris 2017). Black women are often on the frontline of the battle for food justice in their communities and are frequently mobilized through their positions as mothers to their families or to the community. Because of the hypervisibility of white people (often white women) in food justice projects, contributions made by Black women are sidelined or made invisible. Yet women of color like Abby, Lisa, and the women of City Greens are leaders in their community and on the frontline of food justice concerns, demonstrating how Black women occupy roles of significant influence in the food justice movement. My project focuses on particular ways in which Black women mobilize around food issues, challenging the notion that women's food work is apolitical. I look at two food justice organizations—City Greens Market in Forest Park Southeast and United People Market in North County—both of which were founded by and continue to be sustained by Black women.

METHODS

I began by conducting a critical review of literature surrounding the subjects of soul foodways and alternative foodways, looking for potential sites of overlap in the hopes of expanding the meaning of alternative food. I also conducted immersive field research at two alternative food sites in St. Louis. I approached this research through the lens of ethnography, an anthropological method which helped me to develop a rich, immersive understanding of the individuals at my field sites. Because of my commitment to a holistic approach, I utilized mixed methods, including participant observation, short unstructured interviews, and long semi-structured interviews. This approach allowed me to make unexpected observations outside the realm of any single method.

My approach was informed by the field of Black feminist anthropology, which attempts to reorient traditional anthropology away from its colonialist tendencies. For contributors to the volume *Black Feminist Anthropology* (ed. McClaurin 2001), what this often looks like is taking on an approach per which researchers see their commonalities with the researched as assets rather than detriments. Johnnetta B. Cole defines feminist anthropology as weaving into traditional ethnography "an analysis that is informed by a sense of the importance of 'race' and gender" (quoted in McClaurin 2001, p. 57). Black feminist ethnography is inherently political, because it participates "in some way in the struggle against racism, sexism, and all other systems of inequality" (Ibid). An implicit definition suggested by many of the authors in the volume is that Black feminist anthropology is anthropology conducted by Black women. As a white woman, I certainly do not presume to be a Black feminist anthropologist.

My first site of research, City Greens Market, is a 501(c3) community food cooperative started by a group of women in the Forest Park Southeast neighborhood (FPSE). According to their website, City Greens' mission is "to provide access to fresh, quality and affordable produce to neighbors, to promote healthy living in the

community, and to provide space for members to interact.” The women who started City Greens, called the Midtown Mamas, meet weekly at Midtown Community Services (also known as “Midtown”), a local community hub which also hosts a men’s club, a youth group, summer camp, and an outreach program for pregnant women and newborns. In 2008, the Midtown Mamas decided to address the lack of healthy food options in their neighborhood by starting a small fresh food market in the basement hallway of Midtown. Since its inception in the hallway of Midtown, the market has known various locations—the basement of Midtown, a mobile market, and now a storefront on Manchester Avenue—and various degrees of availability, growing from one day of operation per week to five. The market is financially independent, having split from its sponsor, Catholic Charities, in 2016. Interviews with full- and part-time employees and volunteers were key sources of information for this project. The informants I had at City Greens were instrumental in helping me paint a picture of the market’s history and mission, as well as their personal perceptions of the roles of race, gender, and other identities within food justice.

United People Market is a new project in an unincorporated part of North St. Louis County near Ferguson and Dellwood. The founder and director of the market, Abby, is on the board of directors for City Greens along with her husband. Before the inception of the market, Abby and Lisa surveyed the neighborhood to gauge interest for an organic food co-op in North County. As of March 2018, United People Market is open one day per week. It is supported by City Greens, receiving produce from them, and run by volunteers and the director’s family. The market operates out of the Greater St. Mark Family Church, a social justice-oriented Baptist congregation which was an important site of resistance in the aftermath of the murder of Michael Brown in 2014. During my time at United People Market, Abby was focused on establishing community partnerships so she could tap into networks of people that the market would be able to serve. Both she and her husband noted the importance of working with other women of color, who often hold powerful sway in their communities.

The bulk of my research consisted of long, semi-structured interviews. My questions focused on life stories, constructing oral histories of City Greens and United People, and perceptions of race, gender, and age dynamics within the food justice movement in St. Louis. I entered each interview with a set of slightly different questions depending on the person’s role in the market, but was prepared to change the course of the interview depending on what the participant wanted to talk about. Interviews lasted between 30 minutes and three hours. I conducted interviews onsite at neutral locations, mostly at United People Market and City Greens. I recorded each interview on my iPhone.

I felt that the more I was able to make myself visible in the community, the more receptive informants would be to me. Since I am studying communities where people are used to being researched and may be skeptical of researchers, I wanted to be cognizant of the ways in which I might be perceived by identifying myself as a researcher and subvert those perceptions. This is another reason that spending eight hours a day at City Greens was important to my project. I attended two community “coffee talks” at Midtown to make myself visible as someone with a stake in the community, rather than a dispassionate researcher. I also did some of my own networking within the community food movement in St. Louis, meeting with a representative from the St. Louis Food Policy Coalition, to begin to become a part of the community of researchers dedicated to food

justice, a community to which I am also an outsider. After my official research period concluded, I continued to stay involved with City Greens as a grant writing volunteer. My visibility helped me to establish common ground and rapport with market personnel and community members. By continuing to involve myself with City Greens, I subvert the expectation that researchers are disinvested with the communities they study. It is my goal to remain actively involved with City Greens as long as I live in St. Louis.

FINDINGS AND ANALYSIS

A central thread through my project is naturalization, or the ways in which linking identity with inequality “naturalizes” social difference and limits the potential for radical reimaginings of equality and food justice. The conversations I had with my informants “denaturalized” the assumptions that Black foodways are unhealthy, that food work is women’s work, that alternative food is for white people, and that parenting is apolitical. Based on my findings, I argue for an explicitly feminist food justice movement that regards the roles Black women play in their communities as vitally important. I argue for a movement that centers the legacies of Black alternative foodways and Black women-centered community organizing as the building blocks for food sovereignty.

Towards Redefining The “Alternative” In “Alternative Food”

Through a review of literature, I found that deriving power from alternatives to the food system has a strong history in Black communities because the food system was not designed to meet their needs. John T. Edge distills the power of the alternative in one salient example; in the antebellum days, when slaves would cook greens for their masters, the masters would only allow the slaves to drink the potlikker, the liquid substance at the bottom of the pot. Unbeknownst to them, this liquid was more nutrient-rich than the greens themselves (Edge 2017). Over the following centuries, other institutions have demonstrated how Black communities can derive power from opting out of the mainstream food system. In 1920s Chicago, recent African-American migrants from the South opened up a variety of restaurants and grocery stores, helping to create a Black metropolis in which migrants “resisted ‘bending down’” by “exercising their freedom to spend hard earned wages on what they wanted” (Poe 1999, p. 6). In the South in the 1960s, house restaurants provided an informal economy for Black women to garner income independent of white dollars (Edge 2017). The Black Panther Free Breakfast Program, established in 1969, served children nationwide without government dollars, eventually putting enough pressure on the government to increase funding for children’s food (Patel 2011). These examples are just some of the ways Black Americans have resisted white supremacy in the food economy. Melissa Danielle (in Harper 2009) cites this history in her appeal towards an ethic of Black veganism, writing, “We can choose to create health-supportive lifestyles that take cues from our cultural heritage—communal living, susus, bartering, creating relevant community-based businesses, potlucks, daycare co-ops, eating locally and seasonally, establishing food-buying clubs or food co-ops, and growing our own foods,” (n.p.). Danielle’s argument shows potential for a culture of Black alternative food that both celebrates historical Black foodways and strives towards an ethic of health.

In founding City Greens, the Midtown Mamas were clearly determined to “take

cues from [their] cultural heritage.” To Brenda, one of the store's founders, the store is “alternative” to the mainstream food system because it is community-conceived and run. “When we were in the basement, it was staffed with volunteers of the neighborhood. When we had discussions, it was staffed full of people in the neighborhood. So the community always had an input on what was in the store. And if you couldn't afford something, we always tried to find a supplement to assist people” (Stokes, B. 2017). Unlike corporate supermarkets, an integral part of City Greens' mission has always been responsibility towards the community, even when it compromises profit.

Patrice, a longtime City Greens volunteer, shed some light on why the community garden associated with City Greens has been a particularly important site for her as she grows into food justice activism. “What I love about it is everyone comes in and helps,” she said. “We're not just working in the garden. It's our garden” (Edwards 2017). This sense of ownership that Patrice describes underscores the importance of community members feeling that entitled to the sites of alternative food production.

While the (white) alternative food movement romanticizes agriculture by branding urban farms as blank slates with the potential for the “novelty” of growing one's own food, the history of slavery and sharecropping suggests that sites of food production are not the “blank slates” that these projects assume (Woods 1998 and Ramirez 2014). Abby spoke to this dynamic in our interview. “A lot of Black people don't want to garden, or, as they say, ‘dig in the dirt.’ Because of their heritage, because of slaves and because their parents made them do it, or their grandparents” (Harris 2017). Through alternative food projects, Black communities can regain autonomy over sites of food production.

Reformulating Essentialism Through Food Work

Black women are at the helm of healthy food activism in their communities. They occupy multiple, overlapping roles which intersect with food injustice: subject, parent, and centerwoman. Like the naturalness of the food itself, the women behind City Greens perceive there to be a natural connection between women's temperament and community food work. This perception is characteristic of essentialism, which is the belief that “all women share certain experiences because of biological similarities” (Mascia-Lees and Black p. 15). Kelly, United People Market's garden manager, demonstrated an essentialist understanding when speaking to the leadership of the food movement, saying, “I think it's led more by women. I think because women carry a mothering type of nature. Even if you're not a mother, being a woman, you come with caring for others” (Roper 2017). Within the realm of City Greens and United People, the perception that certain identities are “natural” in alternative food spaces, such as femininity and whiteness, limits the possibilities for radical futures within the movement. But there is also power to be found in these women's insistence on politicizing “women's work.”

Black women who participate in community food work must reckon with the conflicting meanings of essentialized Black women's work and food sovereignty. Rafia Zafar (1999) writes that “for a twentieth-century African-American female to publicly announce herself as a cook means she must engage with the reigning ghosts of American racism; she must tackle literally visceral ideas with metaphor, individual agency, and historical memory” (p. 450). For Black women to participate in food work, they must contend with, among other things, the controlling image of the mammy, defined by Patricia Hill Collins (2000) as “the faithful, obedient domestic servant” who was

“[c]reated to justify the economic exploitation of house slaves and sustained to explain Black women's long-standing restriction to domestic service” (2000, p. 72).

One way the women challenged the conflation of community food work with the image of the mammy was by repositioning community food work as radical self-care. Rebecca, City Greens' former co-director, discussed the ways in which a desire to improve her health mobilized her into food justice activism. “My sister died, my mom survived lung cancer, my dad died of lung cancer, my sister died of pancreatic cancer, my niece just died of diabetes, and it'll be three years since my sister died,” said Rebecca. “So all of that took place and it's like, it's gotta be linked to diet. So I started caring” (Stokes, R. 2017). Rebecca changed her whole diet and continues to be conscious of ways to eliminate toxins. Kelly spoke about how her own shift in diet acted as a bridge between her and other people:

When I was in nursing school, I was actually 150 pounds heavier. And when I got out of nursing school, I was like, oh my god, I'm gonna have diabetes, hypertension, but I just lose weight, that will give me a start. And for losing the weight, instead of just exercising, I decided to do a complete diet change. I stopped eating red meat when I was 18 but I didn't want to eat fast food. I didn't want to eat a lot of sugar. So I took all those things out of my diet, I took bread out of my diet, and I was able to lose 150 pounds. And during my weight loss mission, other women were like, ‘oh, you lost weight, tell me how to lose weight,’ and helping others just somehow made me passionate about food and its importance to our bodies. (Roper 2017)

Rebecca and Kelly show that a healthy diet can simultaneously be a political act and an act of self-care. By aspiring towards healthy bodies, Rebecca and Kelly reject the association between Blackness and an unhealthy diet. Their words suggest that having control over one's body is another facet of self-determination essential to Black liberation. Their weight loss, and subsequent healthy food activism, is a manifestation of the personal being made political. Kelly also describes how “helping others” became an extension of helping herself. The relationship between carework and activism characterizes the way in which women often mobilize around social causes.

In the interviews I conducted, women were able to identify leaders or centerwomen in their communities who generated community interest and investment in causes by tapping into their various social networks. Informants often carefully distinguished between the leadership of these women and the leadership of elected officials, which they considered to be less radical and effective. Many women suggested that there was something “natural” about their own leadership abilities that enabled them to rise to positions of influence in their communities. The potential for “natural leadership” gives Black women a positive framework within which they may enact confidence, as opposed to the “angry Black women,” a common cultural image that polices Black women's outspokenness. Patrice discusses how white supremacy affects the ways in which Black women feel that they can enact confidence. “We need to be heard,” Patrice said. “We need to quit being so quiet and doing it just because somebody said so. That matters to me.

For women to know that. Like I said, I have been a single mother. You can have anything anybody else has, but it just might take a little bit longer to get” (Edwards 2017). Melissa Harris-Perry (2011) writes that Black women often show the “pattern of assessing themselves as gentle, thoughtful, and kind while believing that others more frequently considered them aggressive and brash” (p. 89), suggesting that the tendency to keep one’s head down is an attempt to combat others’ perception. The possibility for a Black woman to be a “natural leader” allows her to appropriate assertive leadership qualities in a non-detrimental way. Inscribing women as leaders gives them the grounds to advocate for themselves. Telling women they are “natural leaders” has a far different material effect than telling them they need to keep their heads down “just because somebody said so.”

Another role subject to essentialism that many women inhabit is that of the mother. I found that when speaking about carework, my informants talked about the work of “parenting” as well as the work of “mothering,” a discursive distinction signaling that these two types of carework, while deeply entwined, are categorically different. For example, here, Patrice discusses her decision to work hard so her children could focus on high school:

I’ve always taught my kids, your high school diploma belongs to me. Your college diploma belongs to you. Because me as a parent, and as a single parent, I went out, worked hard, made sure you had everything that you needed so you could go and get that education. You didn’t have to work. I did all that because I wanted you to get your education, so to prove to me that I’ve done my part, your high school diploma belongs to me. (Edwards 2017, emphasis mine)

In describing how she was able to provide for her children, Patrice positions herself as a parent rather than a *mother*. She later emphasized that it is not a clean trade-off, that the roles “go together” (Edwards 2018). Patrice perceives motherhood and parenting to be distinct, yet constantly in conversation with each other. Although she sees herself as a mother first, the realities of being a single parent require her to occasionally step outside the work of nurture and moral upbringing to engage in the gender nonspecific tasks of working outside the home and disciplining children (Edwards 2018). As single parents, Patrice and many of the other women must contend with the category of “mothering work.” By categorizing some of their work as “parenting,” they acknowledge its difference from “mothering” but still include it in the more expansive category of carework. In another instance, when Patrice discusses how she became a community advocate, she says, “I saw women and men when a lot of them hadn’t been nurtured by a mother or a grandmother.” When a parent is “nurturing,” Patrice uses the language of mothering and motherhood. The idea that mothering and parenting go together insists that women can and do participate in the work of nurturing their children while participating in externalized forms of carework, like working outside the home or advocating for changes in the community.

This externalized carework which Patrice and many of the other women deem “parenting” evokes Nancy Naples’ definition of “activist mothering” as “all actions, including social activism, that [address] the needs of their children and community” (p. 448). By leaning into “parenting,” when the women breach gender roles by working

outside the home or advocating for a better community, their actions are automatically subsumed under the “parenting” category and they no longer feel the need to justify them. The different ways in which the women invoke “parenting” as an alternative to “mothering” represents the feeling that “mothering” discourse cannot capture the full extent to which women perform carework. By removing gender from the equation, the women also demand that others perceive their labor as legitimate and intentional, rather than simply an extension of motherhood.

CONCLUSIONS

Julie Guthman (2011) argues that “many of the discourses of alternative food hail a white subject and thereby code the practices and spaces of alternative food as white” (p. 264). When we remake the alternative food subject as the Black women, the approach to food politics becomes less “messianic” (Ibid). I argue that a Black women-centered form of organizing around food would preclude the concerns about inclusion that foreground debates in the food justice movement. If we devote more resources to free spaces where Black women can meet and collectively identify their community’s needs, then they will conceive of how best to address their own concerns. Community food projects that already exist should attempt to locate centerwomen in their communities who can mobilize many women and families around the issue of food. By engaging children in food education, these projects can tap into broad networks of community women concerned for their children’s welfare.

Food work is primarily women’s work; most women I interviewed agreed with this. But it is not so clear to me whether it should remain that way. Patrice talked about how, in recent years, she’s seen men become more involved with food work. “Women have always seemed like, for our culture, to take charge because it was all for men to get jobs or different things, so women had to make up for that,” she says, alluding to the work of survival that encompasses everything outside of being a breadwinner. “And now that the door is slowly opening and the men are coming in and finding out that, our women have been doing it for so long, come on in and help them out...I’m just glad to see them coming in” (Edwards 2017). I think Patrice is right to celebrate the trickling of men into food work. I do not necessarily think it’s a problem that the “door is opening slowly.” Because women have been doing this work for so long with so little political recognition, it’s important for men to be cognizant of that. Historically and currently, there is a lot of unrecognized power in the ways Black women connect over food. Reworking essentialism in the food movement rests not only upon making food work more gender inclusive, but also upon making visible the important work that Black women are doing and have been doing for generations. Whether by watching one’s mother can and preserve food as Brenda did, doing cooking demonstrations like Patrice did, or reminiscing with another community leader about a shared upbringing in the south as Abby did, women contribute much to cultural foodways by preserving traditions and knowledge.

As more men become engaged in food justice issues, Black women stand to lose their claim over the issues of—and therefore the solutions to—food injustice. Lower-income Black mothers who maintain their own gardens, who can and pickle to make food last longer, and who cook for their neighbors when times are hard, are rarely recognized for their contributions for food sovereignty in Black communities. The involvement of men

in food justice projects politicizes and legitimizes food issues, while women's everyday work is sidelined because community food work is still considered an extension of domesticity unless it is performed by men. I want men to ask themselves how they can contribute meaningfully to food justice projects without erasing the historical and contemporary food work of women of color.

This process of questioning the space one takes up in the food movement and “stepping back” accordingly is one way that Black women on the frontlines of food injustice will come to be regarded as vital knowledge sources for transforming food politics. Another way in which food justice projects can center Black women who experience food injustice is by prioritizing them in the hiring process and appointing them to organizational boards. This prioritizing needs to go beyond tokenizing. All that Rebecca has accomplished by helping to reopen City Greens and serving as its co-director did not make her immune to discrimination from other board members when the board was predominantly white, underscoring the need to actively recruit a diverse board. “What I had to say wasn't important and they didn't want to hear me talk. They wanted to hear Daniel talk. And every time we went to a meeting to say what we were doing, what we needed from them, [they wanted to] shut the Black woman up” (Stokes, R. 2017). That has likely changed since the board has become more diverse. According to City Greens' internal data, 73% of board members are low-income, 65% of the board is African-American, 25% are Caucasian, 5% are Asian-American, and 5% are two or more races. And Rebecca is now the president of the board, a position that confers respect. Other organizations might take cues from the diversification of City Greens' board and the appointment of Black women as more than just tokens, but as key informants who experience the effects of food injustice and strategize against it daily.

At a recent grant-writing session, I was chatting with Daniel and Adam, the market's current co-directors, about what City Greens brings to the neighborhood (beyond food access). We talked about how the market is a “space for neighbors to interact” like it says on the website, but more explicitly, “a space for all neighbors to interact,” regardless of social difference. What FPSE needs is more of these “free spaces”—public places for neighbors to interact where social change can be conceived of and brought about. That space might function as a shared kitchen where people can learn how to cook delicious greens without meat. Or a space for communal eating in the spirit of a house restaurant or a lunch counter. Or maybe it looks like a community garden where women grow kinds of vegetables that they ate growing up. Or it could simply be a space where women gather once a week to talk about the labor of care work. The food justice movement needs more spaces for neighbors to interact.

Tracy Poe (1999) discusses these spaces of interaction, or “commensality” as “one of the most important features of Southern African American culture” (p. 11). The communal style of eating, which can be traced back to life in African villages, is central to traditions of Sunday dinners, picnics, fish fries, and barbecues. To claim a Black sense of ownership over a communal food space like City Greens or United People Market is to map this shared history of commensality onto a type of space that has historically been hostile to Black people. For Abby, learning to farm and produce food was part of her own path to self-sufficiency; it was something she wanted to do. “I wanted to learn how I was gonna be able to put this big spread of food on the table three times a day,” she said. “[My grandparents] raised animals so they could feed themselves and

they had a smokehouse...they slaughtered their animals and that was very interesting to me. Opposed to seeing my mother go to a grocery store that didn't have any Blacks [working] in it" (Harris 2017). For Abby, self-sufficiency meant an alternative from the racism of the commercial food industry. It was a way for her to produce and consume food that was wholly her own without someone else's stigma attached to it. Abby and the other women's work of procuring, preparing, and sharing food in ways that speak to self-sufficiency and the alternative assert their exceptional capability to determine their own food system. Yes, we all have to eat. But just because we all do it does not mean it's apolitical. As these Black women have shown, you are the best person to identify the change you need in your community. That change can start with food.

Some names have been changed to protect the privacy of individuals.

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SUMMARIES OF STUDENT WORK

TOWARD A BETTER UNDERSTANDING OF...

MONITORING AND EVALUATION OF THE NUTRITION PROJECT, A PROJECT OF UGANDA DEVELOPMENT AND HEALTH ASSOCIATES

Sophie Abo

Mentor: EA Quinn

This research project aimed to monitor and evaluate the efficacy of Uganda Development and Health Associates' (UDHAs) Nutrition Project. GlobeMed at Washington University in St. Louis has partnered with Uganda Development and Health Associates for the last eight years, funding the Nutrition Project since its inception. The Nutrition Project aims to eliminate malnourishment in children under five years by increasing nutritional and breastfeeding knowledge, uptake of antenatal care visits, and improved home and health sanitation in the Bukooma Sub-County of the Luuka District, Uganda. The Nutrition Project carries out its activities through a network of 35 community health workers and a central Health Center III staffed by a nurse and lab technician. The goal of this research project was to identify successes, failures, and barriers to nutrition in the Luuka District by assessing knowledge of breastfeeding practices, maternal and childhood nutrition, diet diversification, and general health and sanitation in project beneficiary households. This evaluation was completed through a mixed method design that included key informant interviews with local professionals and government officials, focus group discussions with the 35 community health workers, and beneficiary household surveys. This research illuminated the strength of community health worker led interventions and identified organizational shortcomings that can be modified to improve project efficiency.

BURKHOLDERIA BACTERIA ARE GENERALIST INVADERS OF DISTANTLY-RELATED SOCIAL AMOEBAE THAT SOMETIMES ALSO ESTABLISH COOPERATIVE FARMING INTERACTIONS

Omowumi Adekunle and Rory Mather

Mentors: Debra Brock, Joan Strassmann, and David Queller

One of the big surprises in studies of life is how many of an organism's traits come not from itself but from the microbes it harbors. These relationships can be both beneficial and disadvantageous. Examples include how *Rhizobia* bacteria can perform nitrogen fixation for its legume host and how *Salmonella* bacteria can infect the small intestines of mammals and cause disease. This discovery is still revolutionary, and it is not always known whether host-symbiont relationships are generalizable or specific. Recently, the social amoeba *Dictyostelium discoideum* was discovered to have a symbiotic relationship with *Burkholderia* bacteria. Previous work has shown that colonization with certain *Burkholderia* species causes *D. discoideum* to carry not only *Burkholderia*, but other bacteria as well in a stable association. What is unclear is if this symbiotic relationship expands beyond the *D. discoideum* species boundary. To test this, we are colonizing five other *Dictyosteliaceae* species of which *D. discoideum* is a member. We will use two symbiotic *Burkholderia* isolates from each of three different *Burkholderia* species known to form stable associations with some clones of *D. discoideum* and then passage them to determine if this new association is stable. We are also testing to see if colonization affects the fitness of Dictyostelids. We measure fitness as the total spores produced by a Dictyostelid clone. We have already performed this experiment on two members of *Dictyosteliaceae*: *Dictyostelium mucoroides* and *Polysphondylium violaceum*. We found that both are able to carry *Burkholderia* and that this carriage decreases the fitness of both strains. This means that the ability of *Burkholderia* to invade other species exists, but that the cooperative aspects of the interaction have not evolved.

IDENTIFYING POTENTIAL CROSS-TALK BETWEEN THE FASTED LIVER AND DYSFUNCTIONAL HEART

Oyinkansola Adenekan

Mentor: Brian DeBosch

Heart disease is the leading cause of death in the United States. The goal of our research is to discover pathways and potential targets for the prevention and reversal of heart disease. Previous work from our lab has shown that trehalose, a disaccharide sugar, triggers the fasting response in cells. Additionally, recent research has shown that the liver's fasting response is therapeutic in a heart failure context. We found that trehalose protects against heart failure in mice with transverse aortic constriction (TAC), a model of heart dysfunction. Now, we are studying which mechanisms trehalose may act through to prevent heart failure. Our current hypothesis is that crosstalk between the "fasted" liver and failing heart leads to the improved condition of the heart.

We took two approaches to discovering potential crosstalk between the liver and heart: studying particular factors released from the liver and identifying potential interactions between secreted factors from the liver and receptor factors in the heart. Identifying potential interactions between the organs using RNA-sequencing data is the most promising approach, and we have identified potential interactions between the organs. Looking forward, we will continue to identify factors and/or groups of factors of interest and conduct validating experiments on the factors we are identifying.

PARTIAL KNOCKDOWN OF PUTATIVE MTSA2 GENE SUPPORTS ITS ROLE IN 6mA ADENINE METHYLATION OF THE SOMATIC GENOME IN *TETRAHYMENA THERMOPHILA*

Matthew Agritelley and Antiana Richardson

Mentor: Douglas Chalker

DNA methylation can confer heritable epigenetic information critical for proper reading of the genetic code. Methylation on the fifth carbon of cytosine (5mC) has been broadly studied for its roles in gene regulation and epigenetic inheritance. In contrast, much less is known about the importance of methylation on the sixth nitrogen of adenosines (6mA) in DNA or RNA. 6mA is the only DNA modification known in the model organism *Tetrahymena thermophila*, whose nuclear dimorphism provides a unique context for studying epigenetic regulation. In this ciliate, 6mA is found exclusively in the somatic nucleus, which may suggest that it participates in the control of gene expression. The enzyme(s) responsible for this modification remain undiscovered. Methyltransferase targeting position N-Six of Adenine 2 (*MTSA2*) is a putative gene in *T. thermophila* that belongs to a larger family of genes theorized to encode proteins that add 6mA to DNA or RNA. *MTSA2* contains a highly-conserved MT-A70 domain with known function as the S-adenosylmethionine binding subunit of mRNA methyltransferase in eukaryotic mRNA. We examined *MTSA2*'s function using a localization assay of a yellow fluorescent protein construct and assessed relative levels of 6mA by generating an *MTSA2* knockout (KO) strain. We found that *MTSA2* localizes to the macronucleus during growth, supporting its role as a DNA methyltransferase. Moreover, *MTSA2* KO strains showed a substantial decrease in 6mA relative to wild type (WT) strains. Interestingly, it was difficult to generate strains in which all of the copies of the *MTSA2* were knocked out in the polyploid (50N) somatic macronucleus. These KO strains appeared to grow more slowly than strains containing a greater number of WT copies. These results suggest that *MTSA2* appears to be important or even essential for cell growth. Together these data show that *MTSA2* likely functions as a primary 6mA methyltransferase in *T. thermophila*.

TRACKING THE LOCALIZATION OF CpsA, AN ESSENTIAL VIRULENCE FACTOR OF *MYCOBACTERIUM TUBERCULOSIS*

Nashwa Ahmed

Mentor: Jennifer Philips

Tuberculosis, an infectious disease that affects one third of the world's population, is caused by the pathogenic bacterial species *Mycobacterium tuberculosis* (*Mtb*), which grows within macrophages. Recent studies have identified that the membrane protein CpsA plays an essential role in *Mtb*'s ability to evade degradation by the host cell. Successful clearance of *Mtb* from infected cells requires triggering of the lysosomal trafficking pathway, LAP, that depends on reactive oxygen species generated by NADPH oxidase. CpsA, however, blocks this response by inhibiting NADPH Oxidase and thus LAP, enabling *Mtb* to evade the immune response. Currently, however, the localization of CpsA within the cell is unknown.

To clarify the mechanism of action of CpsA, we must pinpoint where it is located within the bacterial cell. To accomplish this, we will engineer plasmid-derived CpsA-GFP and CpsA-mCherry fusion proteins, introduce them into competent *Mycobacterium smegmatis* cells, and localize the encoded proteins *in vivo*. This approach will uncover the precise intracellular location of CpsA, clarifying whether it localizes uniformly throughout the membrane, or is localized to a specific region of the cell. Furthermore, we will be able to determine whether the protein is present within the host cytosol during infection.

Because CpsA alters host cellular trafficking in order to evade the immune response, advancements in our knowledge about the functional properties of this protein should enhance our understanding of host innate immunity.

THE EFFECTS OF *Dictyostelium discoideum* ON *Burkholderia* DISPERSAL

Moid Ali

Mentor: Joan Strassmann

Defined as the long-term, intimate association between organisms, symbiosis and its study has thus far largely focused on the evolutionary impact on the host while neglecting the consequences on the associated symbiont. While the role of microbes has been established as an important force in eukaryotic evolution, understanding the impact of eukaryotes on prokaryotic evolution has lagged behind. Recent publications from the Queller Strassmann Research Group center on the phenotypic advantage granted to *Dictyostelium discoideum* host amoebas from the symbiotic association with *Burkholderia* bacteria. Examining the selective advantages or disadvantages conferred upon *Burkholderia* in this relationship may help illuminate the evolutionary forces at the core of this symbiosis. Here, we have developed two novel experimental assays to detect novel traits associated with *Burkholderia* when associated with host amoebas. The Movement Assay measures horizontal distance traveled by the microbes while the Fly Wash Assay measures microbial ability to make contact with host vectors. Together, our findings indicate that host association may aid in *Burkholderia*'s ability to access and disperse to new spaces with high variability across the tested strains.

THE EVOLUTION OF CHEMICAL DEFENSES IN WHITE CLOVER: WHEN AND WHERE DOES CYANOGENESIS MATTER MOST?

Brenda Alvarado

Mentors: Kenneth Olsen and Sara Wright

Cyanogenesis (the production of HCN upon tissue damage), is a polymorphic trait in white clover, with both cyanogenic and acyanogenic types being found in nature. This trait has also been associated with local climatic adaptation in white clover, due to the repeated documentation of clinal patterns worldwide. That is, the proportion of cyanogenic plants found in white clover populations increases dramatically from cooler to warmer climates. The goal of this study was to determine the effects of cyanogenesis variation on white clover fitness at early life stages, specifically germinant and seedling survival. Seeds were collected from 100 female parent seeds from each of three sites across a latitudinal gradient: Duluth, MN, Saint Louis, MO, and Gainesville, FL and were planted at each of the three sites, as well as in the WashU greenhouse as a control. They were left to germinate and grow to the seedling stage in the field, and semi-weekly photographs were used to quantify germination and survival rates at each site. Surviving seedlings were classified according to cyanotype to ask whether the proportion of the locally adaptive cyanotype at each field site increased in frequency relative to the greenhouse control group, which would suggest that the evolution of cyanogenesis clines occurs early in the white clover life cycle.

STREAMLINING ENROLLMENT IN EARLY CHILD CARE CENTERS USING STABLE MATCHING

Rishab Arora, Julia Burns, Melissa Crombie and Mo Wu

Mentor: John McCarthy

This project applies the classical stable matching algorithm in mathematics to early child care center enrollment. The “stable marriage” algorithm, first outlined by Gale and Shapley, gives an optimal stable pairing of men and women based on their rankings of one another. Such an algorithm is applicable here because for a center with multiple classrooms and age groups, “pairing” exiting and incoming students optimally is the key to achieving full enrollment. The primary aspects of our study are a discussion of the current problems with enrollment at University City Children’s Center, and the creation of precise “ranking” criteria by which the algorithm determines the best fit students. The modified algorithm in this study accounts for multiple possible cases of incoming students, depending on the ages of the children at the time they enroll. Our work streamlining enrollment is essential to daycare functioning because it ultimately improves the quality of student care. We are finding that this is a highly effective application of stable matching, and we hope to further develop our solution into a program easily usable by child care centers.

THE EFFECTS OF GERMLINE SEQUESTRATION ON MULTICELLULARITY

Odion Asikhia

Mentors: Joan Strassmann and David Queller

There have been many transitions in the history of evolution. For example, the transition of prokaryotes to eukaryotes, asexual to sexual populations, primate to human societies and so forth. We are specifically interested in the transition from unicellular to multicellular organisms. This transition is particularly interesting because multicellularity requires an immense amount of *cellular cooperation*. Our previous research focused on how relatively simple mechanisms such as growth and dispersal affected the evolution of multicellularity.

In this study, we investigated the importance of germline sequestration (differentiation). A germline is the cellular lineage of an organism. Germ cells, distinct from other cells, pass their genetic material to following generations. The segregation of germline cells happens early in development. Previous research suggests the presence of germline cells play a role in the transition to multicellularity. The goal of our experiment is to manipulate the germline cells and observe how they influence the presence of multicellularity.

We created multicellular pseudo-organisms using *Dictyostelium discoideum* and 3D printed plates. *D. discoideum* is a eukaryote that transitions from a unicellular amoeba to a multicellular slug to form a fruiting body when starved. A fruiting body consists of an upright stalk (composed of dead cells) with a mass of surviving cells at the apex. A key characteristic of multicellularity is cooperation. We grew the pseudo-organism with three different life cycle structures over many generations. We theorize that the presence of cheaters, which are non-cooperative, should break down the multicellular system, but some types of germline sequestration pattern may prevent this from occurring.

RYBOSOMAL RNA-PROCESSING PROTEIN: HOW DOES IT AFFECT THE GROWTH OF *PLASMODIUM FALCIPARUM*?

Yolotzin Avila-Cruz

Mentor: Eva Istvan

Malaria continues to be a ravaging disease that approximately half the world is at risk of and it mainly affects children under the age of five. Currently, there is no cure for malaria, but drugs and a vaccine help combat the disease. Unfortunately, the parasites are developing resistance to drug therapies and the only approved vaccine shows at best a fifty percent efficiency. Understanding how the parasites thrive is crucial to developing effective therapies.

This research, which identifies genes essential for parasite survival, is a key prerequisite for the development of new and improved treatments for this disease. In our lab, we work with *Plasmodium falciparum*—the most multidrug-resistant parasite of malaria. Our focus is to understand whether an amplification on chromosome 10 is responsible for fast growth. To solve this, we have selected a protein-coding gene, RPP, from that chromosome to monitor its growth against a normal growing parasite. If we find that the parasites with the gene do indeed grow at a faster pace than the normal ones then we will have identified a new target for drugs for our fight against malaria, a disease that has shaped—and will likely continue to shape—human evolution.

HEURISTIC APPROACH TO SPIKING NEURAL NETWORKS

Bryce Bagley and Blake Bordelon

Mentor: Ralf Wessel

The discrepancy between the time encoded (TE) and the rate encoded (RE) models of computation in neural networks motivates the investigation of weight optimization in spiking neural networks. Optimized TE networks would not only provide a faster alternative to traditional RE systems but also could offer insight into the mechanisms of neural coding in biological systems, in which many computations are dependent on precise timings of individual spikes. We apply heuristic algorithms to optimize the weight matrices of leaky integrate and fire (LIF) networks. Spike trains were produced from both small world LIF model networks with light Gaussian input currents and from calcium microscopy measurements of the mouse visual cortex. Each of these spike trains serve as goal spiking behavior for each application of the optimization algorithm. The proposed algorithm first optimally matches corresponding output spike trains of a naïve network and with the goal spike trains. By making small, targeted variations to the presynaptic weights, we then eliminate spikes in the naïve network that were unpaired or produce new spikes in the naïve network outputs to match those unpaired in the goal outputs. For both the model data and the data from biological measurements, the algorithm does reproduce statistical features in the outputs including inter-spike interval and CV distributions, suggesting that the algorithm often reduces to optimizing the rate of firing. In addition, we found that post-optimization inter-spike interval histograms tended towards exponential distributions. However, the precise reproduction of spike times remains elusive. Further inquiry could indicate if improved versions of our algorithm or other similar heuristics can be used to reproduce exact spike timings.

AFTER THE CRASH: TREATMENT OF MOTOR VEHICLE ACCIDENT-ASSOCIATED PTSD USING ART THERAPY

Sarah Banks

Mentor: Eileen G'Sell

Post-traumatic Stress disorder (PTSD) is a psychiatric disorder that results from experiencing or witnessing traumatic or life-threatening events, and affects more than 2% of the population. While commonly assumed to be a result of assault or wartime trauma, it can also likely be a result of motor vehicle accidents. While there are a number of treatments, optimal treatment strategies have not yet been standardized in practice. To explore art therapy's potential effectiveness for treating motor vehicle related PTSD, I examined various studies on PTSD treatment and conducted a cross-analysis of research literature. Eye movement desensitization and reprocessing (EMDR), the most widely accepted therapeutic modality, utilizes Alternating Bilateral Stimulation (ABS), a technique not specific to EMDR. EMDR has not been found to be ultimately effective for various lesser-known symptoms of PTSD such as avoidance of talking about or being reminded of the traumatic event, negative alterations in thoughts and mood, emotional numbing, trouble processing trauma, and hyperarousal symptoms. I researched whether art therapy, which can also utilize ABS, might be well suited to address these other symptoms of PTSD. Art therapy may also allow patients a nonverbal method to communicate and reprocess their trauma, thereby offering a potentially more comprehensive approach to treating trauma symptoms. The Broca's area of the brain is an area wherein PTSD-related injury has been frequently associated with some of these lesser known symptoms. Art therapy appears particularly well suited to healing injury to this region. Thus, art therapy, at least as an adjunct to EMDR, should be part of the therapeutic approach, especially in those motor vehicle victims whose Broca's area has been impacted.

SOYBEAN-DERIVED HUMAN EGF ENHANCES WEIGHT GAIN AND LEAN MUSCLE MASS IN MALNOURISHED MICE

James Bao

Mentor: Brad Warner

Chronic undernutrition is a significant contributor to mortality in children and has both short- and long-term effects on growth and development. Poor sanitation often accompanies poor nutrition and has been shown to contribute to repeated exposures to enteric pathogens. The combination of undernutrition and chronic intestinal infection leads to a syndrome of malabsorption and increased intestinal permeability called environmental enteropathic dysfunction (EED). Due to the shown effects of Epidermal Growth Factor (EGF) on enhancement of gut barrier function and growth in weanling models of stress-induced undernutrition, transgenic soybean-EGF was used to mitigate EED. C57BL6 mice were bred and 10 days after birth dams were given either standard chow or a protein deficient isocaloric diet (RBD), until weaning at day 21. Mice were randomized to receive soybean-EGF or vehicle via oral gavage for 21 or 42 days. We assessed weight gain, body composition, intestinal morphology, intestinal permeability, gene expression, food intake and metabolism. Male mice treated with soybean-EGF gained significantly more weight after six weeks and had increased lean mass and decreased fat mass compared to vehicle gavaged controls. Female mice did not demonstrate these findings. We found that neither diet nor soybean-EGF caused significant differences in intestinal morphology or intestinal permeability despite differences in tight junction gene expression in mice on RBD. Soybean-EGF treatment enhances growth and lean mass in male protein deficient malnourished mice. Regional basic diet alone does not alter intestinal morphology or intestinal permeability as measured by dual sugar absorption test.

ISOLATION, SEQUENCING, AND ANNOTATION OF BACTERIOPHAGE GILSON

Morgan Batley, Ahmed Hanafy, Nupur Singh, and Nathan Soria

Mentors: Kathy Hafer and Chris Shaffer

Bacteriophages are one of the most prevalent biological entities in the world, yet only a small fraction of the species in existence have been discovered. Although some phages are used for therapeutic uses, much more research is required before this practice becomes widespread. After directly isolating an environmental soil sample containing Phage Gilson at 38.647 °N, 90.311 °W just off the side of Forsyth Blvd. in St. Louis, MO, we were able to infect bacterial host *Streptomyces griseofuscus* and purify our phage to a high titer of 5.11×10^{10} and extract its DNA. Through analyzing restriction enzyme digests from gel electrophoresis, we identified that the enzyme *BamHI* did not cut the DNA while enzyme *EcoRI* cut to give an estimated genome of 70,684 base pairs. Using electron microscopy we determined that the phage has an icosahedral head shape with a long, flexible tail. After sending our samples to the Washington University School of Medicine's sequencing facility, we measured a head length of 87 nm, head width of 79 nm, and tail length of 321 nm. After sequencing the genome, Phage Gilson was found to have a genome length of 128,338 base pairs with a fixed, terminally redundant end of 788 base pairs. Several tRNA clusters were also found in Gilson's genome around 5 kbp, and throughout 65 kbp - 105 kbp. Using online tools such as PECAAN (Phage Evidence Collection and Annotation Network), we analyzed coding potential, gap scores, Shine-Dalgarno scores, and DNA BLAST results to determine the presence of 231 genes in the Gilson genome. DNA Master was used to find any gray holes—genes we may have missed in the initial positional annotation. By annotating the positional and functional parts of a novel phage, such as Phage Gilson, we will have a more complete understanding of how to use different bacteriophages' functions in modern science.

50 STATES OF PURPOSE: A STUDY OF PURPOSEFUL LIVING IN THE UNITED STATES

Gemma Baugh

Mentor: Patrick L. Hill

Purpose is a higher-order construct that guides the development of goals and goal-oriented behaviors, providing individuals with a sense of meaning. Individual-level research has demonstrated the role of purpose in short- and long-term functioning, with many positive outcomes. This understanding of purpose has the potential to inform other disciplines including public policy, but first we must study purpose at the group level to understand how it functions within communities, not just within the individual.

We used survey data representing 51 different entities (the 50 U.S. states and D.C.) collected primarily in 2015 by Gallup, the U.S. Census Bureau, the Bureau of Labor Statistics, and the CDC. We selected three survey items from Gallup to assess the average level of purpose among citizens in each U.S. state and analyzed potential purpose correlates also aggregated at the state level by calculating zero-order correlations between purpose and each of these variables followed by partial correlations controlling for age and income.

Purpose varied from state to state, with West Virginia holding the lowest purpose score (3.68), compared to Alaska with the highest score (3.98). Many individual-level correlations were supported by our analysis, including correlations between purpose and health, affect, and financial status. Lower purpose scores were associated with more health problems and negative emotions. Higher purpose scores were associated with lower income inequality, greater numbers of high school and higher education graduates, and higher rates of happiness.

Though additional research is needed to pinpoint the directionality of our state-level purpose correlations, we have demonstrated that higher levels of purpose will be seen in tandem with other advantageous social, financial, and health conditions. These findings highlight further avenues for purpose research and suggest that public health officials or other policy-makers may seek to promote purpose as a way to increase other beneficial societal outcomes.

THE APPLICATION OF POLY ACRYLIC ACID AS A pH SENSITIVE HYDROGEL IN WGM RESONATORS

Zaneta Belay

Mentor: Lan Yang

In today's day and age, we have made so many advancements in the field of biocompatible medical devices. Some of the most widely used biocompatible material are hydrogels. Their unique properties such as high water content, softness, flexibility, and biocompatibility have made hydrogels very popular. Currently, hydrogels have a well-established role in the manufacturing of contact lenses, hygiene products, tissue engineering scaffolds, drug delivery systems and wound dressings. Many hydrogel-based drug delivery and scaffolds have been designed, studied and in some cases even patented, however, not many have reached the market. Because hydrogels have a large resemblance to living tissue, it opens many opportunities for applications in biomedical areas, particularly internal drug delivery.

A key component when using hydrogels in drug delivery is understanding how the gel reacts in various environments. Often times when placed in a different environment the hydrogel will start to swell or shrink. Swelling of the gel is extremely important for the release of the drug into the body. We have decided to focus on how changes in pH affects the hydrogel. After much trial-and-error it has been found that poly acrylic acid (PAA) serves as a pH-sensitive hydrogel. Because this creates an extremely acidic solution, when the gel is in a basic or even neutral environment the hydrogel swells to three times its original size. Because we need to be able to electronically control the hydrogel, another important component is the gel's ability to retain the light properties of a microresonator, which is something that has not been perfected, but has strong promise for future projects.

THE EFFECTS OF FIBROBLAST CO-CULTURE ON HELa TUMOR CELLS

Alex Benton

Mentor: Gary Patti

Tumors *in vivo* interact with the surrounding tissue, which are often cancer-associated fibroblasts. *In vitro* co-culture experiments of tumor cells with these fibroblasts provide a better understanding of these cells' interactions in a physiological system. It is suspected that fibroblasts can have a significant effect on the growth of tumor cells. My studies quantified the effect of 3T3 fibroblasts on the proliferation of HeLa, a human tumor cell line, and qualitatively observed these effects. Proliferation was measured using a Cytation³ imaging machine and compared in different co-culture conditions, while time-lapse video of these conditions was recorded with an Etaluma Lumiscope³ prototype. Different co-culture conditions had dramatically different effects on the HeLa cells that either increased or decreased proliferation. These results aim to generally establish trends in co-culture for other investigations that will be conducted in the Patti Lab.

EMOTION REGULATION AND AUTHENTICITY

Jessica Birg

Mentor: Tammy English

Research has shown that suppressing emotions can have negative social and psychological consequences. Subjective inauthenticity (the feeling of being “fake”) has been found to mediate the link between frequent use of suppression and poor social functioning; however, it is still unknown if suppression influences others’ impressions of one’s authenticity. In the present study, we aimed to test if suppression influences both subjective feelings and impressions of authenticity. We hypothesized that people who suppress during a conversation with a stranger will rate themselves as being more inauthentic than those who do not suppress, because they will be unable to show their true emotions. Partners of suppressors will also rate the suppressor as being more inauthentic, because they will be able to sense that their partner is trying not to be expressive. We recruited 142 undergraduate students from Washington University in St. Louis to form a set of 71 zero-acquaintance dyads. Students were instructed to share a personal negative event with their interaction partner; one participant sometimes received additional instructions to either suppress or exaggerate their emotions during the conversation. Exaggeration was used as a contrasting condition, in which we instructed students to express their emotions visibly to their interaction partner. After the conversation, participants answered questions regarding their authenticity as well as their impressions of their partner’s authenticity. Results from APIM analyses indicated that those who suppressed during the conversation felt less authentic than those who did not, which is consistent with the prior literature. However, there were no significant results for exaggeration or impressions of partner authenticity. By looking at how unacquainted students rate themselves and each other on authenticity, we hoped to gain an understanding of the social consequences of suppression at more than one level.

