Presenter(s): Afzal, Nasrin, Postdoctoral research fellow; Kavya Parekh, Bindu Srinivasa, Zheng Liu, Carmen Mannella, W. Jonathan Lederer, and M. Saleet Jafri
Title: Understanding the Role of Mitochondrial Cristae Structure on Energy Metabolism through Simulation
Poster Location Number: 1
Keywords: Multiscale modeling, Cardiac cell mitochondria, Computational biology
Abstract: Mitochondria are double membrane intracellular organelles that provide the ATP to meet the energy demands of the cell. Mitochondrial dysfunction has been implicated in diverse disease including neurodegenerative pathologies, heart diseases and many more. In rat cardiac ventricular myocytes, due to the large energy demand of a beating heart, mitochondria comprise 30-40% of cell volume and number approximately 20,000 per cell. Within each mitochondrion, the inner mitochondrial membrane (IMM) provide a base for electron transport chain (ETC) and ATP Synthase proteins. The interior topology of mitochondria is a complex mixture of tubular and lamellar "inner membranes" that form the cristae and appear to change under varying metabolic conditions and in disease. Despite their clear importance, how this inner membrane organization affects function is completely unknown. A large part of this problem is that the dimensions of the structures are small and, apparently, dynamic. Therefore, an integrated modeling and experimental study is being pursued by us to develop fundamental understanding of the interplay of mitochondrial organization with its metabolic function. To this end, our previously published model (Nguyen et al., 2007) for mitochondrial energy metabolism will be integrated and be upgraded to take account of our new data on both activity-dependent regulation of ATP production and cristae structure. To ensure model sharing, the model for mitochondrial energy metabolism has been ported to the NIH-supported Virtual Cell (V-Cell) Computational Platform. Serial electron micrographs that we have prepared have been analyzed to delineate mitochondrial cristae shape and structure. This project is aimed to capture the two-dimensional and three-dimensional structure and dynamic of the mitochondrial cristae in simulations. By this means the measured structure will inform the computed metabolic function and the current and future metabolic measurements will be used to constrain the model.

Presenter(s): Akhlaghi, Nima, PhD Candidate;
Title: Differentiation of Hand Motions by Imaging Residual Limb Muscles of Transradial Amputees Using Ultrasound Imaging.
Poster Location Number: 26
Keywords: Rehabilitation, Bioengineering, Prosthetic Control, Imaging
Abstract: Introduction: With the recent developments in the electro-mechanical design of upper extremity prosthetics, the need for more advanced control strategies for such prosthetics has increased. Current commercially available prostheses, based on myoelectric control, have limited functionality; this leads to many amputees abandoning their use. Myoelectric control using surface electrodes has a number of limitations, such as low signal to noise ratio and lack of specificity for deep muscles. To address these limitations, and enable more intuitive dexterous control, our research group is investigating a new strategy for sensing the muscle activity based on ultrasound imaging. In previous work, we demonstrated that using ultrasound imaging on able-bodied participants; individual finger flexion could be classified offline with 97% accuracy; and 15 different complex grasps (e.g., power grasp and pinch) could be decoded with 91% accuracy. Also, the real-time image-based control of a virtual hand showed an average classification accuracy of 92%. The objective of this study is to investigate the feasibility of ultrasound-based sensing strategy of residual muscles’ activity in transradial amputees for upper extremity prosthetic control.

Material and Methods: Dynamic ultrasound images of the residual limb were acquired from two trans-radial amputees, using a SonixOne ultrasound system with a 5-14MHz linear probe. The probe was placed on the residual limb to visualize the forearm flexors. The participant was first asked to perform different hand motions (e.g., individual finger flexions and finger point) while ultrasound sequences were acquired for offline analysis. These images were analyzed to map the muscle activity pattern based on the change in ultrasound echogenicity of the contracting muscles during different hand motions performed by participants. Activity patterns were generated by aggregating differences between consecutive frames. The correlation coefficient for the different movements was evaluated as a proportional graded signal.

Results and Discussion: In the image sequences acquired from the first amputee, our method was able to classify four grasps (grip with index point, grasp, thumb and little finger flexion, and wrist pronation) and seven different grasps in the second
amputee (five individual digit flexion, grasp and wrist flexion). Figure 1 shows the activity patterns (top row) and proportional graded signal (bottom right) generated during the performance of 7 different hand motions by the second participant. The confusion matrix represents the cross-correlation between these 7 different hand motions. In this pilot study on trans-radial amputees, our results demonstrate that the residual muscles' functions can be visualized and classified to differentiate between different complex grasps using ultrasound imaging with small crosstalk between the motions performed. Furthermore, visual feedback of the ultrasound images accelerated the training of the amputee to perform the different motions.