PERFORMING CULTURE IN THE TOURIST CITY: THE CONSTRUCTION OF ESSENTIALIZED IDENTITY IN CUZCO, PERÚ

Gabriela Bloom

Mentors: Ignacio Sánchez Prado and Javier García Liendo

This work analyzes the construction of regional identity in Cuzco, Perú and how this essentialized identity is commodified to define the ideal tourist encounter. The *indigenismo* and *neoindianismo* intellectual movements in the twentieth century shaped regional Cuzco identity as one in which the grandeur of the Inca Empire is valorized and celebrated and the present indigenous and mestizo experience is marginalized as socially inferior. Through the tourism industry, these attitudes of the Cuzco elite have propagated in the performance of culture. The sanitization and negotiation of public spaces serves to preserve an essentialized image of the physical space and the social composition of Cuzco in order to meet the tourists' expectations. Local policies serve to eradicate tourist spaces of individuals who are perceived as dirty and unrefined. The mediated physical space and social composition of Cuzco suspends the tourist city in time and prevents *cuzqueños* from accessing the tourist space. Ritualized performances such as *Inti Raymi*, the annual Festival of the Sun, also demonstrate the priorities of the cultural elite to preserve an essentialized *cuzqueño* identity rooted in the glory of Inca traditions. The historical and cultural context of the creation of these rituals impacts how *cuzqueños* interact with and interpret the staged performance. Both the twentieth-century construction of identity by the Cuzco elite and the tourism industry seek to create a specific, mediated image of Cuzco that is divorced from social and cultural realities of the region. The tourism industry relies upon the commoditization of this essentialized identity, and the performance of staged authenticity legitimizes the elite construction of culture and identity.

NATURALIZING SCALES OF INJUSTICE IN JORDANIAN WATER

Seth Blum

Mentor: Jeremy Caddel

Several hydropolitics scholars have noted that the literature on Israeli-Jordanian hydropolitical relations suffers from a curious disengagement from social justice questions and methodologies. While much has been written on the procedural and substantive fairness of the 1994 treaty, as well as the process of its negotiation, the uneasy naturalization of a fixed ratio of water allocation and the adherence to a data-based system borne out of procedural fairness had escaped investigation. Furthermore, there is a lack of mixed methods or digital humanities approaches to the study of discourses and practices of water scarcity in Jordan. Academics, the Ministry of Water and Irrigation, and donor organizations have used GIS to improve the efficiency of water distribution, but there has been no effort in the critical literature to spatially document changing scales and their relationship to discourse.

My summer research grounded an interest in distributional justice and inequality in access a more concrete project with a robust methodological framework. Over the summer, my interest shifted from interest in indicators determining access to green space to a different set of quantitative indicators determining quality of life—water allocations and international water treaties. The preparatory work required to site, understand, and propose such a project consumed much of my research time over the summer.

IMAGINATION MAY OVERRIDE SPONTANEOUS RETRIEVAL OF PROSPECTIVE MEMORY INTENTIONS

Casey Bowen

Mentor: Julie Bugg

Prospective memory (PM) is often studied as the ability to carry out relevant intentions. This study focuses on the gap in the PM literature concerning one's ability to forget a previously relevant intention. There are two phases of the experiment; the active and the finished phase. In the active phase, participants encode the PM intention of pressing the 'Q' key when salient target words are presented during a lexical decision task. In the finished phase, the participant is instructed that the previously relevant intention is now irrelevant. The participant then undergoes two blocks of the lexical decision task while being probed for the response (pressing the 'Q' key). The present study analyzes two types of forgetting practice, which we believe will lead to a significant difference in commission errors (how many times a participant performed an irrelevant action). In the imagination condition, participants walk through an imaginary example of forgetting the previously relevant intention. In the control condition, participants are explicitly told they should not press the 'Q' key when presented with the target words, but they are given no practice (real or imaginary). Commission errors are recorded and analyzed for each condition using Chi-Square and T-Tests. Results support our hypothesis that there is a decline in executive control from older to younger adults. Younger adults also show a significant reduction in commission errors from the control condition to the imagination condition. We find a numeric trend in a reduction in commission errors in older adults, but not a significant difference. Based on these results, and the previous literature, we have reason to believe that imagination practice helps a participant deactivate a previously relevant intention. This could have major implications when applied to real life tasks, such as implementing a smooth change to a new medication prescription.

MASTERY MOTIVATION IN CHILDREN: CAN INCREASED TASK DIFFICULTY ENHANCE TASK COMPETENCE?

Casey Bowen and Alyssa Hunt

Mentor: Laura Hennefield

Children's motivation to master a task could be malleable based on the task's difficulty, and understanding how to intentionally enhance children's motivation could provide educators with effective strategies to ultimately strengthen learning outcomes. The goal of the present study is to determine whether the initial difficulty of a task impacts children's motivation to complete and master the task, thus serving as a desirable difficulty for children. Children ages 3-8 completed a building task in which they replicated a set of block buildings, beginning with either initially difficult models or initially easy models. Children's persistence to complete the set and their ability to replicate the models correctly were measured as indicators of the child's mastery motivation. The findings demonstrated that younger children, but not older children, were more affected by the initial difficulty of the task, such that younger children who started with the initially easy models demonstrated greater competence than younger children who began with the initially difficult models. Therefore, our results reveal that younger children may be more motivated and thus learn more effectively by starting with easier tasks and working their way up to harder tasks. In this way, task difficulty could be an effective pedagogical strategy to enhance younger children's motivation and subsequent overall performance.

BUYING BREATH:
A STUDY OF THE JUXTAPOSITION OF YOGA
AS A COMMODITY, A BIOPHYSICAL WORKOUT, AND
A QUASI-RELIGIOUS EXPERIENCE IN YOGA TEACHER
TRAININGS IN MIDWEST AMERICA

Sarah Burack

Mentor: Rebecca Lester

This study explores how yoga teachers, working in an increasingly competitive market, learn to integrate the discourses of biophysical health, quasi-religious, spiritual philosophy into a lifestyle that is sold to the general public for consumption. By focusing on yoga teacher training programs as a node of information exchange and transfer, this study hopes to shed light on the mechanisms of experiential learning. The singular governing body of certification, Yoga Alliance, which in itself calls to question issues and benefits of standardization and democratization of an ancient Indian practice, requires 200-hour certification courses to teach about emotional and physical stress through a combination of anatomy, yogic philosophy, and nonviolent communication. The environment (social, political, digital) surrounding an individual is intrinsically entwined with the biophysical body, the theological body, and the body as a commodity. This study argues that individuals will consequentially teach yoga to the general public based on their individualized experience: the standardized course work, the intentionality of instructors, and the media surrounding their practice. Understanding yoga teacher trainings can tell us about attempts to handle chronic stress in contemporary American culture. I conclude that individuals are driven by aesthetic, and the means of relaxation and fostering community are shifting from organized religion to a pick-and-choose body of influences. Studies of yoga needed to further implement this health trend into mainstream public health ought to not look at the dichotomy of yoga as a physical practice versus a metaphysical experience, but rather an integrated, holistic practice that develops in a manner that is specific to time, community, and individual. Data was collected through participant observation and semi-structured interviews with women training to become yoga practitioners and certified teachers who train them for a total of 12 participants from three different studios in St. Louis, Missouri, from June 2017 to August 2017.

DRIVING GENE EXPRESSION IN THE HETEROCHROMATIC ENVIRONMENT OF THE FOURTH CHROMOSOME OF *D. MELANOGASTER*

Jacob Cantrell

Mentors: Sarah C. R. Elgin and Elena Gracheva

Genomes of higher eukaryotes can be divided into two fundamental and dynamic subtypes: euchromatin and heterochromatin. In general, genes that are active in a euchromatic environment are silenced when transposed to heterochromatin. However, heterochromatin is not devoid of actively functioning genes. The main goal of our project is to identify regulatory elements that drive transcription of heterochromatic genes. The fourth chromosome of *Drosophila melanogaster* represents an excellent model for this study: ~80 genes within this heterochromatic domain are expressed.

Insertion of an *hsp70-white* transgene, which results in a uniform red eye phenotype when present in euchromatin, into a heterochromatic region on the fourth chromosome results in sporadic silencing, or Position Effect Variegation (PEV). We replaced the *hsp70* promoter of *hsp70-white* with a 5' genomic fragment of a highly-expressed fourth chromosome gene, *Rad23*. Insertion of the *Rad23-white* transgene into the same location switched the *hsp70-white* PEV phenotype to a uniform full red eye, suggesting that the *Rad23* fragment is sufficient to drive strong expression of the euchromatic white reporter. A series of experiments with reporter constructs containing fragments of varying lengths of the *Rad23* promoter region is helping us identify the minimal length of the *Rad23* promoter fragment to drive white expression. The removal of a 250 bp *Rad23* promoter fragment bringing an upstream 1360 transposon closer to the TSS did not result in silencing of the white reporter. An additional construct where a 100 bp *Rad23* promoter fragment replaces the corresponding portion of the *hsp70* promoter in the *hsp70-white* transgene resulted in the loss of PEV, but low level expression (light orange eyes). Additional experiments to identify the essential elements of the 5' noncoding regulatory region of the *Rad23* gene are underway.

SOIL RESPIRATION IN NATIVE TALLGRASS PRAIRIES UNDER CLIMATE CHANGE: THE ROLE OF ABOVE AND BELOWGROUND DIVERSITY

Erin Carroll

Mentor: Scott Mangan

Understanding how climate change may alter ecosystems' ability to function is crucial to securing the many ecosystem services provided to humans. It is well-established that an ecosystem's capacity to function, and thus the ecosystem services it provides to humans, is positively related to its biodiversity. However, how climate change influences interactions among members of different trophic levels to influence ecosystem functions is not well-understood yet. In this study, we explore how increased soil microbial diversity and plant diversity interact under drought conditions to influence soil carbon respiration in native Tallgrass Prairie ecosystems. Grasslands play an extremely important role in the global carbon cycle, storing more than twice as much carbon in the soil as the atmosphere. Our results show significantly higher soil respiration rates in more diverse plant communities only in the presence of a diverse live soil microbial community, while this positive plant diversity effect disappears in soils lacking a diverse live soil microbial community. Under drought conditions, we found soil respiration rates decreased in the absence of live soil biota relative to well-watered conditions. However, drought conditions had no effect on respiration rates in the presence of a diverse soil microbial community. These results suggest that soil microbes play a key role in maintaining the positive relationship between diversity and ecosystem function, potentially stabilizing ecosystem function and securing the delivery of ecosystem services under climatic stresses.

THE ROLE OF SOIL MICROBES AND PLANT DIVERSITY IN POLLINATION AND SOIL CARBON SEQUESTRATION UNDER CLIMATE CHANGE

Erin Carroll and Savannah Fuqua

Mentor: Scott Mangan

It is well-established that an ecosystem's functioning, and thus the services it provides us, is related positively to its biodiversity. Further, it is known that soil microbial communities play an important role in maintaining this relationship between plant diversity and ecosystem functioning. How the relationship between soil microbes, plant diversity and ecosystem functioning will be affected by a changing climate, however, remains unclear. In order to explore these interactions we examine how pollination and soil carbon sequestration, two important metrics of ecosystem function, are affected by plant community diversity, drought, and soil microbial communities within the context of native tallgrass prairies. Specifically, as previous data has shown that soil microbes have a strong influence on the fecundity of individual plant species in this system, we attempt to determine whether this is through a direct effect on plant fitness or an indirect effect by mediating plant-pollinator interactions. Additionally, as our lab has shown with past data that systems with live soil microbial communities continue to sequester carbon under drought conditions better than systems with sterile soil, we examine how the same measurements are affected by different gradients of plant community diversity.

GENE MUTATIONS ASSOCIATED WITH DYSTONIA-PARKINSONISM DO NOT IMPAIR PLA2G6 PHOSPHOLIPASE ACTIVITY

Sthitadhi Chakraborty

Mentor: Paul Kotzbauer

Mutations in the PLA2G6 gene have been identified in autosomal neurodegenerative diseases, such as dystonia-parkinsonism and infantile neuronal dystrophy (INAD). Those with dystonia-parkinsonism develop a parkinsonian movement disorder between the ages of 15 and 30. The PLA2G6 gene encodes an enzyme known as calcium-independent phospholipase A2 beta (iPLA β), which hydrolyzes the sn-2 acyl groups of phospholipids and lysophospholipids, producing free fatty acids. In previous studies we found that PLA2G6 mutations associated with INAD cause loss of function for the enzyme, but PLA2G6 mutations associated with a dystonia-parkinsonism phenotype do not impair the catalytic function in A2 phospholipase and lysophospholipase assays. Due to the recessive nature of dystonia-parkinsonism, we hypothesize that mutations in PLA2G6 cause loss of PLA2G6 function. In this study, we investigated the A1 phospholipase activity of PLA2G6 and whether dystonia-parkinsonism mutations impair this aspect of PLA2G6 function.

We produced wild-type (WT) PLA2G6 and mutant PLA2G6 proteins in HEK293 cells by transient transfection of expression plasmids. The A1 phospholipase activity (hydrolysis of the sn-1 acyl group) was measured in sonicated cell extracts using the fluorogenic phospholipase substrate, *PEDA1*, at 37°C. We find that after controlling for enzyme concentration, catalytic activity of mutant PLA2G6 proteins is not significantly different from WT. Some mutations even have slightly greater catalytic activity for *PEDA1* when compared to WT.

These results were compared to previous studies involving mutations in *PLA2G6* and their association with diseases such as INAD and dystonia-parkinsonism. The findings solidified the notion that dystonia-parkinsonism mutations do not directly impair *PLA2G6* catalytic activity in a significant manner, and therefore may impair PLA2G6 function by other mechanisms.

USING CAVE BACTERIA TO INHIBIT *PSEUDOGYMNOASCUS DESTRUCTANS*, THE WHITE NOSE PATHOGEN

Austin Chan

Mentor: Joshua Blodgett

Pseudogymnoascus destructans, the causative fungus of White Nose Syndrome (WNS), has rapidly spread across North America, endangering many species of bats through accelerating their use of stored fuels during hibernation. Bats diagnosed with WNS have faced greater than 90% mortality in caves. In hopes of controlling this fungus, we screened cave bacteria for antifungal compounds inhibitory to *P. destructans*. Actinomycetes, a widely-distributed family of filamentous bacteria, have a long history of producing antibiotics. They have been known to synthesize a great variety of our current day antibiotics and serve as an important discovery platform for new antibiotics. With this reasoning, we performed enrichments to isolate cave actinomycetes, amassing a library of over 500 individual strains. To screen for antibiotic activity, we tested organic extracts from spent culture media against the yeast *Saccharomyces cerevisiae* and *P. destructans*. Extracts giving the strongest inhibition were subjected to further analysis by mass spectrometry (MS), chromatography (HPLC) and additional bioassays. Additionally, we are collaborating with the Doering Lab (WUSM) to screen our extracts against *Cryptococcus neoformans*, a facultative intracellular pathogen that causes severe brain and lung infections in humans. Within our library, we discovered 56 actinomycetes that have pronounced antifungal activity. Broadly, we found some are active against all three indicator organisms, while others were more selective against *P. destructans*. These studies are foundational towards identifying specific antibiotic compounds and strains for the environmental control of WNS.

EXPERIMENTAL VERIFICATION OF METALLIC GLASS PREDICTION FROM LIQUID DATA

Ryan Chang

Mentor: Ken Kelton

Unlike ordinary metals with crystalline atomic arrangement, metallic glasses or amorphous alloys, have a disordered atomic arrangement with local order extending to nearest and next-nearest neighbors only. From a practical standpoint metallic glasses have many desirable technological advantages over normal, crystalline, metals that make them of potential commercial and military interest. They are much stronger than normal metals and can be processed into intricate shapes using techniques that are similar to those used to prepare polymeric materials. However, the process of metallic glass formation and of how a liquid transforms into a glass (the glass transition) are incompletely understood. Our goal is to go beyond the trial and error methods commonly used to predict whether a liquid can make a good glass, and to devise an algorithm for identifying good glass formers that does not require measuring T_g (the glass transition temperature) beforehand.

We propose that the critical casting thickness (d_{max}), which is a glass forming ability indicator, is correlated with T_g and T_g/T . Based on this we can derive a predictive formula for glass formation. Further, we have shown that T_g/T^* , T_g/T_A , and the liquid expansion coefficient are correlated with T_g . This allows us to predict T_g before making any glass; it can be predicted based on only the liquid data. Using the predicted T_g and the correlation between $\log(d_{max} \cdot d_{max})$, T_g , and T_g/T^* , glass formability can be predicted from liquid data alone. Our work will tell us whether our predictive algorithms are capable of pointing to good glass formers and, if so, giving an accurate value for T_g , using only data from the high temperature liquid. Our studies of adding element to destroy the icosahedral structure in alloys will also tell us whether the predictive algorithm needs to correct for a liquid structure term.

LINKING CIRCADIAN CLOCKS TO MAMMALIAN OVULATION

Sneha Chaturvedi

Mentor: Erik Herzog

Most biological processes are regulated by an internal circadian rhythm, critical for synchronizing cellular, organ, and bodily functions with the outside environment. One such process is the ovulation cycle in female mammals, regulated to occur when the oocyte is mature and at the optimal time of day, when sexual motivation and bodily activity peaks. The suprachiasmatic nucleus (SCN), located in the hypothalamus, is the main pacemaker in mammals, dictating the overall circadian rhythm of the body. VIP neurons, found mostly in the core region of the SCN, synchronize the overall rhythm of the SCN, taking in light cues from the outside environment. Given that ovulation is regulated by circadian rhythms, we think VIP neurons, named for their release of vasoactive intestinal peptide, may help regulate ovulation in mammals. VIP neurons connect synaptically with GnRH neurons, which regulate the release of luteinizing hormone (LH), and a surge of LH at the right time stage of the cycle triggers ovulation. We hypothesize that VIP neurons, through VIP release, send signals to GnRH neurons to contribute to the circadian timing of LH release and ovulation. To test this, we will observe how stimulation of VIP neurons affects ovulation of female mice. By optogenetically inducing VIP neuron stimulation out of phase with the normal circadian cycle in vivo, we will test whether VIP stimulation is by itself sufficient to trigger LH release and induce ovulation. Discovering the impact VIP neurons have on ovulation will not only provide important insight into how the circadian clock controls the timing of impact other circadian regulated circuits in the body. Understanding how circadian circuits work can help with diseases caused by a disruption in the normal circadian cycle, and in this case, how disruptions can affect reproduction and fertility.

ENCODING THE EXPECTATION OF A SENSORY STIMULUS

Alex Chen

Mentor: Barani Raman

Most organisms possess an ability to differentiate unexpected or surprising sensory stimuli from those that are repeatedly encountered. How is this sensory computation performed? We examined this issue in the locust olfactory system. We found that odor-evoked responses in the antennal lobe (downstream to sensory neurons) systematically reduced upon repeated encounters of temporally discontinuous stimuli. Rather than confounding information about stimulus identity and intensity, neural representations were optimized to encode equivalent stimulus-specific information but with fewer spikes. Further, spontaneous activities of the antennal lobe network also changed systematically and become negatively correlated with the response elicited by the repetitive stimulus (i.e., 'a negative image'). Notably, while response to the repetitive stimulus reduced, exposure to a novel cue generated undamped and even exaggerated spiking responses in several neurons. In sum, our results reveal how expectations regarding a stimulus is encoded in a neural circuit to allow response optimization and preferential filtering.

A CLICKABLE NEUROSTEROID ANALOGUE RETAINS NMDA RECEPTOR ACTIVITY AND ACCUMULATES IN NEURONS

Daniel Chen

Mentor: Steven Mennerick

NMDA receptors (NMDARs) are glutamatergated ion channels that play important roles in the neurobiology of higher organisms. Abnormal NMDAR function is implicated in a multitude of cognitive defects, including depression, autism, schizophrenia, Alzheimer's disease and epilepsy. Therefore, these receptors represent important therapeutic targets for many CNS disorders. Steroidlike compounds, such as pregnenolone sulfate and 24SHC, have been shown to be especially efficacious in the positive and negative modulation of NMDARs. However, the mechanisms by which these compounds are trafficked or compartmentalized in neurons are unknown. These mechanisms are highly relevant in a clinical context, as they correlate to the onset, duration, and intensity of a drug's effect. Thus, further knowledge of compartmentalization mechanisms is needed for the synthesis of more efficacious drugs. In order to investigate the cellular trafficking of these drugs, we will develop "tagged" biological analogues. These analogues will contain: 1) a chemical handle, permitting click chemistry, and 2) a fluorescent diazirine group, facilitating high-resolution cellular imaging and Colocalization of the compounds within the cell. Since these analogues are structurally similar to natural compounds, we expect they will behave comparably in their access to and actions at NMDARs. Ultimately, they will be used as probes of cellular compartmentalization, providing insight into the trafficking of natural neurosteroids at NMDARs. To assess the biological activity of these analogues, we will treat hippocampal neurons with an analogue coapplied with NMDA. For those analogues that potentiate or depress NMDA function, we will label them with a photolabeling diazirine group and analyze them with *in situ* photolabeling. This will inform our understanding of active and passive compartmentalization mechanisms on a cellular level. We hope that this understanding of psychoactive drug pharmacokinetics will aid in the synthesis of new drugs.

A P-ELEMENT MOBILIZATION SCREEN IN *DROSOPHILA MELANOGASTER* USING A TRANSGENE CONTAINING GAA REPETITIOUS SEQUENCE

Frank Chen, Mitchell Grinwald, Mikayla Johnson, and Kendra Woodruff

Mentor: Sarah C. R. Elgin

Eukaryotic genomes are packaged in euchromatin and heterochromatin. Heterochromatin is mainly located around centromeric and telomeric regions of the chromosomes, and plays a crucial role in maintaining genome stability. While euchromatin is enriched with genes, heterochromatin consists primarily of repetitious sequences and has relatively few genes. Heterochromatic regions have compact nucleosomal arrays, rendering DNA inaccessible to the transcriptional machinery. Placement of euchromatic genes into heterochromatin results in sporadic gene silencing (Position Effect Variegation). Expansion of a GAA triplet repeat results in local heterochromatin formation in humans, causing Friedrich's Ataxia. Our research employed the model organism *Drosophila melanogaster* and utilized a *P*-element transgenic construct containing 310 copies of GAA located upstream of the reporter gene *hsp70-white*, which is required for fly eye pigmentation. The presence of the GAA repeats results in PEV of *hsp70-white* when the transgene is located at the base of the second chromosome. Insertion of *GAA₃₁₀hsp70-white* into several other locations did not produce a PEV phenotype. We conducted a large-scale genetic mobilization screen aimed at identifying new genomic locations of the transgene which give a PEV phenotype. Using stable fly lines containing either the functional *P*-element transposase or our reporter, we performed genetic crosses to mobilize the construct and observe its transposition pattern. We determined chromosomal locations of new insertion sites using genetic tools, and then mapped the sites on the molecular level. Our results show that most insertion sites resulting in variegation occur in hot spots in telomeric and pericentric regions of the second and third chromosomes; three sites were found on the heterochromatic Y chromosome, but none were observed in the heterochromatic fourth chromosome. Variegating transposition sites account for 4.3% of the total number of mobilizations detected. Our next goals are to confirm GAA dependence and investigate which factors affect GAA-mediated heterochromatin formation.

TFEB-DEPENDENT INDUCTION OF THERMOGENESIS BY TREHALOSE

Phillip Chen

Mentor: Brian DeBosch

Trehalose is a disaccharide that has been used in neurodegenerative studies due to its ability to induce autophagy—the critical homeostatic process by which organelles, lipids, and proteins are degraded in the cell. We have demonstrated the beneficial effects of trehalose on aspects of the metabolic syndrome, such as non-alcoholic fatty liver disease (NAFLD). Trehalose achieves this by blocking the transport of glucose and fructose via glucose transporter 8 (GLUT8) to trigger a starvation-like response. The metabolic effects of trehalose in the liver and for the whole body are largely unknown. In this project, we showed trehalose's ability to induce hepatic starvation response and trigger downstream TFEB-dependent thermogenesis. Performing *in vivo* mouse experiments, we found that white adipose tissue (WAT) uncoupling protein-1 (UCP1) levels increased with trehalose treatment and thermogenesis simultaneously increased. UCP1 mediates heat and calorie dissipation by decreasing the proton gradient in oxidative phosphorylation, leading to futile cycling. We determined mechanistically that the TFEB, PGC1 α , and FGF21 pathway, which are all upregulated in energy-deficient situations (e.g., trehalose treatment), are mediators of WAT (UCP1) levels. *In vivo* experiments with TFEB-deficient mice transfected by adeno-associated virus 8 (AAV8) with TBG promoter, a virus specifically targeting hepatocytes, mitigated heat release and trehalose-induced PGC1 α and UCP1 in WAT. Furthermore, ATG16L1, an autophagy protein complex, was dispensable for trehalose-induced thermogenesis. The data serves to demonstrate that trehalose's therapeutic effect on diabetes, obesity, and metabolic syndrome are not necessarily dependent on autophagy; rather there are other mechanisms such as TFEB-dependent induction of thermogenesis involved.

HIGH PROTEIN DIETS INDUCE AUTOPHAGIC DISRUPTION IN MACROPHAGES OF ATHEROSCLEROTIC LESIONS

Sunny Chen

Mentors: Xiangyu Zhang and Babak Razani

High-protein (HP) diets have long been touted as an effective weight-loss strategy. However, its long-term effects on cardiovascular disease have been inconclusive. Recent clinical and *in-vitro* studies have linked these diets to higher incidences of cardiovascular-related mortality and increased atherosclerotic lesion size. Atherosclerosis is a leading cause of cardiovascular disease, characterized by the accumulation of plaque along the arterial vasculature. The progression of lesions can increase the chances of acute cardiovascular events such as heart attack and stroke. There is mounting evidence that implicates the dysfunction of autophagy, a cellular degradative process that prevents accumulation of cytotoxic aggregates, with lesion progression. Taking this into account, the objective of this study was (1) to investigate the relationship between HP diets, autophagic dysfunction, and increasing lesion size and (2) to provide a mechanistic basis for HP-diet induced disruption of autophagy.

We conducted this investigation using a combination of *in-vivo* and *in-vitro* studies. Amino acid uptake by macrophages was analyzed using mass spectrometry. mRNA and protein levels were measured with quantitative PCR, Western Blot, and immunofluorescence techniques.

Our results suggest that protein-rich diets increase differential amino acid load into macrophages of atherosclerotic lesions. Two amino acids, leucine and glutamine, are found in high concentrations in lesional macrophages. Both stimulate independent biochemical pathways that aggravate autophagic disruption. Leucine inhibits autophagy through the induction of mammalian target of rapamycin complex 1 (mTORC1), while glutamine-mediated inhibition stymies the transcription rate of a key autophagic chaperone, p62/SQSTM1. These findings provide a mechanism to account for HP diets' proatherogenic qualities and highlight the crucial role autophagy plays in modulating atherosclerotic progression.

JUVENATION'S MASKS: FROM MARY PICKFORD TO "LITTLE FRESH MEAT"

Tina Chen

Mentor: Christopher King

Dr. Gaylyn Studlar, program director of the Film and Media Studies Department, conducted research on juvenation in the era 1910-1968 of Hollywood cinema. Juvenation is the phenomenon where actresses portray young characters throughout their acting career even when they mature, as this attracts a larger male audience. In her book "Precocious Charms: Stars Performing Girlhood in Classical Hollywood Cinema," Dr. Studlar examines actresses who became victims of male gaze in the form of juvenation. Upon conducting an interview with her, I posed the question: is juvenation limited to only female actresses in twentieth-century Hollywood? Could it be relevant in twenty-first century in a different region and gender population? Through visual and textual analysis and observation of peers, I study several young male celebrities who are at the height of their fame today, including Luhan, TF Boys, Ning Zetao, and G-Dragon. These men/boys are classified as "Little Fresh Meat," a term used to signify their youth and innocence. They are all targets of juvenation, though analysis of each case shows that their juvenation comes in different forms: some of the celebrities gain popularity based on athleticism while others could be subjects of a female gaze. In analyzing the condition, I question the root of male juvenation and conclude that it could be influenced by foreign culture, affected by a population's own culture, or provide a way for females to challenge patriarchy. By examining juvenation in a different region of the world and a different gender group, my research shows that the audience's obsession over youth culture is already rooted in human nature and influences the trends in societal values. Regardless of the region, era or gender, it is a universal phenomenon.

ISOLATION AND GENOMIC ANALYSIS OF PHAGE PUMPKINSPICE

Brandon Chia, Mackenzie Cunningham, Paul Rice, and Tiana Saak

Mentors: Kathy Hafer and Chris Shaffer

Our objective is to isolate and characterize a novel bacteriophage, a virus that infects bacteria, to add to the knowledge base of both bacteriophage genetics and molecular and microbiology. The bacteriophage studied in-depth here is PumpkinSpice, isolated from the bacterial strain *Streptomyces griseofuscus*. PumpkinSpice is one of the first phages to be isolated using this bacterial host strain. To carry out this project, we collected an environmental sample from the Washington University in St. Louis campus just outside of Dardick House from which we isolated and purified phage PumpkinSpice. From there, we extracted PumpkinSpice DNA, performed gel electrophoresis to gain an initial genome size estimate, and took electron microscopy photos to determine the phage's physical structure. The electron microscopy results showed that PumpkinSpice had a flexible tail that was approximately 319 nm long and an icosahedral head that was approximately 76 nm wide (left-right) and 78 nm long (top-bottom). These results lead us to believe that PumpkinSpice is a Siphoviridae. After sequencing, it was found that the PumpkinSpice genome is 132,480 base pairs in length, with 246 protein-coding genes and 44 tRNA-coding genes. PumpkinSpice also has a direct terminal repeat that is 12,588 base pairs long. After our wet lab experiments, PumpkinSpice was sequenced and we positionally annotated its genome using tools like protein Blast and auto-annotation programs Glimmer and GeneMark. We are currently working on functional annotations to determine the specific purpose of the genes found in PumpkinSpice. PumpkinSpice is hypothesized to be a lytic phage based on the small, clear plaques. PumpkinSpice belongs to the BE2 cluster, with high similarities to bacteriophages Starbow, Tom Sawyer, and Wipeout.

EVOLUTION OF SOCIALITY: USING WILLIAMS-BEUREN SYNDROME TO IDENTIFY CONSERVED “SOCIAL GENES”

Iris Chin

Mentor: Yehuda Ben-Shahar

The prevalence of sociality and social behaviors in diverse animal genera hints toward the existence of a conserved “genetic node” which plays a role in the biological networks that drive interactions between animals and their social environments. Williams-Beuren Syndrome (WBS) is a human neurodevelopmental disorder linked to the hemizygous deletion of 26-28 genes on chromosome 7 (the ‘WBS region’). Along with an array of physiological and developmental symptoms, individuals with WBS display stereotypically hyper-social profiles. In addition, 7q11.23 duplication disorder, characterized by chromosomal duplication of the WBS region, is associated with Autism-spectrum phenotypes. This ostensible negative correlation between gene dosage of the WBS region and human sociability makes the affected genes prime candidates for investigation while studying the processes that drive animal sociality. Remarkably, a majority of the genes in the mammalian WBS region are conserved in the *Drosophila melanogaster* genome. In this project, I systematically downregulated the expression of *Drosophila* WBS homologs in the nervous system using a transgenic RNAi approach, and tested the effects of gene knockdown on fly sociability by employing a “social-space displacement” assay. My studies revealed that knockdown of at least two WBS-related genes, *frizzled* (*fz*) and *eukaryotic translation initiation factor 4H1* (*eIF4H1*), produced social displacement phenotypes significantly different from that of wild type control animals. However, *fz*-knockdown flies also displayed generally abnormal locomotion, which may explain, at least in part, the observed “social space” phenotype. Regardless, these data suggest that at least one of these genes may have a conserved function in the biological network responsible for social behavior.

COMPARATIVE FUNCTIONAL ANNOTATION OF MOOSE SWISS CHEESE, ROHR, AND BIG MAU

Rehan Choudhury, David Plant, Eric Sallinger, and Tara Suresh

Mentor: Chris Shaffer

This experiment was a part of a larger movement to annotate and explore phages and their diversity using a consortium of students and resources. Soil samples were collected around Washington University's campus, from which phages were subsequently isolated and purified; these phages genomes were sequenced, and eventually annotated. We report here on the annotation of phage Moose, Swiss Cheese, Rohr, and Big Mau all belonging to the A1 subcluster. They are all lysogenic as evidenced by the presence of an Integrase and the presence of small, cloudy plaques. The length for all four genomes are 52,695 bp, 51,439 bp, 53,483 bp, and 52,632 bp, respectively. All four have similar number of protein coding genes (95, 95, 93, and 94, respectively). Functional annotations based on similarity at either the primary or secondary amino acid structure were assigned to some but not all genes in these phages. Each phage also has interesting functional annotations that are not commonly found in other phages, including Transposase, RNA sigma factor, Recombination directionality factor, and Immunity Repressor. Comparison within the four phages revealed that Moose and Swiss Cheese are more similar to one another, as are Rohr and Big Mau for both the numbers of genes, their functional annotations, and the number of tRNA present for each phage. Due to low numbers of tRNA in their respective genomes, all four can be considered to be not very virulent.

NMD GENE SCREEN

Abigail Chua

Mentor: Abigail Cheruiyot

Nonsense mediated mRNA decay (NMD) is a surveillance pathway that regulates the number of cellular RNAs and, therefore, gene expression. The pathway recognizes premature termination codons (PTCs) in order to start degradation of RNAs encoding potentially harmful proteins. Considering the overall mechanism of NMD, we are trying to figure out the genes that have affiliation with the pathway. Though there are several genes that have already been identified in inactivation of NMD, there are still many that have not been discovered yet. With this data, we hope to include it in several cancer therapeutic strategies.

We will be using the You Lab's NMD fluorescence (U2OS) reporter cell line to measure the intensity in NMD knockout. A second reporter via a tethering system was tested as well to test genes involved with the spliceosome complex, however, due to several insufficient outcomes in our tethering experiments, we have decided not to use genes associated with the spliceosome complex. The genes that we predict to be associated with NMD will then be quantified using Western Blot analysis. Our main focus will be those genes encoding proteins from the U2:SF3B complex and U2:SF3A complex as fold change values via guide RNAs of these two complexes look promising where fold changes greater than 1.5 are considered significant.

MONITORING AND EVALUATION OF THE YOUTH RESOURCE CENTER, A PROJECT BY UGANDA DEVELOPMENT AND HEALTH ASSOCIATES

Anand Chukka

Mentor: Shanti Parikh

We performed a monitoring and evaluation of the Youth Resource Center, a sexual and reproductive health initiative run by Uganda Development and Health Associates. This project intervenes in primary and secondary schools in the Iganga and Luuka districts of Eastern Uganda and attempts to increase sexual and reproductive health knowledge among students. The topics covered are related to HIV/AIDS prevention, STI/STD prevention, sexual violence, and general healthcare. This education is delivered through five initiatives: peer health educators, patron teachers, sensitization lectures, anonymous health boxes, and health posters. The evaluation was conducted over two months using a survey handed out to 238 students in six different secondary schools in these two districts, two focus group discussions held with Peer Health Educators (PHEs), and general observations from working with this project for two months. Due to a lack of standardization with the survey distribution, we were unable to garner definitive results but this study has informed areas of concern with the project, including: high scores related to menstrual education and stigma reduction and safe sex practices, and low scores related to sexual violence and malnutrition. This study will hopefully inform future evaluation efforts and provide a preliminary look at the effectiveness of this initiative.

CIViC: BRIDGING THE GAP BETWEEN CLINICAL TREATMENT AND CANCER RESEARCH

Kaitlin A. Clark

Mentor: Malachi Griffith

Precision, or personalized, medicine seeks to tailor clinical treatment based on each person's genomic makeup. In the context of cancer, this often involves modifying disease treatment based on the presence and absence of known cancer-causing mutations. The biomedical literature describing these associations is huge. But, currently, the publications explaining genotype-phenotype correlations exist largely in private or encumbered databases resulting in extensive repetition of effort and lack of public access to clinically-actionable data, which in turn reduces the effectiveness of precision medicine. Realizing the potential power of precision medicine requires this information be centralized, vetted and interpreted for clinical application and public access.

The Clinical Interpretations of Variants in Cancer (CIViC) project aims to enable precision medicine by providing an open access knowledgebase for clinicians, researchers, and patients to input submission data, vet this information, and learn about the clinical significance of cancer genome alterations.

My project focusing on curating information on the VHL gene, which, when mutated, causes von Hippel-Lindau disease, is underway. Von Hippel-Lindau disease (VHLD) is a rare, autosomal dominant disease affecting 1 in 36,000 people worldwide and manifests as hemangioblastomas of the central nervous system and retina, renal cell carcinomas, and pheochromocytomas. I seek to curate a large and growing dataset on VHL gene alterations, VHLD, and VHLD patient outcomes in order to link actionable genetic data to clinical practice. Specifically using the CIViC platform, I will summarize patient genotypes, their related phenotypes, and any findings for better prognosis and/or diagnosis of VHLD for each available publication.

From the curation of this information, we hope to create a more comprehensive and readily accessible understanding of the clinical relevance of VHL gene variants and their impact on disease phenotype and treatment, taking us a step closer to realizing the power of precision medicine.

FRAGILITY OF METALLIC GLASSES AND THE T_A/T_g RATIO

Julia Cohen

Mentor: Ken Kelton

A liquid's viscosity, η , increases exponentially as its temperature decreases towards the glass transition temperature, T_g , defined as the temperature at which the shear viscosity reaches a value of 10^{12} Pascal-seconds (Pa·s). However, for different liquids, there are large disparities in the exact temperature dependence of the viscosity. When $\log_{10}(\eta)$ is plotted versus the reduced temperature T_g/T , some liquids have a linear (Arrhenius) viscosity temperature dependence, while others are highly nonlinear (super-Arrhenius). This departure from Arrhenius behavior is known as the liquid's kinetic fragility (denoted by the letter m), and is typically characterized by the slope of $\log_{10}(\eta)$ at T_g , $m = \frac{d \log(\eta)}{d(T_g/T)}|_{T=T_g}$. Kinetic fragility has been correlated with various fundamental properties of the liquid, including its rate of structural ordering, the character of its interaction potential, and how well it forms a glass. Recently, kinetic fragility has also been related to the so-called Arrhenius crossover temperature, T_A , below which the liquid begins to exhibit cooperative properties. The Kelton Research Group has previously argued that the ratio T_A/T_g is correlated with m ; however, the data have significant scatter in the relationship. This could be due to the data spanning disparate families of liquids, ranging from silicate, molecular, network, polymer, and metallic, and could also be due to differences in quantitative methods used to measure m , T_g , and T_A . Thus, it would be instructive to limit the study of the relationship between m and T_A/T_g to a small family of similar liquids and use identical methods to determine m , T_A , and T_g for all liquids in the study. This research focuses on this study.

POTENTIAL MECHANISM OF NEONATAL BLOODSTREAM INFECTIONS FROM A MOUSE MODEL

Paige Coughlin

Mentor: Rodney Newberry

Bloodstream bacterial infections that can result in septic shock are a common cause of death in NICU patients. Improvements to hygienic techniques have failed to lower the rate of sepsis in patients. Recently, we have shown several species of bacteria colonizing the GI tract are able to gain access to the body via goblet cells, an epithelial cell that lines the intestinal tract and secretes mucus. We investigated if bacteria could cross goblet cells in infant mice, and found both commensal bacteria and bacteria isolated from pediatric sepsis patients could cross goblet cells in mice between day 10 and 21 of life. Additionally, we found both bacteria could also colonize organs distant from the gut. Thus, bloodstream infections in infant mice could be initiated from bacteria colonizing the intestine. We then asked what prevented bacteria from crossing the intestine prior to 10 days of life. To answer this, we analyzed levels of EGF, a protective protein secreted in the breast milk of nursing mothers, and counted the number of bacterial colonies present in several mouse organs from day 5 to day 21 of life. We found an inverse correlation between the amount of EGF present in breast milk and number of colonies of bacteria in the infant mice. Therefore, nursing infants may be able to prevent other strains of bacteria from translocating from the intestine. In the NICU, patients often lack access to breast milk, suggesting this may allow them to be susceptible to sepsis. In the future, we hope to utilize a mouse-model to control levels of EGF in the mice while infecting them with sepsis causing bacteria isolated from human patients to analyze the ability of EGF to prevent bacterial translocation from the gut.

MIND THE GAP: UNDERLYING ISSUES AND NEW OPPORTUNITIES FOR THE MARTA SYSTEM AFTER THE COLLAPSE OF INTERSTATE-85

Megan Craig

Mentor: Eileen G'Sell

In surveys of cities with the worst traffic congestion, Atlanta is nearly always ranked within the top 10. Despite daily standstill traffic, there have been few attempts to improve and expand the Metro Atlanta Rapid Transit Authority (MARTA) system to alleviate the crowded roads. At its inception in the early 1970s, deep-seated racism within the metropolitan counties prevented MARTA from expanding into suburban Atlanta. Even though there have been large demographic shifts in these counties, MARTA has not expanded to meet the demands of the growing population. The lack of public transportation is especially detrimental to lower-income populations, many of whom do not have access to private transportation. On March 31st, a 180-foot section of Interstate-85, a crucial avenue into the city, collapsed, forcing hundreds of thousands of people to find alternate commutes. Although the inadequate MARTA system originated from racism, the collapse of I-85 spurred MARTA advocacy groups and incited public support for the expansion of public transit.

The conclusions drawn in this paper are from analysis of historical documents, case studies, and articles. I begin by exploring the circumstances surrounding the creation of MARTA that prevented it from expansion into the metro area. Then, I examine the negative effects that lack of effective public transportation has on impoverished communities. Finally, I analyze the increasing popularity of groups that support MARTA expansion after the collapse of I-85 occurred.

The population of Atlanta is predicted to continue increasing for the foreseeable future. Due to the sprawling nature of the city, more and more people will settle in metro counties and commute to the city, adding thousands of cars to the road. To remain competitive as a desirable place to live, it is crucial that Atlanta expand their public transportation system and increase accessibility to those living outside the city.

PARKINSON'S DISEASE FIBRILS: ANALYZING AGGREGATION GROWTH PROPERTIES IN A CELL SYSTEM

María I. Dabrowski

Mentor: Paul T. Kotzbauer

Parkinson's disease (PD) is the second most common neurodegenerative disease in the world. It occurs when neurons in the substantia nigra degenerate, leading to tremors, rigidity, slow muscle movement, and other physical and cognitive impairments. As of right now, there is no way to accurately diagnose PD prior to a post-mortem autopsy. In approximately less than 1% of PD patients, mutations in alpha-synuclein cause the protein to aggregate. There are five known mutations, and each cause slightly different aggregation outcomes depending on how the proteins misfold and clump together into fibrils. The purpose of our experiment is to generate these mutations in a cell system and test the cells to see how wild-type (WT) and mutated alpha-synuclein-expressing cells cause aggregation of the protein. Doing this in a cell system instead of in vitro will allow us to see how cellular lipids and proteins influence monomeric proteins to become integrated into fibrils, and how the aggregation properties differ across mutations. Additionally, completing experiments within a cell system will indicate what natural mechanisms cells have to remove or degrade monomers and fibrils, and how these removal pathways might be impacted by mutations. Studying the varying aggregation morphologies and growth patterns of these mutations will be a step in the right direction toward diagnosing PD and developing better treatments.

ROLE OF HEME DETOXIFICATION PROTEIN IN *PLASMODIUM FALCIPARUM* HEME METABOLISM

Varun K. Dalmia

Mentor: Daniel E. Goldberg

The malaria parasite, *Plasmodium falciparum*, exports hundreds of proteins into its host erythrocyte, modifying it in many ways critical to the parasites survival and replication. Of the many modifications made to the host erythrocyte, the degradation of hemoglobin and the metabolism of heme is crucial to the biology of the malaria parasite. During its intraerythrocytic stages, the parasite sequesters heme from hemoglobin into hemozoin crystals stored in a lysosome-like compartment called the food vacuole to prevent free heme toxicity. Jani et al. identified a novel parasite protein potent in converting free heme into hemozoin, which they termed Heme Detoxification Protein (HDP). Using Cas9 guide RNAs known to successfully target the locus, we were unable to disrupt the locus and insert a drug selection cassette to create an HDP knockout line, supporting evidence that HDP is essential to parasite intraerythrocytic stages. Using a CRISPR/Cas9 introduced regulatable aptamer knockdown system to inhibit translation of HDP mRNA, we have found that parasites in the knockdown condition are unable to survive. However, there is a significant delay in observing this, suggesting that HDP has a low turnover rate, and is passed on to daughter parasites. Using these lines, we are currently performing hemozoin quantification experiments, allowing us to quantify the effects of HDP knockdown on parasite hemozoin levels.

HDP does not contain a protein export element (PEXEL) signal sequence, a motif frequently found on *Plasmodium* proteins that are transported out of the parasitophorous vacuole. Jani et al. described a circuitous trafficking pathway taken by HDP, however, the evidence was not strong in supporting this conclusion. By tagging HDP with a Neon Green tag in HSP101 export regulatable parasite lines, we hope to also elucidate HDP's trafficking pathway via live microscopy.

SENSING A FEAR OF DEMISE:
RESEARCHING THE INTERSECTION BETWEEN
RELIGION AND COLONIALISM IN THE DYING DAYS
OF THE BRITISH EMPIRE

Paul d'Ambrosio

Mentor: Monique Bedasse

This historical research project looked into the relationship between the British Empire in its dying days and one of its colonies: Jamaica. The Caribbean island was ruled by the British for more than 300 years, only gaining independence in 1962. The project primarily focused on the middle of the twentieth century, and it paid extra attention to British perceptions of local religious and political movements that could have been seen as threats to British rule. Evidence consisted of documents originally written for public consumption, such as newspaper articles, as well as formerly private documents, such as declassified government archives. Over the course of the project, it was determined that large scale movements of any kind were viewed by the British as troublesome, but that the Rastafari Movement was given special attention by British intelligence services because of its fierce left-wing, anti-colonialist platform. Evidence was also found that U.S. intelligence was also concerned that Rastafari may cause Jamaica to become a Communist country. The British viewed the Jamaicans as inherently ignorant, and they were concerned that enough ignorant people could be “fooled” by Rastafari and become radical threats to British rule. This project found many connections between racism and paternalist colonial administrative practices, which the British used to justify cracking down on a movement that they were afraid could topple their power.

USING THE CRISPR/Cas9 SYSTEM ON MURINE CYTOMEGALOVIRUS

Trenton Dawson

Mentor: Wayne Yokoyama

The CRISPR/Cas9 system is a recently developed tool to quickly edit genomes. While most CRISPR research examines eukaryotic genomes due to their DNA repair processes, this project examines the use of CRISPR on murine cytomegalovirus (MCMV). The goal of this work was to familiarize ourselves with using the system on a virus. Since the CRISPR/Cas9 system cuts the DNA in a precise location but NHEJ is an imprecise method, the method of inactivation is largely unknown. Genes can be inactivated but their exact inactivating mutation can be quite unpredictable. We hope to use our findings to better characterize the molecular events that are occurring. Gene inactivation using the CRISPR/Cas9 system has extensive applications in the field of health and genetic research. Studies such as those described above examining the method of gene inactivation will help us to determine exactly how this complex functions.

Since the herpes viral family is non-zoonotic, trial and manipulation of the human herpes virus is difficult. Murine cytomegalovirus falls in the herpes cluster and provides a convenient and accessible analogue due to its remarkable similarity to human herpes virus and mouse host. After optimizing MCMV knockout methods, we explored the virus's immunoevasion capabilities through its ability to downregulate MHC-I receptors and elude NK cells. Using the CRISPR system on non-eukaryotic genomes, specifically those that evade the immune system with unknown molecular pathways, provides insight into viral-host interactions and using the CRISPR tool in novel ways.

TENXSIM: SIMULATOR FOR PURE AND HETEROGENEOUS GENOMIC SEQUENCE WITH 10X GENOMICS

Guanlan Dong

Mentor: Li Ding

Next-generation sequencing has become the major sequencing technology nowadays, however, limitations still exist, such as the short read length in Illumina and the high error rate in PacBio. 10X Genomics addresses both problems with its microfluidic droplet technology where an additional barcoding system is attached to Illumina reads, so that one can obtain long and accurate DNA fragments. There have been numerous simulators developed for sequencing technologies. However, these tools mainly assume a haploid reference genome and a simulator for 10X sequencing has not yet been developed. Therefore, we present *tenxsim*, a software written in python that can perform *in silico* 10X sequencing simulation for both pure and heterogeneous genomes. It can serve to benchmark 10X experiments and optimize relevant software. We used the experimental data from Zheng et al. (2016) as a bench mark to design the simulation process. We synthesized a random DNA genome as the reference, out of which we created two FASTA files with single nucleotide variants (SNVs). These two FASTA files represented two alleles in a diploid sample genome. From the sample genome, high molecular weight (HMW) DNA regions were generated with sizes selected from a normal distribution. Then we sonicated HMW DNA into fragments and attached a unique 16bp barcode to fragments from the same HMW DNA. Finally, fragments with attached barcodes would go through *in silico* Illumina sequencing and be aligned to the reference genome to create a BAM file with barcode information. Our next goal is to use the barcode information to link short reads into long DNA molecules, so that we can reconstruct sample haplotype tree and phase discovered SNVs. Furthermore, we will introduce heterogeneous cancer genome simulation to see if *tenxsim* can identify cancer clonality.

GENOMIC ANALYSIS OF MYCOBACTERIOPHAGE, KRADAL: EVOLUTIONARY INSIGHTS WITHIN THE RECENTLY DISCOVERED BM CLUSTER

Aja Drain, Lauren Kang, Tuka Mousa, and Jerry Sun

Mentor: Chris Shaffer

The goal of this research was to isolate and characterize a novel bacteriophage and deduce the position and functionality of its genes. Phage KRADAL was isolated through direct isolation with host bacteria *Streptomyces griseofuscus*, purified through five rounds of purification, amplified to create a high-titer lysate, and characterized through transmission electron microscopy. Phage DNA extracted from the high titer lysate was also characterized through gel electrophoresis of various restriction enzyme digests and subsequently sequenced. This process of phage isolation, purification, and characterization revealed that KRADAL forms very small (< 2 mm in diameter), circular, and clear plaques. Transmission electron microscopy revealed that it has a flexible tail and a rod-shaped head, in contrast with the more common icosahedral head. The phage genome is 184,673 base pairs long with a 1053 base-pair terminal repeat, and genomic analysis has placed KRADAL in phage cluster BM. The phage shares distinct Gene product similarities with two phages: JustBecause and Satis. For example, gel electrophoresis of KRADAL's DNA and that of other rod-shaped phage revealed similar restriction enzyme digest patterns. We performed positional and functional annotation on the middle section of the phage genome (from base 60,409 to 149,338) utilizing computational tools including PECAAN, DNA Master, GBrowse, and NCBI/PhagesDB BLASTX searches. In total, the middle section of KRADAL has 168 protein-coding genes. Functional annotation will be performed on these genes in order to discern any possible functions of these proteins. This research adds to the limited body of knowledge currently available about the genomes of rod-shaped phages in general, and more specifically, the BM cluster. This research can reveal differences in protein function that differentiate rod-shaped phages from icosahedral phages.

BUFFERING AGAINST HEAT, DROUGHT, AND FUNGUS IN WHITE CLOVER: DOES CYANOGENESIS PLAY A ROLE?

Maya Dutta

Mentor: Ken Olsen

As sessile organisms, plants are particularly vulnerable to increased drought and heat caused by anthropogenic climate change. Thus, the ability to adapt or exhibit plasticity in a changing environment is particularly important. In this research, I studied the ability of a widespread plant, white clover (*Trifolium repens*), to withstand heat/drought stress and fungal pathogens, and I further asked how these stressors might interact with a well-studied chemical defense trait (cyanogenesis). White clover is polymorphic for cyanogenesis (the production of hydrogen cyanide upon tissue damage), with both cyanogenic and acyanogenic individuals present in populations. Cyanogenesis is considered locally adaptive due to the repeated evolution of cyanogenesis clines, where higher proportions of cyanogenic plants are found in warmer and drier climates. Leveraging an F2 population of white clover plants currently growing at Tyson Research Center, I conducted an observational study during a natural period of heat and drought from late June through early August 2017. Plant height and green surface area were measured at three time points throughout the drought period, and fungal presence/absence and degree of infection were quantified. Here I present preliminary observations from one of the three replicate plots under study; analyses are ongoing. Future work may include genetic mapping to identify genetic regions that contribute to the variation we find in these traits.

CYTOCHROME P450 ONTOGENY AND DRUG REACTIONS IN CHILDREN

Jack Elliott-Higgins

Mentor: S. Joshua Swamidass

Administration of prescription drugs to children raises unique issues. Children and adults have functionally different metabolic compositions, which can lead to unexpected reactions. While clinical testing predicts risk in adults, this risk assessment is not sufficient to predict outcome in children, as researchers cannot perform these clinical tests on subjects with pre-adolescent enzyme composition. It is simple, however, to determine the typical enzymatic makeup of a child and, with this data and a knowledge of the enzymes involved in producing toxic metabolites causing adverse drug reactions (ADRs), to predict which drugs will cause ADRs in children. To construct this predictive model, we used data from the Accelrys reaction database to build metabolite trees for specific drugs with documented effects on children. These trees contain all reaction records with a parent metabolite matching our query, and these reaction records point to data for enzyme, isoenzyme, species, and more. We used an in-house reactivity prediction program to assess the most reactive metabolites in the tree and matched these results to external sources to confirm that the search was turning up valid results. Using this, we correctly identified the most reactive metabolites for the anti-convulsants Valproate, and Phenytoin, the sedative Midazolam, and cough medicine Dextromethorphan. With this information demonstrating our method's effectiveness, we set out to restructure how the user interacts with Accelrys. It is packaged as an unformatted collection of raw reaction files, so we parsed these files for all useful information and imported this information to a neo4j graph database. This database allows us to rapidly query over the entire database and filter for the species and isoenzymes of interest, yielding more robust metabolite trees. With further testing and knowledge of enzymatic makeup, targeted queries of this database will be useful in predicting drug reactions as a function of age.

EXPLORING THE ROLE OF miRNA IN REGULATING CD36 FAT ACTIVITY

Thom Ellison

Mentor: Terri Pietka

Obesity-driven metabolic complications such as diabetes and heart disease are major public health issues in the United States. To treat these issues, it is important to understand the regulation of proteins involved in fat metabolism. One such protein, CD36, has been extensively linked to fat metabolism in laboratory mice. However, its regulation after being transcribed is not well understood. MicroRNA molecules, miRNAs, can regulate protein activity by the process of mRNA silencing: binding to and destabilizing the mRNA, decreasing the level of protein transcribed. The mRNA transcript for CD36 has two untranslated regions (UTRs), one long and one short. Previous studies have linked lower levels of transcripts containing the long UTR to metabolic disease or dysfunction. In addition, the long UTR has been found to contain binding sites for the miRNAs studied, suggesting that mRNA silencing is possible. However, the results do not support this hypothesis. pmirGLO plasmids containing the long or short UTR were introduced into HEK293 cells via transfection, as were the appropriate miRNAs. The UTRs were first cloned into pmirGLO as a short string of nucleotides, then as a longer string which contained more of the surrounding wild-type sequence. CD36 activity was then tested via luciferase assay, and there was no consistent change in activity in any case. This result indicates the binding sites in the long UTR are competed for by another molecule in the cell, possibly the RNA-binding protein MBNL1. This method of regulation thus remains under investigation.

INTERSECTION OF LAW AND LOCAL UNDERSTANDINGS OF DOMESTIC VIOLENCE IN IGANGA, UGANDA

Nicolette Esparza

Mentor: Shanti Parikh

The passing of Uganda's Domestic Violence Act of 2010 marked a concrete action taken by the government that acknowledged Uganda's households as among the highest rates of African countries in domestic violence. The law outlines domestic violence as any threatening or harmful set of behaviors or actions from a perpetrator that takes away a survivor's sense of security or safety. The law is thorough in defining each word and the mediums in which domestic violence can occur in a romantic and familial relationship between individuals. After seven years, the law has been addressed with much more scrutiny as the culture of relationships and the rates of violence have not seen any significant change. I conducted 34 interviews over the course of 10 weeks and three focus groups with five individuals per group in rural and peri-urban areas in the greater Iganga District. The interviews were made up by local leaders, key informants, community members, and employees in the criminal justice system. The three focus group interviews were accomplished with five young adults 18-25 years old per group. The lack of implementation of government funded programs and grass roots initiatives left local communities to carry out the same lifestyle and set of cultural expectations. There was little to no consideration of the traditions and systematic barriers in place that contributed to these high rates of violence. From those interviewed, I gathered that there remains a disconnect between what is interpreted as violence at local levels. Survivors of domestic violence take many avenues before approaching the criminal justice system with their case. These avenues vary in education on the law and possibly fall into perpetuating harmful notions and expectations, Uganda is not unique in its struggle for education and justice. Without a change in culture and advocacy surrounding the Domestic Violence Act, domestic violence continues to impact and silence voices in communities.

ISOLATION, PURIFICATION, AND GENOMIC ANALYSIS OF THE NOVEL BACTERIOPHAGE KRADAL

Adeshola Fanegan, Katie Gemperli, Sofia Kling, and Jesse Yavner

Mentor: Chris Shaffer

Kradal, a novel bacteriophage isolated from the host *Streptomyces griseofuscus*, was isolated from a direct environmental sample collected just outside of Gaylord Music Library (38.6465 °N, 90.3112 °W) at Washington University in St. Louis, MO. Kradal was analyzed throughout five main phases: isolation, purification, amplification, extraction, and characterization via electron microscopy and gel electrophoresis, as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science (SEA-PHAGES) program sponsored by the Howard Hughes Medical Institute and Graham Hatfull at the University of Pittsburgh. Kradal produces uniformly circular, small, clear plaques when infecting *Streptomyces griseofuscus*. Additionally, electron microscopy classifies Kradal as a Siphoviridae phage with a prolate head measuring approximately 291 nm by 44 nm and a flexible tail with an average length of 280 nm. Through genetic sequencing using the Illumina Shotgun method, Kradal's genome length was determined to be 186,383 base pairs, which is the second longest sequenced phage genome to be sequenced in the SEA-PHAGES program. Kradal is closely related to the bacteriophage Satis, displaying similarity across 99% of the genome and in the same cluster, BM. Kradal's genome contains 335 protein coding genes, of which our group analyzed from 1-85 and from 254 to the end of the genome. Thirty-five of the genes in these sections of the genome run in the forward direction while 132 run in the reverse direction. Due to the novelty of Kradal, evidence from functional annotation and comparative gene analysis is limited. We are currently comparatively analyzing Kradal with Satis and various other *Streptomyces* phages with similar morphology and sequence to Kradal.

COLLECTIVE MEMORY, CHINESE NATIONAL NARRATIVE, AND THE CENTURY OF HUMILIATION

Jacob Finke

Mentor: James Wertsch

In U.S. discourse regarding China, there is an under-emphasis placed on the Chinese Century of Humiliation. The Century of Humiliation is the period from 1840 to 1950 during which China was continually under occupation by foreign powers. This research attempts to draw attention to the importance of the Century of Humiliation in shaping the births of the Communist Party of China and the People's Republic of China. This research also attempts to understand how the Century of Humiliation continues to shape popular discourse in China to this day. The following conclusions were drawn from two in-person interviews with Chinese university students and detailed observational research at Chinese museums, memorials, and monuments in mainland China. The findings of this paper emphasize the importance of the Century of Humiliation to both the Communist Party of China and the general Chinese population. The Century of Humiliation serves as a founding myth for the Communist Party of China, justifies its foreign policies, and is a source of animus regarding the Japanese and Sino-Japanese relations. There are also pointed differences in how the Western-focused Century and Japanese-focused Century are remembered. These findings all have important meaning for Sino-U.S. relations, as the Century of Humiliation and its memory is still alive and well in the Chinese national narrative propagated by the Communist Party of China. This national narrative informs policies toward the United States. Understanding the Century of Humiliation and its place in China's national narrative is necessary for American public policy and discourse when regarding Sino-U.S. relations in the twenty-first century.

ORTHOGONAL METAL TEMPLATING STRATEGIES FOR THE SYNTHESIS OF POLY[n]CATENANES

Jeremy Fisher

Mentor: Jonathan Barnes

Polymers have the potential to benefit society in various ways such as health, safety, energy saving, and material conservation. The field of synthetic polymer chemistry has recently experienced rapid growth. With the continuing expansion of the material properties of polymers, an increased level of control over the underlying architecture of polymers is in great demand. A particularly relevant topic is the type of chemical linkage in the backbone of such polymers. The typical polymer contains a series of monomeric precursors covalently bonded to form either linear or branched architectures. These covalent bond linkages restrict the polymer, severely limiting flexibility. Although the usefulness of non-covalent mechanical linkages is clear, relatively little literature exists that explores it as a viable option for synthetic polymer chemistry. One type of non-covalent mechanical linkage consists of monomeric ring structures mechanically interlocking with one another to create a structure similar to that of an everyday chain. This category of molecules is called mechanically interlocked molecules (MIMs). The first MIM was made in the early 1960's with the synthesis of the first [2]catenanes, where [2] refers to the number of cyclic monomeric precursors [n] incorporated into the molecule. Though MIMs have been around for around 50 years, they were only starting to be used as subunits in polymers in the past two decades. This 30-year gap resulted from reports of poor yield in the synthetic routes that were explored to produce MIMs. Sauvage and co-workers broke this streak and revitalized the area of research by using metal-ligand coordination chemistry between Cu(I) and phenanthroline-based ligands to develop the first template-directed synthetic protocol. We plan on utilizing this orthogonal metal templating strategy to develop the first ever controlled synthetic route to a poly[n]catenane.

DIFFERING MEASURES OF PARENTAL ANTISOCIAL PERSONALITY AS PREDICTORS OF CHILD ABUSE AND NEGLECT

Lauren Fournier

Mentors: Christina N. White and Thomas F. Oltmanns

Antisocial personality disorder (ASPD) is a personality disorder characterized by maladaptive externalizing behaviors such as repeated arrest, deception, impulsivity, and aggressiveness. These unpredictable and often harmful characteristics can create substantial concern for the wellbeing of individuals in close relation to those with ASPD, such as family members, friends, and romantic partners. Though the relationship between ASPD and child abuse has been examined, most previous research has focused on childhood abuse as a predictor of antisocial behavior. In contrast, very little research has investigated parental antisocial personality as a predictor of child abuse and neglect. The present study compared several measures of antisocial personality (self-report, structured interview, and informant-report) as predictors of five types of child abuse and neglect (emotional abuse, physical abuse, sexual abuse, emotional neglect, and physical neglect).

Intergenerational data collected from the St. Louis Personality and Aging Network (SPAN) study (N=265) was used to conduct hierarchical regression analyses. The SPAN study is a longitudinal study of personality and health in older adults (G1) and has expanded to investigate the children of these G1 participants (G2). We hypothesized that higher scores on all measures of ASPD would predict higher scores of emotional, physical, and sexual abuses in G2s. Results partially supported hypotheses, showing antisocial personality to be a significant predictor of all types of child abuse and neglect. However, with the exception of structured interview predicting physical neglect, only informant-report was a significant predictor of child abuse and neglect outcomes. Informant-report significantly predicted scores on all types of child abuse and neglect. In combination with literature supporting child abuse as a predictor of APSD, these results establish an understanding of ASPD as an important factor in a cycle of abuse. Moreover, these results highlight the importance of informant-report in ASPD research.

TIME-DEPENDENT EFFECTS OF APOE REDUCTION USING ANTISENSE OLIGONUCLEOTIDES IN A MODEL OF β -AMYLOIDOSIS

Caroline Francis

Mentors: David Holtzman and Phat Huynh

Extensive clinical studies have established the Apolipoprotein E (*APOE*) gene on chromosome 19 as the strongest genetic risk factor for late-onset Alzheimer disease (AD). Using human *APOE* knock-in mice, it was previously demonstrated that *ApoE*-hemizygous APP/PS1 mice have significantly less amyloid plaque deposition and microglial activation compared to their homozygous littermates. Since apoE levels were lower in *ApoE* hemizygous mice for their entire life, it was not clear from a mechanistic and therapeutic perspective whether lowering apoE levels pharmacologically in adult animals would affect amyloid deposition. Here, we utilize an apoE antisense oligonucleotide (ASO) to reduce apoE expression in the adult APP/PS1-21 mice homozygous for the human $\epsilon 4$ allele of *APOE*. Despite achieving reduction of apoE expression by more than 50% starting at the onset of amyloid deposition, no reduction of A β pathology is detected when mice were assessed at four months of age. Though there was not an overall reduction in amyloid deposition, there was a clear effect of reducing apoE4 on A β plaque morphology. Interestingly, ASO treatment starting after birth led to a strong and significant decrease in A β pathology when mice were assessed at four months of age. These results suggest that apoE levels can strongly affect the initiation of A β pathology *in vivo* but that once A β plaque pathology is present, reducing apoE does not have a strong effect on further amyloid deposition. This previously unknown age-dependent effect of apoE in the early stages of A β plaque formation suggest the important implication that decreasing brain apoE levels would be useful for primary prevention of amyloid deposition but not for decreasing or removing amyloid plaques once they have begun depositing.

COMPARATIVE ANALYSIS OF TRANSCRIPTION START SITES AND CONSERVED MOTIFS IN *DROSOPHILA* F AND D ELEMENTS

Ben French and Jon Zielke

Mentor: Sarah C. R. Elgin

The *Drosophila melanogaster* Muller F element is unusual in that this chromosome is packaged mostly as heterochromatin, but contains ~80 protein-coding genes. Past studies have shown that classical markers of heterochromatin (e.g., HP1a) are depleted at the transcription start sites (TSS) of active F element genes, which suggests that the factors that regulate F element gene expression are located near the TSS. To define search regions for efforts to identify potential regulatory sites, we manually annotated the TSS positions of genes on the *Drosophila biarmipes* F element (118 TSS) and on a euchromatic region at the base of the D element (258 TSS). These TSS annotations are based on multiple lines of evidence (e.g., sequence homology, RNA-seq data, RNA polymerase II ChIP-seq data). We analyzed promoter shapes (i.e., peaked, intermediate, broad) and the distributions of transcription factor binding sites (TFBS) for these TSS. We found that a substantially greater proportion of D element promoters are classified as peaked compared to F element promoters in both species. To further characterize core promoters of F element genes, we partitioned the *D. biarmipes* F element promoters based on known TFBS observed in the *D. melanogaster* orthologs. We then analyzed each sub-population (partition) using the MEME suite to identify known and novel motifs in the promoters of *D. biarmipes* F element genes. For the dl, twi, Med, da, Udx, zfh1, hb, and Med + dl partitions, no significant motifs (E-value < 1E-05) were found. The most significant motif discovered by MEME was for the zfh1 partition, with an Expect value of 4.3E-04. A Tomtom search of this motif against the FlyFactorSurvey database did not show any significant matches to known TFBS (false discovery rate < 0.01). Hence this motif might be novel.

ARE POPULATIONS MORE STABLE AT THE CENTER OF THEIR GEOGRAPHIC RANGE? A TEST USING BIG DATA SETS

Savannah Fuqua

Mentor: Carlos Botero

The prediction that species are more abundant and stable at the center of their geographic range has been assumed for several decades. This pattern is thought to reflect the environmental gradient underlying the species ranges, as populations can persist in higher numbers in areas that better meet their ecological requirements. As conditions become less suitable, populations will become less abundant. Additionally, population stability is predicted to follow a similar pattern, with populations becoming increasingly variable the closer they are to the edge of a range. Despite the general acceptance of this principle, it has not been rigorously tested using large data sets. Using data from the North American Breeding Bird Survey and BirdLife, we tested whether two important components of population stability—persistence and variability—were correlated with the population's distance from the edge of the species' geographic range across approximately 400 bird species. For approximately 35% of species studied, the distance from the edge of the geographic range was significantly positively correlated with population persistence; however, there were no broad trends in the variability of populations across species' ranges. Given the general acceptance that populations are more abundant at the center of their geographic range, we also tested whether population variability was correlated with population abundance. We found that for 40% of species studied population variability was significantly negatively correlated with population abundance. Our data suggest that a population's location within a species' geographic range could have important implications for the stability of the population. Further studies are needed to make more precise predictions about population stability, which have the potential for important real-world applications in predicting species' responses to climate change and for making conservation plans.

IMPROVING THE GENOME ASSEMBLIES OF MULTIPLE *DROSOPHILA* AND BACTERIOPHAGE SPECIES

Margaret Gaggioli

Mentor: Sarah C. R. Elgin

Sequencing technologies have advanced rapidly in recent years, substantially reducing the cost of whole genome sequencing. However, these technologies are not perfect—manual inspections and targeted resequencing are required to produce high quality assemblies. During Summer 2017, we improved the genome assemblies of 25 bacteriophage and two *Drosophila* species (*Drosophila ficusphila*, *Drosophila eugracilis*). The *Drosophila* species are being used in motif finding through phylogenetic footprinting. For the phage project, we characterized the physical ends and resolved low quality regions within the assemblies so that the high-quality sequences can be used in gene annotations and submitted for publication. The first step for both projects involved the use of Consed to identify consensus errors, low quality regions, and gaps within the draft assemblies. We then attempted to resolve these problematic regions using bioinformatics and wet-bench techniques. Initial assessment revealed 34 gaps in the Muller F and D elements of the two *Drosophila* species. Many of these gaps are located within repetitive regions and might have resulted from misassembly. Using Consed, we resolved one gap by rearranging the available Illumina and 454 sequencing reads. The remaining gaps are caused by missing data and require additional sequencing to resolve. We used Consed to design primers on both sides of each gap and the region was then amplified using PCR. If gel electrophoresis analysis determined that the desired PCR product had been generated, then the samples were sent for sequencing. Between both species, we resolved two gaps using this approach but four attempted gaps remain unresolved. There were no gaps in the phage projects and we were able to resolve consensus errors and low-quality regions using bioinformatics and wet-lab techniques. Thus the phage genomes are finished, but more remains to be done in the *Drosophila* projects.

HISTORY OF COMMUNITY-BASED SYSTEM DYNAMICS

Krista Galleberg

Mentor: Peter Hovmand

System dynamics is an applied field of systems thinking and has been used to solve real-world problems, such as issues in industrial management, environmental policy, and health care policy. One of the recent innovations in the field of system dynamics is the emergence of *community-based system dynamics*, which is system dynamics for community building and social justice. Community-based system dynamics builds capacity within marginalized communities to solve systemic problems facing their community by teaching the tools and language of system dynamics to members of the community. My research project explores the origin and development of the field of system dynamics, with special attention to the emergence of community-based system dynamics. It attempts to situate community-based system dynamics within the context of SD's history. My project also considers potential synergies between community-based system dynamics and education, especially the policy, theory, and practice of PK-12 classroom teaching in the United States.

ANALYSIS OF IMMUNOLABELED NEURONAL CELLS IN A RODENT MODEL OF INTERVERTEBRAL DISC DEGENERATION

Matthew Gayoso

Mentor: Elizabeth Leimer

Sensory nerve infiltration of the intervertebral disc (IVD) is a potential contributor to low back pain with IVD degeneration. Molecular changes of dorsal root ganglia (DRG) in a model of IVD degeneration may reveal a role for sensory nerve activation and infiltration. Quantifying such changes using immunohistochemical (IHC) techniques would be valuable for understanding the underlying disease mechanisms. However, image segmentation of neuronal structures has proved challenging. As a result, attempts to quantify IHC fluorescence intensity of neuronal targets are often not well described, leaving specific methods and sources of bias unknown. This project's objective was to develop a quantitative image processing method to analyze immunolabeled rat DRG neurons in a rodent model of IVD degeneration. All DRG sections were imaged via confocal microscope, stained for IHC targets, and analyzed using ImageJ. The methods developed in this project were semi-automatic, requiring the manual segmentation of neurons in the image. Additional processing included automatic thresholding algorithms and built-in ImageJ functions. The applied algorithms were qualitatively chosen based on their ability to output results with the least error. The examined neuronal parameters were cell area, maximum cell diameter, percentage of positive antibody staining, and fluorescence intensity. Analysis also included the density of satellite cells. Furthermore, all methods developed in this project output continuously distributed data. In contrast with discrete grading scales often used to assess IHC sections, continuous data can enable the use of more powerful statistical tools and potentially provide more insight. In addition, these methods potentially reduce the sources of bias, with the largest one being the manual segmentation of neurons. These methods are also able to detect neuronal cellular changes in a model of IVD degeneration between treatment groups at 20 weeks post-surgery.

GENOMIC ANALYSIS OF CD56^{BRIGHT} AND CD56^{DIM} NATURAL KILLER CELLS

Joe Germino

Mentor: Marco Colonna

Natural killer (NK) cells are a vital part of the innate immune system, playing a role in early response to infection through their ability to produce cytokines and lyse cells. NK cells have been shown to be composed of two subtypes: CD56^{dim} cells are found in the blood and are strongly cytotoxic while CD56^{bright} cells are localized to lymphoid tissues and secrete inflammatory cytokines.

A debate exists over the developmental relationship between CD56^{bright} and CD56^{dim} cells: one model proposes that CD56^{bright} cells are a precursor of differentiated CD56^{dim} cells, but another proposes they differentiate independently from a common progenitor and may interchange. To gain a better understanding of these NK cell subtypes, we profiled the transcriptome of several innate lymphocytes. We used these data to identify genes differentially expressed between the two NK cell subtypes and determined that CD56^{bright} cells have an expression profile that resembles immature NK cells. By using uniquely expressed genes to profile the different NK cell subtypes, we learned more about how they interact with each other providing information about their function in early immune responses. In addition, ATAC-seq data identifying regulatory elements located within open chromatin and CHIP-seq data identifying regulatory elements that are H3k27 acetylated were generated. This chromatin state information was used to profile genes in NK cells as poised, active, or off; giving insight as to how restricted the expression in each subtype is, providing further evidence to determine their lineage.

An understanding of the differences between NK cell subtypes and their relationships can provide insight to the development and function of the innate immune system. The differences between CD56^{bright} and CD56^{dim} cells may be essential to an effective NK cell response and their failure to function properly could result in a weakened immune system that is unable to fend off pathogens.

A STRUCTURAL AND GENOMIC INVESTIGATION OF NOVEL BACTERIOPHAGE KROMP

Laura M. Goh, Benjamin L. Kelsky, and Muhammad Mousa

Mentors: Kathy Hafer and Chris Shaffer

The novel bacteriophage Kromp was isolated from a sample of rotting moss as part of the SEA Phages undergraduate research program. The sample was collected on September 4, 2017 in Forest Park, at 38.6409 °N, 90.2992 °W. It was then enriched in a bacterial broth before initial plating in a *Streptomyces lividans* bacterial lawn; after several rounds of purification, a high-titer lysate of 1.0×10^{11} plaque forming units (pfu)/mL was produced. Kromp creates an atypical plaque morphology in which surviving bacterial cells populate cloudy plaques and produce red pigmentation. Through electron microscopy, Kromp was determined to have a head with an average width of 66 nm and height of 63 nm, and a tail length of 230 nm. Many of its outward characteristics, such as its small, icosahedral head and long, striated tail, are prototypical of *Streptomyces* phages; however, Kromp also expresses a number of unique qualities that make it a bioinformatically interesting topic of study. The Kromp genome is 58268 base pairs in size and contains 96 protein-coding genes, a single tRNA-coding gene, and an unusually high GC content of 71.4%. Certain areas of the genome possess previously unobserved qualities, such as gene cluster 65-67, where evidence suggests that there are fully overlapping genes in multiple reading frames. Gene 17 spans an open reading frame (ORF) of 4815 bp, comprising 8.3% of Kromp's total genome size, making it nearly three times as long as the second-largest Kromp gene. Studying the genomic characteristics of novel bacteriophage such as Kromp contributes to a deeper understanding of phage genetic diversity, evolution, and functionality.

CHANGES IN ECM DISTRIBUTION DURING SMALL INTESTINAL ADAPTATION FOLLOWING MASSIVE SMALL BOWEL RESECTION

William Hyunhak Goo

Mentor: Brad Warner

Short gut syndrome (SGS) is defined as insufficient intestinal length to meet the nutritional and metabolic demands of a patient. Causes range from necrotizing enterocolitis and congenital malformations (children) to inflammatory diseases and cancer (adults). In these diseases, small bowel resection is performed to cut out the damaged and unrecoverable portion of the small intestine (SI), resulting in SGS. In an adaptive physiological response, the body increases the length of intestinal villi and the depth of crypts within remaining short intestine, thereby increasing absorptive mucosal surface area. This regenerative physiological response is called “intestinal adaptation,” but the genetic and molecular mechanisms that drive this adaptive response are poorly understood. Extracellular matrix (ECM) is known to play key roles in many developmental and regenerative processes. We hypothesize that the ECM plays a critical role in the intestinal adaptation response to SGS. In support of this model, our lab found that following SI cytotoxic damage and RNA-seq analysis, ECM related genes were the most highly upregulated class of genes among all gene ontology categories. My research focuses on analyzing changes in ECM during SI adaptation following massive small bowel resection (SBR). To address the role of the ECM in the regenerative response to SGS, we will track the localization of key ECM proteins before SBR and four days after SBR to compare the composition and distribution of the ECM during the adaptive response. Our approach will provide a clearer view of the role of the ECM in the intestinal adaptation following the SBR. A better understanding of SI ECM regenerative processes may inform new therapies for neonatal, pediatric, and adult patients suffering from SGS.

INVOLVEMENT IN SPORTS, HIPPOCAMPAL VOLUME, AND DEPRESSIVE SYMPTOMS IN PREADOLESCENT CHILDREN

Lisa Gorham

Mentor: Deanna M. Barch

Recent studies have found that higher levels of exercise are significantly associated with lower depression among young people. A few studies suggest that exercise may cause changes in hippocampal volume, but little research has been done in preadolescent children. To better understand the relationship between involvement in sports, hippocampal volume, and depressive symptoms in young children, we examined data from a nation-wide sample of 4,525 children ages 9-11 years who completed surveys, interviews, and an MRI scan for the Adolescent Brain and Cognitive Development Study. The parents of the children completed the Child Behavior Checklist, providing data about the child's depressive symptoms, and the Sports and Activities Questionnaire, which provided data about the child's participation in 23 sports. Children also took part in a structural MRI scan, providing us with measures of bilateral hippocampal volume. Analysis of the data showed that involvement in sports was negatively correlated with depressive symptoms in boys only ($p < 0.001$), but was positively correlated with hippocampal volume in both boys and girls ($p = 0.020$). Hippocampal volume was negatively correlated with depressive symptoms in boys only ($p = 0.026$), and served as a partial mediator for the relationship between involvement in sports and depressive symptoms in boys. Moreover, these relationships held even when correcting for SES, race, age, and total brain volume. Thus, these findings help illuminate a potential neural mechanism for the impact of exercise on the developing brain. More research is needed to understand the causal relationships between these variables and to help explain the difference in results between boys and girls, as this could have significant public health implications.

TRACKING TRANSCRIPTION FACTORS: VALIDATING THE BRD4-HYPB CALLING CARD SYSTEM *IN VITRO*

Lucia Grandison

Mentors: Joe Dougherty and Darshan Sapkota

Transcription factors play critical roles in the development of nearly all cell types. While methods currently employed to study transcription factor binding events are limited to only tagging transcription factors bound to the DNA when transcription was halted, a new technology known as the calling card system is able to exhaustively record the memory of transcription factor binding events. Calling card technology harnesses the functionality of genetic transposable elements to identify the targets of DNA binding proteins. When a transposase is fused with a transcription factor, the transposon enzyme will deposit its genetic cargo close to the tagged transcription factor's binding site. Thus, one can track transcription factor binding by looking for transposon insertions.

The purpose of this research project was to assess the functionality of the Brd4-HypBase calling card construct. To create this construct, the general transcription factor Brd4 was fused with a HyperpiggyBac (HypB) transposase and a DHFR degradation domain (DD), all of which was put under the control of a Tet-On promoter. This construction, in theory, would allow for the tight regulation, both transcriptionally and post-translationally, of the Brd4-HypB construct using doxycycline (Dox) and trimethoprim (Tmp), respectively. After culturing primary astrocytes from neonatal mice carrying the TetOn-Brd4-HypB-DHFRDD allele, qPCR and Western blot analyses were performed on cells treated with one of the four combinations of Dox and Tmp to compare the amounts of Brd4-HypB mRNA and stabilized Brd4-HypB protein in treated vs. untreated cells. The qPCR results indicated no significant difference between the amounts of Brd4-HypB mRNA in cells treated with Dox compared to untreated cells, indicating a possible issue with the promoter. Similarly, the Western blot results indicated no significant difference between the amount of Brd4-HypB protein detected in cells treated with Tmp vs. untreated cells.

TRANSLATION OF MASTER REGULATOR GCN₄ IS RESISTANT TO eIF₄E MEDIATED INHIBITION OF CAP RECOGNITION IN *SACCHAROMYCES CEREVISIAE*

Alison Greenlaw

Mentor: Hani Zaher

In Eukaryotes, mRNAs possess a 5' 7-methylguanosine cap, which stabilizes the mRNA and recruits the ribosome to initiate translation. However, not all genes require the cap to be translated. There are several mechanisms by which mRNAs can be translated without cap recognition. Cap-independent translation in eukaryotic systems has not been comprehensively characterized but is implicated in cellular functions such as stress response, apoptosis, and cell cycle control. Studies of cap-independent translation in eukaryotes have the possibility to unearth key conserved regulatory mechanisms in gene expression. We used ribosome profiling to map ribosome protected RNA fragments, providing a comprehensive view of transcripts that are actively translated. We used a *Saccharomyces cerevisiae* strain with a conditional mutant for eIF4E, the eukaryotic translation initiation factor responsible for cap recognition and binding, to halt cap-dependent translation under non-permissive conditions. In this way, we are able to locate genes which can be translated in a cap-independent manner. Our findings indicate that master regulator GCN4 can be translated cap-independently and was an interesting gene with significantly increased translational efficiency. GCN4 is a key transcription factor that activates over 50 genes in amino acid biosynthetic pathways in response to amino acid starvation—we saw a corresponding increase in mRNA from amino-acid biosynthetic genes in the GCN4 regulon. GCN4 is a well-known model for translational regulation and is activated by inhibition of eIF2 α by phosphorylation. When eIF2 α is phosphorylated, it inhibits ternary complex formation, allowing the ribosome to scan through upstream open reading frames to reach the true start codon. Via western blotting we found that our observed increase in translational efficiency was independent of eIF2 α -P. Our investigation further underscores the importance of GCN4's role in the stress response and complicates the accepted model of translational regulation. This work yields novel understanding of stress-mediated translational control in eukaryotes.

INSECT DIVERSITY SURVEY OF WHITE CLOVER IN WILD VS CULTIVATED ENVIRONMENTS

August Gremaud and Alex Mahmoud

Mentor: Sara Wright

This project was designed to complement a common garden experiment being conducted by the Olsen Lab at Tyson Research Center. In that study, white clover plants are being surveyed for leaf herbivore damage to determine whether cyanogenic plants (those that produce HCN following tissue damage) receive less damage than acyanogenic plants. However, the research gardens being used do not fully represent the local environment for a variety of reasons. Our goals here were to determine whether there were differences in insect diversity and trophic structure between the research gardens and mowed areas where white clover grows naturally at Tyson. Between June and August 2017, we captured insects in both environments seven times using 12" sweep nets. Insects were classified according to their taxonomic families, or more specifically when possible. We found that although the insect abundance was reduced by approximately half in the research gardens, the most abundant species and the trophic structure remained similar. Family differences were also determined between the two environments, which shed some light on potential differences in predation that wild clover experience but garden-grown clover does not. Overall, we expect that herbivore leaf damage in the research gardens will be lower than in more natural settings, which may impact the interpretation of those data.

AMPLIFICATION OF MOTIVATED BEHAVIORS THROUGH MU-OPIOID SIGNALING IN THE NUCLEUS ACCUMBENS

Anthony Guglin

Mentor: Michael Bruchas

Motivation, or the desire to obtain rewarding stimuli, is an integral part of human psychology, and appears to be mediated by complex interactions in the mesocorticolimbic pathway in the brain. The mu-opioid receptor system plays a role in modulating motivated behaviors. Here, we genetically and pharmacologically manipulated mu receptors to test whether they are involved in baseline or hyper-motivated behaviors using food intake and social interaction behavioral paradigms. Under baseline conditions, global knockout mice (KO) and wildtype mice consumed the same amount of food and socialized to the same degree. After 24 hours of food deprivation or one week of social isolation, wildtype mice increased their intake by 300% and interactions by 150%. By contrast, KOs didn't show any increase in motivated behaviors. The nucleus accumbens (NAc), located on the ventral forebrain, is involved in generating intense motivation. The two major types of neurons in the NAc that contain mu-receptors are enkephalin releasing and dynorphin releasing neurons. Mice that were bred to delete mu-receptors on all enkephalin neurons (*Oprm1^{fl/fl}* x *enkephalin-cre*) showed a decrease in food deprived intake and social interactions after isolation by 50% compared to wildtype mice. By contrast, mice bred to delete mu-receptors on all dynorphin neurons (*Oprm1^{fl/fl}* x *dynorphin-cre*) showed an increase in motivated behavior similar to that seen in wildtype. Concurrently, a separate group of *Oprm1^{fl/fl}* mice received local viral infusions of a cre containing virus to selectively delete mu from accumbens neurons. Surprisingly, we didn't see the same blunting of motivated behaviors observed in *Oprm1^{fl/fl}* x *enkephalin-cre* mice. In contrast, deleting mu receptors off of incoming neurons that project to NAc blunted motivated behaviors. Finally, we injected a fluorescently tagged retrograde virus into the NAc of *Enkephalin-cre* mice and found that the paraventricular nucleus of the thalamus (PVT) most robustly projects into the NAc.

DEVELOPMENT OF *IN VITRO* FLUORESCENCE POLARIZATION ASSAY CHARACTERIZING THE INTERACTION BETWEEN NIPAH VIRAL PROTEINS

Laura Hagenah

Mentors: Gaya Amarasinghe and Daisy Leung

Nipah virus (NiV) is a highly pathogenic, zoonotic virus that currently has no drugs or vaccines available for treatment. Within the viral RNA-dependent RNA polymerase complex (viral RDRP complex) of NiV, the interaction between the nucleocapsid protein (N) and the polymerase cofactor (P) is essential for viral RNA synthesis. Due to the critical nature of this interaction, we are developing a fluorescence polarization assay (FPA) to characterize this protein-protein interaction, which can be used to screen for inhibitors that target the interface between the NiV N and P protein. These inhibitors could have the potential to be developed into antiviral treatments for NiV or other *Henipaviruses*.

THE ART OF TERROR: ICONOCLASM IN MODERN RADICAL ISLAMIC TERRORISM

Christopher Hall

Mentor: Lee Epstein

Contemporary terrorism has received a great deal of attention in the news media and academia. These analyses tend to focus on the political and economic motivations of terrorists which, while important, are missing a significant aspect of modern terrorism. Looking at major terrorist actions from 2000 to 2017 I find an observable pattern of iconoclasm in modern radical Islamic terrorism. I define iconoclasm as the purposeful destruction of objects of perceived value, symbolism, or cultural unity for political ends. I find this strategy of iconoclasm to arise from a combination of economic and political grievances among Arab populations as well as the allure of Western culture. Those looking to position themselves in opposition to the West realize that Western cultural or “soft” power is a powerful draw for mainstream Arabs, and thus seek to destroy objects that symbolize this power. In so doing, these radical Islamists are seeking to deny Arab populations alternative visions for the future of the Middle East, thereby strengthening their claims to legitimacy. These findings further our understanding of the motivations and strategies of modern radical Islamic terrorism, and in so doing shed light on the strategies required to effectively combat this phenomenon.

MICROTOROID RESONATORS FOR MICRORNA QUANTITATION

Gabriela Hall

Mentors: Lan Yang and Abraham Qavi

Increasing the rapidity, reliability, sensitivity, and cost-effective nature of biological assays for medically relevant molecules holds great potential to improve medical practice and make it more widely available. Many researchers have tapped into the potential of microresonators for ultra-sensitive detection and assays of proteins, oligonucleotides, pH, temperature, and chemicals. Microresonators provide highly sensitive detection on the order of picomolar concentrations, cheap and fast fabrication, recyclability, label-free detection, rapid detection time, accuracy in complex media, and multiplexing. Examples of microresonators include microrings, microspheres, and microtoroids.

To detect particles using microresonators, targets bind to the chemically altered surface and change the path of light traveling through the microresonators. This change is measured and used to detect individual particles or small concentrations of particles. The surface chemistries can be altered to optimize binding of a specific target biomolecule by attaching the appropriate functionalization, blocking, and probe chemistries. My research seeks to optimize surface chemistry and microfluidics while using a toroidal microresonator to detect specific miRNA's. Since miRNA's have recently been found to regulate multiple cancers and diseases, a cheaper, faster, and more accurate assay to analyze miRNA's would be beneficial.

ISOLATION AND ANNOTATION OF BACTERIOPHAGE YABOI

Molly Harback, Michael Hogarty, Rocio Rubiano, and Richa Sinkre

Mentors: Kathy Hafer and Chris Shaffer

We present here an investigation into the largely untapped diversity of bacteriophage. In the experiment, a bacteriophage, dubbed Yaboi, was collected from a mulch sample from the median of Wydown Blvd at 38.6434 °N, 90.3157 °W, isolated, and purified using the bacterial culture *S. lividans*. A high titer lysate of 7.4×10^{10} pfu/mL was achieved through collecting plate lysates. A restriction enzyme digest of Yaboi genomic DNA with endonuclease *Bam*HI did not cut, and the restriction enzyme *Hind*III produced 19 bands during gel electrophoresis. Transmission Electron Microscopy of bacteriophage Yaboi revealed an icosahedral head and long, flexible tail. The head length was determined to be 86 nm, the head width 74 nm, and the tail length 413 nm. Preliminary analysis suggested that the phage was temperate, as it created bullseye plaques, with a clear center followed by a ring of bacteria, and then another clearing. Yaboi's genome length is 131,251 bp, with a direct terminal repeat of 12,433 bp, and 251 genes. The GC content is 49.3%. Yaboi's cluster determination was BE2. In positional annotation, some unusual genes were found with little BLAST similarity to previously described phage proteins, and these included the gene at 11,219 to 11,007; 65,450 to 65,701; 85,405 to 85,560; and 117,859 to 111,359. Characterization of novel phages such as Yaboi creates a larger database with which researchers can compare other phages. Uncovering genetic variety in such a vast population of organisms allows for advancements in fields such as medicine and agriculture to develop, giving rise to technologies such as bacterial infection detection and vaccines.

EMPLOYING HUMAN INDUCED PLURIPOTENT STEM CELLS (hiPSCs) TO MODEL NF1-ASSOCIATED LOW GRADE GLIOMAS

Kelly Hartigan

Mentor: David Gutmann

Neurofibromatosis type 1 (NF1) is a clinically heterogeneous cancer predisposition syndrome caused by a germline mutation in one of the two alleles of the *NF1* gene. Low grade gliomas (LGGs), particularly in the optic pathway, are common in patients with NF1 (15-20%). These tumors arise when the remaining allele is somatically inactivated in glial progenitor cells. *Nf1* genetically-engineered mouse (GEM) models have been employed to study NF1-associated LGGs; however, there are still a limited number of therapeutic targets available. This lack of clinical translation could reflect species-specific differences between rodents and humans or the use of “knockout” mutations in the mouse models, whereas patients with NF1 harbor a diverse number of germline *NF1* gene mutations. To study the importance of the germline mutation to LGG development and progression in human cells, the Gutmann Laboratory has created a collection of human induced pluripotent stem cells (hiPSCs) with NF1 patient mutations and hiPSC-derived cerebral organoids. Using this resource, we have generated mixed cerebral organoids comprised of hiPSCs homozygous for patient-specific *NF1* mutations and hiPSCs heterozygous for distinct *NF1* mutations spanning the *NF1* gene. Our preliminary results demonstrate that these mixed organoid cultures exhibit histological characteristics of NF1-LGGs. Future experiments employing this model will evaluate the differential effects of *NF1* mutations on LGG formation and growth.

IDENTIFYING NOVEL EPIGENETIC DEPENDENCIES IN PRE-LEUKEMIC HEMATOPOIETIC STEM CELLS

Emily Haussler

Mentor: Grant Challen

The DNA methylation modifying enzymes DNMT3A and TET2 are essential for proper differentiation of hematopoietic stem cells and are frequently found to be mutated in blood cancers. Although their functions in regulating DNA methylation have been characterized, a specific connection between methylation patterns and altered gene expression has not been established to explain the observed disease phenotype. We hypothesize that *Dnmt3a* and *Tet2* mutant HSCs are dependent on other epigenetic regulators to corrupt normal hematopoietic pathways. If this is the case, inhibition of the chromatin modifiers on which driver mutations *Dnmt3a* and *Tet2* depend could represent a novel therapeutic strategy for reducing the propagation of pre-leukemic HSC populations and preventing the onset of hematological malignancies. To test this hypothesis, we employed a CRISPR-Cas9 based negative selection screen on cells derived from DNMT3A-null and TET2-null HSCs, targeting 180 chromatin modifying genes. Results were obtained from three biological replicates, and those genes showing significant fold depletion over time in *Dnmt3a*-null or *Tet2*-null cells were selected for further investigation as potential therapeutic targets. Specifically, *Esco1*, *Brd2* and *Zmynd8* are being considered for future directions. Ultimately, we conclude that our negative selection CRISPR screen is optimized to detect those genes potentially showing an epigenetic dependence with DNMT3A and TET2 in hematopoiesis, and that functional studies *in vivo* are needed to validate and further define our *in vitro* findings.

SEQUENTIAL EXPRESSION OF *let-7* AND *E93* DURING THE LARVA TO PUPA TRANSITION IN *DROSOPHILA*

Michaela Henderson

Mentor: Ian Duncan

Whether transitioning from larva to pupa, or child to adolescent, animals proceed through distinct stages during their development. How such transitions are specified is poorly understood. In many animal forms, the transition from juvenile to adult development is controlled by accumulation of the *let-7* micro-RNA. In *Drosophila*, adult development also requires the transcription factor *E93* which is expressed specifically at the pupal stage. To determine the relationship between *let-7* and *E93*, I have focused on the mushroom bodies (MBs) of the brain. MBs are generated by neuroblasts, stem cells that divide to produce neurons throughout larval and pupal development. Neurons generated at the pupal stage produce distinct adult lobes of the mushroom body. In pupae, *E93* is expressed in a ring of neurons immediately surrounding each neuroblast, whereas *let-7* is expressed in an adjacent outer ring of neurons. Two models could explain these expression patterns: 1) neurons express *E93* soon after birth, but then transition to expressing *let-7* as they become displaced from the neuroblast by later-born neurons; or 2) neuroblasts generate *let-7*-expressing neurons early in metamorphosis, and then switch to generating distinct *E93*-expressing neurons. These models were distinguished by permanently marking cells that have expressed *E93* at any time in their developmental history. The experiment was to use *E93-Gal4* to drive expression of yeast Flippase which then permanently activated GFP expression by the excision of a cassette containing a transcriptional stop. The results support model 2; green fluorescence was restricted to *E93-Gal4*-expressing neurons, with no fluorescence seen in *let-7* expressing neurons. These observations indicate that the transition from larval to adult development in the mushroom body occurs in two steps, with neuroblasts first generating *let-7*-expressing neurons, followed by the production of *E93*-expressing neurons. Experiments are under way to determine the fates of each of these neuronal types.