Conclusion: Our preliminary results demonstrate the feasibility of using ultrasound imaging for control of upper extremity prostheses. We anticipate that this strategy will be a significant improvement over conventional myoelectric based control of prosthetics, as well as robots and other actuated exoskeletons. Further data collection and real-time classification is ongoing and will be presented in future work.

Presenter(s): Aralar, April, Graduate Research Assistant; Matthew Bird, Graduate Research Assistant
Title: Ultrasound Characterization of Interface Oscillation as a Proxy for Ventriculoperitoneal Shunt Function
Poster Location Number: 48
Keywords: Ultrasound, Diagnostic Imaging, Noninvasive
Abstract: Objective: Ventricular shunts are a mainstay of hydrocephalus treatment, but the detection of its clinical failure often relies on circumstantial evidence. A direct, non-interventional method for reliably evaluating CSF function does not exist due to the difficulty of measuring in vivo flow characteristics. The objective of this study is to apply a novel method of ultrasound monitoring to characterize the oscillation observed during pulsatile CSF flow and failure states, in an in vitro and cadaveric model.
Method: In this proof-of-concept report, ultrasound is utilized to noninvasively monitor the shunt valve and characterize its mechanical response to different flow conditions. In vitro and in situ testing was carried out by running deionized water through a VPS system using a pulsatile flow generator to replicate the flow rates expected in vivo. Different flow conditions were then tested: no flow, normal flow, proximal blockages, and distal blockages. Ultrasound data taken from the pressure relief valve were analyzed to determine differences in displacement of valve components over time between flow states.
Conclusions: Each of the aforementioned flow conditions were found to have a distinct displacement profile, showing that ultrasound imaging of the pressure relief valve can be used to easily differentiate between flow conditions that mimic physiologic shunt function and failure. Ultrasound monitoring may be a promising approach to determine if shunt revision surgery is required.

Presenter(s): Ashkezari, Seyedeh F.S., M.S.; Juan R. Cebral, PhD; Bong Jae Chung, PhD; Fernando Mut, PhD
Title: Hemodynamic Characteristics Associated with Growth Rate of Cerebral Aneurysms
Preferred Medium: Presentation
Poster Location Number: 49
Keywords: Cerebral Aneurysms, Hemodynamics, Growth, Computational Fluid Dynamics
Abstract: Background and Purpose A cerebral or intracranial aneurysm is a cerebrovascular disorder in which a weak spot on a cerebral artery dilates and results in a localized balloon filled with blood. It is estimated that approximately 2-5% of the population (around 15 million people in the United States) have at least one cerebral aneurysm [1-4]. Although many studies have identified the growth of a cerebral aneurysm as a strong risk factor for future rupture, the pathophysiology by which aneurysms grow is poorly understood. In fact, determining growth rate of unruptured aneurysms often requires follow-up for a long period of time so that significant growth could be observed and many clinicians recommend treating aneurysms that have been enlarged during the follow-up periods, which results in fewer longitudinal follow-up imaging data being available to study the growth and possible associated hemodynamic variables.
The purpose of this study is to use computational fluid dynamics (CFD) simulations to understand how the hemodynamic environment of the aneurysm changes as the aneurysm grows and to identify hemodynamic characteristics that are associated with aneurysm growth rate by artificially mimicking the aneurysm growth in time.
Materials and Methods
3D models which outlines the aneurysm and selected vessels were generated and CFD simulations were performed for 7 large aneurysms (mean aneurysm size: 17.2±4.9 mm, mean aneurysm aspect ratio: 16.5 ± 4.8 mm) at basilar artery tip (BA-tip) based on 3DRA images [5]. In the next step, the resulting 3D models were manually manipulated, cut, and smoothed (if necessary) to
Preliminary Results
In all the seven aneurysms, the mean velocity (VE), viscous dissipation (VD), and mean wall shear stress (mean WSS), which is defined as the time average of the spatial-averaged WSS, decreased as aneurysms grew in time; i.e. from the first stage (small aneurysm) to the sixth stage (enlarged aneurysm). Moreover, vortex coreline length (CORELEN), which provides a measure of the complexity of the aneurysmal flow structure either increased as aneurysms grew or increased and then decreased during time. The above results indicate that different hemodynamic characteristics may be associated with aneurysm growth.