MORE THAN CAUCASIAN COPYCATS: CULTURAL BEAUTY STANDARDS BEHIND SOUTH KOREAN COSMETIC SURGERY

Alice Herrmann

Mentor: Eileen G'Sell

The Seoul Metro subway system, which transports 2.9 billion passengers annually, plans to ban all plastic surgery advertisements by the year 2022. In the year 2015, 445,144 aesthetic procedures were performed in South Korea. What factors are responsible for this obsession, and how is it influenced by the West? Though much literature exists to examine the presence of Western beauty ideals in Asia, little has been written to analyze the existence of these standards in advertisements. I consider three Korean cosmetic surgery advertisements to determine whether they promote strictly Western appearances or are also rooted in Korean beauty ideals and marriage rhetoric. An advertisement for the Louivin Dental Clinic presents “before” and “after” pictures of a woman who does not appear more Caucasian after surgery, but is represented by colors and symbols to be happier and more feminine, and to have higher social and economic statuses. A second advertisement, for Grand Plastic Surgery, utilizes the Western symbol of an engagement ring, but promotes cosmetic surgery and improved appearance as necessary to finding one’s ideal spouse, a belief not specific to Western countries. Finally, another Grand Plastic Surgery advertisement incorporates the image of a sheet mask, a popular Korean skincare product, representing a mathematical, cookie-cutter approach to Korean beauty. I conclude that though some aspects of Korean plastic surgery, such as double eyelids and flattened cheeks, stem from a Western basis, the controversial subway advertisements do not emphasize a Western appearance as a prominent goal. Still, it is clear why many subway riders take issue with these posters, which target young women by presenting plastic surgery as necessary to represent one’s character and find a spouse. It remains to be seen whether banning the ads will stem the tide of desire for cosmetic surgery.

ISOLATION AND GENOMIC CHARACTERIZATION OF STREPTOMYCES PHAGE CIRCINUS

Alice Herrmann, Amy Kwan, Caelan Miller, and Brandon Tang

Mentors: Chris Shaffer and Kathy Hafer

A major goal of phage biology is to understand how the phage genome interacts with its bacterial host and how these interactions drive evolutionary change. Isolation and genomic characterization of environmental phages allows for this continuation of research into phage infection mechanisms. *Streptomyces* Phage Circinus was isolated from environmental sampling at the coordinates 38.6032 °N, 90.2616 °W near Seed Sprout Spoon in St. Louis, MO. Subsequent plaque assays and streaking with *Streptomyces griseofuscus* ensued to ensure presence of phage, with Circinus displaying clear, stellar plaques. Four rounds of purification and subsequent webbed plating were performed to achieve a high titer lysate of 6.0×10^9 pfu/mL. Transmission electron microscopy revealed that Circinus has an icosahedral head with a non-flexible tail with an average horizontal head, vertical head, and tail measurements of 85 nm, 80 nm, and 358 nm, respectively. Through genomic sequencing, Circinus was found to have a genome of 126,383 base pairs with a direct terminal repeat of 2050 base pairs and a G-C content of 52.9%. The draft annotation of Circinus contains 216 protein-coding genes with 33 tRNA genes. Circinus belongs to the BK cluster and BK2 sub cluster and shows a high level of similarity with the phage BillNye. Through meticulous manual annotation, our group found that the genome organization of Circinus is comprised predominantly of forward-strand genes, with a total of 10 reverse strand genes, split into a cluster of eight at 2620 bp to 6112 bp, with two scattered at 70279 and 119711 bp. By comparing similar proteins of previously annotated phages, we seek to discern the functions of the genes found in phage Circinus.

INVESTIGATING SEX DIFFERENCES IN THE BRAIN TUMOR MICROENVIRONMENT

Cameron Hill

Mentor: Joshua Rubin

The risk of cancer increases with age, and senescent cells accrue in the body with age. Cellular senescence is an anti-cancer response that arrests cells in response to potentially oncogenic stresses, such as DNA double strand breaks, oxidative stress, or oncogene activation. Although cellular senescence protects an individual cell from propagating, it can be harmful to surrounding cells. Senescent cells exhibit the senescence-associated secretory phenotype (SASP), which can have deleterious effects, such as promoting inflammation or tumor progression, and stimulating cell proliferation. The link between the increased development of cancer with age and the accumulation of senescent cells has been documented in breast cancer; however, it has not before been considered for brain tumors. Glioblastoma (GBM) is the most frequent primary malignant brain tumor in adults. Patients with GBM have a dismal prognosis, with a median survival of about one year. Glioblastoma arises preferentially in men, with a male to female ratio of 1.6. Furthermore, increasing age is a greater risk factor for males than for females in developing GBM. Therefore, the question remains whether the senescence response and the SASP in the brain, specifically in astrocytes, differs between males and females. My aim is to characterize the threshold of the cellular senescence response in male and female mouse wild-type (WT) astrocytes in order to illuminate whether the SASP microenvironment contributes to 1) males' higher susceptibility to developing brain tumors as they age in comparison to females and/or 2) differences in growth of male and female GBM cells. Thus, I developed a protocol for inducing and characterizing senescence in mouse astrocytes by causing oxidative stress via hydrogen peroxide and staining for senescence associated β -galactosidase, a marker of cellular senescence. My results indicate that male astrocytes undergo oxidative stress induced senescence at a higher frequency than females. Elucidating the sex differences in the senescence response and the SASP will allow for a better understanding of GBM biology and ultimately uncover novel targets for GBM treatment.

DISCOVERY AND GENOMIC ANALYSIS OF BACTERIOPHAGE HIYAA

William J. Hsaio, Julia K. Lieu, and Zoe Chunqi Tian

Mentors: Kathy Hafer and Christopher Shaffer

A major goal of isolating and annotating novel bacteriophages is to identify possible evolutionary relationships between various phage. Phage Hiyaa is a newly isolated bacteriophage of the host *Streptomyces lividans*. It was isolated from a dry and sandy soil sample collected along Big Bend Boulevard between open ends of Forest Ridge Place in St. Louis, MO, near the Washington University in St. Louis campus. Hiyaa was plaque purified, amplified, and sequenced using a shotgun approach. Its plaque morphology is small (pinprick to 1 mm in diameter) and turbid. Hiyaa has a hexagonal head with average dimensions of 76 nm x 73 nm (measured from the top of the head to the point where the tail attaches to the head and between the widest points of the head) with a distinctly striated tail with average dimension of 148 nm long as determined from electron microscopy imaging. Hiyaa's genome is 83,219 base pairs in length and has circularly permuted genome ends. It also contains 123 protein-coding genes and 3 tRNA genes. Using BLAST, which compares the genomes of various phages, Hiyaa shows no significant similarities with other phages; therefore, Hiyaa does not currently have any closely-related phage and most of the annotated genes cannot be recognized to have conventional functions. Additionally, the distance between genes in the Hiyaa genome is much larger than previously described in most phage with an average of 83 base pairs (with a total range of -65 bp to 628 bp) contrasting with the normally accepted range of -10 bp to 50 bp. Further investigation of these novel gene sequences provides insights on Hiyaa's unique mechanisms for surviving and expands the existing evolutionary tree of bacteriophages.

ROLE OF CHMP5 IN ENDOSOMAL TRAFFICKING

MaeMae Huang

Mentor: Phyllis Hanson

The Endosomal Sorting Complex Required for Transport (ESCRT) machinery is a set of proteins that help with the formation of intraluminal vesicles (ILVs) inside of endosomes. A complex of this machinery, ESCRT-III proteins, are thought to drive the membrane remodeling and fission required for this process. One ESCRT-III protein, CHMP5, is essential for life but has been shown to not be required for ILV formation, so its specific role in endosomal trafficking is unclear. In this study, we used siRNA to transiently deplete CHMP5 in cultured human cells. We found that CHMP5 depleted cells had an accumulation of enlarged swollen particles (diameters greater than 480nm) that were positive for late endosomal marker LAMP1 and an increase in the number of small LAMP1 endosomes (diameters less than 300nm). In CHMP5 depleted cells, large endosomes were also shown to uptake FM dye and stain positively for CD63, suggesting that they are full of ILVs—which agrees with previous reports. We thought that this increase in ILVs might be due to impaired lysosome formation or degradative capacity. We found that Magic Red, a marker for degradative capacity, was present, and even increased, in CHMP5 depleted cells, indicating that lysosome formation was not impaired. The large swollen endosomes were MR negative which suggested that they are likely late endosomes. Given that lysosome formation was not impaired, we then looked at the maturation of late endosomes. This process involves a well-characterized recruitment of retromer, a complex that removes early endosomal membrane cargo from the maturing endosome. We found that SNX1 and VPS35, the co-localization of which is required for a functional retromer complex, were less co-localized in CHMP5 depleted cells. All together, these data suggests that CHMP5 depletion does not affect lysosome function, but may impair the maturation and fusion of late endosomes with lysosomes.

gRNA DESIGN PIPELINE

Shrikar Iragavarapu

Mentor: William Buchser

In recent years, CRISPR-Cas9 has made the headlines in both the general worldwide media for good reason. It is an invaluable tool for both *in vitro* and *in vivo* genome editing, used by scientists around the world to break, insert, or remove genes of interest. As a result, the technique allows scientists to study particular genes and create a variety of cell lines used today. The strands of RNA crucial to the functioning of CRISPR-Cas9, called single guide RNAs (gRNAs), can be designed in the lab to target particular genes. However, current methods of designing gRNAs that have high efficiency and specificity are still imperfect. My project is to create an algorithm that can predict the activity score/effectiveness of any gRNA sequence, based on an experimental dataset with over 3000 gRNA sequences and their corresponding activity scores. In order to do this, certain features of the gRNAs nucleotide sequence were analyzed for a possible relationship with their corresponding overall activity scores. Using R, a linear model was determined based on the dataset of 3000 gRNA sequences and corresponding activity scores, indicating the possibility of activity score prediction based solely on gRNA nucleotide sequence. Future direction includes incorporation of additional gRNA features into the existing algorithm and to consider indel pattern for each gRNA in order to increase the predictive accuracy of the algorithm.

DENDRITIC CELLS INDUCE MEMORY-LIKE CHARACTERISTICS IN ACTIVATED NATURAL KILLER CELLS

Devika Jaishankar

Mentor: Todd Fehniger

Natural killer (NK) cells are innate lymphocytes that defend host cells against pathogens and malignancies through their robust cytokine production and cytotoxic properties. One method of enhancing anti-tumor functionality is through the generation of cytokine-induced memory-like NK cells, a promising therapeutic approach for the treatment of hematologic cancers through adoptive cellular transfer. Memory-like character in NK cells has been thoroughly documented upon the pre-activation of naïve NK cells with exogenous cytokines (IL-12, IL-15, IL-18), but further investigation into mechanisms underlying NK cell biology and memory-like modulation is required, especially in the physiologic context. Dendritic cells are innate effector cells and antigen-presenting cells that produce abundant cytokines, including IL-12/15/18 and have been implicated in the physiologic mechanism of NK cell activation. To study the effects of dendritic cell stimulation and cytokine production on memory-like NK cell differentiation, dendritic cells were first generated *in vitro* from peripheral blood mononuclear cells and matured in the presence of CD-40 ligand expressing leukemia cells and cytokines. Mature dendritic cells were irradiated and subsequently co-cultured with naïve, autologous NK cells in a brief 'pre-activation,' which was followed by a cytokine-washout and seven-days rest *in vitro* permitting NK cells to return to their basal state. It was found that upon subsequent re-stimulation with tumor targets or cytokines, dendritic cell-activated NK cells showed enhanced IFN- γ responses as compared to control NK cells. These findings suggest that NK cells previously stimulated by dendritic cells express similar characteristics to memory-like NK cells generated by incubation with purified cytokines alone, thus exhibiting superior anti-tumor effects over control NK cells when measured by flow cytometry. Future work aims to use cytokine-blocking assays and *in vivo* models to further elucidate the role of dendritic cells and pro-inflammatory cytokines in physiologically inducing memory-like NK cell functionality.

PEXRAP-MED19 INTERACTIONS

Nitya Janardhan

Mentor: Irfan Lodhi

PexRAP (peroxisomal reductase activating PPAR γ) is a peroxisomal protein involved in lipid synthesis, and improved glucose metabolism. Recently, research conducted at the Lodhi Lab has discovered that PexRAP has concurrent transcriptional regulation roles as well—suggesting that it may affect metabolism by regulating adipose tissue development at the transcriptional level. Previous experiments have demonstrated that an interaction exists between PexRAP and Med19, a mediator complex subunit. This project investigated the interactions that occur between Med19 and PexRAP in order to better understand their role in adipogenesis and transcription regulation throughout the body, and the overall metabolic pathways in which this interaction could occur. Bioinformatics analysis revealed that this interaction likely occurs within the N-terminus of the PexRAP protein. The focus of this project was to first optimize a mammalian 2-hybrid assay in order to confirm the previously determined interaction. This project resulted in the development of a robust protocol to determine protein-protein interactions within mammalian cells, which was then used to test the interactions between PexRAP and Med 19 *in vivo*. In addition, a secondary project was also completed, through which purified PexRAP antibody was extracted and tested from rabbit serum, for use in further experiments.

INVESTIGATING *MYCOBACTERIUM SMEGMATIS*' ELECTRON TRANSPORT CHAIN THROUGH USE OF CHEMICAL INHIBITORS

Keshav Jayaraman

Mentor: Christina Stallings

Mycobacterium tuberculosis has infected approximately one out of every four people globally as reported by the CDC. One possible source for an antibiotic solution is the Electron Transport Chain. Using *M. smegmatis* as a model organism, I investigate the mycobacterial electron transport chain using known chemical inhibitors and identifying whether they have a specific target within the electron transport chain. Two oxidoreductases of interest include *qcrB* and *cydA*. My current research involves work with the CWHM1023 (CB81-family) chemical inhibitor. It is hypothesized that this compound acts through targeted inhibition of the *qcrB* oxidoreductase. This hypothesis is based on prior experiments showing a decrease in ATP levels of *M. smegmatis* following exposure to CWHM1023, as well as the discovery of a mutation in *qcrB*, $\text{QcrB}^{\text{A178T}}$, conferring resistance to CWHM1023. In an effort to confirm this hypothesis, various deletion mutants of *qcrB* and *cydA* in *M. smegmatis* have been constructed using novel phage recombineering methods. These mutants are then complemented with either empty vector, the original deletion, or a mutant version of the deleted sequence ($\text{QcrB}^{\text{A178T}}$) in an effort to confirm with certainty the targets of CWHM1023. To test the effects of CWHM1023 on the various strains, I utilize the Microplate Alamar Blue Assay (MABA), which tests for respiration levels of bacteria through quantification of the reduction of blue-colored Resazurin to the pink Resorufin. Numerous MABA experiments have thus far been conducted, and have provided promising data supporting *qcrB* as the target of CWHM1023. However, current research directions involve cloning of new complement strains that account for possible genetic polar effects given the existence of *qcrB* and *CydA* in operons. Confirmation of *qcrB* as the target of CWHM1023 will provide novel understanding of the organization of the mycobacterial electron transport chain, and ways by which it may be inhibited.

ELUCIDATING HOST/MICROBE INTERACTIONS BY
COMPARING ANCESTRAL AND EVOLVED
BURKHOLDERIA RESISTANCES TO
DICTYOSTELIUM DISCOIDEUM

Cara Jefferson

Mentors: Joan Strassmann and Tyler Larsen

Complex relationships shape how species evolve. *Dictyostelium discoideum*, a social amoeba, is an excellent evolutionary model because its behaviors provide insight on altruism, self-sacrifice, cooperation, and how these behaviors evolve. Studies found that *Dictyostelium* survival improves when evolved in the presence of *Burkholderia*, its intracellular symbiont. However, little is known about how *Burkholderia* and *Dictyostelium* adapt to each other. Specifically, I ask whether *Burkholderia* resistance, using maximum growth rate as an estimate of fitness, to *Dictyostelium*, increases or decreases when *Burkholderia* is evolved in the absence of *Dictyostelium*. Slow growth in evolved *Burkholderia* compared to ancestral *Burkholderia* may indicate that, when isolated from *Dictyostelium*, *Burkholderia* lost adaptations that improved its resistance to *Dictyostelium*. Thus, the presence of *Dictyostelium* would motivate *Burkholderia*'s resistance adaptations. Alternatively, fast growth in evolved *Burkholderia* compared to ancestral *Burkholderia* suggests evolved *Burkholderia* acquired new or better resistance adaptations in the absence of *Dictyostelium*. This result would indicate *Dictyostelium* inhibits *Burkholderia* resistance adaptation. Addressing fitness adaptations specifically due to the laboratory environment, I show that evolved *Burkholderia*, when plated without *Dictyostelium*, grows faster than ancestral *Burkholderia*. Adaptation to the laboratory environment caused an increase in evolved *Burkholderia* growth rate relative to the ancestral growth rate; I used this data to establish a baseline for determining variation in resistance to *Dictyostelium*. To assess *Burkholderia* resistance, I will then compare growth rates of evolved *Burkholderia* to ancestral *Burkholderia* growth rates in the presence of *Dictyostelium*. The data collected from this project will provide insight on how evolution influences existing host/microbe interactions.

INVESTIGATION OF THE ANTERIOR LATERAL LIGAMENT

Matthew Jenkins

Mentor: Spencer Lake

Currently there is a hot debate on the existence of the anterolateral ligament (ALL). Some studies argue the ALL exists in every human knee, while others argue the ALL does not exist. The ALL originates at the lateral epicondyle of the femur, and inserts at the anterolateral aspect of the proximal tibia. Proponents of the ALL believe it to play a crucial role in post anterior cruciate ligament (ACL) reconstruction knee stability. The goal of this study was to determine if the ALL is a true ligamentous tissue or just a thickening of the anterior lateral capsule (ALC). To test for the existence of the ALL, we harvested 13 ALC, lateral collateral ligament (LCL), and ALL tissue samples from human cadavers with ages ranging from 35-48 (4 M, 9 F). These samples were tested through stress-strain mechanical tests using the quasi-linear viscoelastic (QLV) model and a quantitative polarization imaging technique. In doing this real-time collagen alignment analysis we hoped to compare the ALL to the ALC and LCL tissues, paying particular attention to the parameters of average angle of polarization (AoP) and standard deviation degree of linear polarization (DoLP). Results show that the ALL is not a ligamentous tissue. The ALL demonstrated significantly lower toe and linear region moduli in addition to lower levels of collagen alignment (i.e., lower degree of linear polarization (DoLP) values and more distributed angle of polarization (AoP) values) compared to the LCL. In some cases the ALC tissue was significantly stronger and more aligned than the ALL. These results suggest against the existence of the ALL as an important structural ligamentous tissue.

CHANGING DOMINANCE HIERARCHIES: COMPETITION BETWEEN *DICTYOSTELIUM DISCOIDEUM* IN THE VEGETATIVE STATE

Daniela Jimenez

Mentors: Joan Strassmann and David Queller

Dictyostelium discoideum is an excellent model for studying cooperation and conflict. When these amoebae starve, they aggregate to form a multicellular slug then a fruiting body. *D. discoideum* genotypes compete for space in the fruiting body, which contains reproductive cells, and avoid forming the stalk cells, which will die. Most studies have focused on competition when these amoebae aggregate and become multicellular, however, they spend most of their life in the unicellular stage. Therefore, it is necessary to develop techniques to study interactions during the relatively understudied unicellular, vegetative state.

The sex locus for *D. discoideum* provides a stable genetic marker to identify a clone. By taking advantage of distinct regions within the sex locus, I have developed quantitative PCR assays to track and quantify *D. discoideum* clones in mixed genotype interactions. Previous studies found a linear dominance hierarchy among *D. discoideum* clones during their multicellular phase. Clones at a disadvantage in the multicellular stage may have advantages at other stages, which could explain how this linear dominance hierarchy is stable. Therefore, competition experiments are underway to determine whether the same dominance rankings are evident earlier in the lifecycle. Preliminary results suggest that there is competition between clones in the vegetative stage and dominance rankings differ from those previously found. In a 50:50 mix during the vegetative state, a clone previously ranked last outcompeted a clone previously ranked fourth. We calculated relative fitness and found a range of 0.54 to 1.04 meaning that all clones except for one were negatively impacted by the presence of a competitor. Additional competition experiments are being conducted for a complete comparison to the previously constructed multicellular dominance hierarchy. These shifting competitive advantages provide insights into how competition changes across different lifecycle stages and could explain how the diversity observed among *D. discoideum* is maintained.

LEGITIMACY AND CONSTRAINT: THE FAILURE OF MULTILATERALISM IN SEATO

Syrus Jin

Mentor: Elizabeth Borgwardt

The Southeast Asia Treaty Organization (SEATO) was one of several multilateral alliances built by the United States in the early Cold War. However, SEATO never became an effective alliance because it lacked the foundations for strong multilateralism. This work uses international relations theory as a starting point to evaluate SEATO's failings, and delineates the relationship between postcolonialism, American identity, and the flaws of American Cold War strategy in Asia to SEATO's ineffectiveness. American strategic and identity concerns invariably inhibited the benefits which SEATO could deliver for its members. The need for the United States to maintain its policy autonomy trumped any interest in empowering the organization. SEATO was tainted by the legacy of colonialism, and its small membership was unable to form a cohesive base that could either balance the United States or deliver collective goods to its members. By design, SEATO's constraints, and its legitimacy as a multilateral institution, were limited, preventing it from being effective in its own right or valuable as a legitimizing tool for American interventionism. Explaining SEATO through these lens in turns explains the contours of future U.S. policy in Asia in the Cold War and beyond, and the difficulties which policymakers face in attempting to build a legitimate multilateral institution.

THE EFFECTS OF INCREASED SPONTANEOUS ACTIVITY ON POTENTIATION OF THE GABA_A RECEPTOR BY ALLOSTERIC MODULATORS

Alexander Johnson

Mentor: Gustav Akk

The γ -aminobutyric acid Type A (GABA_A) receptor is the major inhibitory ion channel in the central nervous system. Its activation leads to cellular inhibition or dampening of the effects of excitatory ion channels. Many anesthetics drugs, such as the intravenous anesthetic propofol, directly activate or potentiate the response of the GABA_A receptor to its endogenous ligand GABA. Previous studies have identified amino acid residues whose substitutions have divergent effects on direct activation and potentiation by propofol. For example, the gain-of-function α_1 (L263S) mutation enhances receptor activation by propofol but reduces its ability to potentiate GABA-elicited currents. These observations have sometimes been interpreted as different structural elements underlying direct activation and potentiation. In this study, I tested the hypothesis that changes in receptor spontaneous activity affect observed potentiation. We employed the concerted transition model, a simple four-parameter function introduced by Monod, Wyman, and Changeux, that allows us to analyze and predict the behavior of the GABA_A receptor in the presence of one or more activators. The model predicts increased direct activation and reduced apparent potentiation as the level of spontaneous activity increases. The predictions were confirmed by two-electrode voltage clamp electrophysiology experiments on $\alpha 1\beta 3$ and concatemeric $\alpha 1\beta 2\gamma 2L$ GABA_A receptors.

THE ROLE OF RET-GFL SIGNALING ON BLADDER SENSATION

Amulya Joseph

Mentor: Judy Golden

Visceral pain conditions such as interstitial cystitis/painful bladder syndrome (IC/PBS) affect nearly one million U.S. adults, and present a significant depression in quality of life for these patients. Treatment options for IC/PBS are limited and often ineffective, due in part to the preferential study of pain in the somatic system. One pathway that has a demonstrated role in the modulation of pain is the RET-GFL neurotrophic signaling pathway. RET is the co-receptor for the GDNF family of ligands (GFLs), a group of neurotrophic factors with functional roles in renal development, enervation of the gastrointestinal tract, and neural growth and survival. Notably, GFLs have been shown to reverse neuropathic pain when supplied exogenously to damaged sensory neurons and prevent the establishment of neuropathic pain; RET-GFL signaling has also been shown to modulate somatic sensation. However, the role of RET-GFL signaling on visceral sensation has yet to be firmly established. Our aim was to characterize the effect of endogenous RET-GFL signaling on bladder sensation. We found that attenuation of RET-GFL signaling decreases the visceromotor response to noxious bladder distension *in vivo*. *In vitro*, bladder afferents that express RET were more likely to respond to capsaicin, the agonist for TRPV1, a channel implicated in bladder pain, than bladder afferents that do not express RET. Furthermore, there is a trend that bladder afferents expressing RET have higher peak responses to capsaicin than bladder afferents that do not express RET. Finally, afferents expressing RET are significantly more likely to respond to mustard oil, the agonist for TRPA1, a channel also implicated in bladder pain, than afferents not expressing RET. This data taken together suggests that the RET-GFL pathway may be a plausible therapeutic target for IC/PBS and other visceral pain conditions.

AN INVESTIGATION OF THE ROLES OF MATERNAL AND FETAL CLOCKS IN DETERMINING GESTATION LENGTH

Pranita Kaginele

Mentor: Sarah England

Preterm birth is one of the leading causes of infant mortality in the United States. Shift workers are especially prone to preterm birth, especially those that consistently engage in rotating night shift work, possibly due to their constantly changing schedules that disrupt their circadian rhythms. Circadian rhythms are regulated by a group of clock genes. *Per2* (Period 2) is a core clock gene that helps regulate functions about a 24-hour period. A family in Utah has a mutation in the *Per2* gene (serine to glycine) that leads to an advanced sleep phase disorder and causes one to be an extreme “early bird.” Members of this family consistently go to bed around 7 p.m. and wake at 2 a.m. the human *Per2* mutant gene (*hPer2*) was inserted into a mouse strain to create a mouse model to mimic the human phenotype, the *hPer2* short mouse. Previous studies have shown that the circadian periods of *hPer2* short mice (21.6 hours) have shorter gestation lengths (17.5 days) compared to wild-type mice (with 24 hour circadian periods and gestation lengths of 19.5 days). We aimed to determine if the circadian period of the mother or fetus drives the timing of the birth. *In vitro* fertilization techniques have an increased risk of shortened gestation length in humans, so we first conducted control studies using wild-type embryos from wild-type donor dams and wild-type recipient dams. We found no significant difference in gestational length between naturally bred dams (19.5 ± 0.257 days, $n=13$) and dams that received embryo transplants (19.67 ± 0.155 , $n=7$). This result suggests that the IVF protocol does not shorten pregnancy length in mice. Further studies will include transferring wild-type embryos into short dams and short embryos into wild-type dams to better understand whether fetal or maternal clocks determine gestation length.

USING MAGNETIC RESONANCE ELASTOGRAPHY TO TEST BREAST TUMOR STIFFNESS

Joshua Katz

Mentor: Gregory Longmore

Women with breast cancer rarely die from primary breast tumors, rather, they die from the spread or metastasis of the tumor to other organs. It is now understood that non-tumor cells, growth factors, chemokines and cytokines, and physical properties of the tumor microenvironment/extracellular matrix (ECM), or stroma, all influence tumor progression to metastasis. In breast tumors, these stromal components differ from their normal tissue counterparts in composition, structure, physical properties, and function. My research focuses on testing bulk tumor stiffness in order to better treat tumor metastasis.

Collagen fibers are the most abundant protein in the ECM and in the tumor stroma. Increased collagen typically leads to increased tissue stiffness. This is critically important for cancer etiology and treatment because increased collagen deposition is often associated with poor prognosis for cancer patients. Work from many labs reveals the amount of collagen, the fiber alignment of individual collagen strands, and their thickness all contribute to altered mechanical properties (i.e., increased stiffness) of breast tumors that promotes metastasis.

My research seeks to find a better more comprehensive way to quantify bulk tumor stiffness. We will use magnetic resonance elastography (MRE) to assess tissue stiffness, and specifically, its impact on tumorigenesis. The first part of the experiment which would look at tissue between *Coll1a1tmJae* mice and control FVB mice would provide information to see if MRE is a viable option to detect tumor stiffness, as it should be detected that *Coll1a1tmJae* have increased tissue stiffness. The second part of this experiment which looks at tumors in these mouse models would help to determine if MRE is a viable option in order to test tumor stiffness. The purpose of the final experiment between MMTV-PyMT and *Her2(neu)* mice would be to develop predictive algorithms in order to comparatively and quantitatively measure tissue or tumor stiffness.

IDENTIFYING PROTEIN THAT ASSOCIATE WITH ADAMTS-A IN THE CENTRAL NERVOUS SYSTEM

Prajwal Keranahalli

Mentor: James B. Skeath

AdamTS-A is an extracellular metalloprotease that cleaves proteins in the extracellular matrix to anchor cells in place and control tissue structure in the *Drosophila* nervous system. Past research in our lab showed that AdamTS-A inhibits collagen IV accumulation in the ECM, but the molecular interactions between these proteins are not well defined. My research focuses on identifying proteins that associate and interact with AdamTS-A. To do this, I am using the yeast two-hybrid system to identify proteins that interact with different regions of AdamTS-A. Identifying proteins that interact with AdamTS-A will help us clarify the exact mechanism through which AdamTS-A preserves nerve cord structure. In addition, through genetic studies our lab found that Papillin (Ppn), another ECM protein, acts opposite to AdamTS-A to regulate tissue structure. By designing antibodies to track the protein distribution and localization of Ppn we can learn if Ppn colocalizes with other key ECM proteins. The antibodies will also help us understand how AdamTS-A processes and inhibits Ppn accumulation in the CNS ECM. Cellular migration plays a major role in head and neck cancer metastasis therefore elucidating the mechanisms that allow cells to spread great distances is an important step in developing treatments. There are several mammalian AdamTS genes that may play a role in maintaining CNS structure just like AdamTS-A in *Drosophila*.

DEEP TISSUE IMAGING USING SILVER SULFIDE NANOPARTICLES

Daniel Khan

Mentor: Bryce Sadtler

Silver sulfide nanoparticles show promise as fluorescent probes for imaging deep tissue injuries due to their emission in the near-infrared region of the electromagnetic spectrum and low biological toxicity. However, a common problem among many nanoparticles, including silver sulfide, is that the individual nanoparticles tend to cluster together and aggregate into larger structures. To examine both the fluorescence properties of silver sulfide nanoparticles and their assembly into larger structures, we first synthesized colloidal silver sulfide nanoparticles of different sizes using dodecanethiol as a capping ligand. The resulting nanoparticles were washed with isopropanol to remove excess dodecanethiol and then stored under different atmospheric environments. Nanoparticles stored in an argon environment were observed to assemble into highly ordered structures (supercrystals), while nanoparticles stored in an oxygen-rich environment remained as individual particles around 5-6 nm in diameter. Using X-ray photoelectron spectroscopy, it appeared that the assembly of silver sulfide could be prevented by the surface oxidation of the nanoparticles. This could explain why supercrystals were not observed when the nanoparticles were stored in an oxygen-rich environment. Electron microscopy was used to show that the supercrystals possessed well-defined morphologies that resembled either “octahedrons” or “stars”. We are currently testing what factors affect the final morphology of these supercrystals such as reaction temperature, reaction time, and ligand concentration. Scanning electron microscopy was used in conjunction with different chemical analysis techniques (infrared spectroscopy, raman spectroscopy, nuclear magnetic resonance) to identify a strong correlation between the quantity of surface ligands and the supercrystal morphology.

DISSECTING A FEEDING CIRCUIT BETWEEN THE EXTENDED AMYGDALA AND PARABRACHIAL REGIONS

Kate Kimbell and Hannah Oden-Brunson

Mentor: Michael R. Bruchas

The bed nucleus of the stria terminalis (BNST) is a structure in the limbic system of the brain known to integrate information related to external threats, while the parabrachial nucleus (PBN) in the brainstem is involved in metabolic signaling, taste sensation, and feeding. Due to these combined roles, the interactions between these two regions may strongly influence food-seeking and exploratory foraging-like behaviors. This project investigates the anatomical structure and behavioral responses associated with the neural circuit projecting from the BNST to the PBN through GABAergic (inhibitory) and glutamatergic (excitatory) neurons.

To understand these BNST-PBN anatomical connections, we utilized cutting-edge retrograde viral tracing methods to identify the source of projections onto the PBN. These tracers showed both GABAergic and glutamatergic neurons projecting from the BNST onto the PBN. For investigating the behavioral implications of this circuit's actions, we injected cre-dependent viruses into the BNST of VGLUT-Cre and VGAT-Cre mouse lines to selectively express an inhibitory optogenetic proteins in either glutamatergic and GABAergic projections. We then used fiber optic implants to deliver optogenetic stimulation directly to these neuronal projections. In doing so, we found that activation of these GABAergic neurons in the BNST-PBN circuit results in increased feeding and an increased exploratory behavior, and mice showed a robust place preference for this activation. Alternatively, activation of the glutamate neurons decreased feeding, and mice showed a strong aversion to activation of these neuronal projections in the PBN. These findings implicate a mechanism by which the brain balances metabolic needs with external threats, and further analyses to explore these interactions are ongoing.

MULTI-FUNCTIONAL SUPRAMOLECULAR
METAL-BINDING NANOCOMPONENTS:
SYNTHESIS AND STUDY OF
THIACALIX[4]ARENE DERIVATIVES

Troy K. Kincaid

Mentor: Jonathan C. Barnes

Recently, the rise in bacterial resistance rendering both new and old antibiotics ineffective has driven researchers to explore supramolecular molecules as a novel means to target and treat infection. The current work of the Barnes Research Group focuses on combating antibiotic-resistant bacteria via the potent combinatorial treatment of antibiotics with metal ions. In this study, we aimed to investigate the metal-binding nanocomponent of a multi-functional polymeric platform, a thiacalix[4]arene ring. Specifically, a series of modifications along the upper-rim of the ring were constructed to optimize the metal-ion binding and solubility properties of the nanocomponent. This library of derivatives was synthesized in order to enhance the bactericidal activity of the drug-delivery platform, while reducing the system's cytotoxicity.

QUANTIFICATION OF DNA ORIGAMI DYNAMICS USING MOLECULAR ORIENTATION ESTIMATION

Eshan King

Mentor: Matthew Lew

DNA origami is a burgeoning method of folding DNA into arbitrary 2D and 3D nanoscale conformations. Researchers can design origami using commercially available software to fit a broad array of needs, such as DNA scaffolds to hold other molecules in place, nanoscale masks for photolithography, DNA nanorobots, or drug delivery capsules.

Many authors claim that under certain environmental conditions, such as low concentrations of magnesium chloride, DNA origami becomes more flexible. However, the evidence presented is mostly concerned with the static or ensemble conformation of DNA origami through TEM imaging or small-angle X-ray scattering, providing only a loose, subjective measure of flexibility.

There is a need for more direct quantification of the mechanical properties of DNA origami, namely elasticity. Understanding how the elasticity of DNA origami structures changes under different environmental conditions, such as changes in temperature, pH, or metal ion concentration, is crucial for understanding the limitations of DNA origami and building more advanced models of higher order structures.

In this project, we have successfully synthesized DNA origami nanopillars labeled with fluorescent molecules. The nanopillars include biotin modifications at the bottom for attachment to modified substrates, allowing the nanopillar to stand upright. Two Cy5 molecules are attached to the top and bottom of the nanopillars. By studying the orientation distribution of the fluorophores, we hope to infer the range of bending that the nanopillar attains, allowing for more direct observation of the change in flexibility of the nanopillar under different environmental conditions. For instance, we expect the nanopillar to access a greater range of bending at lower concentrations of magnesium chloride, as other researchers have reported that this increases the flexibility of the nanopillar. In addition, we hope to develop a simple model for DNA origami bending, allowing for quantification of the mechanical properties of the DNA origami nanopillars under different environmental conditions.

DESIGN AND USE OF A BILATERAL GRIP STRENGTH DEVICE FOR ASSESSING FORELIMB FUNCTION IN RODENTS

Griffin Kivitz

Mentor: Spencer Lake

Post traumatic joint contracture (PTJC) is a debilitating condition that effects up to 50% of patients after suffering an elbow dislocation or fracture. We sought to make limb-specific longitudinal strength measurements to assess how PTJC affects elbow joint function, however commercially available devices compute an average value across both limbs. A custom grip strength device was developed to track individual limb function during rehabilitation in our unilateral elbow injury model. In this study, we describe the novel grip strength device and demonstrate its use by showing functional differences between injured limbs and control/contralateral limbs in our rat model of PTJC.

Long-Evans rats received a clinically relevant elbow injury. After recovery, grip strength measurements were obtained using our custom grip strength device. The grip strength device consists of two sets of metal rungs, or ladders, each held in place by a linear slide and connected to separate load cells. This setup allows for the measurement of individual limb strength, important for tracking progression/recovery of a unilateral injury, and for variability in the pronation-supination positioning of the rungs.

The grip strength measurements indicated a significant loss of strength in the injured limb without causing any loss of strength of the contralateral limb. These findings prove our model of PTJC to be effective, and future work includes tests to track recovery of limb strength postimmobilization in both the pronated and supinated positions. We will also make longitudinal measurements to evaluate the effectiveness of therapy strategies looking to reduce or prevent PTJC in our rat elbow model.

USING A METHANOGENIC ARCHAEON TO CREATE A GENETICALLY TRACTABLE AOM SYSTEM

Bryan Ko

Mentor: Arpita Bose

Methane is a potent greenhouse gas and a major contributor to climate change, with a global warming potential (GWP) much greater than CO₂. Thus, understanding the various biological sources and sinks of methane is critical. One such sink is the anaerobic oxidation of methane (AOM) carried out by microbes that oxidize methane to CO₂. AOM is commonly linked to nitrate reduction in freshwater environments, and sulfate reduction in marine environments by sulfate reducing bacteria (SRB). Studies on AOM are limited as these anaerobic methane oxidizers (ANME) have never been successfully isolated, so there is no direct way to test various theories concerning potential methane oxidation pathways. A well characterized methane-producing archaeon, *Methanosarcina acetivorans*, exhibits limited methane oxidizing capabilities and is closely related phylogenetically to ANME organisms. In an effort to make a genetically tractable AOM system, here we show that a co-culture of *M. acetivorans* and *Desulfosarcina variabilis*, an SRB commonly found with ANME in nature, oxidizes methane and reduces sulfate. In addition, this co-culture exists in an aggregate formation similar in size and shape to ANME-SRB aggregates found in nature. We also identified an oxidase in *M. acetivorans* that could allow methanogens like *M. acetivorans* to oxidize methane anaerobically by coupling it to oxygen reduction or by transferring electrons to its syntrophic partners in nature. Given that *M. acetivorans* is very genetically similar to an ANME strain, this co-culture is a viable substitute for an ANME-SRB co-culture, and will be used to test various theories about the specific energetic and metabolic pathways for methane oxidation, and the morphological and energetic basis of the ANME-SRB syntrophic relationship.

USING IMMUNOPRECIPITATION-TANDEM MASS SPECTROMETRY TO DETERMINE THE PROTEOFORMS OF APOE IN DENSE CORE NEURITIC PLAQUES

Vishal Krishnan

Mentor: Randall Bateman

Alzheimer's disease (AD) is known as the leading cause of dementia in the elderly. This disease is characterized by a severe neuronal loss and the development of extracellular amyloid plaques and intracellular neurofibrillary tangles. In our project, we will be focusing on amyloid plaques which are comprised partly of the Apolipoprotein E protein (APOE). APOE is recognized as a major genetic risk factor for the late onset of AD.

The Holtzman Lab recently developed an anti-APOE antibody that binds to the dense cores of amyloid plaques but not soluble APOE. However, the specific proteoform of APOE that the APOE antibody binds to is still unknown. The project will be divided into two main parts. This part of the project involves immunoprecipitation (IP) method development. Specifically, I worked on optimizing the Solid Phase Extraction protocol. We used a fixed Equimolar mix of ApoE3 and ApoE4 with 13C/15N-Arg as a standard. We then spiked in increasing amounts of purified native ELISA protein standard APOE. After analysis using mass spectrometry, we plotted the peak ratio which results in a linearly increasing graph. There were three potential protocols: the amyloid beta protocol, APOE protocol, and the alpha synuclein (aSyn) protocol. I was to test which of these protocols were optimal. Based on the results, it was found that the APOE protocol was optimal, although the aSyn protocol also worked well.

This project has many future potential implications. The method can allow us to discover which proteoforms of APOE are bound by the antibody, which can lend further clarity to many of the current APOE focused projects being conducted. An understanding of this would also help offer insight into APOE's role in AD pathology and ultimately provide an assessment of the potential for anti-APOE immunotherapy as a therapeutic approach for the treatment of AD.

THE EFFECT OF VARYING TUNGSTEN OXIDE MORPHOLOGIES ON PHOTOCATALYTIC ACTIVITY FOR CARBON DIOXIDE REDUCTION

Christina Krucylak

Mentor: Bryce Sadtler

Tungsten oxide is a cost efficient and environmentally friendly semiconductor photocatalyst that can reduce the amount of carbon dioxide in the atmosphere, by converting carbon dioxide into useful chemical fuels. There are many different crystal structures and compositions of tungsten oxide, which vary in their photocatalytic activity. In this project, we varied the synthesis conditions and then characterized the samples to identify which conditions led to samples with active morphologies for photocatalysis. The four distinct morphologies based on different alcohol solvents and tungsten precursor concentrations were nanoscale rods, wires, stars, and platelets. We used X-ray diffraction and transmission electron microscopy to characterize the samples. Among the four morphologies, tungsten oxide nanowires had the highest photocatalytic activity based on the dye transformation of resazurin, a non-fluorescent molecule, to resorufin, a fluorescent molecule whose presence was measured with fluoresce spectroscopy. The most promising nanowire samples were then used in the reduction of carbon dioxide to formic acid and ethanol. Continued work will be focused on increasing the yield of product formed from this carbon dioxide reduction and producing methane gas by working to increase the oxygen vacancy concentration on the tungsten oxide nanowires.

CLINOPYROXENE'S ROLE IN THE IRON ISOTOPE COMPOSITION OF LUNAR MARE BASALTS

Ethan Kuehl

Mentor: Michael Krawczynski

The Moon is hypothesized to have formed approximately four billion years ago during a giant-impact between a Mars sized object and Earth. Material ejected from both objects accreted to form the Moon, producing enough heat to form a widespread lunar magma ocean. One consequence of the magma ocean is that the Moon's heterogeneity was preserved. Lunar mare basalts, which are partial melts of the Moon's mantle, have a non-uniform composition that is differentiated by both the abundance of titanium and iron isotope composition. High-calcium pyroxene is an important phase that crystallized during the magma ocean period on the Moon. It is therefore possible that high-calcium pyroxene crystallization imprinted a distinct Fe-isotope signature on magma ocean cumulates, and subsequently, the mare basalts.

We conducted experiments that produce two phases: pyroxene and glass (quenched melt) at lunar mantle conditions. The experiments can be grouped into two broad groups: low pressure and high pressure. Low pressure experiments mimic clinopyroxene (cpx) crystallizing at shallow depths in the lunar magma ocean, whereas high pressure experiments replicate clinopyroxene crystallizing at greater depths in the lunar magma ocean. In both cases, not all of the melt crystallizes into clinopyroxene and the residual magma quenches to a glass. By analyzing both the cpx and glass from these experiments in a multi collector inductively-coupled mass spectrometer, we are able to determine the difference in Fe-isotope composition between cpx and glass. This isotopic fractionation allows us to test whether cpx crystallization from a melt is responsible for the varied Fe-isotope compositions in lunar mare basalts. The results of this research will provide data necessary for determining and modeling the evolution of the iron isotope composition of the lunar mantle.

CHILDREN'S GENDER STEREOTYPES AND SCIENCE LEARNING

Daniel Lagoni, Gavin Rackoff, and Mia Shoshany

Mentor: Laura Hennefield

Recent research has demonstrated that children as young as five years old hold the stereotype that males are more competent than females in the field of science. Our study tested whether 3- to 8-year-old children apply this stereotype when judging the credibility of scientific claims made by men and women. In the first phase of the study, children heard a man and a woman present pairs of opposing testimonies about toys and science, and indicated which testimony from each pair they thought was right. Boys and girls were expected to endorse testimonies from the male informant more frequently when learning about science than when learning about toys. When accounting for the influence of children's age, there was a significant interaction between children's gender and the subject of informants' testimonies. The data suggested that girls endorsed the male informant's testimonies more frequently when learning about science than when learning about toys. Furthermore, as girls' ages increased, they were more likely to endorse the testimony of the male informant when learning about science. The first phase of the study provided initial evidence that gender stereotypes affect girls' judgments of the credibility of scientific claims throughout early childhood. The second phase of our study is currently exploring whether 4- to 8-year-old children rely more strongly on gender stereotypes when informants are introduced as "scientists." We expect that both boys and girls will endorse the male scientist's testimonies significantly more frequently when learning about science than when learning about toys. We also expect that this pattern will increase with age.

THE ROLE OF NF- κ B p65 IN SUBARACHNOID HEMORRHAGE INDUCED SECONDARY BRAIN INJURY

Molly Lawrence

Mentor: Itender Singh

Subarachnoid hemorrhage (SAH), primarily caused by rupture of a cerebral aneurysm, refers to the extravasation of blood into subarachnoid space between the pial and arachnoid membranes. With high mortality and morbidity rates, the initial hemorrhage itself is often fatal, but the primary cause of poor outcomes is through the secondary brain injuries that develop in the days following SAH. There are two separate categories of these damages, distinguished as early brain injury (EBI) and delayed cerebral ischemia (DCI). Occurring 1-3 days following SAH, EBI presents as neuroinflammation, cerebral edema, and blood-brain barrier (BBB) disruption. DCI, the more common and devastating category, describes the slower onset damages, 4-12 days post-SAH, including microcirculatory deficits and large artery vasospasm. There is strong evidence that vascular deficits are the main cause of these secondary brain injuries, with blood-brain barrier (BBB) disruption leading to EBI and large artery vasospasm leading to DCI. Several previous studies have shown that a strong genetic risk factor for these poor outcomes after SAH is the presence of apolipoprotein E4 allele. The APOE4 linked pathway involves cyclophilin A (CypA), a cell signaling molecule that causes inflammation through activation of transcription factor nuclear factor kappa-light-chain-enhancer of activated B cells (NF- κ B) p65 and resulting induction of matrix metalloproteinase-9 (MMP9) and BBB disruption. However, the role of CypA in secondary brain injury has not yet been clearly established. Early findings showing high levels of CypA in rodents after SAH, we hypothesize that the CypA- NF- κ B p65 -MMP9 pathway plays a critical role in SAH-induced EBI and DCI.

With CypA inhibition and MMP9 knockouts displaying reduced post-SAH BBB leakage and vascular deficits, our objective for this study was to confirm the role of NF- κ B p65 in this pathway. To assess this, wild-type C57BL6 mice were administered a pharmacological inhibitor of NF- κ B p65, ammonium pyrrolidinedithiocarbamate (PDTC), via intraperitoneal injection the day of SAH surgery and daily for three days following (Day 0 - Day 3). Cognitive and motor skills of the mice were assessed Day 0 - Day 3 via neuroscoring and rotarod along with their littermate controls (also administered SAH). On Day 3, the mice were sacrificed by India ink-gelatin perfusion, which fixes and stains the brain vessels to allow imaging and measurement of the middle cerebral artery to assess vasospasm. The mice with p65 inhibition showed significantly less cognitive impairment and vasospasm than their littermate controls, corroborating our hypothesis of the role of the transcription factor in the induction of post-SAH deficits and suggesting p65 to be a promising potential therapeutic target for SAH.

NEW TANDEM TRANSFORMATION OF α , β
UNSATURATED S-PHENACYL THIOESTERS TO
DIHYDROTHIOPHENE DERIVATIVES VIA
CATALYTIC ACYL TRANSFER

David Leace

Mentor: Vladimir Birman

Our group has recently focused on utilizing electron rich Amidine Based Catalysts (ABC's) to develop tandem transformations of α , β unsaturated thioesters. Until now, the scope of this reaction had been limited to S-aryl thioesters. As an extension to this study, we explored the possibility of activating the less reactive S-phenacyl thioesters in the hope of achieving a similar transformation. We found that under similar conditions, an unexpected product had formed indicating the reaction proceeded via a new mechanistic pathway involving an intramolecular proton transfer. A preliminary study revealed that when a chiral ABC was employed, the same reaction exhibited promising enantioselectivity (55% ee). Substrate scope and mechanistic implications of this newly discovered tandem transformation will be discussed.

THE RELATIONSHIP BETWEEN ANTICIPATORY PLEASURE AND EFFORT-BASED DECISION MAKING

Annie Lee

Mentor: Deanna Barch

The willingness to exert effort in one's daily life is an essential component in leading a healthy lifestyle in order to pursue goals and complete everyday tasks. One must be willing to invest effort to complete daily tasks, such as driving to the grocery store or dedicating time to finish homework. One potential underpinning mechanism for such effort allocation in individuals may be anticipatory pleasure, the experience of pleasure one feels when anticipating future rewards. The Effort-Expenditure for Rewards Task (EEfRT) was conducted to examine effort allocation in response to different levels of reward, effort level (hard or easy), and probability of receiving the reward. The Temporal Experience of Pleasure Scale (TEPS) was administered to measure each individual's capacity to experience anticipatory pleasure. I hypothesized that the more an individual experiences looking forward to engaging in a certain pleasurable future activity, in other words, having higher trait levels of anticipatory pleasure, the more willing he or she will be to exert effort and choose the hard task to receive a monetary reward. Results showed that participants chose the hard task more often when the reward value and probabilities were high. However, contrary to what was predicted, a negative relationship between anticipatory TEPS scores and percentage of hard task choice, suggesting that participants who reported having less anticipatory pleasure in daily life tended to choose the hard task. This data indicates that further studies should be conducted in order to examine the relationship between anticipatory pleasure and effort-based decision making in the general population.

IDENTIFICATION OF CARDIOVASCULAR DISEASE ASSOCIATED GENETIC VARIANTS IN A POPULATION WITH AFRICAN ANCESTRY

Jae Hee Lee

Mentor: Nathan Stitzel

Cardiovascular disease (CVD) is the leading cause of death in the United States, regardless of ethnicity and gender. Coronary heart disease (CHD), the most prevalent form of CVD, kills 370,000 people each year. A wide variety of CVD conditions including CHD are heritable, meaning DNA variation can influence disease risk. Identifying specific variants and genes that underlie the inheritance of CHD has the possibility to reveal insights into human biology and disease pathophysiology. Many known genetic variants associated with CVD only focus on a population of European ancestry. Those with African ancestry have disproportionately high susceptibility to CVD, and thus, it is crucial to identify specific CVD-related variants for this population.

In order to do so, differences in p-values between European and African CVD markers at known loci were analyzed. Regions with non-significant p-values in one dataset and statistically significant ($p < 1 \times 10^{-5}$) in the other were specifically targeted. Number of alleles and allele frequencies of these variants between populations of African ancestry and those of European ancestry were compared, and the functions of each variant were identified.

Such study of genetic variants will assist in more efficient methods and tools such as genome wide association studies for identifying CVD-related genes that are specific to those of African ancestry. This information will also help generate more advanced medical applications for diagnosing and treating the disease. Finally, it will further enhance genetic risk scoring for CVD in individuals of non-European ancestry.

STAT3 SIGNALING MEDIATES FAK INHIBITOR RESPONSE AND RESISTANCE IN PANCREATIC CANCER

Kyung Bae Lee

Mentors: Hong Jiang and David Denardo

Pancreatic cancer is not responsive to targeted therapy. This may be due to the presence of a uniquely fibrotic and immunosuppressive tumor microenvironment present in pancreatic ductal adenocarcinoma (PDAC). Critical obstacles to targeted therapy in PDAC tumors include the dense desmoplastic stroma that acts as a physical barrier to drug delivery and the high numbers of tumor associated immunosuppressive cells. In our previous study, we identified hyperactivated focal adhesion kinase (FAK) activity in neoplastic PDAC cells as a significant regulator of the fibrotic and immunosuppressive tumor microenvironment (TME). FAK inhibition (VS-4718) significantly limited tumor progression, and prolonged mice survival. Herein, we observed that STAT3 signaling was constantly activated in non-responsive and rebounded tumors, suggesting STAT3 signaling pathway regulates FAK inhibitor (FAKi) response and resistance.

We proposed that overcoming STAT3 reactivation upon FAK inhibition would enhance pancreatic cancer sensitive to FAK inhibitor. Together, our data indicate that STAT3 inhibition sensitizes PADC to FAKi and overcomes FAKi resistance.

EXPLORING THE FUNCTION OF SRSF1 RRM1 DOMAIN IN SPLICEOSOME ASSEMBLY

Charlie Lenihan

Mentor: Kathleen Hall

In eukaryotic cells, the spliceosome plays the pivotal role of determining which segments of pre-mRNA make it to the ribosome to be translated (exons) and which get snipped out during mRNA processing (introns). Many small proteins, known as splicing factors, function to guide the spliceosomal complex in choosing the splice sites at which to excise an intron. One of the more ubiquitous splicing factors is Serine/Arginine-Rich Splicing Factor 1 (SRSF1, a.k.a. ASF1 or SF2), which is made up of two RNA-Recognition Motif (RRM) domains and one Serine/Arginine-Rich (RS) domain. Though it is well established that SRSF1 recruits the spliceosome to the 5' splice sites of introns by means of interaction with the pre-mRNA transcript at the Exonic Splicing Enhancer (ESE) sequence and with the RRM domain of the U1-70K protein of the spliceosome's U1 snRNP, the exact mechanism of binding remains unclear. Here we report that SRSF1's first RRM (RRM1) is capable of binding to both the ESE RNA sequence and the U1-70K separately, with preliminary data suggesting that simultaneous binding to both ESE RNA and U1-70K in the form of ternary complex.

URBAN ROOF FARMS AS FOOD PROVIDERS IN FOOD DESERTS: A CASE STUDY OF URBAN HARVEST STL'S STRENGTHS, WEAKNESSES, AND FOOD FLOW IN DOWNTOWN ST. LOUIS

Marissa Lerner

Mentor: Scott Krummenacher

Studies of urban agriculture have long investigated crop variety, socioeconomic effects of urban agriculture, and the its impacts on food justice. Less is known about the potential of rooftop farming, a subset of urban agriculture, to both provide subsistence to, and distribute food into, urban food networks, specifically those in food deserts. Using Urban Harvest STL (UH) as a case study, this work examines a rooftop farm's role in an urban food network. Through interviews with network organizations and GIS mapping of providers, distributors, and food deserts, this research identifies UH's food network and its strengths and weaknesses in serving the local food-insecure population. This research quantitatively demonstrates the role of rooftop farming to urban food production and food justice in a local St. Louis Food Network. Additionally, it highlights focus areas for analyzing small-scale urban food networks. Future studies should investigate the production capacities of rooftop farms, barriers to implementing rooftop farms, and ways that rooftop farms interact with, rather than work in isolation from, the greater urban food network. This research provides novel insight on rooftop farm potential in urban agriculture, as well as methods for identifying urban agriculture's strengths and weaknesses in food desert-heavy urban food networks.

TOWARD A BETTER UNDERSTANDING OF...

RUSSIA:
A EURASIAN ANOMALY
Jacob Levitan

Mentor: James Wertsch

The purpose of this work is to conduct an analysis on Russian culture. Russian culture has for centuries invited multiple attempts to define it, without any single theory ever attaining a permanent dominance accepted by the majority of people. This work will look at definitions of various civilizations, as well as the history of Russia and personal field notes from a summer spent by the author in Russia, traveling from Smolensk to Vladivostok.

INVESTIGATING THE ROLE OF METABOLITES IN MAINTAINING STEMNESS IN HUMAN ADULT STEM CELLS

Kevin Li

Mentor: Tim Peterson

A major goal of regenerative medicine is to understand the unique characteristics of adult stem cells that result in their flexible and adaptive functions. Adult stem cells divide indefinitely and can differentiate into organ-specific cell lines to replace aging or damaged cells. Previous studies on the optimization of adult stem cell therapy have focused on the use of specific activator genes to turn on relevant stem cell genes, which may be inconvenient when considering costs and its resulting effect on the accessibility of stem cell therapy. The purpose of this project is to study the activation of key genes relevant to adult stem cells and develop natural metabolite treatments to maintain stemness in adult stem cells. To determine a set of relevant adult stem cell genes, we use a Python script to compile a ranked list of terms associated with “stem cell metabolism” and narrow down highly characterized genes, including the well-known Yamanaka factors. For initial screenings of these genes, we use a luciferase reporter assay to analyze the activation pathways across several human cell lines. Different reporter genes are activated with specific activator genes via transfection experiments, and the resulting readout is quantified using a luminescence plate reader. Reporter activation is optimized by varying the dosage ratios of reporter and activator and cross-referencing with data in current scientific literature. Metabolite screenings of these optimized reporters are then conducted to find a minimal combination of metabolites that can be used to produce similar activation patterns. This study finds that while combinations of natural metabolites have the ability to activate stem cell genes of interest, the activation level is not as prominent as that of specific activator genes, suggesting further research on the effect of metabolites on stem cell gene biochemical pathways.

STRATEGIC PROSPECTIVE MEMORY MONITORING IN OLDER ADULTS: THE TIME COURSE OF MONITORING DEACTIVATION AND REACTIVATION

Peeta Li

Mentor: Julie Bugg

Strategic monitoring refers to using contextual information to increase attention in contexts in which targets are expected to appear (expected context) or decrease attention in contexts in which targets are not expected to occur (unexpected context). Prior research has shown that using a blocked procedure in which contexts changed every 10 trials, both younger and older adults could strategically monitor in response to simple (e.g., color) and complex (e.g., color and location) contextual cues. In younger adults, strategic monitoring was evidenced by a quick deactivation of monitoring in the first trial (i.e., faster responding) followed by a reactivation of monitoring across the last few trials (i.e., slower responding) in blocks with unexpected contexts. However, to date no research has examined the time course of strategic monitoring in older adults. In the present study, we therefore investigated older adults' ability to strategically monitor in response to complex (Experiment 1) and simple (Experiment 2) blocked contextual cues by examining the time course of monitoring deactivation (Experiment 1) and reactivation (Experiment 2). Experiment 1 showed that using a complex contextual cue, older adults could identify unexpected contexts and deactivate monitoring within the first trial, which is very similar to the time course found in previous research with younger adults. Experiment 2 replicated this pattern using a simple contextual cue. However, there was no evidence for reactivation of monitoring at the end of the block in preparation for the upcoming block with expected context. These findings suggested that strategic inhibitory (deactivation) processes generally remain intact with increased age whereas strategic preparatory (reactivation) processes may not.

CONDITIONAL DENSE LINEAR REGRESSION

Zongyi Li

Mentor: Brendan Juba

Our research follows Juba's recent work on Conditional Sparse Linear Regression, where given some examples, the algorithm finds a subset separated by a k -DNF condition, and a linear regression fit with low loss on the subset. The main shortcoming of his algorithm is that it only works if there exists a sparse regression fit. To extend the setting from to dense setting, we introduce and modify the techniques from Charikar et al., which at a high level, obtains a list of candidate parameter vectors by repeatedly finding the best parameters for each data point, and clustering the data by these parameters. Their algorithm could not be applied to linear regression since individual points do not give nontrivial estimates of the regression parameters. But, it seems that by considering the collection of points satisfying a term instead of individual points, we can obtain an algorithm that finds a list of candidate regression fits. From this list of candidate regression fits, we can find one that, on a subset of essentially the same size, obtains at most polynomially larger loss.

GAUSS BONNET ON 2-ORBIFOLD

Zongyi Li and Bohan Lu

Mentor: Xiang Tang

This summer we researched on 2-orbifold Gauss-Bonnet Theorem. The Orbifold Gauss-Bonnet theorem has been first developed by Sakate in 1957. In this program, we studied textbooks and papers on topology and geometry, and rediscovered these interesting theorems of orbifolds. In the first half of the research, we reviewed the classical Gauss-Bonnet theorem on smooth Riemann surfaces; in the second half, we presented an elementary proof of the Gauss-Bonnet theorem on orbifold Riemann surfaces. Specifically, we give detailed proofs of 1. classical Gauss-Bonnet theorem, 2. classification of finite subgroups of $O(2)$, 3. Integral of curvature on 2-orbifold is well-defined, and 4. Gauss-Bonnet for compact 2-orbifold, along with plenty of examples and illustrations.

ANALYSIS OF THE EFFECTS OF ACTIVE IMMUNIZATION WITH A β ₁₋₄₂ PEPTIDE OF *APPPS1* TRANSGENIC MICE AT THREE AND NINE MONTHS OF AGE

Jenny Lin

Mentor: Anne Fagan

The brain chemistry of individuals with Alzheimer disease (AD) begins to change years before cognitive symptoms appear, making preclinical stages crucial for intervention. Identifying biomarkers is integral for diagnosis and prognosis during this time, as clinical signs and symptoms are unapparent; the two most highly validated biomarkers, amyloid- β (A β ₁₋₄₂) and tau, are associated with the two hallmark pathologies of AD, amyloid plaques and tau tangles, respectively. Studies suggest amyloid plaque formation is a key driver for AD, so potential treatments that prevent amyloid pathology during preclinical stages are important to investigate.

A transgenic mouse model was used to mimic these types of treatments. These mice overexpress human AD-causing mutations in amyloid precursor protein and Presenilin-1 (*APPPS1*), and develop aggressive amyloid plaques around six weeks of age. *APPPS1* mice were immunized monthly with human A β ₁₋₄₂ peptide (or PBS as a sham treatment) to elicit an immune response creating anti-A β ₁₋₄₂ antibodies that, in other mouse models, reduced amyloid plaque load significantly. Blood was drawn to obtain anti-A β ₁₋₄₂ titers to evaluate the immune response of the mice, and half of the brain was homogenized to measure A β ₁₋₄₀ and A β ₁₋₄₂ concentrations using ELISA; the other half was sectioned and immunostained for A β to quantify amyloid plaque load. CSF was collected for future evaluation of potential downstream effects of immunization.

A β ₁₋₄₀ and A β ₁₋₄₂ concentrations in brain tissue and amyloid plaque load were not statistically different between immunized and sham-treated groups, indicating the immunization was ineffective in altering amyloidogenesis. The immunization resulted in very low anti-A β ₁₋₄₂ titers, meaning a weak immune response was mounted. This could be because the immunizations started at four weeks of age, before the immune system is fully developed. Further work is needed in other models that develop amyloid plaques later to test anti-A β treatment effects in a setting mimicking preclinical trials.

EMPHATICALLY NEITHER WHITE NOR BLACK

Alice Liu

Mentor: Tina Shen

The depth of African slavery's influence in America has established a black versus white foundation for racial discourse. The tensions between these two racial groups have, in part, shaped the social outcomes of other minority groups based on which side they are associated with. This research examines the "white" perception of Asian Americans and its cultivation of widespread Asian American political docility and the continuation of a limited racial discourse through generations. An analysis of testimonials from children of the 1992 LA riots reveal that stereotypical perceptions of other races determined the subjects' interpretation of who was at fault. These personal narratives also demonstrate that the riots were a turning point for Asian American representation in political discourse. Drawing from theories such as the bimodal racial modal and racial triangulation provided Asian immigration and non-confrontational cultural values as potential justifications for contemporary Asian American racial involvement. Finally, recent exit poll data demonstrated positive trends in overall Asian voting, but rates of voting were disproportionately low among non-East Asian subgroups. Political engagement and participation in racial discourse remain to be prevalent issues across all racial groups, especially amongst the minorities who are dismissed under an umbrella group and lack the ability to assert their political agendas. This paper is an effort to explore the root of the Asian American political docility and how American society continues to view racial discourse and the potential implications of this limited lens.

FUNCTIONALIZED PEG HYDROGEL SCAFFOLDS FOR NUCLEUS PULPOSUS CELL ENCAPSULATION

Benjamin Liu

Mentor: Lori Setton

Lower back pain associated with old age can commonly be attributed to degeneration of the nucleus pulposus (NP) region of the intervertebral disc (IVD). Specifically, age may lead to biochemical changes, leading to a dehydration of the inner gelatinous nucleus pulposus (NP). This may in turn lead to reduced mobility and shock absorption, increasing the risk for tissue fragility and disc damage. Injectable biomaterials that mimic the mechanical properties of a healthy disc capable of stimulate healthy cell growth have generated a lot of interest towards developing a noninvasive treatment. Our aim was to fabricate polyethylene glycol (PEG) hydrogels with NP cells and test its abilities as an injectable cell carrier for potential use for an IVD treatment. Homogenous initial cell dispersion throughout the hydrogel to increase possible cell interaction and cell viability were the main criteria by which the hydrogels were judged. To gather this data, PEG hydrogels were fabricated through Michael addition using either an 8-arm PEG-Acrylate or an 8-arm PEG-Maleimide crosslinked with PEG-dithiol. Porcine NP cells were suspended in media and mixed with the dithiol precursor prior to the addition step to incorporate NP cells into the complete hydrogel. The 3D dispersion of the cells throughout the hydrogel was analyzed using z-stacks generated through confocal microscopy and immunostaining. An acidic pH PEG-maleimide protocol was found to be the most practical in terms of handling. Using this protocol, a preliminary three-day time-lapse study of the hydrogels was conducted using a live/dead assay. The data suggests that the embedded NP cells remained viable in media and a degree of clustering was shown. These results show that the fabrication of cell containing PEG-hydrogels maintains cell viability and evenly diffuses cells throughout which are positive traits for a potential cell carrier.

CPG-STIMULATED MOUSE B CELLS REQUIRE GLUTAMINE METABOLISM AND mTORC1 ACTIVATION FOR CYTOKINE PRODUCTION

Emily Liu

Mentor: Alfred Kim

Effector functions of immune cells have demonstrated a dependence on specific metabolic pathway utilization. The metabolic pathways B cells need to acquire effector functions are unknown, but may uncover how B cells acquire pathogenic features associated with autoimmune diseases. Thus, we sought to identify the metabolic requirements of B cell effector function in mouse B cells.

B cells were isolated from the spleens of C57Bl/6J mice using negative selection magnetic beads. B cells were then activated overnight with CpG, which activates B cells through TLR9. B cells were incubated overnight with pharmacological inhibitors, which was used to prevent utilization of one of three main carbon sources: UK5099 prevented pyruvate transport into the mitochondria, etomoxir inhibited fatty acid oxidation, and BPTES inhibited glutaminolysis. To control for off target effects, glutamine titration and galactose replacement experiments were performed. The XF Seahorse Analyzer was used to measure oxygen consumption rate (OCR) and extracellular acidification rate (ECAR) as surrogates for mitochondrial respiration and aerobic glycolysis, respectively. ELISA was used to measure cytokine secretion. We also interrogated the role of mTORC1 activation in cytokine secretion; Western blots for phosphorylation of Akt and S6K, upstream and downstream proteins of mTORC1 respectively, were used to examine mTOR activation.

We found that CpG activation of B cells was reliant on glutamine and drove mTOR activation, both of which were capable of driving glycolysis and mitochondrial activity. Glutamine and mTOR activation were also required to produce the inflammatory cytokine IL-6 and immunosuppressive cytokine IL-10, although differentially: while IL-6 required mTOR and glutaminolysis, IL-10 only required glycolysis. Finally, mTORC1 activation was independent of glutamine, indicating that mTORC1 activation is likely driven directly by TLR activation.

B cell activation and cytokine secretion both exhibit a dependence on glutamine utilization and mTOR activation, which drives glycolytic and mitochondrial activity. Production of cytokines also is dependent on these processes, but in a complicated fashion. These data suggest that inflammatory responses may be dependent on glutamine and mTOR activation, while immunoregulatory responses are dependent on glycolysis. Future steps will be to perform metabolic flux studies to determine the metabolic pathways necessary for B cell cytokine production. These results may result in more specific immunomodulatory therapies for autoimmune diseases.

A NOVEL AUTOMATED HUMAN BRAIN TUMOR CLASSIFICATION FRAMEWORK BASED ON DIFFUSION MRI

Xiran Liu

Mentor: Jr-Shin Li

As cancer stays to be a major public health problem worldwide, being able to discriminate among different tumor pathologies are of great importance for the evaluation of tumors and the analysis of cancer. Brain tumor is the third deadly cancer for adults and first deadly cancer for children in the United States. Malignant brain tumor has poor prognosis. With the innovative diffusion MRI histology (D-Histo) imaging technique which generates feature maps that help better differentiate between pathologies in tumor, we apply machine learning techniques to MRI data and classify tumors into designated categories. In this study, we develop techniques specifically to differentiate brain tumor pathologies. Our techniques can classify the selected brain tumors into high cellularity tumor, tumor necrosis, and tumor infiltration with accuracies over 90%, 92% and 83% respectively and these designated categories are clinically important prognosis factors. We see the potential of this classification framework in the analysis of human brain tumor, as well as other types of tumors.

NEONATAL AND FAMILY PREDICTORS OF SOCIAL-COMMUNICATION IMPAIRMENTS IN VERY PRETERM CHILDREN AT AGE FIVE

Karen Lob

Mentor: Cynthia Rogers

Very preterm (VPT) infants have a higher risk of social-communication deficits. Social-communication deficits are a key characteristic of autism spectrum disorder (ASD) and studies have shown an association between increased cerebrospinal fluid (CSF) volume and the risk of ASD. However, this association has not been examined in VPT children, who are prone to social-communication deficits. This study investigated whether CSF volume based on neonatal MRI and social-communication deficits at age five years in both VPT and full term (FT) children were correlated. This study also examined the extent to which infant medical complications, social adversity and parental involvement in early learning influenced social-communication problems. CSF volume at birth was calculated by using Advanced Normalization Tools (ANTs) software. At five-year follow-up visits, parents completed the Social-Communication Impairment scale of the Social Responsiveness Scale (SRS-2) and the Parental Involvement in Developmental Advance (PIDA) section of the StimQ-Preschool, which measure social-communication problems and parental involvement in developmental advances respectively. Results found that VPT infants had significantly higher CSF volume than FT infants after adjusting for total intracranial volume ($p < 0.001$). At age five, VPT children had significantly higher SRS-2 scores ($p = 0.03$) and significantly lower PIDA scores ($p = 0.02$) than FT children after adjusting for social background. A multivariate regression model assessing the extent to which CSF volume ($p = 0.8$), total intracranial volume ($p = 0.6$), infant medical complications ($p = 0.4$), social adversity ($p = 0.6$) and PIDA scores ($p = 0.004$) influenced SRS-2 scores found that parental involvement in early learning were associated with most of the variation in SRS-2 scores ($\beta = -0.38$, $p = 0.004$). These findings add to research explaining the differences in developmental outcomes of VPT and FT infants and suggest that further research should be conducted to understand how a supportive learning environment may support brain development and early social-communication skills.

HYPOXIA TOLERANCE AND RESPIROMETRY IN MORMYRID ELECTRIC FISH

Emily Lopez-Ichikawa

Mentor: Bruce Carlson

Animals, such as humans, that have evolved to have a large brain relative to their body size likely do so at a cost. Larger brains require more resources than smaller ones, and the leading hypotheses explaining how organisms can allocate more resources to the brain are that a species must either increase its overall consumption or must reduce resources used in other high-demand organs, such as the gut. We hypothesize that, while species-wide evolutionary adaptations may involve a tradeoff of resources allocated to different “expensive” organs, within a highly encephalized species, organism with a smaller brain to body ratio will have a lower rate of oxygen consumption and higher hypoxia tolerance. To test this, I carried out research on the mormyrid family of electric fish, which contains species that vary in level of encephalization. Thus, they are an ideal system to explore the tradeoffs of evolving a large brain relative to body size. To determine whether a larger brain correlates to an increased oxygen consumption and decreased hypoxia tolerance within a species, I performed respirometry and hypoxia experiments on fish with varying brain to body mass ratios from multiple species of mormyrids with differing degrees of encephalization. The results of these experiments are likely to contribute to our understanding of the evolutionary tradeoffs of extreme encephalization, such as that observed in humans and mormyrid fish.

ELUCIDATING THE ROLE OF A LYSYL OXIDASE POLYMORPHISM IN RISK FOR CORONARY ARTERY DISEASE

Sofia Luna and Salwa Mikhail

Mentor: Nathan Stitzel

Cardiovascular disease (CVD) is the leading cause of mortality in the United States and is heritable. Identifying human genetic differences associated with CVD such as coronary artery disease (CAD) has the potential to identify genes and pathways with direct relevance to disease. Functional studies can then be used to discover the mechanisms through which these genes affect the heart and vasculature. Recent studies have robustly associated a naturally occurring human genetic polymorphism (R158Q) in the gene lysyl oxidase (*LOX*) with increased risk of CAD. *LOX* is synthesized intracellularly and then released into the ECM where it is cleaved into a pro-peptide and an enzymatic peptide. The polymorphism in *LOX* alters the coding sequence of the pro-peptide region of the gene, leading us to question whether the increase in atherosclerosis is due to altered enzymatic activity of the protein or from altered function of the pro-peptide itself. To study this, we cloned murine *Lox* cDNA into the pCMV6-Myc-His vector and used site-directed mutagenesis to insert the mutation of interest at site 152, which is the analogous position in murine *Lox* corresponding to amino acid 158 in human *LOX*. We then subcloned the pro-peptide regions of both wild-type and 152Q *Lox*. Next, we were able to transfect PP-*Lox* into cultured cells and purify each protein from the media. We are assessing whether the PP-*Lox* polymorphism affects cell growth in a BrdU proliferation assay. To determine if the PP-*Lox* polymorphism altered enzymatic activity, we are performing an activity assay with the purified full length wild-type and 152Q *Lox* proteins. We hypothesize that intracellular signaling in proliferation pathways will be altered in the 152Q PP-*Lox* when compared to the wild-type while the enzymatic activity will be unchanged. By studying the genetic basis of CAD our findings have the potential to reveal novel biology and new therapeutic targets.

NEUROMARKERS OF PREOPERATIVE INFLAMMATION AND DEVELOPMENT OF POSTOPERATIVE DELIRIUM FOLLOWING CARDIAC SURGERY

Anhthi Luong

Mentor: Ben Palanca

Delirium is a temporary neuropsychiatric disorder defined by an acute or fluctuating disruption in attention and cognitive processes. The incidence approaches 50% for major surgery and may signal a greater postoperative risk of cognitive and functional decline. The underlying mechanisms and individualized preoperative risk markers for delirium remain unclear.

To further our understanding of this disorder, pre-operative MRI was utilized to assess NII markers that may demonstrate associations with the incidence and severity of delirium after surgery. We hypothesized that higher inflammatory markers in specific white matter regions (e.g., corpus callosum, cingulum, internal capsule) will relate to an increased probability of developing postoperative delirium.

Six patients were recruited at Barnes-Jewish Hospital as part of an ongoing investigation (NCT03110185) to evaluate the relationship between postoperative delirium and markers of distributed patterns of correlated brain activity. Inclusion criteria included age ≥ 60 , English-speaking, and scheduled cardiac surgery requiring cardiopulmonary bypass. Preoperative imaging was conducted within one week of surgery on a 3T Siemens Skyra scanner. Delirium determination relied on the Confusion Assessment Method (CAM). Patients were evaluated with the CAM on three consecutive days within the first eight days after surgery. Diffusion data were processed using custom scripts for motion, group registration, and tract-based spatial statistics. NII-derived metrics of anisotropy and diffusivity were used to examine white matter integrity and markers of neuroinflammation.

Two patients developed delirium. Group maps will be generated to assess differences among patients with and without delirium. We expect this approach will highlight brain regions that may predispose individuals to delirium via markers of cellular inflammation. This will also provide preliminary support toward the use of NII as sensitive neuroimaging modality for the development of postoperative delirium.

IN VIVO EVOLUTION OF NOROVIRUS CAUSES PHENOTYPIC VARIATION

Larissa Lushniak

Mentor: Megan Baldrige

Norovirus (NoV) infections are the most common cause of acute nonbacterial gastroenteritis worldwide, and pose significant economic health burdens. Even after symptomatic infection resolves, shedding of infectious virus can persist for weeks in healthy hosts and months in immunocompromised hosts. Viral mutation in these immunocompromised hosts may allow for emergence of more pathogenic variants. Strains of Murine Norovirus (MNoV) also persist, providing a useful murine model for NoV infection. We study two strains of MNoV—CW3, which infects acutely, and CR6, which infects persistently. We seek to understand how viral evolution is regulated by the immune system, and whether immunocompromised hosts and/or immunoprivileged tissue sites alter viral evolution. Additionally, we hypothesize that acute viral strain CW3 was originally derived from mutation of persistent strain, such as CR6, in an immunocompromised host. We report that intracranial inoculation and passaging of a persistent MNoV strain in *Stat1*^{-/-} mice lead to significant phenotypic shifts, including loss of persistence and the development of lethality after oral inoculation. Using Nextera sequencing methods, we have been performing deep sequencing of the MNoV viral genome in order to identify viral genotypic changes in the ssRNA genome that correlate with these phenotypic shifts. The identification of critical residues in the MNoV genome will help us to understand how pathogens mutate in immunocompromised hosts, and may provide key insight into viral evolution of human NoV.

NICOTINAMIDE AS A NEUROPROTECTIVE AGENT IN MOUSE MODELS WITH DELAYED HYPOXEMIA FOLLOWING TBI

Alan Makedon

Mentor: Stuart Friess

Traumatic brain injury (TBI) is one of the leading causes of death and disability in children. Despite advances in care, morbidity following TBI remains high. Following the initial primary injury, critical secondary injuries develop from multiple mechanisms including hypoxemia, ischemia, hypoglycemia, and excitotoxicity. Treatment of secondary injuries to TBI patients provides a unique opportunity for therapeutic interventions and to overcome the narrow temporal window of efficacy of many therapeutics. Nicotinamide has been shown to provide neuroprotection when administered early after TBI in animal models. The hypothesis of this ongoing study is that NAD treatment before delayed hypoxemia in mice with TBI would reduce axonal injury and neuronal death. Twenty 8-week-old C57/B6 male mice underwent controlled cortical impact (CCI). Twenty-four hours following CCI, the mice were subjected to 60 minutes of hypoxemia (8% FiO₂) treatment. Mice were randomly assigned to receive nicotinamide 500 mg/kg IP or an equivalent volume of saline 2 hours before hypoxemia. Mice were sacrificed 24 hour after hypoxemia. The brains of the mice were extracted and sectioned into 50 μ m slices to be used for immunohistochemistry. We stained the slices for beta amyloid precursor protein (β -APP), NF200, and 4-HNE. Previous studies have suggested that these biomarkers are highly expressed short term following TBI. We also stained the slices with Fluoro-Jade C. Anterior white matter sections of the corpus callosum were analyzed with ImageJ and the Fluoro-Jade slides were scanned with a confocal. We found little distinguishable change between treatment/vehicle groups for β APP and NF200 staining. However, our ImageJ protocol has not been correlated with stereology, the current gold standard for quantification. The remaining stains are still in progress of analysis. Furthermore, we began testing a second cohort with longer-term survival to analyze neuronal death.

EARLY SPRINGS CAUSE POPULATION GROWTH IN NORTH TEMPERATE RESIDENT BIRDS, POPULATION DECLINES IN MIGRANTS

Lily Malcolm

Mentor: Carlos Botero

Anthropogenic climate change is altering the seasonality of climate and driving changes in the seasonal timing of biological events of many species. The magnitude of such phenological changes can vary greatly among species, particularly if they respond to different environmental cues when making reproductive decisions. Phenological mismatch occurs when asymmetric phenological responses to climate change cause important species interactions to become asynchronous. Secondary consumers, such as birds, may be particularly vulnerable to such mismatch because they can respond to changing climatic cues differently than their food sources. Migratory birds are expected to face additional risk due to their limited ability to respond to the local climate conditions of their breeding grounds while they are in their wintering range. To determine the extent to which phenological mismatch is causing population changes in more than 1,000 north temperate birds, I generated a north temperate map of potential mismatch based on temporal changes in heat accumulation. Using ordinal regression analysis, I tested for a correlation between the degree of mismatch within each species' range and its conservation concern. I found that non-migratory species experiencing the severest degree of mismatch tended to show positive population growth and be of least conservation concern while migratory species experiencing severe mismatch tended to show negative population growth and be of greatest conservation concern. These results may be explained by the greater potential for resident species to adjust their breeding to an earlier spring, allowing residents a longer breeding season overall. Migrants may be unable to advance their phenology to match that of their breeding grounds, leading to disrupted species interactions and population declines. Understanding the complexity of the consequences of phenological mismatch on both resident and migratory birds will be important for informing and directing efforts to conserve these species in the future.

ENUMERATION AND ANALYSIS OF ACTINOMYCETES ISOLATED FROM A SMALL GLADE SOIL VIA MORPHOLOGY, MYCELIA, SPORES, MEDIA-DEPENDENT MORPHOLOGY, ANTIBIOTIC ACTIVITY, AND PHYLOGENETIC ANALYSES

Lily Malcolm, Erica Ryu, and Carrie Stump

Mentor: Joshua Blodgett

Actinomycetes are valuable bacteria because they produce many biological products that we can use. As a result, the isolation of actinomycetes from the environment has been a focus of research for decades. In this experiment, we exposed dilutions of soil sample taken from a small glade to different treatments and then plated them on different media with different antibiotics to determine which media and treatment combination gave the highest relative percentage of actinomycetes. We selected 15 strains from the environmental plates and characterized them via an analysis of their morphology, mycelia, spore production, 16s rDNA sequences, and antimicrobial production. Generally, the HV medium was the best for actinomycete enumeration with the HV-Nal/NHS combination giving the highest relative percentage of actinomycetes. Our analysis of the selected environmental strains revealed that all 15 strains are distinct (but not definitively identified) *Streptomyces* species. All 15 strains had characteristic actinomycete morphology. One of our key observations to arise from this study is that while the environmental isolation media chosen did not often result in a high relative percentage of actinomycetes, they did enable the isolation of a diverse subgroup of *Streptomyces* species. However, the lack of isolation of non-streptomycete actinomycetes could indicate that these media are not as effective at isolating a diverse group of actinomycetes. Our results suggest that these methods are effective for diverse actinomycete isolation, which will be beneficial for isolating novel species in the future.

PHONEME ADAPTATION FROM EXPOSURE TO ACCENTED SPEECH

Sabina Maniak

Mentor: Kristin Van Engen

Perceptual learning from exposure to non-traditional speech has been documented within very controlled training conditions: studies have manipulated the perception of ambiguous speech sounds by carefully controlling their placement in words and non-words, or moved listeners' consonant category boundaries by presenting lists of words produced by an accented speaker. This study investigates perceptual learning based on exposure to Spanish-accented English presented in the form of a story. Spanish has lower voice onset times (also known as "VOT"—the amount of time between voicing and articulation of a produced sound) for its stop consonants than American-English; the VOT boundary between /b/ and /p/ phonemes in American-English falls around +25 ms, while the boundary in Spanish can range anywhere from +14 ms in Castilian listeners to (-10)-(-5) ms in Latin American Spanish Listeners.

In this study, subjects performed an initial syllable categorization task in which they identified sounds from a /b/-/p/ VOT continuum. They then listened to one of two stories read by a Spanish-accented talker (either a condition in which /b/ and /p/-initial words were present, or a condition in which they were not). Afterward, they repeated the syllable categorization task. The results from these categorizations indicate that exposure to characteristic Spanish-accented /b/ and /p/-onset words (average VOTs of -80 ms and -1ms, respectively) shifts listeners' perceptual boundaries downward, and, further, that listeners generalize this perceptual shift into their /b/-/p/ categorizations even when only exposed to words starting with other stop consonants.

THE (UN)REPRESENTATIVENESS OF DISAGGREGATED NATIONALLY REPRESENTATIVE SURVEYS AT POLITICALLY RELEVANT SUB-NATIONAL LEVELS

Bradley Mankoff

Mentor: Matthew Gabel

While public opinion surveys, especially around election season, can be useful tools for campaigns interested in gauging public opinion, even the world's finest surveys fail to remain representative at most relevant sub-national levels. Since American elections are won state-by-state and the main American elections survey ANES (American National Election Survey) is only representative at the level of the nation as a whole, various statistical techniques have been employed to attempt to ameliorate this issue. While survey weighting schemes succeed in turning a non-representative sample into a representative one, these schemes are only applied one time, at the national level and toward the goal of making the sample nationally representative. Dr. Matthew Gabel's and my research project was to determine the extent to which this actually is a problem and also to characterize the scope of the problem—how many researchers have fallaciously disaggregated samples to the sub-national level or given up in route? Though the project isn't complete, my role was to conduct a broad review of the efficacy of disaggregated survey data by comparing survey data to the “true” value of the nation's own census. We found that indeed survey weights fail to keep a sample representative at relevant sub-national levels.

UNDERSTANDING NESTMATE RECOGNITION CUE DEVELOPMENT IN *APIS MELLIFERA*, HONEYBEE

Katelyn Marcus

Mentor: Yehuda Ben-Shahar

In eusocial insects, nestmate recognition (NMR) is an adaptive behavior used to recognize and reject intruders, both conspecific and from different species. NMR cues in honeybees and most eusocial insects are composed of cuticular hydrocarbons (CHC), whose overall profile is specific to bees of the same colony and differs between colonies. The broadly accepted 'gestalt' model of NMR cue development states that colony-specific cues represent an emergent uniform mix of chemicals that are passively derived from the hive's environment and its individual members. Preliminary data from the Ben-Shahar Lab, however, indicate that the CHC profile of individual worker bees develops in association with their age-dependent division of labor via a two-phase process. In the first phase (2-8 days old), total non-specific CHC amount is built up, and in the second phase (between 16-19 days old, the age at which bees begin to forage) CHC profiles become colony specific, which we hypothesize is specifically used to gain access back into the natal hive. We sought to behaviorally test this hypothesis by determining at what age a bee is recognized as either a nestmate or an intruder by members of a colony. To do this we collected bees at various ages and tested their acceptance rate at their native versus an unrelated hive. We found that bees of all ages are accepted into their native hive. In contrast, bees are accepted unrestricted into an unrelated hive through 14 days of age, but bees of foraging age (21 days old) are rejected from entering an unrelated hive. Together with our previous findings about the age-dependent chemical maturation of individual CHC profiles, my data suggest that within honeybee colonies, NMR does not develop via a passive gestalt mechanism, but instead, actively develop in association with the behavioral development of individual worker honeybees, with a mature signal specifically present only in foraging bees.

DEVELOPMENT AND FIELD DEPLOYMENT OF THE VOLATILITY AND POLARITY SEPARATOR-AEROSOL MASS SPECTROMETER

Riley Martell

Mentors: Brent Williams and Michael Walker

It has been widely recognized that organic aerosol (OA) particles make up a large fraction of submicron particulate mass which impacts both human health and global climate radiative forcing. The formation of secondary organic aerosol (SOA) has recently been recognized as a major contributor to much of the total atmospheric OA, but uncertainty remains surrounding its formation mechanisms, chemical precursors, and the influence of anthropogenic and biogenic emissions. Although controlled lab experiments are crucial to gaining an understanding of these processes, *in situ* field measurements are necessary for identifying SOA formation sources and transformation pathways in the atmosphere. The field deployment of the Volatility and Polarity Separator-Aerosol Mass Spectrometer at the Jefferson Street site in Atlanta, Georgia, aims to answer some of these questions.

The VAPS-AMS is a modified version of the previously developed thermal desorption aerosol mass gas chromatograph (TAG) system with major changes targeting improvement in time resolution and mass throughput. The VAPS-AMS system aims to obtain volatility and polarity resolved data with the increased total OA mass analysis. The Jefferson Site field campaign marks the first deployment of the VAPS-AMS for *in situ* measurements following a variety of hardware modifications. Data analysis for the VAPS-AMS ambient sample is performed using a variation of traditional factor analysis called Positive Matrix Factorization (PMF) which explains the data by a certain number of factors, giving each factor its own profile and details its contribution to the total OA over time. The VAPS-AMS collected ambient sample data through August 24. Pre-processing steps and preliminary analysis of the data has begun; however, a more complete analysis including PMF will be the next step as the project continues.

HESS J1844-030: A NEW GAMMA-RAY BINARY?

Hannah McCall

Mentor: Manel Errando

Gamma-ray binaries are comprised of a massive, main-sequence star orbiting a neutron star or a black hole that generates bright gamma-ray emission. Only six of these systems have been discovered. Here we report on a candidate stellar-binary system associated with the unidentified gamma-ray source HESS J1844-030, whose detection was revealed in the H.E.S.S. galactic plane survey. Analysis of 60 ks of archival *Chandra* data and over 100 ks of *XMM-Newton* data reveal a spatially associated X-ray counterpart to this TeV-emitting source ($E > 10^{12}$ eV), CXO J1845-031. The X-ray spectra derived from these exposures yields column density absorption in the range $n_H = (0.4 - 0.7) \times 10^{22} \text{ cm}^{-2}$, which is below the total galactic value for that part of the sky, indicating that the source is galactic. The flux from CXO J1845-031 increases with a factor of up to 2.5 in a 60-day timescale, providing solid evidence for flux variability at a confidence level exceeding 7 standard deviations. The point-like nature of the source, the flux variability of the nearby X-ray counterpart, and the low column density absorption are all indicative of a binary system. Once confirmed, HESS J1844-030 would represent only the seventh known gamma-ray binary, providing valuable data to advance our understanding of the physics of pulsars and stellar winds and testing high-energy astrophysical processes at timescales not present in other classes of objects.

SELECTIVE ISOLATION AND CHARACTERIZATION OF ACTINOMYCETIC STRAINS FOR BIOTECHNOLOGICAL APPLICATIONS

James McMullen, Eric Song, and Marcus Wargel

Mentor: Joshua Blodgett

In this series of experiments, fifteen bacterial strains were isolated from environmental soil samples using methods tailored to selectively recover actinomycetes, a type of filamentous, gram-positive bacteria that has many applications in the biotechnology industry for molecule and drug synthesis. The methods for recovery included heat shock of the soil samples and CaCO₃ treatment combined with various agar growth media. The strains were subsequently identified by gene sequencing of their 16S rDNA, and additional efforts were made to document the morphology and growth of these bacteria: both to confirm their standing as actinomycetes and to more closely describe their characteristics. Using the 16S rDNA sequences, phylogenetic trees were constructed from a wide variety of known *Streptomyces* species, and the environmental strains were placed within the trees to illustrate the evolutionary diversity of these isolates. The antimicrobial capabilities of the strains were tested due to the substantial potential of actinomycetes for generating drugs as secondary metabolites, and in preparation for further engineering of these strains to achieve more efficient drug production. Actinomycetes have been previously demonstrated to produce polycyclic tetramate macrolactams (PTMs) and piperazic acid, both of which have critical bioactivity. Degenerate primers were designed to specifically recognize PTM or piperazic acid gene sequences, and these primers were subsequently used to identify possible producers of such bioactive molecules among the environmental strains. Finding novel or higher activity producers of PTMs and piperazic acid could have considerable implications for the pharmaceutical industry in the years to come.

BEING PULLED IN THE WRONG DIRECTION? TRADITIONAL SPORTS BENEFITS VS. ENJOYMENT

Lucy Meehan

Mentor: Eileen G'Sell

Today's fast-paced culture is responsible for young adults feeling that they must be certain of their college choice, major, internships, and career choices, however, this trend is also increasingly prevalent in youth sports. At younger and younger ages, children are solely dedicating themselves to one sport in an effort to maximize their success, but this specialization is proving itself both physically and mentally detrimental.

In my analysis, I first investigate how researchers, including kinesiologist Andrew Driska, tend to focus on the beneficial aspects of youth sports participation, such as developing worth ethic and accountability, but fail to ask whether children truly enjoy sports. After surveying approximately 40 student-athletes at Washington University in St. Louis, a Division III school that is prohibited from offering athletic scholarships, I examine why student-athletes still participate in sports and their attitudes towards sports participation. I then examine how more rigorous practice schedules and individual sport demands practically force children to choose a single sport while also increasing sports injuries. I also examine how increased specialization is prevalent across society, namely in higher educated by encouraging students to bypass general education requirements by accumulating pre-matriculated Advanced Placement credits in high school. Finally, I question the accelerated college athletic recruiting process by asking how both athletes and colleges can be sure of how the athlete will contribute to the college athletic program early in their high school career; recruiting athletes earlier into high school also contributes to the pressure to specialize with hopes of receiving an offer to play college athletics.

Understanding the increased specialization and its impacts on children can help parents, coaches, and educators to understand the pressures these children are facing and to help them better cope with the accompanying challenges while also attempting to return to a carefree culture to youth sports.

CELL-FREE HEME EXHIBITS DOSE DEPENDENT LETHALITY IN A MURINE MODEL OF SEPSIS

Sahil Mehta

Mentor: Kenneth Remy

Sepsis is a disease caused by invasive infection, which causes systemic inflammation and leads to greater than four million deaths worldwide. About 50% of critically ill children suffering from sepsis in the U.S. receive a blood transfusion during their stay in the ICU. Recent research has led to mounting evidence indicating that RBC transfusions in patients with sepsis are associated with altered immunity and worsened outcome. Transfusion in sepsis is associated with dysregulated immunity. During transfusion, some donor RBCs lyse, generating microparticles and free hemoglobin (Hb), which then release cell-free heme (CFH) into plasma. In septic adults, increased plasma Hb and depletion of the CFH scavenger, hemopexin (Hpx), are associated with increased mortality. Recent work (in animals) indicates that CFH in plasma may directly activate TLR4, the LPS receptor. As such, heme release in excess of plasma binding capacity has the potential to worsened inflammation and may influence survival.

We used a murine cecal ligation, puncture (CLP) model of sepsis, and mimicked RBC transfusion via exogenous, commercially obtained heme. After initial LD50 heme studies without sepsis, we conducted heme dose response preliminary studies in B6/C57 strain mice and CLP (n=29) for 72 hours. After CLP (50% ligation-21G single puncture), each mouse was either injected via tail vein with PBS (control) or heme (10 μM , 50 μM , or 500 μM ; n=9, 8, 10, 2 respectively). At 2 hours and 24 hours. post-CLP, heme measurement were obtained and each animal was re-dosed with PBS (control) or respective heme.