Conclusion and Future Work
Understanding the cerebral aneurysm growth rate is important for improved patient management as it makes it possible for us to predict the rupture risk. In future we want to investigate the aneurysm growth rate in other brain locations to understand the hemodynamic changes that are associated with aneurysm growth and to see whether there is any dependence between aneurysm’s location and growth.

References

Presenter(s): Ayhan, Miranda, PhD Student; Kaitlyn Power, Deyra Carranco, Emily Metz, Fatima Siddiqui, Farishta Boura
Title: NeuroMorpho.Org: The Study of Neuronal Morphology Through Digital Reconstruction
Poster Location Number: 27
Keywords: computational neuroscience, big data, neuroscience
Abstract: In all biological systems, form denotes function. Neuronal morphology is important in the understanding of the nervous system. Morphology examines the cellular level of neuronal anatomy and its functional mechanisms. Understanding how populations of neurons encode information and guide behavior is a major focus of systems neuroscience. More data on the morphologies of neurons leads to deeper conceptual understandings in regards to the brain. Currently, the standard for quantifying cellular neuroanatomy is through three-dimensional digital reconstructions. These digital files are standardized and centralized in NeuroMorpho.Org, the world’s largest database of publicly available digital reconstructions of neuronal morphologies.
NeuroMorpho.Org is a user friendly web-based platform for freely sharing these data in an expert system online. The accumulation of neuromorphological tracings generated every day is growing exponentially. By compiling this information, the data can be better utilized world-wide by allowing large scale analyses and international collaboration to answer more and bigger questions about neuronal morphologies. As Data-Processors, we use both automation and manual editing to standardize and correct data received from laboratories around the world. Once pre-processed, inspected, edited as needed, error-checked, and post-processed, the data are ready to be uploaded onto the website. All neurons are accompanied by details on the animal species, brain region, cell type, and the experimental collection methods. Ultimately, big data neuroscience and the processors who curate every single neuron enable the formation of connections all across the neuroscience community.

Presenter(s): Barclay, Alex, Graduate Student; NA
Title: Lack of HIV-1 Transcriptional latency: exosomes from uninfected cells activate hiv-1 transcription
Poster Location Number: 28
Keywords: HIV-1, exosome, latency
Abstract: HIV-1 infection causes AIDS, infecting millions worldwide. It can persist in a state of chronic infection due to its ability to become latent. We have previously shown that there is a link between HIV-1 infection and exosome production.
Specifically, exosomes were shown to transport viral proteins and RNA from infected cells to neighboring uninfected cells. These viral products could then elicit an innate immune response, leading to activation of the TLR and NF-kB pathways. In this study, exosomes from uninfected cells were observed to increase short and long-length viral transcripts from latent wild-type HIV-1-infected cells. A possible mechanism for this finding revealed that the exosomes potentially cause an increase in RNA Polymerase II activity within the infected cells. These viral transcripts, which include TAR and a novel RNA termed “TAR-gag”, can then be packaged into exosomes and potentially be exported to neighboring uninfected cells, leading to increased cellular activation. Collectively, these results imply that exosomes from uninfected cells could activate HIV-1 from latency in infected cells and that a true transcriptional latency may not be possible in vivo, especially in the presence of cART.