All heme administered animals died by 61 hours (mean $40.4\text{h} \pm 12.5$) in a dose dependent fashion, while controls had a 45% survival. Circulating heme levels were lowest among controls. Spleen, liver, and lung tissue samples showed an increase in apoptosis and tissue denudation as dosage of heme was increased.

We demonstrate that three separate doses of heme given in a CLP model of murine sepsis has 100% lethality. Future studies will carefully investigate innate immune phenotype during sepsis evolution and evaluate the utilization and timing of administration of CFH and potentially scavengers (i.e., Hpx) to improve survival.

NANOSTRUCTURED POLYANILINE/PLA COMPOSITES FOR ELECTROCHEMICAL ENERGY STORAGE IN FLEXIBLE CONDUCTIVE THIN FILMS

Dominique Meyer

Mentor: Julio D'Arcy

A major goal of conducting polymer research involves designing scalable and inexpensive light-weight energy storage technologies. Polyaniline is useful in these applications due to its simple protonic doping mechanism and large electroactive surface area, allowing a high conductivity, response time, and sensitivity. Furthermore, development of a flexible polyaniline dispersed solution would allow for drop casting of a conductive liquid, thus providing a highly customizable energy storage device that can be ready overnight. Polylactic acid (PLA), a flexible plastic that is widely available and inexpensive, could be used to develop polyaniline+PLA composite films, characterized by a polyaniline nanofiber percolation network, and could achieve the goal of both high flexibility and energy storage capacity.

To develop such a conductive material, polyaniline was first synthesized via a robust oxidation process involving interfacial polymerization. Formation of the nanofibers in the doped hydrophilic state immediately leave the interface site, allowing for continuous fiber development instead of secondary growth. The lyophilized powder product was incorporated into solutions along with a dispersant, a plasticizer, a fluorosurfactant, and PLA. Using these substituents, solution ratios and processing order were altered to develop superior drop-casted films. Quality of the resulting film was based on homogeneity, flexibility, conductivity, optical micrographs, and two-point probe analysis.

Optimization determined a composite solution for a conductive and partially flexible film. However, the high degree of homogeneity and flexibility for widespread energy storage application was not obtained with these substituents and process design, limiting the current direction of this research. Furthermore, incorporation of flexible components into the film sacrificed the desirable properties of the polyaniline, thus reducing energy storage capabilities. Continued development of a flexible and conductive polyaniline liquid requires further optimization, likely involving different substituents and a different method of film synthesis.

DISRUPTION OF CELL SIZE HOMEOSTASIS IN (p)ppGpp-DEFICIENT *ESCHERICHIA COLI*

Teran Mickens

Mentor: Petra Levin

Under constant environmental conditions, the processes of cell growth and cell cycle progression are coordinated to ensure that cells of the Gram-negative bacterium *Escherichia coli* divide at midcell after adding a constant volume between birth and division. As long as these processes are properly coordinated, cells maintain size homeostasis, exhibiting very little variation in the size of dividing and newborn daughter cells.

Precisely how cells maintain homeostasis is not fully understood, but the signaling nucleotides guanosine pentaphosphate or tetrphosphate ((p)ppGpp), appear to play a critical role. (p)ppGpp is a global regulator of biosynthetic pathways that is synthesized in response to nutritional stress. The intracellular concentration of (p)ppGpp rises following carbon, nitrogen, phosphorus, and iron deprivation, or reductions in fatty acid synthesis, which triggers a rapid and global downregulation of ribosomal and transfer RNA synthesis to slow down biosynthetic pathways. This is accompanied by (p)ppGpp-dependent modulation of DNA replication initiation, elongation, and cell division.

While (p)ppGpp is studied as a mediator of stress responses, cells unable to synthesize (p)ppGpp ((p)ppGpp⁰) exhibit a number of phenotypes under relatively stress-free conditions, including an average increase in cell size and disruption of size homeostasis. To further our understanding of how (p)ppGpp acts to maintain size homeostasis, we will analyze various cellular parameters of (p)ppGpp⁰ cells, using live-cell imaging and cell segmentation software to quantify single-cell growth rates, cell size at birth and division, and to characterize the positioning and dynamics of the cell division machinery.

SAMPLE FABRICATION OF NIOBIUM THIN FILMS

Elizabeth Montesano

Mentor: Erik Henriksen

Over the summer, I worked I the Henriksen research group developing a recipe to create strain-free niobium samples. In order to make the samples, I was trained to work in the clean room on the physical vapor deposition (PVD) system (also known as a sputter coater), used to deposit thin metallic films. I used the sputter coater in the clean room to deposit niobium onto a thin film of Kapton (a high temperature polymer) in a vacuum chamber. To develop a strain-free recipe, I looked at Henriksen's previous research (dating to the late 1990s) on the topic to guide the experiments I ran. In the experiments, I systematically varied the deposition rates and background argon pressures, while depositing niobium films of identical thickness onto Kapton strips. By noting whether the films bend up or down after deposition, the intrinsic tensile or compressive strain of the film can be determined. I aimed to make films that did not bend in any way after the deposition to achieve strain-free niobium films.

MICRORNA-150 PROMOTES PATHOLOGICAL ANGIOGENESIS IN AGE-RELATED MACULAR DEGENERATION BY TARGETING STEAROYL-CoA DESATURASE-2

Harsh Moolani

Mentor: Rajendra Apte

Age-related macular degeneration (AMD)—a prominent cause of blindness in older adults—primarily affects the macula, the cone-concentrated area of the central retina. Previous studies have shown that macrophages play a pathogenic role in various diseases associated with aging, including AMD. In order to better understand mechanisms that regulate macrophage aging and the impact of aging on macrophage functionality, we explored the impact of certain microRNAs (miRNAs), key post-transcriptional regulatory factors that have been shown to be dysregulated in patients with advanced AMD, on various metabolic and lipid properties of macrophages. Since one significant difference between old and young macrophages is a shift from an M1-like pro-inflammatory phenotype towards an M2-like proangiogenic phenotype, identifying key miRNAs may provide potential causes for the phenotypic changes. We determined that miR-150 is upregulated in old macrophages and contributes to transcriptomic changes with lipid trafficking and metabolism genes. By detecting specific gene targets for miR-150, we were able to refine our search for potential mechanisms. We identified that stearoyl-CoA desaturase-2 (Scd2), an imperative gene in lipogenesis and biosynthesis of membrane phospholipids, was directly regulated by miR-150. In order to replicate the impact of miR-150 on Scd2, we knocked down Scd2 in murine macrophages and observed that numerous pro-angiogenic factors—contributors to advanced wet AMD—are upregulated. Furthermore, macrophages with a knock down of Scd2 were less capable of inhibiting injury-induced angiogenesis by using an injury-induced choroidal neovascularization model compared to normal macrophages. These results lead to the conclusion that microRNA-150 impacts the pathogenesis of AMD and may serve as a therapeutic target to slow and prevent progression of AMD.

TRANSITION METAL COMPLEXES OF THE N4PicTs LIGAND FOR CARBON DIOXIDE REDUCTION

Emily Morgan

Mentor: Liviu Mirica

One of the most important environmental issues today is finding ways to reduce the amount of carbon dioxide that humans produce and release into the atmosphere. A possible solution to this problem is to find an efficient way to convert captured carbon dioxide to other compounds; however, carbon dioxide is not a very reactive molecule, so it is difficult to produce conditions under which these reactions are possible. Therefore, our lab has worked to develop transition metal catalysts that make the reduction of carbon dioxide more accessible.

Previously, our lab has used variants of the N4 ligand system to stabilize various oxidation states of different transition metals, especially nickel and palladium, and has investigated the catalytic properties of the resulting metal complexes. After developing the N4PicTs ligand, we have characterized the complexes of this ligand with Mn^{II} , Fe^{II} , Co^{II} , Ni^{II} , Cu^{II} , Zn^{II} , and Pd^{II} in terms of both their structural and chemical properties. Additionally, we have used electrochemical techniques to analyze their potential to serve as catalysts for carbon dioxide reduction. So far, the Fe^{II} , Co^{II} , Ni^{II} , Cu^{II} complexes show some potential for this type of chemistry. Our goal is to further study these reactions in order to optimize them and determine their efficiency.

ASSESSING NEUROINFLAMMATION IN OBESE INDIVIDUALS USING DIFFUSION BASIS SPECTRUM IMAGING (DBSI)

Tatianna Murphy

Mentors: Sarah Eisenstein and Tamara Hershey

Today in the United States, more than two-thirds of adults are overweight or obese. Obesity is associated with chronic systemic inflammation affecting many organs in the body. However, there has been little research in humans on whether inflammation is also present in the brain. My research seeks to determine if obese individuals have increased brain inflammation compared to controls. Previous studies using magnetic resonance imaging (MRI) and diffusion tensor imaging analyses (DTI) have found altered white matter integrity in the brain associated with obesity. However, these traditional diffusion analysis techniques confound axonal and extra-axonal (e.g., inflammation) effects in the brain. To separate the inflammation from axonal integrity, we used the recently developed Diffusion Basis Spectrum Imaging (DBSI) analysis approach. DBSI allowed us to measure indices of edema and cellularity (both associated with neuroinflammation) and axonal integrity in healthy normal-weight controls and obese individuals. Using Tract-Based Spatial Statistics to control for multiple comparisons, we found that obese individuals had higher edema and cellularity and lower axonal integrity metrics compared to normal-weight individuals. These results suggest that obesity increases brain inflammation and decreases axonal integrity in the brain. Future research will determine the specific clinical variables (e.g., insulin resistance, body fat) that are related to degree of brain inflammation in obesity.

ECOLOGICAL DRIVERS OF LOCAL ADAPTATION IN WHITE CLOVER: HERBIVORES OR WINTER TEMPERATURES?

Samantha Myers

Mentor: Sara Wright

Trifolium repens (white clover) is a widespread species that displays local climatic adaptation related to cyanogenesis (the production of cyanide upon tissue damage). Cyanogenesis is polymorphic in white clover, with cyanogenic and acyanogenic individuals present in populations, and higher frequencies of cyanogenic plants are found in warmer climates. While this clinal pattern has been documented worldwide across latitudinal and altitudinal gradients for over 60 years, the exact ecological factors that drive the evolution of cyanogenesis clines remain unresolved. Leveraging reciprocal common gardens that are currently growing in Duluth, MN, St. Louis, MO, and Gainesville, FL, this project was conducted to test two hypotheses that might explain the low frequency of cyanogenic plants in cold climates: the autotoxicity hypothesis (cyanogenic plants might harm themselves when tissue is ruptured due to low winter temperatures) and the energetic trade-off hypothesis (when herbivore abundance is low, chemical defense is too energetically-costly to be favored). To test these hypotheses, we measured leaf herbivore damage and a variety of fitness traits, including floral production and vegetative surface area at crucial points in the growing season at all three sites. Our preliminary conclusions suggest differences in rates of herbivory between the sites, including variation between cyanotypes within each site. Analyses are ongoing and will include digital picture analysis to quantify vegetative tissue area before and after the winter seasons in Duluth and St. Louis to test for autotoxicity.

STRUCTURAL EFFECTS OF NEURODEGENERATION IN SPORADIC CREUTZFELDT-JAKOB DISEASE

Jaimie Navid

Mentor: Beau Ances

This study investigated structural brain changes associated with sporadic Creutzfeldt-Jakob Disease (sCJD) in 11 autopsy-confirmed cases assessed at Barnes-Jewish Hospital. The processes that promote the spread of pathology in patients with sCJD remain unclear with important implications for diagnosis and treatment. Accordingly, we identified regions most affected by sCJD by measuring cortical thickness for various brain regions, parsed using Freesurfer. We compared these values to 22 age- and sex-matched, cognitively normal controls. Significant decreases in cortical thickness were noted in the superior and inferior temporal gyri, fusiform gyrus, precentral and postcentral gyri, precuneus, caudal middle frontal gyrus, superior frontal gyrus, superior and inferior parietal lobules, lingual gyrus, supramarginal gyrus, transverse temporal gyrus, paracentral lobule, entorhinal cortex, insula and pars opercularis ($p < 0.01$) compared to controls. Our results confirm that cortical thickness decreases with sCJD. Certain brain regions appear to be disproportionately affected, identifying areas of apparent selective vulnerability to sCJD-mediated brain changes. We compared the cortical thickness of the 17 ROIs for slow and fast disease progression using a t-test. Cortical thickness tended to be highest in controls and smallest in long-duration sCJD subtypes (MV2, VV2, MM2), while thicknesses of shorter duration subtypes (MM1, MV1, VV2) fell in between those of controls and long duration subtypes. This was a general trend for the ROIs but not always the case. More research is needed before a definitive conclusion can be made regarding the relationship between neurodegeneration and disease duration. Additionally, we found no correlation between the thickness of significant regions and CSF Tau, confirming CSF Tau is not a specific biomarker for regional patterns of atrophy in patients with sCJD. We conclude that the temporal and posterior areas of the brain are selectively vulnerable to neurodegeneration causing cortical thickness decreases in patients with sCJD. This knowledge can improve CJD diagnosis and aid in treatment options in the future. In subsequent projects, volume measurements may be the best way to see early changes associated with CJD but more longitudinal studies are needed.

SYNAPTIC DEPENDENT AMYLOID- β GENERATION IN VIVO IN ALZHEIMER'S DISEASE MOUSE MODEL

Derrick Ogola

Mentors: John Cirrito and Carla Yuede

Alzheimer's disease (AD) is the most common cause of dementia and is pathologically characterized by toxic amyloid- β (A β) oligomers and plaques. Extracellular accumulation of A β peptide in the brain appears to precipitate disease onset and the cognitive AD-associated pathogenic cascade. In humans and transgenic models of AD, brain regions with the highest levels of synaptic activity show the greatest amount of A β plaques, suggesting A β production is closely linked to synaptic transmission. To determine whether changes in synaptic activity alter the amounts A β in the brain, we developed novel micro-immuno-electrode (MIE) technology that detects A β in the brain ISF with high temporal resolution in the hippocampus of living mice allowing us to examine rapid A β kinetics. We custom designed a 3D-printed adaptor to connect the MIE to an injection port which enables us to measure A β and locally deliver drugs directly to the dentate gyrus. With these technologies, we pharmacologically manipulated synaptic activity by delivering excitatory and inhibitory drugs. Here, we show that changes in levels of A β are closely related synaptic activity in the brain, where large increases in synaptic activity rapidly brought forth higher A β levels in the mouse brain, while inhibition of nonspontaneous synaptic activity decreased A β levels *in vivo* in a concentration dependent fashion. These findings highlight a close temporal relationship between synaptic activity and A β generation in the brain.

REFORMED TAXONOMIC GROUPING OF *GARDNERELLA VAGINALIS* BASED ON COMPUTATIONAL AND FUNCTIONAL CHARACTERIZATION OF CARBOHYDRATE METABOLISM

Niamh O'Grady

Mentor: Amanda Lewis

Bacterial Vaginosis (BV), a shift from a *Lactobacilli* dominated vaginal flora to a polymicrobial imbalance involving Gram-variable and Gram-negative bacteria, is a common vaginal condition for women of reproductive age. BV predisposes women to several adverse reproductive health outcomes including higher risk of sexually transmitted infections, pelvic inflammatory disease, infertility, and preterm birth. *Gardnerella vaginalis*, one of the most frequently isolated bacterial species from women with BV, is poorly understood in the possible roles it plays in the condition. Although there have been attempts to classify *G. vaginalis* in the past, currently available methods remain inadequate for distinguishing *G. vaginalis* from related bacteria and differentiating between strains. In this work, I report a new method of combining bioinformatic analysis of genomes and experimental validation of predicted functions of genes across the strains of *G. vaginalis* in the areas of 1) core genes, already established in identifying different clades of *G. vaginalis*, 2) sialic acid liberation and foraging from sialoglycans, theorized to be involved in the degradation of mucus in the vagina during BV, and 3) broader carbohydrate metabolism, to group *G. vaginalis* strains in appropriate clades. From this classification, clades 1, 2, and 3 emerge as sialic acid consumers through sialylate lyase, while only selected strains from clades 1 and 2 are equipped to cleave sialic acid from glycans using a sialidase. Clade 1 strains also appear to have the capability to consume carbohydrates on a broader scope as compared to the other clades. Overall, the unification of functional and genomic studies of *G. vaginalis* improves on the classification from the conventional methods in microbiology, leading to better distinctions between strains. Further, this approach suggests that *Gardnerella* have varied metabolic adaptations, which may be helpful to understand the broader biology and pathogenesis of *Gardnerella*.

DECAFFEINATED TEA INTAKE AND MAMMOGRAPHIC DENSITY IN PREMENOPAUSAL WOMEN

Victoria Olojo and Valerie Otti

Mentor: Adetunji Toriola

Higher mammographic breast density is associated with an increased risk for breast cancer. As a result, detecting causes of increased density may provide insight for breast cancer prevention. Few studies have assessed the relationship between tea and coffee intake and mammographic density. Thus, we investigated the associations of coffee and caffeinated and decaffeinated tea intake with volumetric mammographic density measures.

We recruited 383 premenopausal women who had a routine screening mammogram at the Breast Health Center, Washington University in St. Louis, MO, from December 2015 to October 2016. Amount of coffee and caffeinated or decaffeinated tea intake were self-reported. We evaluated mammographic density measures: volumetric percent density (VPD), dense volume (DV), and non-dense volume (NDV) using Volpara. Multiple quantile regression models were used to evaluate the associations of coffee and caffeinated and decaffeinated tea intake with volumetric mammographic density measures.

Coffee and caffeinated tea intake were not significantly associated with VPD or NDV. However, the amount of decaffeinated tea intake per week was positively associated with VPD and inversely associated with NDV. There was no significant relationship between coffee or tea intake and DV. Compared with women who drank decaffeinated tea less than once a week, those who drank decaffeinated tea once or more than once a week had an average 12.5% decrease in NDV (p -value = 0.04). Additionally, drinking decaffeinated tea once or more than once a week was associated with an 11.8% increase in VPD (p -value = 0.042), compared to those who drank decaffeinated tea less than once a week.

Decaffeinated tea intake was correlated with higher VPD and lower NDV. Based on our results, limiting the intake of decaffeinated tea may be useful in decreasing breast density in premenopausal women.

INTERROGATING MECHANISMS OF HUNTINGTON'S DISEASE BY DIRECT NEURONAL REPROGRAMMING OF PATIENT FIBROBLASTS

Hannah Olsen

Mentor: Andrew Yoo

In Huntington's disease (HD), expansion of CAG codons in the huntingtin gene (HTT) leads to the aberrant formation of protein aggregates and the differential degeneration of striatal medium spiny neurons (MSNs). Modeling HD using patient-specific MSNs has been challenging, as neurons differentiated from induced pluripotent stem cells are free of aggregates and lack an overt cell death phenotype. Here we generated MSNs from HD patient fibroblasts through microRNA-based direct neuronal conversion, bypassing the induction of pluripotency and retaining age signatures of the original fibroblasts. We found that patient MSNs consistently exhibited mutant HTT (mHTT) aggregates, mHTT-dependent DNA damage, mitochondrial dysfunction, and spontaneous degeneration in culture over time. We further provide evidence that erasure of age stored in starting fibroblasts or neuronal conversion of presymptomatic HD patient fibroblasts results in differential manifestation of cellular phenotypes associated with HD, highlighting the importance of age in modeling late-onset neurological disorders.

THE CONTRIBUTIONS OF GENE COPY NUMBER VARIATION TO DROUGHT ADAPTATION IN WHITE CLOVER (*TRIFOLIUM REPENS* L.)

Akash Oza

Mentor: Kenneth Olsen

As sessile organisms, plants are susceptible to changing climates, particularly drought. The accumulation and the use of cyanogenic glucosides have been hypothesized and shown to confer drought responses. However, the role of quantitative variation in these cyanogenic glucosides in confer fitness advantages in response to drought-induced water stress remains unknown. We attempted to address that question using white clover (*Trifolium repens*) plants. White clover, a widespread perennial legume, is polymorphic for cyanogenesis—the production of HCN upon tissue damage. The presence of two genes, *Ac* (conferring cyanogenic glucosides) and *Li* (conferring linamarase) are both required for an individual to be cyanogenic. Both genes also demonstrate quantitative variation. In this study, we used a 65-day growth chamber experiment to expose two replicate white clover (*T. repens*) cuttings of 98 plants (N = 196) from nine genotypic groups to either a drought or non-drought watering treatment. We measured vegetative growth, fecundity, leaf relative water content, isotopic composition, and terminal survival. We found that white clover plants exposed to drought displayed lower fitness than plants not exposed to drought. Moreover, individuals possessing cyanogenic glucosides (*Ac*) demonstrated lower vegetative fitness under water stress compared to those lacking cyanogenic glucosides. Individuals possessing more copies of the *Ac* gene were not found to have higher fitness under water stress. Finally, individuals with higher copies of the *Li* gene demonstrated higher fitness regardless of being exposed to water stress. Overall, our findings suggest that quantitative variation in cyanogenic glucosides may not confer a fitness advantage in response to drought-induced water stress under controlled growth chamber conditions, counter to previous findings. Moreover, the role of copy number for the *Li* gene in conferring fitness advantages presents avenues for further studies.

LOCALIZATION IN DISORDERED CLASSICAL MAGNETS

Jordan Pack

Mentor: Erik Henriksen

Localization is an important concept in physics: in conducting materials, it describes the phenomenon where conduction electrons can become localized in space in the presence of disorder. Although it is most often studied in the context of charge or spin degrees of freedom, it is known to be a general property of waves traveling in a disordered media. Here, we measured localization in a lattice of permanent bar magnets, each one inch long, that are able to rotate freely but in fixed positions. With these magnets, we have measured the collective motion that results from the impetus of one rotating magnet at the edge of a square lattice, and in square lattices where each point has been shifted a small amount in a random direction. These measurements reveal the presence of localization by the damped collective motion of the magnets with increasing disorder. We will also share measurements of response to different frequencies and wave speed using the same freely-spinning magnets arranged in a one-dimensional line.

EXPLORING THE ROLE OF MUTANT-HUNTINGTIN IN THE EARLY TRANSCRIPTIONAL DYSREGULATION OF HUNTINGTON'S DISEASE

John Palucki

Mentor: Hiroko Yano

Huntington's disease (HD) is a progressive and invariably fatal, autosomal-dominant neurodegenerative disorder caused by an abnormal expansion of CAG repeats in the huntingtin gene (*HTT*), which encodes an abnormally long polyglutamine repeat in the HTT protein. Transcriptional dysregulation is an early anomaly in the course of HD progression and has been proposed as an underlying pathogenic mechanism. Accumulating evidence suggests that epigenetic mechanisms including DNA methylation, which control chromatin structure, play an important role in transcriptional dysregulation in HD. A recent genome-wide studies in a cell model of HD and human brain tissues demonstrated that mutant HTT extensively perturbs DNA methylation. Importantly, earlier studies conducted by the Yano Lab demonstrated a requirement for DNA methyltransferases (DNMTs) in mutant Htt-induced transcriptional alterations and neuronal death, which suggests a neurodegeneration mechanism based on DNA methylation-mediated transcriptional repression. However, how mutant Htt causes aberrant DNA methylation and subsequent neuronal dysfunction remains undefined. Our preliminary co-immunoprecipitation experiments revealed an enhanced interaction between DNMT3A and mutant Htt when compared to wild-type. Based on these data and recent published results from Yano Lab, I hypothesize that the mutant HTT activates DNMT3A through interaction with DNMT3A, thereby increasing DNA methylation on specific gene promoters. To map the domain of DNMT3A required for interaction with mutant HTT, I generated a series of DNMT3A deletion mutant constructs. Subsequent binding domain mapping using GST-HTT fusion proteins and DNMT3A deletion mutants, however, provided inconclusive results. Defining the HTT binding domain within DNMT3A may provide the mechanism of how mutant HTT induces aberrant DNA methylation in HD.

CREDIT RISK FOR CUSTOMERS OF A FINANCIAL SERVICES FIRM

Jessica Pang

Mentor: Arun Gopalakrishnan

Financial services rely on credit risk scores in order to assess how likely a customer is to pay his or her bills on time, and thus, calculate profitability. An Asian credit card company assesses its customers based off a calculated risk score. This analysis uses customer and marketing data in order to predict how different customer spending and payment behaviors affect future risk scores. Specifically, the variables we evaluated were current and cumulative payment statuses, share of wallet, and whether a customer paid their bill in full amount at this bank and another bank in Asia. After running ordinary least squares, fixed effects, and random effects models, we concluded that last month's and cumulative payment statuses affect a customer's risk score the most, especially if a customer pays beyond the minimum. After controlling for customer heterogeneity, whether a customer paid their bill in full amount was no longer significant. These models could further be used to try to build more sophisticated models to predict when customers might churn based on risk score. With a better understanding of future risk scores, this can contribute to how the company interacts with its customers and overall lead to higher customer satisfaction and profitability.

OPTICALLY ACTIVE ANGIOTENSIN RECEPTORS

Christina Papari

Mentor: Yehuda Ginosar

Optogenetics is a relatively new field that allows us to better understand receptor signaling by creating chimeric receptors that can be activated by light. Along these lines, we have created optically active versions of angiotensin 1 and 2 receptors (AGTR1/2), by combining the native G protein-coupled receptors (GPCR) with portions of the light-sensitive rhodopsin GPCR, with the hope that this will help elucidate the role of the angiotensin pathway in preeclampsia. Our goal was to determine which amino acid substitutions are necessary and sufficient for the ligand active AGTR1/2 to become optically active (oAGTR1/2) as well as functionally equivalent. We characterized the chimeric receptors through western blot and internalization assays to confirm a functioning GPCR through the G protein and arrestin pathways. Measurement of phosphorylated ERK (p-ERK) levels was done at five different time points in western blots by transfecting HEK cells with oAGTR1/2-GFP. We confirmed that white light confers G protein activation through the MAPK/ERK pathway and achieves the same biphasic levels as its cognate ligand active receptor. We also utilized confocal microscopy to visualize the internalization of the novel GPCR's by arrestin and compared it to the native receptors using the same HEK cells. We confirmed that arrestin dependent internalization of the optically active receptor is achieved by 30 minutes after dosage of white light and parallels the response of its ligand activated native receptor. The assays performed support our hypothesis that the ligand activated AGTR1/2 could be modified to become optically active by changing only a few key amino acids (A/F113E and Y/F296L). The next key step is to characterize the chimeric receptors *in vivo* using Cre recombinase-dependent adeno associated viruses in order to further confirm functional equivalency of the optically active receptors.

INVESTIGATING SLEEP FRAGMENTATION IN MURINE MODELS OF *Nf1*

Kyung Park

Mentor: David Gutmann

Neurofibromatosis type 1 (NF1) is a common monogenic disorder caused by a single germline mutation in the *NF1* gene, affecting 1 in 3,000 people worldwide. Children with Neurofibromatosis type 1 are at increased risk for sleep issues which negatively affect their quality of life, cognitive function, and behavior. Past cross-sectional studies have demonstrated that children with NF1 were more likely to have more sleep disturbances while initiating and maintaining sleep, arousal, and sleep-wake transition. Preliminary studies using genetically engineered mouse (GEM) models of NF1 have shown that female *Nf1*+/+ (wild-type) mice spend less time in non-REM sleep than male *Nf1*+/+ mice, and their male and female *Nf1* mutant counterparts. Leveraging new electroencephalogram (EEG) technologies in collaboration with Dr. Wong's laboratory, the sleep difference between wild-type and their respective mutants was seen, indicating that NF1 plays a major role in sleep fragmentation. The loss of a major sleep pathway regulator, orexin, has been shown to induce sleep fragmentation in mice. Based on these observations, NF1 would be negatively affecting levels of orexin because of the sleep fragmentation that was seen in the mutant mice. To determine if NF1 affected transcription or translation of orexin in the murine brain, hypothalamic orexin expression in wild-type and *Nf1*-mutant mice was assessed by quantitative RT-PCR and Western blotting. Female *Nf1*-mutant mice had much lower levels of hypothalamic orexin compared to *Nf1*+/+ females, while orexin expression did not differ between male *Nf1*-mutant and wild-type mice, indicating that orexin was not causing the sleep fragmentation found in both male and female *Nf1*-mutant mice. Therefore, this study narrowed down potential candidates that could be causing this sleep fragmentation in NF1 mutant mice, which is one-step closer in elucidating the obscure molecular pathway of NF1 and sleep.

COMPARISON OF INNERVATION IN WHITE ADIPOSE TISSUE AND BONE MARROW ADIPOSE TISSUE

SungJae Park

Mentor: Erica Scheller

Peripheral adipose tissue not only acts as an insulating layer to reduce heat loss, but can also act as a site of energy storage, cytokine release, and, in some cases, thermogenesis. Of the different types of adipose tissues, the role and the regulatory mechanisms of white and brown adipocytes have been extensively explored. However, the role and regulatory mechanisms of bone marrow adipose tissue (BMAT) are still not fully understood. Energy release by white adipose tissues and thermogenesis by brown adipose tissues are largely controlled by the central and peripheral nervous systems. We hypothesize that BMAT within the skeleton is also innervated by the peripheral nervous system, similar to WAT and BAT. To test this hypothesis, we developed immunostains specific for peptidergic sensory neurons that express calcitonin gene related peptide (CGRP) and sympathetic efferent neurons that express tyrosine hydroxylase (TH). After comparing innervation levels of stained WAT and tail vertebrae (BMAT) from 13-week-old C3H/HeJ male mice, we observed an association of tyrosine-hydroxylase (TH) positive axons with a subset of bone marrow adipose tissue adipocytes. However, the overall appearance and density of neurons was substantially reduced in BMAT relative to WAT. Sensory innervation was also observed in both WAT and BMAT along the regions of tyrosine-hydroxylase positive axons. Overall, the data suggests that BMAT is innervated by the sympathetic and sensory nervous systems, but the pattern is distinct from that of WAT. In the future, we will define the specific pathways underlying regulation of marrow adipose tissues and their role in maintenance of skeletal and metabolic homeostasis.

THE EFFECTS OF PRESCRIBED FIRE ON HABITAT USE BY WHITE-TAILED DEER

Hanna Peterman

Mentor: Solny Adalsteinsson

White-tailed deer (*Odocoileus virginianus*) play a key role in local disease transmission as hosts for ticks and reservoirs of tick-borne pathogens. Prescribed fire is potentially an effective management tool to mitigate disease risk by reducing tick populations in oak-hickory forests. However, habitat changes resulting from fire may impact how wildlife species such as white-tailed deer use forested habitats, with greater implications for disease risk. We predicted that due to the increased vegetative growth (i.e., food availability) stimulated by fire, deer would show a preference for recently burned forest. Out of 16 paired 2-ha forested plots at the Tyson Research Center, eight plots were burned in March and April 2017. To investigate white-tailed deer's response to prescribed fire, we conducted fecal pellet counts to quantify relative deer use of burned and unburned forest plots. We marked and counted pellet groups along three 2-m by 120-m transects in each of the 16 plots (11,520 m² total), and repeated the sampling twice during Summer 2017. Contrary to our prediction, we observed a trend indicating greater usage of unburned plots relative to burned plots; however, the trend was not statistically significant ($F_{2,29}=1.29$, $P=0.12$). Deer behavior and habitat use varies seasonally, so further data collection will continue in fall and winter months to fully characterize changes in habitat use following prescribed fire. Understanding how prescribed fire affects deer habitat use will inform management strategies aimed at reducing tick-borne disease risk.

THE GREAT DE-ESCALATOR: FDR'S CONFLICT MANAGEMENT STRATEGIES AND THEIR IMPACT ON THE FDR-CHURCHILL ALLIANCE IN WWII

Adam Presswood

Mentor: Maire Murphy

The relationship between FDR and Winston Churchill was not as peaceful or as consistent as much of the literature might lead one to believe. The two men differed radically with regard to their views on colonialism and imperialism, and those differences of opinion often resulted in rifts between the two allies. Unfortunately, those rifts usually occurred during pivotal moments of WWII, such as prior to the Torch operation and during the planning for D-Day. Had it not been for FDR's great skill in bringing Churchill back to the table following their disagreements, the course of WWII could have been very different—and with it the fate of FDR's vision for the post-WWII world.

In exploring this aspect of the relationship between Roosevelt and Churchill, this project will focus on the rhetorical and argumentative approaches and strategies that FDR used to mend rifts between himself and Churchill (accessible for research via primary resources such as FDR and Churchill's diary entries and recorded minutes from various meetings that occurred between the two men and their respective staffs). The project will look at two to three case studies and develop a nuanced characterization or typology of approaches and strategies FDR deployed in particular circumstances when dealing with Churchill. The findings from such an analysis have the potential to complicate, or at least deepen, the understanding we have of the FDR-Churchill alliance, give insight into and provide a more detailed vocabulary for talking about FDR's arts of persuasion, and encourage other scholars to see if those findings are useful in explaining how FDR cajoled, encouraged, and otherwise interacted with other people with whom he needed to work closely.

THE EFFECTS OF MAQUILADORAS IN THE HOUSEHOLDS OF LOWER SOCIOECONOMIC LEVELS IN CIUDAD JUÁREZ

Jorge Puentes

Mentor: Ignacio Sánchez Prado

In the 1960s, workers from the bracero program started to return to Mexico and became stagnated in the U.S.-Mexico border. To solve the unemployment problem that the migration of braceros caused the maquiladora was instituted across the Mexican side of the border. The maquiladora is a translational factory that produces goods for foreign companies while using local workforce. The introduction of these factories led to Mexico becoming one of the biggest markets for cheap labor force and after the implementation of the NAFTA trade deal it did not take long for Maquiladoras to grow exponentially. Today maquiladoras represent one of the pillars of the Mexican economy. However, the economic benefits did not stay at the local level but instead went back to the owners of the maquiladoras and instead negatively impacted the workers of the maquiladoras. In this project, I analyze the factors that currently impact the lower socioeconomic households and tie its roots to maquiladoras. Throughout the different sources analyzed in this research the maquiladoras fostered harmful conditions with its xenophobic, exploitative, and sexist ideals that led to a cycle of violence and extreme poverty that claimed the lives of many a worker in the factories, with a predominance of them being women. Furthermore, the city became unsafe to the point that it was known as the most dangerous city of the world in 2008. At its height Ciudad Juarez saw eight murders a day alone and it can be traced to maquiladoras. However, there is still hope for the city as detailed in this work that through diversifying the economy and improving working conditions of the maquiladora workers the violence and life that the city has gone through will finally stop.

THE COMPLEX EFFECTS OF SIMULATED CLIMATE TEMPERATURE INCREASE ON THE SOCIAL AMOEBA *DICTYOSTELIUM DISCOIDEUM* AND THEIR BACTERIAL ENDOSYMBIONTS

Xinye Qian

Mentor: Joan Strassmann

Environmental stress can result in strong ecological and evolutionary effects on natural populations. Global warming can affect not only individual species but also mutualistic associations. Here, we used the soil-dwelling social amoeba, *Dictyostelium discoideum*, as a model system to simulate how climate temperature increase affects the social amoeba *Dictyostelium discoideum* and their bacterial endosymbionts, *Burkholderia*.

D. discoideum has a very dynamic relationship with bacteria. It predated bacteria, can be infected by bacteria, and can also form symbiotic associations with different bacterial species. *D. discoideum*'s association with bacteria appears to be binary, with some amoebae (called farmers) consistently carrying bacteria through their social life cycles, while others (called non-farmers) do not.

In the first part of our project, we studied the adaptive divergence of thermal tolerance in natural populations of *D. discoideum*. We used clones from two populations that differ in climate and altitude (Virginia, VA, and Texas, TX), and tested them under moderate and thermal conditions using common garden experiment. We found that TX population (the high-temperature origin population), had higher fitness than VA population (the lower-temperature origin population) under the thermal condition, while there was no difference between two populations under moderate condition. These results suggest that *D. discoideum* has diverged in response to temperature mediated selection, with Texas population having locally adapted to thermal stress.

In the second part of our project, we studied how simulated climate temperature increase affects amoeba-*Burkholderia* symbiosis. We mixed and matched *D. discoideum* with two facultative symbionts *B. hayleyi* and *B. agricola*, to see how they affect host's thermal tolerance. We found that *B. agricola* made no difference to *D. discoideum*'s thermal tolerance (both to their native hosts and other hosts). However, *B. hayleyi* significantly decreased *D. discoideum*'s thermal tolerance (both to their native hosts and other hosts). In addition, under thermal stress, *B. hayleyi* killed most of the *D. discoideum* from other hosts and caused a breakdown of symbiosis. This did not happen to their native hosts, indicating potential host adaptation between *B. hayleyi* and their native *D. discoideum* hosts. Taken together, these results suggest the complex effects of climate temperature increase on the amoeba-*Burkholderia* symbiosis.

THE ROLE OF THE RIBOSOMAL RNA IN TRANSLATION QUALITY CONTROL IN *SACCHAROMYCES CEREVISIAE*

Anjana Rajan

Mentor: Hani Zaher

In all domains of life, the ribosome is the machine responsible for translating mRNA transcripts into polypeptide chains. Often, the ribosome encounters a block (for example, a damaged mRNA), which causes the ribosome to stall and stop protein synthesis. To alleviate this, eukaryotic cells evolved a pathway called no-go decay (NGD) to rapidly degrade these defective mRNAs by cleaving the transcript upstream of the stalled ribosome. However, the endonuclease responsible for this cleavage activity is yet to be identified. Previous studies from our lab suggest that the ribosome might be responsible for the cleavage reaction. In particular, I hypothesize that the ribosomal RNA of the small subunit catalyzes the cleavage reaction at stalled ribosomes. To test this hypothesis, I carried out a screen by introducing a mutagenized library of 35S pre-rRNA-containing plasmids into yeast strains harboring an integrated reporter gene subject to NGD. These reporter plasmids contain inhibitory (arginine) codons upstream of the *ade2* gene that stall the ribosome as a proxy for damage. Upon transformation of the library, we selected for white colonies that indicate translation of the *ade2* gene and thus, cleavage inhibition. I am currently attempting to confirm that six of my isolates contain rRNA mutations, that are causative and do not contain secondary mutations. In addition to the screen, 18S rRNA mutants were rationally designed based on their location near the mRNA. One mutant (T1430D) resulted in white colonies, indicating that this region of the ribosome is likely to be important for endonuclease activity. Moreover, western-blotting analysis indicated increased synthesis of the NGD reporter. These preliminary findings provide insight into how quality control mechanisms evolved to integrate into fundamental biological machines. Further delineation of the details of this mechanism will contribute to the understanding of how cells identify and degrade defective biological molecules.

MIR142 LOSS-OF-FUNCTION MUTATIONS PROMOTE LEUKEMOGENESIS VIA DEREPRESSION OF ASH1L RESULTING IN INCREASED HOX GENE EXPRESSION

Rahul Ramaswamy

Mentor: Daniel C. Link

Mutations of MIR142 have been identified in approximately 2% of *de novo* AML and in 20% of diffuse large B cell lymphoma. In AML, the mutations in MIR142 disrupt both miRNA-142-3p and miRNA-142-5p function, suggesting that loss of MIR142 plays a role in leukemic transformation. To test this hypothesis, we first characterized hematopoiesis in Mir142^{-/-} mice, and reported that loss of Mir142 results in an expansion of myeloid progenitors with impaired erythropoiesis and lymphopoiesis.

We examined several putative miR-142 target genes, eventually focusing on ASH1L, a histone methyltransferase that has been recently implicated in MLL-associated leukemogenesis. The 3' UTR of ASH1L contains four putative binding sites for miRNA-142-3p, indicating that this miRNA is critical in its post-transcriptional regulation. Indeed, Ash1L protein levels were 3-fold higher in Mir142^{-/-} mice bone marrow compared to control mice. Since ASH1L is a known regulator of HOX gene expression, we examined HoxA9 and HoxA10 expression in Mir142^{-/-} hematopoietic progenitor subsets. While HoxA9 and HoxA10 expression were not different in hematopoietic stem cells, they were markedly upregulated in myeloid progenitors. For example, in granulocyte-macrophage progenitors (GMPs), HoxA9 and HoxA10 expression were increased 2.86-fold and 34.4-fold, respectively in Mir142^{-/-} versus control cells. Likewise, in megakaryocyte-erythroid progenitors (MEPs), HoxA9 and HoxA10 expression were increased 5.3-fold and 21.4-fold. Dysregulated HoxA9 and HoxA10 expression have been implicated in enhanced self-renewal capacity, and HoxA9 overexpression has been shown to cooperate with mutant IDH1 to induce AML in mice. Collectively, these data suggest a model in which MIR142 mutations contribute to leukemogenesis by de-repressing ASH1L expression, which, in turn, increases expression of HoxA9/10 and enhances self-renewal. Inhibitors targeting ASH1L may have therapeutic benefit in AML characterized by increased HOX gene expression.

CARD-MEDIATED TRANSCRIPTION INITIATION IN *MYCOBACTERIUM TUBERCULOSIS*

Abheek Raviprasad

Mentor: Eric Galburt

Mycobacterium tuberculosis (*Mtb*), the bacteria that causes tuberculosis (TB), infects about one-third of the world's population. People infected by *Mtb* have a 10% lifetime risk of falling ill with TB, making it one of the top ten causes of death worldwide. CarD, an essential transcription factor known to enhance transcription in *Mtb*, could prove to be an important drug target as mutant CarD protein leads to a decrease in antibiotic resistance. The goal of this study is to elucidate the molecular mechanisms behind CarD-enhanced transcription initiation, including its ability to stabilize the RNA polymerase open promoter complex and affect the rates of promoter escape. Using single-molecule magnetic-tweezers assays, DNA tethered between the surface of a glass cover slip and a paramagnetic bead can be manipulated and tracked at constant force. DNA unwinding can be detected on torsionally constrained DNA templates via changes in the end-to-end distance of the tethered DNA.

Preliminary data suggests that CarD acts by increasing the lifetime of the RNA polymerase (RNAP) open complex. Furthermore, DNA extension changes due to promoter opening on positively supercoiled DNA are greater than those on negatively supercoiled DNA. These changes are indicative of DNA compaction possibly stemming from DNA wrapping around the polymerase, consistent with published measurements on *E. coli* RNAP. Additionally, a single trace taken in the presence of CarD and all four rNTPs shows possible DNA scrunching behavior in the process of promoter escape. This occurs during an intermediate state when RNA polymerase remains stationary, while unwinding and pulling downstream DNA into itself before escaping the promoter and beginning processive transcription. Further experiments will be performed as a function of CarD concentration to fully determine the mechanism of CarD in the context of an important human pathogen.

FUNDAMENTAL FREQUENCY (F0) VARIABILITY IN L2 VOCABULARY LEARNING AND L1 WORD IDENTIFICATION

Kyra Reu

Mentors: Mitchell Sommers and Joe Barcroft

This is a psycholinguistic study investigating the effects of variability in fundamental frequency (F0) on second language (L2) vocabulary learning and first language (L1) spoken word identification, specifically for native Mandarin speakers. F0 is an acoustic property of speech that roughly equates to pitch. Previous research has shown that acoustic variability improves L2 vocabulary learning and hinders L1 word identification when it is phonetically relevant to the listener but has null effects when it is phonetically irrelevant. F0 is phonetically irrelevant to native English speakers because pitch does not change meaning in English. However, we predict F0 is phonetically relevant for native Mandarin speakers because Mandarin is a tone language; therefore, we expect to see significant effects of F0 variability on L2 vocabulary learning and L1 word identification. We will ask native Mandarin-speaking participants to learn 24 Russian concrete nouns by listening to the spoken words and looking at pictures of the referents (L2 vocabulary learning). Next, we will ask them to identify 150 disyllabic Mandarin words in noise (L1 word identification). The F0 of each of the pre-recorded stimuli (i.e., Russian or Mandarin words) was digitally altered by $\pm 10\%$, $\pm 20\%$, and $\pm 30\%$. In low variability conditions, all stimuli within a group are presented at the same F0 level; in moderate variability conditions, three different F0 levels are present; and in high variability conditions, all six different F0 levels are present. We predict that higher F0 variability will improve L2 vocabulary learning but hinder L1 word identification. The results of the study could have implications for foreign language instruction for native Mandarin speakers and for understanding how native language background affects speech perception.

TRANSFUSION THRESHOLD VARIANCE BETWEEN CANNULATION TYPE AND DISEASE TYPE IN EXTRACORPOREAL MEMBRANE OXYGENATED PATIENTS

Michaela Reuter

Mentor: Philip Spinella

Extracorporeal Membrane Oxygenation (ECMO) is an increasingly used form of life support, which has also been associated with higher volumes of blood product transfusions. Many studies have shown that greater transfusion volumes are associated with an increased risk for mortality, which causes concern for patients cannulated on ECMO. This study set out to determine which patients would be most affected by this, differentiating patients by cannulation type and disease type. The primary hypothesis was that the thresholds at which patients were transfused would differ between venoarterial and venovenous cannulation, and between cyanotic heart disease, non-cyanotic heart disease, and non-cardiac disease. It was also hypothesized that patient mortality would be associated with higher volumes of blood product transfusion.

In this retrospective study, data was extracted from the PCCM ECMO database. Patient data was analyzed both by each transfusion threshold and by patient mean transfusion threshold. Difference in median transfusion thresholds was determined using a Mann Whitney Test and a Kruskal Wallis Test. The risk of mortality associated with transfusion volume was determined using a logistic regression.

The results of the data suggest that transfusion thresholds vary between blood product type as well as disease and cannulation type, with red blood cell and platelet thresholds varying significantly between cannulation type, and plasma transfusion thresholds varying significantly between disease type. Higher volumes of red blood cell and plasma transfusions are also correlated with higher risk for mortality in these patients.

ERRAND INTO THE PAST:
PERRY MILLER, REINHOLD NIEBUHR, AND THE
INTERPRETATION OF AMERICAN HISTORY

Taylor Reynolds

Mentor: Abram Van Engen

This work argues that Perry Miller coopted Reinhold Niebuhr's vision of American history and secularized it to fit his own projects and perspective. This process is the creation of his metahistorical faith, which I will define as an undergirding set of principles, guided by which the historian chooses facts, imposes narrative, and creates meaning from facts about the past. In contradiction to the majority of the professional field of history at the time, Niebuhr and Miller expressed explicitly their own versions of a metahistorical faith, seeing through history and attempts to discover unchanging features of human nature and unchanging patterns of human history. Their metahistorical faith was an impassioned, realist liberal philosophy of history that presented new answers to the objectivity question in ways that would prove influential across academic disciplines and into the public square. However, many of their students, especially Miller's, adopted their explanation of history without realizing the importance of understanding the undergirding principles of philosophy that guided their historical work. These same students went on to become influential figures in public and foreign policy. With this understanding of history unaccompanied by the necessity of a metahistorical faith to see history through (and see through history), they created all sorts of problems and misappropriations of the past.