Presenter(s): Barksdale, Stephanie, Research Associate; Akanksha Kaushal, Research Associate; Evelyn J. Hrifko, Research Associate; Barney M. Bishop, Associate Professor; Monique L. van Hoek, Professor
Title: Antimicrobial Peptides with Activity in a Murine Pneumonic Tularemia Model
Poster Location Number: 2
Keywords: biothreat, Francisella tularensis, antibiotic, mouse model
Abstract: Our group has previously identified a C-terminal fragment of apolipoprotein C-1 from Alligator mississippiensis with broad-spectrum activity against a range of bacteria, including drug-resistant strains. In this work, we tested this fragment (Ap6) and synthetic derivatives (GATR-1 to -7) against strains of Francisella tularensis to determine activity in vitro and in vivo and to examine mechanism of action. The synthetic derivatives were produced by altering amino acids in the peptide to increase hydrophobicity, positive charge, and hydrophobic moment. The antimicrobial activity of the CAMPs was found to increase as they increased in hydrophobicity and charge, but only to a certain point. We examined the mechanism of action using DISC3(5) and ethidium bromide for membrane disruption and using dimethylmethylene blue for LPS binding. It was found that all of the CAMPs disrupted the bacterial membrane of Francisella and bound this bacteria’s atypical LPS. Altered peptide sequences increased activity of both mechanisms to a certain point. The highest performing CAMPs were tested in a murine pneumonic tularemia model using F. tularensis subspecies holarctica Live Vaccine Strain. All of the tested peptides rescued at least some of the mice. However, GATR-3, a moderately derived peptide, was found to have the most effective activity in vivo. GATR-3 rescued 60% of mice and decreased severity of symptoms over the course of infection.

Presenter(s): Best, Amy, Amy Best, Professor and Chair, Sociology & Anthropology; Margaret Slavin, Assistant Professor, Nutrition & Food Studies; Katie Brennan, Nutrition MS alumna, Nutrition & Food Studies
Title: University Food Provisioning, Health and Student Choice in an Era of Personalized Food Consumption
Poster Location Number: 3
Keywords: diet, young adults, health
Abstract: Dining halls are highly rationalized food provisioning systems. In large public universities, they feed thousands of students daily. Yet, contemporary dining services are increasingly expected to accommodate students’ individualized dietary needs and promote dietary health. Dining services face substantial challenge in providing healthy options that satisfy student food preferences, while also operating within budget constraints. Several broad cultural and economic currents help us understand this. These include a transforming institution of higher education, changing budget realities, a transforming food landscape, the cult of health, drift toward greater personalization, and use of food as identity marker. College food, once easy fodder for being downright dismal, has undergone a remarkable upscaling. As prospective students “shop” for their top-choice colleges, ratings of campus food options increasingly figure into the calculus. It is not surprising then, that dining hall food is increasingly marketed, alongside other university services: state-of-the-art instructional and athletic facilities, modern dorm amenities, and small student-faculty ratios as universities compete to recruit selective students. This poster highlights the dilemmas of institutional food provisioning. It takes as its case dining halls at a large public university and is based on meal assessment surveys collected in dining halls, and focus groups with college students and dining service employees. The research identifies the competing narratives held by students about food provisioning in public institutions, the creative efforts and challenges of dining hall services to promote student wellbeing through food, and quantitative data that demonstrate students are not consuming food in support of dietary health.

Presenter(s): Blower, Ryan, Post-Doctoral Research Fellow; Dr. Monique van Hoek, Associate Professor
Title: Antimicrobial Peptides with Activity Against Bacillus anthracis in vitro and in vivo
Poster Location Number: 4
Keywords: B. anthracis, antimicrobial peptide, cationic antimicrobial peptide, histone, bioprospecting, de novo peptide sequencing

Abstract: In this study, we improve on our previously published “Bioprospector process” and present the results of a process that allows for large-scale identification and de novo-assisted sequencing of newly discovered CAMPs from organisms, specifically Varanus komodoensis (Komodo dragon), using lipobead microparticle capture followed by mass spectrometry with electron-transfer dissociation. Identified CAMPs were then analyzed based on their physico-chemical properties and predicted antimicrobial activity to narrow our selection of CAMPs to synthesize and test against B. anthracis Sterne Strain. B. anthracis is the causative agent of anthrax, a disease which is categorized as a priority A pathogen by the NIAID as it remains an important biodefense threat. The rise of antibiotic resistance has driven research into novel antimicrobial therapies. Cationic antimicrobial peptides (CAMPs) are a part of the innate immune system of higher order organisms that have evolved over time to exert host defense and antimicrobial activity. Twelve CAMPs were selected and produced, named VK-26 through VK-38. These selected CAMPs were analyzed by EC50 and MIC antimicrobial assays. Membrane depolarization and pore formation were performed and correlated with antimicrobial activity. Finally, active antimicrobial peptides were tested in vivo against Galleria mellonella. We identified several komodo-dragon serum peptides with significant and direct antimicrobial activity against vegetative cells of Bacillus anthracis Sterne strain, suggesting they may be good candidates for further development.