EFFECTS OF COMPOSITION AND PROCESSING ON MICROSTRUCTURE OF CuZr BULK METALLIC GLASS COMPOSITES

David Robinson

Mentor: Katharine Flores

The goal of this work was to examine the effect of the concentration of a high melting point element on the crystallization of a bulk metallic glass-forming alloy. Alloys with compositions $(\text{Cu}_{48}\text{Zr}_{48}\text{Al}_4)_{100-x}\text{Nb}_x$, with $x = 0, 0.25, 0.5, 0.75$, and 1 , were cast from the melt into cylindrical rods of 3 and 4 mm diameter using a Cu mold, and their microstructures were characterized in detail. 4 mm diameter specimens of all compositions were found to be fully crystalline. The results for the 3 mm diameter specimens, which cooled from the melt at a higher quench rate, were inconclusive. Optical and scanning electron microscopy (SEM) observations show at least 3 phases, including at least 2 crystalline phases within a matrix of undetermined structure. X-ray diffraction measurements show peaks for 2 phases; B2 CuZr and CuZr_2 . SEM observations of the B2 phase were consistent with the expected spherical shape. Compositional measurements obtained via energy dispersive x-ray spectroscopy (EDS) suggest that the second phase may be CuZr_2 with aluminum substituted for copper. The observed microstructures were similar for all compositions, indicating that niobium content does not have a significant effect on the microstructural evolution of the alloy.

BONE MARROW ADIPOSE TISSUE: WHITE, BROWN OR BEIGE?

Hero Robles

Mentors: Erica L. Scheller and Clarissa S. Craft

The role and regulatory mechanisms of white (WAT) and brown adipose tissues (BAT) have been extensively explored. Previous research has also identified adipocytes within the skeleton known as bone marrow adipose tissue (BMAT). These cells comprise approximately 60-70% of bone marrow in an average adult human. However, despite their prevalence, the function and regulation of BMAT remains poorly characterized. A key question concerning BMAT function is whether it is capable of induced thermogenesis, multilocularity, and UCP1 expression, also known as beiging. Reconstruction of the bone marrow niche via 3D electron microscopy suggests BMAT has an extensive mitochondrial network interspersed around lipid droplets. We also found that BMAT adipocytes in 3-week-old mice are multilocular and resemble BAT. Lastly, we found that CL316,243, a β 3-adrenergic agonist, is capable of inducing lipid remodeling in a subset of BMAT adipocytes. Thus, we hypothesized that BMAT has a distinctive phenotype which, like beige and brown adipocytes, may undergo induced UCP1 expression. To address this, we developed two mouse models of inducible UCP1 expression. In the first, UCP1-Cre drives DTA expression and cell death after β 3-agonist stimulation. In the second, UCP1-Cre drives green fluorescent protein expression (GFP) allowing us to track cells expressing this protein. We found that treatment of adult UCP1-Cre/DTA mice with CL316,243 was associated with loss of inguinal WAT (iWAT) mass, however, we did not observe an increased loss of BMAT compared to control mice with this treatment. Similarly, our reporter mouse model demonstrated that CL316,243 selectively activated GFP in iWAT but not in BMAT. Overall, the data suggests that BMAT adipocytes are capable of induced remodeling, however, they are not true UCP1-expressing beige adipocytes. This supports the paradigm that BMAT adipocytes are a unique subpopulation between white and beige cells and are likely specialized to support cells within the skeletal niche.

ENHANCING PROSTHETIC DESIGN: CHARACTERIZING THE SENSORY CAPABILITIES OF THE MACROSIEVE ELECTRODE USING A RAT MODEL

Luis Ruiz

Mentor: Wilson Z. Ray

There are nearly two million amputees living in the United States today. Predominant causes of amputation include vascular problems caused by diabetes, combat or vehicular trauma, and cancer. Current prosthetic technology does not provide the rich sensory feedback afforded by the body's natural somatosensory and proprioceptive pathways. In the absence of such feedback, excessive visual attention is required.

Truncated peripheral nerves retain the ability to transmit sensory signals to the brain. Prosthetics interfaced with the peripheral nervous system via implanted electrodes can close the feedback loop, enabling more intuitive control of these devices. Our group has recently developed the macrosieve electrode (MSE), which provides fine subfascicular selectivity and mechanical stability, making it an ideal candidate for this task.

My research this summer focuses on measuring detection thresholds for various configurations of MSE activation, i.e., the smallest activating current that is detected with a 75% success rate. Due to the invasive and irreversible nature of MSE implantation, an animal model, namely a rat sciatic model, is necessary. Rats are surgically implanted with an MSE on their sciatic nerve. Wires from the MSE are then routed to the skull and wired to a connector that is part of a headcap secured to the rat's skull. The connector allows us to activate specific nerve regions interfaced with the MSE during training and testing.

Detection thresholds will be determined using a Go/No-Go task paradigm. Within a Skinner Box, a rat inserts its nose into a nose-poke device, and holds it there until stimulus onset (randomized interval). If the rat withdraws its nose within 500 ms of stimulus onset, it receives a reinforcement of sweetened water. Premature withdrawal (i.e., before stimulus onset) results in a 10 s punishment during which the lights are extinguished.

Training will begin with auditory stimuli. Rats that successfully learn this version of the task will be implanted. After recovery, they will resume behavioral training with the addition of electrical stimulation of the sciatic nerve. Over time, auditory stimuli will be phased out, leaving only the electrical stimuli. At this point, proper testing will begin.

Our measurements will establish whether a given current level elicits sensory percepts equally throughout the nerve; whether thresholds change over time post-implantation; and whether thresholds are similar across multiple rats.

THE COMMUNITY MENTAL HEALTH CENTERS ACT: AN EVALUATION OF ITS CONSEQUENCES

Gabriella Ruskay-Kidd

Mentor: Virginia Slachman

On October 1, 1963, President John F. Kennedy signed the Community Mental Health Centers Construction Act (CMHCA). The CMHCA shifted treatment for the mentally ill from state mental hospitals—viewed as toxic and impersonal—to a community setting. As a starting point, I looked at the specific text of the CMHCA and the associated philosophies behind a community-based intervention. The Act was designed to not only reduce the number of patients in mental institutions, but also to promote individualized care, increased social freedom and opportunities, a recognition of cultural and environmental influences on mental health, and active patient participation. I then turned my attention to research regarding the unintended structural flaws and far-reaching consequences of the CMHCA. Training gaps among the staff led to the neglect of many patients with significant and chronic mental illness, and a decreased number of psychiatric inpatient facilities left many without capable supervision or a place to reside. Rates of homelessness, crime, and arrest among the mentally ill reveal the impact the Act had on the lives of many mentally ill individuals, who suffered from harassment and stigmatization, or found themselves in criminal justice settings without adequate treatment.

I finally shifted my focus to researching the key elements of empirically sound treatment that are most effective in mitigating some of the unintended repercussions of the Act. This research is significant in shaping how we think about the treatment and care for those suffering from mental illness. It is crucial that those working with mentally ill clients are trained extensively in evidence-based treatments that reduce relapse rates, decrease stress, and result in higher rates of long-term employment and self-sufficiency. The effects of the CMHCA can allow us to think about the additional responsibilities that accompany a shift into the community setting: the importance of high-quality community housing services for the mentally ill, greater supervision to prevent harassment and vulnerability, and the presence of trained mental health provisions in prisons so the mentally ill can receive proper medication, therapy, and support.

GROWTH FORM AND LEAF TRAITS INFLUENCE SUSCEPTIBILITY TO DROUGHT ACROSS TREE SPECIES

Maya Samuels-Fair

Mentor: Joseph A. LaManna

Anthropogenic climate change is predicted to make natural disasters such as drought more frequent and extreme. More than just a threat to agriculture, extreme summer drought can cause tree mortality and habitat destruction. Though droughts are predicted to worsen with climate change, there is little synthesis analyzing the relative importance of species traits on drought-induced tree mortality. Like forest fires, floods, and invasive species, drought has the potential to be an agent of long-term forest community change due to differential species mortality. The Forest Dynamics Plot at the Tyson Research Center is a large Ozark oak-hickory forest site in which every stem at least one centimeter in diameter at breast height has been tagged, mapped, measured, and identified. These censuses have been conducted regularly over the last decade, capturing the Midwest's largest drought since the Dust Bowl in 1934. We tested the relative influence of three important traits, habitat preference, growth form (canopy vs. understory trees), and specific leaf area (an important trait linked to photosynthetic capability and water retention in leaves) on the mortality of 24 tree species during this severe drought. We found that understory trees had higher mortality than canopy trees over the time period spanning the drought (2011-2015). Because canopy trees generally have deeper roots than understory trees, this result suggests that root depth mediates the susceptibility of tree species to drought. We also found that trees with greater specific leaf area had higher mortality during the drought, suggesting that water loss associated with greater specific leaf area also mediates the susceptibility of tree species to drought. An understanding of how different traits affect mortality of tree species will advance our understanding of how severe drought might affect forest communities in the Ozark region and across the world.

UTILIZING METAL OXIDE NANOPARTICLES FOR PERFLUOROOCTANESULFONATE SORPTION

Daniel Schmucker

Mentor: John D. Fortner

Perfluorooctanesulfonate (PFOS) is a water-soluble compound that is corrosive and toxic to both humans and the environment. PFOS solubilizes in water to form perfluorooctanoic acid (PFOA), which is extremely persistent in the environment. PFOA cannot be separated from water by physical or chemical treatment processes due to its stable composition and solubility. This has led to the study of other unique approaches in environmental nanochemistry that offer potential solutions for PFOS treatment and remediation.

Magnetic metal oxide nanoparticles have shown promise in treating radionuclide contaminated systems due to their high surface to volume ratios, thermodynamically favorable surface chemistries, and enhanced redox potentials. In this unconventional treatment process, iron oxide and manganese iron oxide nanoparticle surfaces are used as foundations for sorption and bind to the compound of interest. Once bound, the magnetic properties of the nanoparticle allow for easy separation from water. This method of nanoparticle sorption is not exclusive for radionuclides and can be engineered to treat many different compounds depending on how the nanoparticles are functionalized. For this reason, functionalized iron oxide nanoparticles also have the potential to treat PFOS contaminated systems.

To observe and optimize the efficiency of PFOS sorption on a nanoparticle, a library of iron oxide of iron oxide and manganese oxide nanoparticles engineered with PEI and CTAB were synthesized. Theoretically, the negative dipole in the PFOA should bond with the positive dipole ends of the PEI and CTAB functionalities due to electrostatic attractions. Iron oxide, manganese-rich iron oxide, and iron-rich manganese oxide were synthesized in various sizes (8nm, 12nm, 16nm, 20nm) and with different PEI and CTAB polymer lengths (.55K, 5K, 25K). Each sample underwent sorption testing in the presence of PFOA at different pH (5,7,9 +/- .2) to determine the optimal conditions for PFOA sorption.

THE CHARACTERIZATION OF E-CIGARETTE USE IN INFLAMMATORY BOWEL DISEASE

Jasmine Serpen

Mentor: Alexandra Gutierrez

E-cigarettes represent a popular method of nicotine replacement and an adjuvant tool to aid in smoking cessation; however, the effect on disease course and smoking cessation efficacy in inflammatory bowel disease (IBD) patients is unclear. The primary aim of this project was to delineate the behavior and pattern of e-cigarette usage in IBD patients. All patients with an IBD diagnosis and self-reported history of e-cigarette use were retrospectively identified from a prospective cohort of IBD patients recruited between 2014 and 2016. Eligible patients who consented to participate were administered a comprehensive telephone questionnaire addressing multiple e-cigarette behaviors including the type and quantity of e-cigarettes used, duration of use, nicotine content, and motivations for use. Kruskal-Wallis and Fisher's exact tests were used to evaluate comparative data, as appropriate. Of 304 patients screened, 49 (16.1%) were eligible for study inclusion. Of those eligible, 27 consented to participate, 14 declined to participate, 7 were unable to be contacted, and 1 yielded insufficient data. Seven (25.9%) were current e-cigarette users and 20 (74.1%) were prior users. Current users were less likely to be current smokers (0% vs 50%, $p = 0.026$) and used e-cigarettes for a longer duration of time (34 vs 6 months, $p = 0.036$). Use of e-cigarettes reduced cravings for regular cigarettes in 21 (77.8%) people with sustained smoking cessation in 17 (63%). Motivation for choosing e-cigarettes over other methods of smoking cessation included poor success of other methods (74%) as well as the appeal of the hand to mouth habit and resemblance to regular cigarettes (64%). IBD patients who used e-cigarettes experienced a reduced craving for regular cigarettes with a smaller but substantial proportion experiencing sustained smoking remission. Larger scale studies are needed to confirm the efficacy of e-cigarettes in smoking cessation among IBD patients as well as determine the impact on clinical course.

FOSMIDOMYCIN RESISTANCE IN STAPH SPP. INFECTING VETERINARY ANIMALS

Ishaan Shah

Mentor: Audrey Odom-John

Organisms synthesize isoprenoids (IPP), an essential secondary metabolite, through one of two pathways: the non-mevalonate (MEP) pathway and the mevalonate pathway. While humans use the mevalonate pathway, many microorganisms, including some of the most important pathogens, use the MEP pathway. This makes the MEP pathway an attractive candidate for antibiotic therapy. One antibiotic, fosmidomycin (FSM), competitively inhibits a key enzyme in this pathway. It was recently reported that the *Staphylococcus* spp. that infect household animals, including *S. schleiferi* and *S. pseudintermedius*, utilize the MEP pathway. This suggests that FSM is a strong candidate for the treatment of these *Staphylococcus* spp. However, the mechanism/s by which FSM resistance may be acquired in these strains is unknown. My project will characterize FSM resistance in *S. schleiferi* and *S. pseudintermedius*. For my project, 12 FSM-R strains of *S. pseudintermedius* and *S. schleiferi* were generated and isolated *in vitro*. FSM resistance in these strains was demonstrated using a Minimum Inhibitory Concentration (MIC) assay. In *S. pseudintermedius*, all FSM resistant mutants express a mutation in *GlpT*, a glycerol 3-phosphate transporter responsible for the uptake of FSM. In *S. schleiferi* some of the resistant mutants have mutations in *GlpT*; other mutations of interest are being analyzed as well. Through this research, we will improve our understanding of the MEP pathway in these emerging pathogenic organisms.

ENDOGENOUS OPIOIDERGIC CIRCUITS INVOLVED IN THERMOREGULATION

Jordan Shaker

Mentor: Michael Bruchas

Native opioid signaling is clinically important. It has been implicated in sleep/arousal, temperature regulation, and the endocrine system. Exogenous opiate administration can have a profound effect on these systems. Although opiates are primarily used medicinally for pain relief, there are a host of negative side effects including a high abuse potential that has contributed to the opioid epidemic of the past two decades. There are three families of endogenous opioid peptides: dynorphin, a ligand of kappa opioid receptor (KOR); enkephalin, a ligand of delta and mu opioid receptors (MOR); and beta-endorphin, which preferentially binds to MOR. The neurocircuitry and sources of endogenous opioids that mediate native regulation of the sleep/arousal, temperature regulation, and endocrine systems remain poorly understood.

To identify the neurons that are the source of endogenous opioids in the preoptic area of the hypothalamus (POA), we used novel retrograde viral tools to selectively label neurons based on projection to the POA and genetic identity (expression of opioid peptide or receptor). We identified that dynorphinergic neurons in the supramammillary nucleus (SuM), a region implicated in arousal and stress, enkephalinergic neurons in the premammillary nucleus (PM), a region associated with reproductive control, and both dynorphinergic and enkephalinergic cells in the parabrachial nucleus (PBN), a region implicated in temperature sensation/regulation, nociception, and arousal, all present to the POA.

We identified glutamatergic neuronal populations in the SuM, PM, and PBN that project to the POA as well, suggesting that glutamate may be the fast neurotransmitter released from the opioidergic cells. We also identified limited local populations of dynorphin and enkephalin in the POA. Our research focused on the PBN inputs to POA, suspecting that the dynorphinergic and enkephalinergic PBN populations may project to the ventral medial preoptic area (VMPO) specifically and may be activated by changes in ambient temperature. Anterograde viral tracing experiments revealed that both populations project to the VMPO. As identified by cFos staining following temperature exposures, 72% and 45% of cold-activated PBN cells were dynorphinergic and enkephalinergic respectively, while 83% and 58% of warm-activated PBN cells were dynorphinergic and enkephalinergic respectively. Excitation of KOR-positive neurons in the VMPO lead to a 3°C drop in body temperature, and along with data showing overlap between these cells and warm-activated cFos cells, this suggests that KOR-positive cells in the VMPO are potentially warm-activated. Moving forward, we plan to use optogenetic techniques to elucidate the functional significance of the identified PBN to VMPO pathways in the context of thermoregulation.

DEVELOPMENT AND CHARACTERIZATION OF TREM2 HEK CELLS AS A MODEL FOR ALZHEIMER'S WITH TREM2 mAb AGONISTS

Nikash Shankar

Mentor: Jason Ulrich

Alzheimer's disease is a neurological disorder that is characterized by two major hallmarks—the extracellular aggregation of beta-amyloid (A β) peptides to form A β plaques and the hyperphosphorylation of microtubule-binding protein tau to form neurofibrillary tangles (NFTs). The R47H loss-of-function variant in TREM2, a microglial transmembrane surface receptor that is important for cell survival and proliferation, was found to strongly increase the risk for developing Alzheimer's. Individuals with the R47H TREM2 variant were also found to have reduced microgliosis around A β plaques. These findings suggest that TREM2 induced microgliosis could protect against the aforementioned neuritic dystrophy and NFT formation, thereby slowing the progression of the disease. However, the specific effects of TREM2 activation still remain unclear. This study sought to establish a HEK cell line that expressed a functional TREM2-DAP12 cell membrane reporter to characterize its efficacy as a model for Alzheimer's, using TREM2 mAb agonists.

After establishing a puromycin kill curve to select 2 $\mu\text{g}/\text{mL}$ of antibiotic as an optimal concentration for cell selection, TREM2-DAP12 transfected cells were tested at this dose to see whether they had been successfully transfected. High survival rates confirmed that the HEK cells had taken up the plasmid construct. A subsequent qPCR on the TREM2-DAP12 transfected cells and control HEK cells revealed that the transfected cells were able to amplify both TREM2 and DAP12 genes, indicating that they readily expressed both genes, in addition to the puromycin resistance gene. It was then discovered via fluorescence microscopy that hamster mAbs raised against the TREM2 receptor did not specifically bind to the TREM2-DAP12 surface receptor. This finding is insufficient to determine if the receptor is expressed on the cell surface and that the tested antibodies were specific to this receptor. Further testing is necessary to confirm the validity of this model via binding effects of the aforementioned agonists.

ADOLESCENT MOTIVATION AND COGNITIVE CONTROL

Katie Shapiro

Mentor: Todd Braver

Research suggests that rewards impact motivated behavior differently in adolescents than in adults. This has real-world consequences, as teenagers may have increased susceptibility to engage in risky decision-making, especially in high-reward situations or emotionally salient contexts. Adolescence is a unique period in human development, marked by new responsibilities such as learning to drive or making consequential decisions about the future. In addition to behavioral evidence, cognitive neuroscience research has revealed differential engagement of reward-processing systems in the adolescent vs. adult brain, coupled with an underdeveloped prefrontal cortex, which governs cognitive control. Cognitive control is the ability to flexibly maintain and rapidly update task representations, allowing an individual to ignore irrelevant stimuli and switch goals when necessary. Previous studies have examined the behavioral aspects of adolescent motivation and decision-making, but none have sought to investigate whether and how adolescents integrate different types of incentives. The following study incorporates both primary and secondary incentives—liquid feedback and monetary rewards, respectively—with a cognitive control task, to test whether adolescent performance is differentially modulated (relative to young adults) by these varying incentive conditions. Three liquids were examined that differ in affective valence, with apple juice as appetitive feedback (positive valence), an isotonic tasteless solution (neutral valence), and saltwater as aversive feedback (negative valence). Adolescents (ages 13-18) performed a novel computerized letter-digit task-switching paradigm, developed by Yee et al. in the Cognitive Control and Psychopathy (CCP) Lab at Washington University in St. Louis, requiring subjects to recruit cognitive control to appropriately update the relevant task goal for each trial. Results will be discussed in relationship to similar studies conducted in the CCP lab investigating a young adult demographic (ages 18-40). More specifically, we will report the effects of primary and secondary incentives and how they influence motivation in combination as well as individually.

IDENTIFYING THE MECHANISMS IN WHICH ZIKA VIRUS CROSSES THE PLACENTA AND INDUCES FETAL INFECTION

Meghal Sheth

Mentor: Indira Mysorekar

Zika virus (ZIKV) is a mosquito borne flavivirus that was first discovered in Uganda in 1947. Between 2007 and 2016, ZIKV has spread to the Americas and ZIKV has been discovered to have a devastatingly profound neurological impact on adults, causing Guillain Barré Syndrome. ZIKV in pregnant women can also induce congenital complications like microcephaly in fetuses. 29% of fetuses in ZIKV infected mothers have shown developmental abnormalities, and no vaccines or therapies have been developed to combat ZIKV infection.

My research sought to understand how ZIKV specifically crosses the placenta and induces infection. The inhibition of furin (FI), a proprotein convertase that has been found to activate viruses like Chikungunya (CHIKV), was assessed due to its ability to decrease the spread of ZIKV. An antimalarial drug, Hydroxychloroquine (HCQ), was also assessed to see if there are therapeutic effects on infected placental trophoblast cells. JEG-3 choriocarcinoma trophoblast cultures were infected with ZIKV and were then co-treated with FI and HCQ. The viral burden was then measured via qRT-PCR. The trophoblast cultures co-treated with the furin inhibitor had no statistically significant decrease in viral burden compared to the ZIKV only treatment, however the HCQ co-treatment did have a significant decrease in viral burden. My findings show that ZIKV infection does not appear to use the furin convertase to induce infection in placental cells. However, HCQ treatment, which blocks autophagy processing required by ZIKV, is effective in limiting infection.

The next step is to better understand the mechanism by which HCQ modulates ZIKV infection and move closer to employing it as a therapeutic avenue to prevent the damaging effects of ZIKV on fetuses.

THE MATERNAL-AGE ASSOCIATED RISK OF CONGENITAL HEART DISEASE IS ASSOCIATED WITH EPIGENETIC MODIFICATION OF THE CARDIAC GENOME IN THE OFFSPRING

Rachel Siegel

Mentor: Patrick Jay

Older maternal age is a risk factor for congenital heart disease (CHD) in humans and a mouse model caused by a mutation of *Nkx2-5*, a cardiac transcription factor. Our lab has shown that the basis of the age-associated risk relates to an unknown maternal factor that interacts with cardiac development in *Nkx2-5^{+/-}* embryos. Voluntary exercise by mouse mothers reduces the risk. The strain background of the mother affects risk too. We hypothesized that these the effects of age, exercise and strain background on risk would be correlated with epigenetic changes in the cardiac genomes of the offspring. We performed reduced representation bisulfite sequencing on the genomic DNA from the hearts of newborn pups. We then looked for CpG methylation patterns that were correlated with the maternal variables related to the age-associated risk of CHD; they could relate to how the unknown maternal factor affects embryonic cardiac development. In a cross that has a significant maternal-age associated risk, the offspring of old and young mothers have opposite patterns of increased or decreased methylation at a few hundred CpG sites. Voluntary exercise by older mothers causes a shift in the methylation profile to a young mother pattern. However, this shift in methylation due to exercise only occurs with the FVB strain of mice and not the A/J strain. Genomic patterns of methylation in the cardiac genome of newborn mouse pups are associated with variables that influence the maternal-age associated risk of CHD. These results suggest that the unknown maternal factor could affect the risk of CHD through epigenetic modification of cardiac developmental genes in the embryo.

THIN FILMS OF ZINC-DOPED GaAs BY RF MAGNETRON SPUTTERING FOR USE IN PHOTOVOLTAIC CELLS

Kirby Simon

Mentor: Elijah Thimsen

Thin film gallium arsenide (GaAs) based devices have the highest energy conversion efficiency among single-junction photovoltaic technologies. However, expenses associated with traditional production methods, such as metal-organic chemical vapor deposition (MOCVD) and epitaxial liftoff techniques, have hindered the widespread use of GaAs in commercial technologies. Radio frequency (RF) magnetron sputtering could offer a lower cost alternative to these methods since it does not require expensive or toxic precursors, such as trimethyl gallium or arsine. However, little is known to date about depositing GaAs by sputtering for photovoltaic applications. This investigation focuses on identifying deposition conditions that result in highly crystalline GaAs layers on glass and single-crystal alumina substrates with controlled doping type and concentration.

Highly crystalline GaAs thin-films were deposited at high RF powers (> 400 W), high temperatures ($> 400^{\circ}\text{C}$), and low pressures (1.1 mTorr). Crystallinity increased with temperature and RF power. As pressure increased, however, a loss of crystallinity was noted in the deposited films. At desirable deposition conditions for a high degree of crystallinity, the gallium-to-arsenic ratio was determined to deviate from stoichiometry. After determining the excess gallium was present as a metal on the film surface, a simple acid etching procedure was devised to selectively remove this metallic gallium and return the film to the stoichiometric ratio of Ga:As. An *in situ* zinc-doping procedure was then investigated to deposit crystalline, p-type films. Keeping RF power and chamber pressure constant, at 400 W and 1.1 mTorr respectively, zinc concentration in the film decreased with increasing substrate temperature. At temperatures upwards of 400°C , the zinc concentration was unmeasurable, indicating the zinc evaporated from the film before being stably incorporated. Despite variability in Hall Effect measurements, hole concentrations were within the desired range (10^{16} - 10^{20} cm^{-3}) and increased with increasing zinc concentration.

CHEMICAL CHARACTERIZATION OF BIOMASS BURNING ORGANIC AEROSOL COLLECTED ABOVE AND BELOW FOREST CANOPY

Skyler Simon

Mentor: Brent Williams

We present chemical speciation of biomass burning organic aerosol produced by a prescribed forest fire on March 20, 2017 at Tyson Research Center. It is important to understand the behavior of these aerosols because they contribute to impaired visibility and human health complications such as respiratory problems. Additionally, atmospheric aerosols are responsible for uncertainty in the global energy balance. Biomass burning organic aerosol varies based on the type of fuel that is burned as well as the fire conditions. In this project, samples were collected on quartz filters at ground level by pump samplers and above the forest canopy by a drone equipped with a pump. Collection occurred at regular time intervals at both levels, so compound evolution over time could be studied in addition to varying compound abundance. The samples were then analyzed using thermal desorption gas chromatography-mass spectrometry with a Filter Thermal Desorption Aerosol Gas Chromatograph (Filter TAG). Individual compounds were identified and integrated using the TERN software package in Igor Pro. Individual compounds behave differently in the atmosphere and are produced in variable quantities, so conclusions are generally drawn on a per species basis. Overall, drone samples tended to show evidence of more aged aerosol, evident in both the higher vanillin and higher m/z 44 signal, which is associated with more oxidized aerosol in TAG data. High abundance compounds included aromatic compounds, which are characteristic of lignin pyrolysis.

BIOCHEMICAL AND STRUCTURAL CHARACTERIZATION OF A HOST PROTEIN THAT BINDS EBOLA VP30

Gabe Small

Mentor: Gaya Amarasinghe

Ebola and Marburg viruses are negative sense RNA viruses that can cause high case fatality rates during outbreaks. Approximately 19 kb genome encodes for seven open reading frames. During virus replication, 7-10 multifunctional proteins are expressed, but viral replication and pathogenesis also require numerous cellular proteins. While the need for host factors in virus replication and pathogenesis has been long appreciated, our understanding of key host-virus interactions during filoviral infection and replication remain incomplete. In order to address this limitation, our collaborators recently performed a proteomic analysis, which identified RBBP6, an E3 ubiquitin ligase, as a cellular interactor of Ebola VP30 (eVP30). eVP30 is a viral protein critical for transcription initiation. In this study, we generated a series of recombinant RBBP6 and eVP30 truncation constructs. We performed in vitro pull-down assays to validate the initial proteomic identification of the eVP30/RBBP6 protein-protein interaction and defined key regions within RBBP6 that are critical for eVP30 binding. Furthermore, using purified eVP30 protein, we generated initial crystals with a RBBP6 binding peptide (RBBP6BP) and are currently refining X-ray diffraction data to develop a molecular model for RBBP6 interaction with eVP30. At the completion, we expect to define a key host-viral interface that modulates viral pathogenesis and define a novel target for potential development of antiviral therapeutics that target filoviruses.

WILKINSON POWER COMBINER EFFECTIVE AT 1-2GHz FOR DATA COLLECTION FROM EM RESONANT CAVITIES

Caroline Smith

Mentor: Jim Buckley

Two large questions in Astrophysics are that of the nature of dark matter in the universe, and discrepancies in the standard model. The ADMX experiment, hosted at the University of Washington in Seattle, is using vacuum sealed resonant cavities cooled to a few milliKelvin to detect the decay of theoretical particles named "axions." These cavities are tuned to frequencies in the range of a few Gigahertz, in line with theoretical predictions about the nature of these proposed dark matter particles which would solve the inconsistencies in the standard model. As lower frequencies are ruled out, new hardware designed for higher frequencies is needed to continue the experiment. This research conducted over the summer develops a preliminary design for a Wilkinson combiner that would be used to combine signals from two different resonant cavities operating between 1-2GHz. Simulations of this combiner show how it behaves slightly differently between the low and high end of the spectrum, but not excessively so. 2.5-D models show a larger reflection coefficient as compared to simulations based on a schematic. This circuit element is part of a larger system of signal detection that, if a signal is detected at all, would effectively prove the existence of an axion particle. This particle would be fundamental in understanding the makeup of our universe, a large fraction of which is occupied by dark matter.

CAN ONE “SNATCH THE SOUND?”: THE IMPACT OF AFRICAN AMERICAN VERNACULAR APPROPRIATION IN POPULAR MUSIC

Taylor Smith

Mentor: Virginia Slachman

In “On Black English,” James Baldwin argues that the African American Vernacular (AAVE) is a language within its own right, divergent from the English language. Referred to as Black English by Baldwin, AAVE functions as both a unifier of diverse African traditions but also as a way African Americans separate themselves from white people. This separation was historically for their protection. The words and phrases that African Americans, during and after enslaved, formed were adopted by white people but often diluted or had a change in meaning all together. These stolen terms became the names of movements and eras, garnering mass dividends for white people. The idea of stolen terms lead to questioning of how Black American and Diasporic intellectual property has been commodified. Black culture has been merchandised by Black and white audiences, in terms of white people appropriating it is often centered around ways in which people fashion and adorn their body. One of the goals of the research was to determine if white people, who have degraded and policed Black expression and creativity, have the right to profit from it. This research attempts to formulate answers through individual case studies of white artists, including Elvis Presley, Iggy Azalea, and Eminem. Their authenticity and potentially the validity of their claim and use of Black cultural elements was largely determined through their personal background, racial interactions and ideals, and their use of the AAVE, in performance and everyday life. The research was conducted through the analysis of academic discourse on race, music, “race music,” and linguistic studies of the AAVE, and is intended as an addition into the overall conversation about anti-Black ideals that shape the capitalist economy and valuing of Black cultural products for Blacks and non-Black peoples.

ON THE STRUCTURE OF ACFER094-07 MATRIX GRAINS AND THE ORIGINS OF COSMIC SYMPLECTITES

Isabella Solaro

Mentor: Ryan Ogliore

Though many studies focus on the intricate chondrules of chondrite, here we study the origin of the enigmatic fine-grained matrix of primitive meteorite in order to determine if it is a pristine sample of interstellar space or formed by processes on the parent asteroid. In this study, we first gathered elemental compositions and high-resolution backscattered electron maps of 25 matrix regions of the carbonaceous chondrite Afer094-7 and used these chemical maps to investigate both the origin of the aqueous imprints on matrix and to detect extremely oxygen-rich symplectites that have been present in other thin sections but never studied in No. 7. Though the initial goal was to analyze the structure of the matrix, the grains were too fine for Electron Backscatter Diffraction (EBSD), so the detection of cosmic symplectites was a viable second option. We first use optical microscopy to detail which large regions did not host chondrites and then located 20x20 micron regions with the finest grains and no inclusions using the Scanning Electron Microscope to collect the backscattered electron images. From these scans, we were able to determine the atomic percent of each element using energy-dispersive X-ray spectroscopy. The atomic percent, normalized to silicon, could be found for each pixel on the scan. Further, ion probe and Auger data were collected for six select regions whose compositions could best be described as chondritic. This study finds that there is a possibility for symplectite inclusions in the matrix based on the compositional data collected and the ion probe data trending toward symplectite levels. Though the study is ongoing, there are clear steps forward; pixel-by-pixel or grain-by-grain analysis can be used to find grains rich in ^{17}O and then can be compared to known isotopic values of symplectites.

ROLE OF LYSOSOME TO NUCLEUS SIGNALING IN MACROPHAGE EFFEROCYTOSIS

Eric Song

Mentors: Trent Evans and Babak Razani

Cell death, or apoptosis, is a routine part of homeostasis; up to tens of billions of our cells die every day and must be properly digested and recycled. Apoptotic cells normally are immunologically silent, unless they are allowed to remain unengulfed for prolonged periods of time, during which they become necrotic and inflammatory. Macrophages are the primary cell type responsible for the timely clearance of apoptotic cells, termed efferocytosis, which involves the recruitment and binding of macrophages, the ingestion of the apoptotic cell, and their digestion in lysosomes. Consequently, increased efferocytosis may reduce disease phenotypes that can occur from uncleared apoptotic cells, which is potentially relevant in the development of translational interventions. One underexplored component of efferocytosis is the maintenance of macrophage lysosomal function despite stress from digesting relatively massive apoptotic cargo. In other contexts, lysosomal stress is known to be sensed by two transcription factors, TFEB and TFE3, which translocate to the nucleus to drive expression of autophagy and lysosomal genes.

In our studies, we are evaluating the significance of TFEB and TFE3 on the effectiveness of efferocytosis. More specifically, we seek to identify how these transcription factors regulate the way macrophages recognize apoptotic cells, the efficiency of their degradation, and the characterization of autophagosomes generated within the macrophages. Preliminarily, we have developed a replicable procedure to use UV light to induce apoptosis in cells, protocols to fluorescently label them, and mouse models with modified TFEB and TFE3 expression for macrophage production, in preparation for both imaging and the quantification of gene expression through quantitative PCR. We plan to apply these procedures over time course experiments to observe how macrophages generate and receive efferocytosis signals. Our hypothesis is that TFEB and TFE3, through the induction of lysosomal-autophagy, are able to modulate the efficiency of macrophages in performing efferocytosis.

TAGLESS AMYLOID BINDING SUPER-RESOLUTION MICROSCOPY

Kevin Spehar

Mentor: Jan Bieschke

Oligomeric amyloid structures are crucial therapeutic and diagnostic targets in Alzheimer's disease and other amyloid diseases. However, these oligomers are too small to be resolved by conventional light microscopy. We have developed a new tool to image amyloid structures on a nanometer scale using standard amyloid dyes such as Thioflavin T, without the need for covalent labeling of the amyloid protein or staining via fluorescently labeled antibodies. Tagless amyloid binding (TAB) microscopy using TIRF microscope and 488 nm laser excitation promises directly image native amyloid in cells and tissues using standard probes at nanometer resolution.

COMPARING STRUCTURAL MRI SEGMENTATION METHODS FOR A BRAIN IMAGING STUDY OF TOURETTE SYNDROME

Shaarada Srivatsa

Mentor: Tamara Hershey

The use of anatomical brain imaging data is important for the insight it provides into brain alterations present in neurodevelopmental disorders like Tourette syndrome (TS). These data include structural volumes and cortical thickness measures. However, it is difficult to obtain these measures accurately in an automated way, as there are a number of software packages for extracting anatomical measures that differ in approach and output. Therefore, the aim of this project is to compare several of these packages to evaluate accuracy. Our ultimate goal is to use these measurements to study the onset of tic disorders and identify predictive biomarkers of TS in children who first experience symptoms (i.e., motor and/or vocal tics). Structural T1-weighted MRI scans were used from 15 participants (ages 5–14 years old; 9 male, 6 female) with recently developed tics. The four segmentation software programs evaluated were FSL FIRST, Freesurfer (both unedited and manually edited segmentations), large deformation diffeomorphic metric mapping solution (LDDMMS), and an online brain volumetry tool called volBrain. We evaluated volumetric measures of structures in the basal ganglia and thalamus. Accuracy was determined by comparing outputs visually to an atlas, and comparing volume output data quantitatively across programs. Thus far, volBrain outputs and edited Freesurfer volume outputs have yielded the most similar and accurate results and both diverged significantly from volume outputs from FSL FIRST and LDDMMS. However, the ability to edit LDDMMS output on Freesurfer could result in more accurate outputs and will be tested. The results from this project will help determine which segmentation method yields the most accurate outputs to examine subcortical volumes in children with new-onset tics over time.

THE “PRIVILEGE” OF HEALTH

Alexandria Staton

Mentor: Virginia Slachman

Racial inequality in the food system is reflected in food injustice, environmental injustice, and the death rates due to diet related diseases, such as certain cancers and heart disease, of African Americans compared to Caucasians. A plant-based diet has been proven to have the ability to prevent and in some cases reverse the effects of certain diseases; however, sustaining a nutritionally adequate plant-based diet is not plausible for African Americans more so than their Caucasian counterparts due to the limited access to resources in many predominantly African American communities. This is reflected in a larger percentage of African Americans living in food deserts and areas with inadequate public transportation than Caucasians. African Americans are also more likely to live in an area subject to the environmental injustice of animal agriculture polluting their air or water supply, in ways such as run off from hog farms or lack of waste treatment from factory farms. Through analyzing multiple studies, it is evident that their inability to access the most cost effective form of disease prevention along with the environmental injustice in these communities are considerable reasons why African Americans are dying from diet related diseases more than other races. In a time where many people's health care is at risk of being taken away, it is important to identify other, cost effective ways for people to manage their health as well as make these options more available to all groups.

INFORMANT REPORTS AND THE ABILITY TO PREDICT PARTICIPANT HEALTH OUTCOMES

Natalie Stephanus

Mentor: Tom Oltmanns

This project looked into how informant reporting on a variety of personality factors affects the ability to predict several health outcomes. The hypothesis was that the type of informant does indeed play a role in how well an informant can predict health outcomes of a participant, and while one type of informant may be better at predicting one health outcome, a different type of informant could better predict another health outcome. Using a mediation analysis, each of these types of relationships (spouse, family, friend, etc.) were looked at as predictors for three outcomes: social functioning, energy/fatigue, and general health change. The NEO-PI that both the informants and participants filled out was also involved in the analysis. In order to do mediation analyses, conditions have to be met involving statistical significance, and a majority of the correlation coefficients from the NEO-PI, the nature of relationship, and the health outcomes were not significant. Because of this, a majority of these mediation analyses could not be conducted fully, leaving the results of this project inconclusive. From the few that were statistically significant, we found that type of informant does have an effect on the ability to predict certain health outcomes.

CAN PRESCRIBED FIRE REDUCE TICK PARASITISM OF BIRDS?

Leslie Sterling

Mentor: Solný Adalsteinsson

Tick-borne diseases spread through enzootic transmission cycles that often involve ticks parasitizing bird hosts. Some avian species are competent reservoirs that amplify the pathogens causing tick-borne illnesses in humans. Prescribed burns in forests have the potential to reduce tick-borne disease risk if they limit interactions between ticks and infectious wildlife hosts. Although prescribed burns are increasingly being used for a variety of habitat management purposes, little is known about how they affect tick-host interactions. We hypothesize that if prescribed fires reduce tick abundance, then birds in burned forest plots will host fewer ticks than birds in unburned forest plots. Experimental forest plots were burned during Spring 2017. To assess avian tick burdens, we captured passerine birds using mist-nets, and removed ticks from each bird in two burned and two unburned plots during July 2017. Overall, we captured 43 birds (9 different species), and we removed a total of 130 larval and nymphal ticks from 23 of the birds. Birds in unburned plots ($n = 26$) had tick burdens (4.19 ± 0.93 ticks, mean \pm standard error) nearly four times greater, on average, than their burn plot counterparts ($n = 17$ birds; 1.18 ± 0.76 ticks). Juvenile birds hosted 4.86 ± 1.20 ticks, while adult birds hosted 1.23 ± 0.38 ticks. We modeled the effects of bird age and plot burn status on tick burden with a negative binomial regression. There are significant effects of both bird age and plot burn status on tick abundance, but no interaction was found between the two main effects. These results show a significant reduction in the tick burdens found on birds in burned plots compared to unburned plots, supporting our hypothesis.

EFFECT OF TEMPERATURE ON MECHANICAL YIELD OF QUARTZ AS MEASURED BY NANOINDENTATION

Ben Strozewski

Mentors: Phil Skemer and Kathy Flores

Formation of tectonic plates is influenced by the mechanical behavior of the lithosphere as well as convective processes in the mantle. The rheology of constituent minerals must be well-constrained in order to understand earth's deviance from the stagnant lid regime. The plastic rheology of constituent minerals has proven difficult to isolate from brittle behavior in traditional experiments. Nanoindentation and microcompression are employed here in order to study the plasticity of quartz at low temperatures ($T/T_m < 0.5$). Tests were performed on the (0001) face of a natural quartz single crystal from 23° to 175°C. Nanoindentation experiments return a reduced modulus and hardness values which are used in determining Young's modulus and yield strength. Multiple methods are analyzed here in order to determine the best way to find yield strength for geologic materials, which are both elastic and hard. Preliminary microcompression tests are also conducted as uniaxial yield strengths are readily returned. Data is then fit to flow laws to determine Peierl's stresses for each set of indents. Peierl's stresses close to 19 GPa are reported, higher than previously measured for quartz. We also demonstrate the need for a refinement of methodology for geologic materials.

ANALYSIS OF NICOTINE METABOLISM BY FLAVIN-CONTAINING MONOOXYGENASE AND CYTOCHROME P450 ENZYME ACTIVITY IN MALE AND FEMALE C57 BLACK MOUSE TISSUES AT DIFFERENT STAGES OF DEVELOPMENT

Carrie Stump

Mentor: A. Joseph Bloom

Nicotine addiction is a major health concern for human populations. Many people smoke; however, people also have difficulty quitting smoking. As a result, it is important that we begin to develop an understanding of the biochemical basis of nicotine addiction. Mice are often used as a good experimental model for nicotine dependence. Flavin-Containing-Monooxygenase protein (FMO) three is known to contribute to nicotine dependence and its expression is known to influence nicotine addiction behavior in humans. This study focuses on the activities of FMOs one and three in male and female C57 Black mouse tissues. As one goal of research in the Bloom Lab is to develop a mouse model for nicotine addiction and withdrawal, understanding how FMO activity varies in different mouse tissues at different stages of mouse development (mouse ages) is critical. Based on prior mRNA studies in 129/SV mice performed by Janmohamed et al., it was hypothesized that FMO one should show activity in all tissues at some level in all stages of mouse development while FMO three should show greatest activity after three weeks of mouse development. Microsomes of mouse brain, liver, lung, and kidney tissues were prepared and then incubated with nicotine in order to elucidate the amount of metabolite from FMO one and three formed. Metabolites were analyzed and quantified by High Performance Liquid Chromatography Mass Spectrometry (HPLC-MS). Results are expected to demonstrate that the activity of FMO one and three matched patterns predicted by the hypothesis.

SYNTHESIS OF LIGNIN MODEL POLYMER

Vicky Su

Mentor: Marcus Foston

In the project of synthesis lignin model polymer, precursors of lignin model polymers and co-polymers containing various monomers and molecular weights are made in order to help monitor and simulate the activity of lignin. Lignin is the only renewable source of aromatics, which is currently treated as waste. Therefore, it's more economically meaningful for second generation to convert lignin. To more efficiently use lignin and to convert it into value-added compounds is economically meaningful for second generation biorefinery. However, the high structural complexity and recalcitrance of lignin makes it spectacularly hard to understand its depolymerization process. In this study, various types of lignin model polymers with only β -O-4 with different molecular weight, topology, and repeating units were synthesized for understanding how the size and topology affect lignin depolymerization in future studies. The synthesis of the model compounds polymer involves using an S₂N reaction adapted from the work of Takao Kishimoto, which includes recrystallization, bromination, column filtration, polymerization, and reduction. 4-hydroxy-3-methoxy-acetophenone, and 4-hydroxylacetophenone were used as starting precursors to simulate the G and H units in lignin, which are the basic components of lignin in nature. The products from each step were tested by Thin-Layer Chromatography and/or Nuclear Magnetic Resonance, and yields were recorded for their purity over the duration of the research period. The majority of my time was devoted to work focusing on repeating the bromination step to generate monomer in large scale and increase its purity through the multiple recrystallizations of the brominated products. It is crucial to build a library of the brominated monomers for further research, and it is necessary to ensure the starting material of the polymerization is pure in order to obtain high yield of polymer in the polymerization step of the brominated products as well. While trying to balance the overall percent yield and the purity of the brominated products, adjustments to the bromination period and filtration methods were made. The optimal percent yield for H brominated monomer is 91.3% after two rounds of recrystallization. Overall, a library of 11.56g of pure brominated H monomer, 6.03g of pure brominated G monomer, and a model of cross-linked H polymer (with 1,3,5-trihydroxylbenzene in 50:1 ratio) were made and tested during the research period, and these products will be applied in the future study.

DESIGN CONSIDERATIONS FOR A QUANTUM HEAT ENGINE AND WORK OUTPUT

Caroline Sullivan

Mentor: Kater Murch

Quantum thermodynamics is a growing field, especially for experimental physicists. While many concept designs for a quantum heat engine (QHE) have been proposed and discussed, most have not yet been experimentally realized. Here we consider several possible designs for a QHE in the lab, as well as a mechanism to extract or measure the work done by the engine. We use an analogy with artificial magnetic substances to conclude that the work done will result in an increased current through the SQUID loop of the quantum bit (or “qubit”), which is the working substance of the engine. Calculations predicting the effect of the generated work on extra elements coupled to the working substance are shown, along with discussion of how these predictions rely on classical vs. quantum concepts, and how one outlook may change the outcome of the experiment.

HUMAN CHORIONIC GONADOTROPIN'S ROLE AS A NEUROPROTECTANT: EXPLORING THE PATHWAYS BY WHICH hCG PROVIDES NEUROPROTECTIVE EFFECTS TO INJURED NEONATAL HYPOXIA-ISCHEMIC CELLS

Sharath Sundaram

Mentor: Rafael Galindo

Human Chorionic Gonadotropin (hCG) acts as a neuroprotectant against the neurodegenerative effects of injured developing neurons in a mouse and in vitro model of neonatal cerebral hypoxia-ischemia. In gonads, hCG-mediated signaling involves the binding of hCG to Luteinizing Hormone Receptors (LHR) and subsequent phosphorylation of ERK1/2 (extracellular signal-regulated kinases 1 and 2) signaling. However, it is not known whether hCG activates the LHR-ERK1/2 cascade in brain or whether hCG-mediated neuroprotection involves this cellular signaling pathway.

We set out to answer the above hypothesis by using neurons, MA-10 cells (mouse testicular cancer cells) as a model for gonad cells, and Y79 cells (human retinoblastoma cells) as a model for neural derived cells. We compared the effects of hCG exposure between these three cell lines to see if the effects were similar across the different types of cells and if they operated under similar pathways. Since ERK1/2 is a known downstream kinase in the LH receptor activation pathway, we used ERK1/2 phosphorylation as a measure of hCG-LHR activation; Via western blot procedure, we compared the activation of LHRs following hCG exposure. To examine the downstream effects of LHR-ERK1/2 signaling and its potential role in neuroprotection, we studied the relative expression of 3 known neuroprotective genes following hCG exposure utilizing real-time quantitative PCR: EGR1 (early growth response 1), VEGF (vascular endothelial growth factor), and LIF1 (leukemia inhibitory factor).

We found that hCG in neurons acts under the LH receptor activation pathway, and that this effect can be modulated pharmacologically with deglycosylated-hCG (dg-hCG). hCG-LHR signaling may involve an increase in the expression of VEGF, EGR-1, and LIF-1. Our results also suggest that there is some endogenous activation of this pathway in normal growing cells, which hints towards its role in the healthy growth and protection of cells naturally.

THE ROLE OF LIPIN 1 IN CARDIAC METABOLISM AND FUNCTION

Alison Swearingen

Mentor: Brian Finck

Lipin 1 is an intracellular protein that dephosphorylates phosphatidic acid (PA) to generate diacylglycerol, which is an important step in lipid metabolism. Exercise, which affects cardiac metabolism, has been shown to increase lipin 1 expression in mice, while heart failure or hypertrophy has been shown to cause decreased lipin 1 expression. We have hypothesized that accumulation of PA in failing heart contributes to cardiac hypertrophy and dysfunction, and thus, the overexpression of lipin 1 in failing hearts will alleviate cardiac dysfunction by reducing PA accumulation. To test this hypothesis, we generated transgenic mice with cardiac specific overexpression of lipin 1 (cs-lipin 1 OE) by using a cre-inducible transgene to examine the effects of this protein on cardiac metabolism and function. The cs-lipin 1 OE mice appear outwardly normal, and H&E staining did not show any architectural abnormalities or inflammatory infiltrates.

Additionally, echocardiographic studies revealed no functional abnormalities in the hearts of cs-lipin 1 OE mice compared to littermate control mice. However, the cs-lipin 1 OE mice have increased heart weight to body weight ratios and increased expression of several genes associated with ventricular hypertrophy at baseline. Following pressure overload on the heart, cs-lipin 1 OE mice have slightly decreased expression of some genes associated with hypertrophy compared to littermate control mice. The cs-lipin 1 OE mice show no change in heart function, architecture, or inflammation as measured by echocardiography and H&E staining when compared to wild type control mice following pressure overload. While contrary to our original hypothesis, these data provide novel evidence that lipin 1 may influence cardiac hypertrophy and function.

SIMULATION OF CHARGE CARRIERS IN SMALL-PIXEL CZT DETECTORS

Jason Tang

Mentor: Fabian Kislat

Hard X-ray astronomy is used to study high-energy astrophysical objects such as neutron stars, black holes, and supernova remnants. The energies of interest are typically in the 5-80 keV range. Cadmium Zinc Telluride (CZT) detectors are often used in X-ray astronomy because they are room temperature semiconductors with excellent quantum efficiency and good energy resolution. Our group is leading the development of new small-pixel CZT detectors with center-to-center pitch of 150 microns, as opposed to the 600-micron pitch in the current NuSTAR space-based X-ray telescope. These smaller pixels will match newly-developed X-ray focusing optics that will allow for much higher angular resolution than NuSTAR. X-rays that hit the detector trigger a chain of interactions, depositing energy into the detector and creating clouds of electron-hole pairs which expand as they propagate in the detector. The electronic signal is generated from charges induced on the pixels due to the movement of these charge carriers. In small-pixel detectors, the charge carriers will induce a charge on multiple pixels, resulting in charge sharing. I will present Monte Carlo simulations of photon interactions inside the CZT detectors and the resulting signals in the pixel electrodes, including these charge-sharing effects. By considering the signals from multiple pixels, we can achieve improved energy resolution, reconstruct the depth of the interactions, and potentially achieve sub-pixel resolution.

LINKAGE OF LIPID-LOWERING, BLOOD PRESSURE, AND ANTIDEPRESSANT MEDICATIONS WITH COGNITIVE AND IMAGING BASED MARKERS OF ALZHEIMER'S PATHOLOGY

Vineeth Thirunavu

Mentor: Tammie Benzinger

The effect of statins, beta blockers, selective serotonin reuptake inhibitors (SSRIs), and other drug classes on Alzheimer's pathology is not well characterized. The objective of this project was to investigate potential relationships between these drugs and certain measures reflective of Alzheimer's pathology. Participants in ongoing studies on aging and dementia from the Knight Alzheimer Disease Research Center at Washington University were selected for this analysis. Medication data was self-reported for all participants, so a string matching algorithm in R was used to correct spellings and classify drugs into different categories (statins, beta blockers, etc). These participants (~13,000) have A β and tau PET imaging, CSF, structural MRI, and clinical dementia rating (CDR) measures. APOE4 status (APOE4 allele increases risk of Alzheimer's disease), gender, and education levels were controlled for. Basic linear regressions and general linear models show that statins delay the onset of dementia associated with Alzheimer's disease, but there is no evidence to suggest that statins slow the progression of Alzheimer's pathology after onset. Additionally, no trend was found between beta blocker usage and Alzheimer's onset or progression of pathology. Genotypic analysis to investigate rates of drug usage between APOE4 carriers and non-APOE4 carriers reveals that proton pump inhibitors (PPIs) are used at a significantly lower rate among APOE4 carriers ($p = 0.00174$), and SSRIs are used at a higher rate among APOE4 carriers ($p = 0.08671$). This uneven usage may serve as a basis for further exploration of the relationship between these drugs and Alzheimer's disease.

DETERMINING THE RECOGNITION REQUIREMENTS FOR HEME ATTACHMENT IN PROKARYOTIC CYTOCHROME *c* BIOGENESIS

Dustin Tillman

Mentor: Robert Kranz

Cytochromes *c* (cyt *c*) play an essential role in many electron transport chains, making it important to understand how this protein is matured. Cyt *c* maturation requires the covalent attachment of heme, via two thioether bonds, at the cysteine thiols of a conserved CXXCH motif. Three pathways, two prokaryotic (Systems I and II) and one eukaryotic (System III), can mature cyt *c*. I focused on System II, in which two integral membrane proteins (CcsB and CcsA) function as the holocyt *c* synthetase. CcsBA is proposed to transport heme from the cytoplasm to the periplasm and then attach it to apocyt *c* at two conserved CXXCH motifs in the di-heme cyt *c*₄. The purpose of this project was to determine the recognition capabilities of CcsBA for apocyt *c* in order to reveal new information about the requirements for heme transfer in prokaryotes. The ability of CcsBA to recognize cyt *c* CXXCH motif variants with altered spacing (CXCH, CXAXCH) or altered amino acid composition (SXXCH, CXXSH, SXXCH, CXXCA) was determined by co-expressing these variants with CcsBA and monitoring the maturation of cyt *c*. We concluded that full length cyt *c* cannot be matured at wildtype levels when either motif is mutated and that variation of one motif does not prevent maturation of the other motif. These results demonstrate, for the first time, that the order of heme attachment is not fixed (neither motif is preferentially matured) and that CcsBA has stringent recognition requirements for heme attachment. Similar variants and experimental techniques will be used to explore cyt *c* recognition requirements for the more complex System I synthetase (CcmF/H), allowing the two prokaryotic cyt *c* maturation processes to be compared and contrasted.

FUNCTIONAL CHARACTERIZATION OF *EDS1*, A PREDICTED YEAST ZINC CLUSTER PROTEIN AND PUTATIVE TRANSCRIPTION FACTOR

Mike Toomey

Mentor: Michael Brent

EDS1 is an uncharacterized putative transcription factor in *Saccharomyces cerevisiae*. Previous studies have indicated that this gene may play a role in the glucose expression pathway, as well as the yeast lysine biosynthesis pathway. With this background, *EDS1* was knocked out in combination with *MIG1*, *MIG2*, *RGT1*, and *LYS14* yeast transcription factors in different experiment conditions, including time courses performed with glucose media and stationary galactose experiments with and without lysine in the media. RNA-Seq and metabolite data were obtained for these different experimental conditions, and preliminary results suggest that Eds1 plays a role in regulating the glucose repression system, and its presence in the cell may affect a number of important regulatory and functional proteins such as a number of glucose-related transcription factors and *HXK1*, a protein which plays a crucial role in phosphorylation of glucose during glucose metabolism.

THE EFFECT OF K_{ATP} CHANNEL MUTATIONS ON INHIBITOR SENSITIVITY: IMPLICATIONS FOR PERSONALIZED TREATMENT OF CANTU SYNDROME

David Tyus

Mentor: Conor McClenaghan

Cantu Syndrome (CS) is a rare, complex disease characterized by a wide array of cardiovascular features caused by mutations resulting in the overactivity of ATP-sensitive potassium (K_{ATP}) channels. K_{ATP} channels are heteromeric complexes composed of pore-forming Kir6.x and regulatory SURx subunits. Currently, no cure exists for CS, but K_{ATP} inhibitors are promising candidates for the treatment of the disease; however, the effect of CS mutations on drug sensitivity have yet to be established. The goal of this project was to test a range of inhibitors against K_{ATP} channel mutations found in CS patients (Kir 6.1[V65M] and Kir 6.1[C176S]) to investigate their potential clinical benefit. K_{ATP} activity in the presence or absence of inhibitors (glibenclamide, repaglinide [both SURx interacting], and terfenadine [Kir6.x interacting]) was determined by measuring the efflux of radioactive $^{86}\text{Rb}^+$ from CosM6 cells transfected with wild type or mutated channels. These results show that these mutations resulted in decreased sensitivity to inhibitors of diverse structural classes which bind to different channel subunits. These findings demonstrate the need for comprehensive studies to investigate the effects of CS mutations on inhibitor sensitivity. Furthermore, these results predict poor clinical outcomes of certain K_{ATP} inhibitors for CS patients, which highlights the requirement for the development of novel inhibitors with new mechanisms of action.

SYMBIOTIC BACTERIA MANIPULATION OF THE HOST INNATE IMMUNE SYSTEM IN THE SOCIAL AMOEBA *D. DISCOIDEUM*

Stacey Uhm

Mentor: Joan Strassmann

Innate immunity is a non-specific immune response that targets agents of harm such as bacteria and acts as the first line of defense for many eukaryotes. The innate immune mechanism has been studied in depth in many organisms, especially humans, and now in the social amoeba *Dictyostelium discoideum*. The innate immune cells in *D. discoideum*, called sentinel cells, phagocytize harmful material inside multicellular aggregates of *D. discoideum* during the social stage. These spent sentinel cells are left behind in trails as the multicellular slug migrates and can be visualized using fluorescent confocal microscopy.

Some *D. discoideum* clones, known as farmers, have a symbiotic relationship with *Burkholderia* spp. These clones carry food bacteria and other kinds of bacteria, including *Burkholderia*, through the social cycle. We have previously reported that farmers have fewer sentinel cells than non-farmers and thus their innate immunity could be impaired. We also reported that farmers exposed to a toxic environment had a higher number of total spore counts compared to non-farmers challenged with toxin. Both farmers and non-farmers showed same level of spore viability regardless of toxin treatment. This equal spore viability result supports the decreased fitness in toxin-challenged non-farmers as being real. However, further research needs to be conducted to test if the differences in sentinel cell number are due to the different phenotypes of the farmers and non-farmers or due to the presence of *Burkholderia*.

Here, we found that the presence of *Burkholderia* leads to a decrease in sentinel cell number in *D. discoideum*. We cured *Burkholderia* from farmer clones and noted an increase in sentinel cell number. Conversely, we also infected non-farmer clones with *Burkholderia* and observed a decrease in sentinel cell number. These data suggest that *Burkholderia* spp. may be manipulating the innate immunity of their host *D. discoideum* to reduce the possibility of clearance during the multicellular stage. Further study of this simple system could lead to insights in how bacteria are able to interact and manipulate the innate immunity of their eukaryotic hosts.

HOW IMPLICIT ATTITUDES PREDICT BEHAVIOR

Gina Vellequette

Mentors: Calvin Lai and Joel Le Forestier

Implicit attitudes are positive or negative evaluations that are relatively unconscious and/or uncontrollable. Implicit attitudes are often assessed with a tool known as the Implicit Association Test (IAT). Research has shown that implicit attitudes as measured by the IAT are related to behavior. Little is known about the pathways by which implicit attitudes may cause behavior. The present study aims to explore how implicit attitudes predict behavior by positioning the measurement of implicit attitudes within the Theory of Planned Behavior (TPB). The TPB states that (explicit) attitudes, subjective norms, perceptions of behavioral control, and intentions are the factors that predict behavior. Our study intends to explore if and where implicit attitudes fit within this model in the prediction of running behavior. By using running behavior, the study explores an important health promoting behavior. 396 participants from the Project Implicit website took two IATs assessing associations between running/exercising and reading/relaxing and the concepts "Good" and "Bad." Participants then completed explicit questionnaires on these topics assessing explicit attitudes, perceived norms, perceived behavioral control, and behavioral intentions. We found that the IAT predicted intentions to run, reports of running in the past week, and moderated the relationship between intentions and behavior. These findings help us understand how implicit attitudes fit into the TPB and contribute to predicting behavior.

EPIMORPHIN REGULATES THE INTESTINAL STEM CELL NICHE VIA WNT4 SECRETION

Courtney Vishy

Mentor: Deborah Rubin

Short bowel syndrome results following intestinal resection as treatment for Crohn's disease or bowel ischemia and presents with malabsorption and intravenous nutrition dependence. Currently, there are few effective treatments, but stem cell therapies have been proposed. Intestinal stem cells reside at the base of the crypt-villus principal unit of the small intestine and are surrounded by a lattice network of stromal supporting cells termed intestinal subepithelial myofibroblasts (ISEMFs). Epimorphin (Epim) is a member of the family of t-SNARE vesicle docking proteins regulating growth factor secretion from ISEMFs. We previously showed that Epim deletion expands stem cell populations *in vivo* and that *in vitro*, this effect is dependent on stromal environmental effects on the stem cell niche. The aims of this project are to determine the mechanism by which Epim modulates the stem cell niche through the stromal microenvironment.

ISEMFs were isolated from WT and *Epim*^{-/-} mouse small intestines by treatment with collagenase and dispase enzymes. ISEMFs were cultured *in vitro* and grown to confluence at which point ISEMFs were harvested for RNA. qRT-PCR was performed to analyze expression of ISEMF marker genes and target genes. Protein expression was analyzed by western blot for genes confirmed to have differential expression.

Epim^{-/-} ISEMFs showed significantly increased ($p < .001$) mRNA and protein expression of Wnt4 compared to WT ISEMFs. *Epim*^{-/-} ISEMFs also showed a trend towards increased ($p = .080$) mRNA expression of Wnt2b, which is being investigated further.

Wnt4 primarily acts in non-canonical Wnt signaling pathways, but has been shown to function in the canonical Wnt signaling pathway depending on cellular context. Wnt4 secretion from mesenchymal cells has been shown to induce epithelial proliferation in both the large intestine and mammary tissue. Thus, we propose Epim deletion induces small intestinal stem cell proliferation through increased secretion of Wnt4 in the stromal microenvironment.

AN ANALYSIS OF FOOD DIFFERENCES BETWEEN RURAL AND NON-RURAL COUNTIES IN MISSOURI

Melinique Walls

Mentor: Christine C. Ekenga

Several studies have documented variances in health outcomes for residents living in rural versus non-rural settings, which may be linked to differences in the food landscape between these two settings. The objective of this study was to determine if there are rural-non-rural differences in the food environment in Missouri. We used 2016 County Health Rankings data to evaluate differences across the three domains of interest (food environment, food insecurity, and access to health food) for rural and non-rural counties in Missouri. This is a cross-sectional study employing chi-square analysis and logistic regression.

We found that there is a significant difference ($p < 0.05$) in the food landscape for rural and non-rural counties. Rural Missouri counties are at increased likelihood of being ranked in the lowest quartile for food environment, food insecurity, and access to health food than non-rural counties. The largest difference was seen in food environment, after adjusting for socioeconomic factors, health behavior factors, and physical environmental factors, with rural counties being 5.40 times ($OR = 5.40$, 95% $CI = 1.08, 27.13$) more likely to be in the lowest quartile than non-rural counties.

Our analysis revealed that rural counties were ranked worse in food environment than non-rural counties. This study highlights the food disparities between rural and non-rural settings and therefore the need to address these disparities to improve the overall health of Missouri residents. Further study of health outcomes in terms of food environment may inform non-clinical approaches to improving health in Missouri.

DOES AN INCREASE IN AVERAGE TEMPERATURE FAVOR SOUTHERN-DISTRIBUTED TREES OVER NORTHERN-DISTRIBUTED TREES?

Emma Waltman

Mentor: Jonathan Myers

Ecological theory predicts that an individual will survive best if it resides in the center its species' geographical range. In determining a species' range, scientists have historically referred to its known native range, determined by decades of observation and mapping. However, global climate change has caused an increase in mean temperature across latitudes, and ecologists have documented associated shifts in species distributions, especially expansions of species' leading edges (i.e., cold limits). As temperatures continue to warm, a species' documented natural range may no longer be the best representation of where its individuals will best survive. According to the National Weather Service, St. Louis has experienced a warming of $+1.41^{\circ}\text{C}$ from 1982-86 to 2012-16. Using census data of a 4 Ha forest plot at Tyson Research Center, we investigated how tree survival has changed during 30 years of warming from the 1980s to the 2010s. We hypothesized that Tyson tree species located at the top third of their native ranges will have higher survival in the 2010s than they did in the 1980s because average temperatures in St. Louis are becoming warmer and therefore are more similar to temperatures at the center of their latitudinal ranges before the warming. Similarly, we hypothesized that tree species in the bottom third of their native ranges will have lower survival in the 2010s than they did in the 1980s, as Tyson's annual temperatures. The results of this study provide insight into how temperate tree species are responding to climate change and has the potential to inform future conservation and reforestation efforts.

EXPLORING THE ANTIMICROBIAL ACTIVITY OF BETA-LACTONES TO COMBAT ANTIBIOTIC RESISTANCE

Anne Wampler

Mentor: Timothy Wencewicz

Antibiotic resistance is one of the world's most urgent health crises. By their very nature, antibiotics tend to select for resistance in bacteria, killing off non-resistant strains in the process of fighting infection and leaving only resistant strains to reproduce, making each successive generation harder to treat. In the past, antibiotic drug development has focused on a small number of classes of antibiotics, directly combating bacterial resistance mechanisms by modifying the functional groups surrounding the drug's active core. However, diminishing returns in the efficacy of these alterations have driven antibiotic drug development to branch out into new classes of antibiotics that hit different targets within the bacteria, circumventing evolved resistance mechanisms. I am studying one such under-explored class: beta-lactones. The beta-lactone ring is a relatively uncommon functional group that is very similar in structure to the beta-lactam active group in common antibiotics such as Penicillin. Although a few beta-lactone lipase inhibitors such as lipstatin, hymeglusin, and ebelactone have been approved for clinical use as anti-obesity drugs, the antibiotic activity of beta-lactones is not well characterized. In order to explore this property, we synthesized a library of simple beta-lactones to test their antimicrobial activity. I used the Mitsunobu cyclization on L-serine followed by an acylation to synthesize simple substituted beta-lactones. These compounds were then assayed with *E. coli* and showed dose dependent activity. This suggests that beta-lactones, even in their simplest form, possess bacteriostatic antimicrobial activity.

THE EFFECTS OF *EL PARTO VERTICAL* ON MATERNAL HEALTH IN PERU, AND THE CONSEQUENCES OF NGO RESPONSE TO THESE TRENDS

Sarah Wang

Mentor: Bradley Stoner

El Parto Vertical, roughly translated into English as “Vertical Delivery,” is the Peruvian traditional form of giving birth. Considered as a more natural form of delivery, *el parto vertical* involves the mother giving birth in a squatting (supported or not), kneeling, and/or standing position. The benefits of *el parto vertical* [B3] have already been well-established around the world, including that the squatting position opens up the pelvic opening to facilitate with birth, that the force of gravity helps the baby descend into the birthing canal with decreased pressure on the mother to push, and countless others. However, Peru continues to be one of the leading countries in maternal mortality. The methods by which I conducted the research included individual interviews, surveys/questionnaires, and participant observation. The primary collection of data consisted of ethnographic field notes. In this research project, I was able to examine and observe the effects and consequences of *el parto vertical* on maternal health in Peru. After spending four weeks in Peru actively pursuing answers to the questions listed above, I found that after giving birth in the hospital, with the option of the position *el parto vertical*, the maternal mortality rate greatly decreased.

UPGRADE OF WIRELESS SENSOR NETWORK TESTBED TO FACILITATE GLOSSY COMMUNICATION PROTOCOL

Xinghan Wang

Mentor: Chenyang Lu

Glossy communication protocol is a novel flooding structure designed by researchers at ETH Zurich and enables unprecedented reliability in wireless sensor networks. In order to combine Glossy and our existing WirelessHART communication protocol for greater network packet successful transmission rate, current hardware and software infrastructures have to be upgraded for greater accessibility and memory capacity. Here in the report we present the transition in both hardware: from Telosb/Tmote Sky motes to Firefly motes, and in software: from TinyOS to Contiki. The reasons and implementations of the transition are explained in detail, then test in Glossy are performed. Moreover, an experiment combining 6TiSCH-RPL and Glossy is conducted, whose success proves the feasibility of incorporating Glossy into the existing WirelessHART standard.

DEVELOPMENT OF DIABETIC ZEBRAFISH MODEL FOR GENETIC SCREENING

Yixi Wang

Mentors: Christopher Emfinger and Colin Nichols

Neonatal diabetes is a rare subset of the disease diabetes and affects an estimated 1 in 250,000 births. As in other types of diabetes mellitus, the body is unable to effectively control blood glucose levels due to a faulty insulin response. The ATP-sensitive potassium (K_{ATP}) channel is instrumental in insulin response, and gain of function mutations in its two subunits, kir6.2 and SUR1, are the primary cause of neonatal diabetes.

Previous studies have shown that the SUR1 subunit, which regulates channel sensitivity, can be targeted with the drug sulfonylurea as a form of treatment for the disease. However, required level of treatment and symptom severity of the studied cases can vary widely. This variation in expression of the mutations can be caused by many underlying factors, some of which may be mutations in other parts of the genome. A possible method to isolate these modifiers is a forward genetic screen.

To do so, we made an inducible neonatal diabetes model. We chose to use zebrafish as our model organism because of their similarities to humans and other practical advantages. We created a kir6.2 gain of function construct and established lines of fish that expressed the mutation. After testing, they have recapitulated several aspects of the disease in humans. In addition, a few assays essential for the screening process have been developed. With these tools, we will be able to identify individuals that deviate significantly in expression of the disease and genotype them to find candidate genes that modulate neonatal diabetes in humans as well. This will improve our understanding of the disease and inform future treatment.

CREATING ELECTROSTATIC HYDROGELS WITH OLIGOVIOLOGEN AND A POLYANION

Andrew Wellen

Mentor: Jonathan Barnes

After previous work utilizing the redox capabilities of oligoviologens to create hydrogels that rely on reduction and π - π stacking as a method of actuation, the oligoviologen platform for gel networking has been proposed for expansion. By taking advantage of the oligoviologen's cationic character, gels whose networks rely on electrostatic interactions between a polycation (the oligoviologen) and a polyanion (poly(styrenesulfonate)) to form polyion complex domains separated by water-soluble chains can be created. Electrostatic gels have been and continue to be pursued for their self-healing capabilities, non-toxicity, scalability, tunability, and high stiffness, toughness, and fracture-resistance. For best gelation, equivalents of polyion that result in balanced charges are required. Important first steps, such as synthesis and purification of oligoviologen, tosyl-end-capped hexaethylene glycol, and tosyl-end capped tetraethylene glycol as well as initial attempts at mixing of the two oppositely charged polyions, have been completed, but a lot of work remains to explore this new area of gel networking. In particular, different molar ratios of polycation and polyanion should be tested to find the combinations that yield the best results while maintaining cost efficiency.

LOW TEMPERATURE FLAME SPRAY PYROLYSIS OF NICKEL-RICH NMC FOR LITHIUM-ION BATTERY CATHODES

Jeremy Wojtak

Mentor: Richard Axelbaum

Energy is one of the major challenges of the twenty-first century for applications including power generation and storage. Developing state of the art materials would facilitate the implementation of renewable energy sources as well as significantly reduce the carbon footprint of the transportation sector. A low cost, robust synthesis process with high reproducibility is required for the production of nanostructured lithium-ion battery cathode materials. Lithium-ion batteries are considered an attractive power source for portable devices, electric and hybrid electric vehicles, and large renewable power facilities. $\text{Li}_{1.2}\text{Ni}_{0.13}\text{Mn}_{0.53}\text{Co}_{0.13}\text{O}_2$ composite materials with layered structures have received attention as high-capacity, low cost, and safe cathode materials for lithium-ion batteries. The conventional synthesis method for these materials is co-precipitation, which has challenges associated with scale up. Therefore a spray pyrolysis synthesis was developed by this group as a scalable, low cost production method. Due to the formation mechanism of the particles, the product contains hollow spheres, which cause low bulk density. Recently, Washington University in St. Louis developed a scaled-up spray pyrolysis process for the synthesis of non-hollow, solid lithium transition metal oxide materials. The method at present is capable of producing high quality battery materials at close to 50 gram per hour scale. In the present study layered $\text{Li}_{1.2}\text{Ni}_{0.13}\text{Mn}_{0.53}\text{Co}_{0.13}\text{O}_2$ material is produced and the electrochemical properties will be discussed.

CHARACTERIZING EFFECTS OF PEVONEDISTAT IN MYELOPROLIFERATIVE NEOPLASMS

Abigail J. Wong

Mentor: Stephen Oh

Myeloproliferative neoplasms (MPNs) are hematologic malignancies that cause uncontrolled blood cell growth and can progress to secondary acute myeloid leukemia (sAML). While there are therapies for AML and MPN patients, only a fraction of them are suitable to the individual, and the progress of standard chemotherapy has remained largely stagnant over the past few decades. Therefore, the investigation of MPN drug candidates such as pevonedistat is imperative. Pevonedistat is a NEDD8 activating enzyme inhibitor currently in clinical trials for AML. The inhibitor is known to impede NF- κ B signaling as well as other signaling pathways associated with MPN pathogenesis; therefore, it is crucial to characterize the effects of pevonedistat on a variety of pathways. While the JAK-STAT pathway is primarily associated with AML and myelofibrosis, inhibition of JAK2 does not completely diminish MPN pathogenesis. Therefore, it is likely that activation of other signaling processes drive cell proliferation in addition to JAKSTAT. Previous studies in the Oh Lab have shown that the NF- κ B pathway is hyperactivated in sAML and MF hematopoietic stem and progenitor cells (HSPC), identifying the NF- κ B pathway as a potential target of pevonedistat. We have found that pevonedistat lowers cell viability in human erythroleukemia (HEL) cell line in a dose-dependent manner. Furthermore, pevonedistat in combination with JNK-IN-8, an inhibitor of the JNK-AP1 pathway, lowers cell viability in an additive fashion. The combination of pevonedistat and JNK-IN-8 may be superior to pevonedistat alone, and thus we are currently exploring this possibility.

ANALYSIS OF DRUG RESISTANT HIV-1 ENV EVOLVING IN THE PRESENCE OF CO-RECEPTOR ANTAGONIST

Ellen Wu

Mentor: Lee Ratner

Little is known about the development of CCR5-antagonist resistant HIV-1 *in vivo*. We analyzed one subject who was found to have both R5 and X4-using virus at virological failure from a phase II clinical trial of Vicriviroc (VCV). The presence of multiple viral tropisms indicates the multiple mechanisms of drug evasion. Our findings may describe the early transition into drug resistance. Studies with VCV based susceptibility assays show that there is a phenotypic difference between the R5 viral populations from week 0 (baseline) and 8 (virological failure). Genotypic analysis of the R5-population overtime suggest that the V1 region may facilitate more effective use of CCR5 or CD4 and may also contribute to VCV-susceptibility.

SYSTEMIC RISK MITIGATION IN DYNAMIC RECEIVERSHIP AND AUCTION MODELS

Kevin Xu

Mentor: Zachary Feinstein

Systemic risk is the risk of a collapse of an entire financial system caused by the failure of individual parts inside the system. Systemic risk is the culprit for many catastrophic financial crises, the most famous one being the 2008 global financial crises in which mortgage market bubble burst directly caused the collapse of investment bank Lehman Brothers. In order to study the systemic risk in financial systems quantitatively, Eisenberg & Noe, proposed a foundation network system of interconnected banks with bilateral obligations in a single type of asset. Bernstein, Banerjee & Feinstein incorporated time dynamics in the model and proposed a foundation mechanism for multi-period clearing. We propose receivership and auction as two specific liquidation assistance models to mitigate systemic risk in an extension of the Eisenberg-Noe model with time dynamics. We found that the receivership model mitigates financial risk and that the auction model increases the wealth of financial networks at current time, but worsen financial health of the system in the future. Studying systemic risk and augmenting Eisenberg-Noe models with realistic financial elements helps researchers in academia and industry to analyze risk contagion and financial crises. Federal banking regulators could benefit from the studies by evaluating financial health of institutions through the models and then adjust financial policies accordingly.

TREATMENT WITH INTERLEUKIN-22 (IL-22) PROTECTS AGAINST NECROTIZING ENTEROCOLITIS (NEC) BY ENHANCING MUCOSAL HEALING

Lily Xu

Mentor: Misty Good

Necrotizing enterocolitis (NEC) is the leading cause of death from gastrointestinal disease in premature infants. NEC is characterized by an exaggerated pro-inflammatory response, gut barrier dysfunction and impaired mucosal healing. Interleukin-22 (IL-22) has been shown to provide gut barrier maintenance and attenuate intestinal inflammation in adult animal models. Therefore, we hypothesized that IL-22 plays a role in protecting against NEC by reducing intestinal inflammation. We evaluated IL-22 as a treatment strategy *in vivo* using a NEC mouse model, which utilizes a combination of formula feedings and hypoxia. We used breastfed (BF) mice as a healthy negative control and formula-fed (FF) NEC mice as a sick positive control. Our results supported our hypothesis of the role of IL-22 in protecting against NEC. We found disruption of the small intestinal architecture in the histology of NEC FF compared to the BF controls. Importantly, in the NEC mice that received treatment with IL-22, we found restoration in gross appearance of the intestine and improvement in the intestinal architecture compared to NEC FF mice and they appeared similar to the BF controls. We further found that treatment with IL-22 increases the expression of CD4+ T helper cells, which suggests that these T helper cells are mediating protection against the intestine. Taken together, we conclude that IL-22 contributes to protection against NEC, which may be related to enhanced immune cell expression in the gut. This raises the possibility that treatment with IL-22 may protect premature infants from NEC.

SYNTHETIC SCHEME OF GRAPHITE OXIDE USING HUMMERS' METHOD

Haoru Yang

Mentor: Julio D'Arcy

Graphite oxide (GO) is an allotrope of carbon comprised of oxygen and hydrogen and it is produced by exposing graphite to strong oxidizing conditions resulting in the attachment of functional groups to the graphitic surface. This process expands the interlayer distance of graphite and makes GO easy to exfoliate into single layers, i.e., graphene oxide sheets. Although the exact structure of GO and the mechanism of its formation are still unclear, various approaches to oxidation have been reported. We chose the Hummers' synthetic method due to its safety and efficiency at oxidizing carbon; this protocol was modified to increase product yield. To determine the best path for synthesis, the product GO was characterized using atomic force microscopy (AFM) and Raman spectroscopy. Through optimization, we managed to exfoliate the product GO without reducing it due to prolonged exposure in heat. Finally, we generated a synthetic protocol to be referenced for future synthesis.

THE IMPACT OF FATTY ACID SYNTHESIS ON CELL SIZE IN *BACILLUS SUBTILIS*

Zhizhou (Jason) Yang

Mentor: Petra Levin

Nutrient availability has a significant impact on bacterial cell size. Generally, bacteria cultured in nutrient-rich environments grow bigger than those cultured in nutrient-poor environments. However, it is unclear whether cell size is determined by specific biosynthetic pathways, or by bacterial biosynthetic capacity as a whole. Previous studies in the Levin Laboratory identified fatty acid synthesis as the major biosynthetic determinant of cell size in *Escherichia coli*, a Gram-negative model bacterium. Here we examined the impact of fatty acid synthesis on cell size in the Gram-positive bacterium *Bacillus subtilis*. We found that significant reductions in fatty acid synthesis reduce the size of *B. subtilis* cells. However, fatty acid synthesis is not the only major contributor to *B. subtilis* cell size. Further investigation of factors including the small molecule (p)ppGpp, a global inhibitor of biosynthesis, is still needed for a better understanding of cell size regulation in *B. subtilis*.

EXPLORATION OF THE ROLE OF THE ANTERIOR AND POSTERIOR CEREBELLAR VERMIS DURING VESTIBULAR STIMULATION

Angela Yim and Ruyan Zhang

Mentor: Pablo Blazquez

An intact cerebellum is essential for accurate spatial navigation. Previous studies in monkeys have demonstrated that the posterior cerebellar vermis (PV), a region that receives strong projections from the vestibular nerve, encodes inertial acceleration information. Remarkably, evidence suggest that this inertial acceleration signal is computed by the PV by combining semicircular canals and otolith related information. In this study we investigated whether other regions of the cerebellar vermis with abundant vestibular inputs, such as the anterior vermis, also perform similar computations. We recorded single unit activity in the anterior vermis (lobules 1 and 2) and posterior vermis (lobules 9 and 10) of mice during vestibular stimulation that stimulate the otolith and semicircular canals, alone or in combination. Mice were implanted with a recording chamber above the cerebellum to allow insertion of tungsten and glass electrodes. To gain insight into the temporal response properties of Purkinje cells, we used vestibular stimulation consisting of sinusoidal translation and rotations at different frequencies (0.18-2 Hz). To gain insight into the spatial response properties of Purkinje cells, vestibular stimulation was done in 3 azimuth orientations (0, +45, and -45 deg direction from the straight orientation). Our data suggest that anterior vermis Purkinje cells carry gravito-inertial information (like the otoliths) while posterior vermis Purkinje cells carry translational information respectively. The strong vestibular response in both anterior and posterior vermis and the differences between both areas suggest that they play important but differential roles in balance and spatial navigations.

CANONICAL WNT SIGNALING AND ITS ROLE IN CARDIAC ARRHYTHMOGENESIS

Tiankai (Kevin) Yin

Mentor: Stacey Rentschler

The Canonical Wnt signaling pathway is a key component of cardiac development, and our lab has previously seen that manipulation of this developmental pathway can lead to phenotypes of arrhythmogenic cardiomyopathy, with a slowed right ventricular conduction velocity and increased susceptibility to ventricular tachycardia. Although the adult left and right ventricular myocytes have different developmental origins, the differences in their physiological properties at baseline and in response to stress have not been well studied. We aimed to look at the role of Wnt in the development and maturation of the heart and differential effects through analysis of adult left and right ventricles where Wnt has been inactivated during development (Wnt Loss of Function (LoF) mice: *Mlc2v^{Cre/+}*; *Ctnnb1^{DM/Flax}*). In electrophysiology experiments performed on these mice, we see a slowed conduction velocity in the right ventricle, and an increased susceptibility to ventricular tachycardia. Previous studies have shown that connexins, sodium channels, myocyte cell size, and fibrosis determine cardiac conduction velocity. I performed immunostaining and Western Blots, and found that myocyte cell size and fibrosis were not affected, while there is a decrease in the Connexin 43 protein in the right ventricle of the Wnt LoF mouse hearts. Interestingly, connexins levels were unchanged in the left ventricle, and conduction velocity was also unaffected. These results suggest that changes in the electrical substrate in the right ventricle is likely responsible for the slowed conduction velocity and therefore could possibly increase susceptibility to ventricular tachycardia.

DISSECTING THE KAPPA OPIOID RECEPTOR SYSTEM IN PAIN INDUCED NEGATIVE AFFECTS

Hye-Jean (Kristine) Yoon

Mentor: Jose Moron-Concepcion

The dynorphin–kappa-opioid receptor (KOR) system produces anhedonia, depressive states and decrease goal-driven motivation, some of the characteristics often reported in patients experiencing pain conditions. Recent evidences have demonstrated that this dynorphin–KOR system in the nucleus accumbens (NAc), a brain structure deeply involved in reward and aversion, plays a major role in the regulation of reinforcing properties and motivation. In this structure stimulation of KOR by dynorphin decreases reward-induced release of dopamine, a neurotransmitter deeply involved in positive reinforcement. Therefore, we hypothesized that this dynorphin–KOR system might represent a necessary and sufficient system to explain the opioid misuse observed in patients experiencing chronic pain. To test our assumption, we primarily studied how pain impacts opioid self-administration in a rat model. After acquiring self-administration behavior using sucrose pellets, rats were implanted with an intra-jugular catheter and, after recovery from the surgery, were exposed to a daily two-hour session of fentanyl self-administration for two weeks. After the animals demonstrate a consistent fentanyl intake, known as a hedonic spot, we induced inflammatory pain using a complete Freund's adjuvant injection in the right hind paw and measured, 48 hours later, the amount of fentanyl consumed by rats experiencing inflammatory versus controls (no pain). Our results showed no changes in the overall consumption; however, the animals experiencing inflammatory pain present bursts of fentanyl self-administration during the session whereas our control animals present a linear and consistent drug consumption. Our result demonstrates for the first time a clear dissociation in how pain affects fentanyl use. With the current opioid epidemic in the U.S., the model we describe here could help future behavior research to better understand the key factors contributing to the opioid misuse epidemic.

INTRA- AND INTERGROUP SOCIAL ANXIETY IN DIFFERENT DEMOGRAPHICS

Lingyan Yu

Mentor: Thomas L. Rodebaugh

People typically report elevated social anxiety when interacting with out-groups (OGs) compared to their in-group (IG), particularly when groups are defined by race or ethnicity. Social anxiety entails both fear and avoidance of social situations, both of which could plausibly be moderated by race. We were thus interested in disassociating anxiety and avoidance in different social contexts and testing how race moderates these relationships. We hypothesized that all participants would be more anxious and avoidant with an OG than with their IG; however, minority participants would exhibit higher anxiety but similar avoidance with an OG compared to nonminority participants. We recruited 47 undergraduates in total. They were first asked to write about their IG and OG members, and then administered the Liebowitz Social Anxiety Scale, which assesses fear and avoidance of different social situations. Each of these situations was framed in both IG and OG conditions and demographic information was collected at the end of the study. Our first hypothesis was confirmed by t-tests comparing anxiety and avoidance between IG and OG: participants reported significantly higher anxiety and avoidance with their OG. Using multilevel modeling, we found that avoidance of IG predicted avoidance of OG and vice versa. Race, the Level 2 predictor, was also shown to have a significant effect on the intercepts when predicting OG anxiety using IG anxiety and predicting IG avoidance using OG avoidance. Results indicate that both anxiety and avoidance are elevated in OG compared to IG. People with minority status are more anxious with their OG but, perhaps counterintuitively, more avoidant with their IG. The study highlights that minority individuals may not experience social anxiety and avoidance in the same way as nonminority individuals when social context is considered.

ULTRASOUND MODULATION ON TRP CHANNELS

Shuming Zhang

Mentor: Jianmin Cui

The grand goal of the project is to develop an acoustogenetic technique for truly noninvasive and cell-type specific neuromodulation. Ultrasound sensitive ion channels will be expressed in mouse brain and focused ultrasound will be used to stimulate brain activities by opening the ultrasound-sensitive ion channels. Our aim during the summer is to identify ion channels that are highly sensitive to ultrasound and suitable to activate excitatory neurons. We aim to test different types of ion channels. The ion channel should be permeable to Ca^{2+} and Na^{+} ions because the opening of these channels will depolarize the membrane and excite neurons. The potassium channels already tested in Dr. Cui's lab are not candidates because they are leak channels and their opening hyperpolarizes the cell membrane. Our designed experimental method, including the experimental setup, is shown in the diagram below. Different channel proteins will be expressed in *Xenopus* oocytes for current measurements. We will apply ultrasound onto the cell containing the ion channel protein of interest and observe if any difference in current flowing occurs between applying ultrasound and without applying ultrasound. Our targeted channels are TRP channels (Transient receptor potential channels), which had been proved to be mechanosensitive channels previously. We have proved some of those channels (Trpv4, Trpc6, Trpv2) can be opened by hypotonic solution, and those current can be significantly enhanced when ultrasound is applied. Our next goal is injecting virus vector containing those DNA into mouse brain for further neuron modulation investigation.

EXPLORING NEURO-IMMUNE INTERACTION IN CHRONIC MIGRAINE

Zhiyu Zhang

Mentor: Yuqin Cao

Migraine is one of the most common neurological disorders. The major symptoms involve severe recurring headache, nausea, and photophobia. Migraine is remarkably common, affecting more than 10% of general population. It can be episodic or chronic. Symptoms of chronic migraine occur at least 15 days in each month for at least three consecutive months. It has been proposed that the nervous and immune systems communicate in the establishment of chronic migraine. My research investigated the relationship between regulatory cells (Treg) and mouse's nociceptive wiping behavior. This sets foundation for the possible engineering of Treg cells in order to prevent or delay the chronification of migraine. Mice were divided into two groups in the experiment. Both were injected with nitroglycerin (NTG, a well-known migraine inducer in human) every other day for 15 days to simulate the frequency of chronic migraine. Group 1 also received injection of interleukin 2 (IL-2), which can boost Treg cell number, every day. While Group 2 only received vehicle. To measure the mice's nociceptive behavior, I ran the Acetone-Induced Hypersensitivity Assay, in which the mouse's cheeks should be shaved beforehand to exposed the skin. Behavior tests were recorded with a video camera and the mouse's behavior was demonstrated in all angles with the help of mirrors. The duration of nociceptive wiping was then quantified using a stopwatch. The result turned out to be a boost in Treg cells which can help suppress migraine chronification. This experiment set a foundation for further research on engineering Treg cells to delay or even treat chronic migraine. Since the acetone hypersensitivity assay was only performed on female mice in our lab, we will also verify the result on male mice in the future.

SYNTHESIS PATHWAYS TO COBALT OXAPENTADIENYL COMPLEXES AS PRECURSORS TO INDUSTRIAL CATALYSTS

Kevin Zhu

Mentor: John Bleeke

Previously, Professor Bleeke's group has studied the synthesis and application of pentadienyl metal complexes. Due to the open ring structure, the pentadienyl ligand can transfer between η^5 , η^3 and η^1 structures. The flexibility of the pentadienyl ligand gives the metal center the ability to catalyze reactions between small organic molecules such as CH_4 and CO_2 and to stabilize unusual bonding interactions.

Replacing a terminal carbon in the pentadienyl with a heteroatom such as O, N or S, however, changes the reactivity and the stability of the pentadienyl-metal complex. Oxapentadienide, which replaces a terminal carbon with an oxygen, has shown ability to react with cobalt phosphine complexes in previous studies. In this research project, previous synthetic routes of oxapentadienide were followed. We tried to recreate the reactions with cobalt phosphine complexes and therefore to confirm the viability of the synthetic pathways of the oxapentadienide reagent. The 2,4-dimethylated oxapentadienide, as a derivative to oxapentadienide, was also reported to react with cobalt phosphine complexes. Previous reported synthesis of 2,4-dimethyl-5-oxapentadienide was recreated. The effect of the methyl groups was worth further study.

Cobalt chlorocobalttristimethylphosphine, $\text{CoCl}(\text{PMe}_3)_3$, has been reported to show η^3 bonding behavior with both oxapentadienyl and 2,4-dimethyl-5-oxapentadienyl ligands. In this project, we try to recreate the synthetic pathway to (η^3 -oxapentadienyl) $\text{Cl}(\text{PMe}_3)_3$ in order to test out the oxapentadienide synthesis. Besides, we attempted to synthesize $\text{CoCl}(\text{PEt}_3)_3$, and tried to combine it to the oxapentadienyl ligand, looking at the effect of the phosphine ligands to the metal center's bonding activity.

In the studies before, iron phosphine was reported to form complexes with pentadienide in η^5 and η^3 behaviors. Therefore, the interaction between iron phosphine and oxapentadienide is another focus of this project.

THE ROLE OF TWIST1 IN MUTANT HUNTINGTIN-INDUCED TRANSCRIPTIONAL ALTERATIONS AND NEUROTOXICITY

Selina Zhu

Mentor: Hiroko Yano

Huntington's disease (HD) is a fatal neurodegenerative disorder caused by an abnormal expansion of polyglutamine repeats in the huntingtin protein (Htt). Transcriptional dysregulation is an early event during HD progression and is thought to contribute to disease pathogenesis. But how mutant Htt causes transcriptional alterations and subsequent cell death in neurons is not well understood. By RNA-sequencing analysis in primary cortical neurons, we found that expression of a mutant Htt fragment leads to robust gene expression changes before neuronal death. Basic-helix-loop-helix transcription factor Twist1, which is essential for embryogenesis and is normally expressed at low levels in mature neurons, was substantially upregulated in mutant Htt-expressing neurons in culture and in the brains of HD mouse models. Knockdown of Twist1 by RNA interference in mutant Htt-expressing primary cortical neurons reversed the altered expression of a subset of genes and, importantly, abrogated neurotoxicity. We investigated the possible interaction between Twist1 and DNA methyltransferase (DNMT3A and DNMT1) both in HD mouse models at endogenous level, and in 293le cells overexpressed by PEI co-transfection. Together, these results suggest that Twist1 is an important upstream mediator of mutant Htt-induced neuronal death and may in part operate through epigenetic mechanisms.

DEVELOPMENT OF A PEDIATRIC HYDROCEPHALUS SEVERITY INDEX (PHSI) TO PREDICT LONG-TERM CLINICAL OUTCOMES

Sophie Zimbalist

Mentor: David Limbrick

Hydrocephalus is a disorder of cerebrospinal fluid physiology resulting in abnormal expansion of the cerebral ventricles and increased intracranial pressure. Despite its prevalence, there is little information on clinical outcomes in children treated for hydrocephalus or how neurosurgical practices affect outcome. The goal of this study is to create a composite index for classifying the severity of disease at baseline and predicting outcomes among children treated, in order to inform both treatment and research for this condition. The Hydrocephalus Outcome Questionnaire will be administered in person or online to the parents of 150 patients between the ages of 5-18 years who are followed at the Neurosurgery Clinic at St. Louis Children's Hospital for hydrocephalus. Potential risk factors will be identified on retrospective medical record review. We will create a clinical prediction rule, called the PHSI, to stratify patients on likelihood of experiencing poor long-term outcomes after surgical treatment. We will use a combination of bivariate analysis and clinical reasoning to restrict the number of factors for further analysis, and multivariate logistic regression to build a predictive model for poor outcomes. Creation of the PHSI will involve assigning integer values to adjusted odds ratios for significant risk factors at a 95% confidence level. We anticipate risk factors including signs and symptoms at onset (bulging fontanel, splayed sutures, papilledema, up-gaze palsy, headache, vomiting, lethargy), head circumference above the 97th percentile, frontal-occipital horn ratio greater than 0.4, etiology of meningitis or neonatal intraventricular hemorrhage, central nervous system comorbidities (seizures, Chiari malformation, scoliosis, periventricular leukomalacia), preoperative infection or sepsis, and frequent shunt revisions or infections, will be predictive of long-term clinical outcome. We hypothesize a PHSI would be a major advance in clinical hydrocephalus research as it will be a valuable tool for stratifying patients and aiding prognosis in clinical situations.



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