Presenter(s): Cannice, Sydney, Student; Richard Fab sitsz, PhD, CHHS [PI]; Seth Hudson, CVPA; R. Kevin Mallinson, PhD; Paul Rogers, PhD, CHSS; Naomi Watanabe, PhD, [Japan]

Title: Video Gaming and Its Effects on Well-Being Among George Mason University Students

Preferred Medium: presentation or poster

Poster Location Number: 19

Keywords: video games, student wellbeing, health effects

Abstract: Participation in video games is trending higher around the world, particularly among young people. Attention within the research community has focused on pre-adolescents and adolescents, with less emphasis on the effects of video gaming on the wellbeing of college students where the freedom to participate is greatly increased. A convenience sample of George Mason University students (N=216) was recruited on campus (primarily in the student union) in the Fall 2016 semester; the sample included males (n=158, 73%) and females (n=58, 27%) who identified as regular video game players. Survey results addressed time devoted to gaming, activities interrupted by gaming, and overall effects of video gaming on study habits, social relationships, and wellbeing. Time devoted to gaming: Men reported playing video games for an average of 13.5 (SD=5.04) years while women reported playing video games an average of 12.1 (5.65) years (p=.11). Average weekly play did not differ significantly between men [12.3 (11.4) hours] and women [10.0 (11.7) hours] (p=.20). Furthermore, average weekly time reported watching others play video games was 3.97 (5.51) hours for men and 5.69 (8.60) hours for women (p=.09). Activities interrupted by gaming: At least once in the last thirty days, 71% of the respondents reported choosing to play games rather than sleep and 41% reported choosing to play games rather than eat a meal. Similarly, at least once in the last thirty days, 69% of the respondents reported choosing to play video games rather than study and more than half reported choosing to play video games rather than attend a social engagement. About 25% of the respondents reported choosing to play video games rather than work at least once in the last thirty days; this result may be misleading because many students did not work during the school year. Effects of video gaming on study habits, social relationships, and wellbeing: Overall, 51% of men and 39% of women thought their video gaming enhanced their relationships with others; 10% of men and 21% of women thought it interfered with their relationships with others (p=.054). Overall, approximately 6% of the sample reported that video gaming enhanced their study habits; then again, nearly half reported it interfered with their study habits (p=.79). Regarding overall wellbeing, one half of the respondents reported that video gaming improved (37%) or greatly improved (13%) their wellbeing. Conversely, about 7% of men and 14% of women thought video gaming reduced their wellbeing (p=.55). Considering that the weekly time burden equals – or exceeds – class time and that video gaming interferes with relationships and academic studies, these findings support further investigation of the effects of video gaming on the wellbeing of college students.

Presenter(s): DeMarino, Catherine, MS;

Title: Antiretroviral drugs alter content of exosomes from HIV-infected cells

Poster Location Number: 29

Keywords: HIV, exosome, antiretroviral

Abstract: HIV-1 is a complex retrovirus that produces chronic infection affecting approximately 40 million people worldwide and is responsible for 1.1 million new infections each year. To date, the most effective treatment of HIV is a combination of several antiretroviral drugs (cART), which lowers viral titers and reverses pathology (1-3). Here we investigated the effect of cART on the content of exosomes released from HIV-infected cells. We have previously shown that HIV-infected exosomes contain a non-coding RNA, which has been shown to elicit responses in recipient cells. In our most recent data, we found
altered levels of genomic RNA while other RNAs, such as TAR RNA, remained unaffected by the addition of cART treatment in both cell lines and primary macrophages. More recent experiments in our lab have shown that several other FDA-approved drugs have the ability to alter the content of exosomes released from HIV-infected cells. Furthermore, we will discuss how these findings on cART-altered exosomal content can be applied to general viral inhibitors (i.e. interferons) which is normally used in the treatment of HIV and many other infections both in vitro and in vivo. Collectively, these data imply that when patients are under antiretroviral therapy, they still release exosomes which may cause cytokine storm associated with neurocognitive and immunological dysfunction.

Relevant Manuscripts

Presenter(s): Detmer, Felicitas, MsC; Bong Jae Chung, PhD, Fernando Mut, PhD, Christopher Putman, MD, Juan R. Cebral, PhD
Title: **Large scale, multi-center analysis of hemodynamic and morphological risk factors for aneurysm rupture**
Poster Location Number: 46
Keywords: CFD, aneurysms, hemodynamics

Abstract: **Background and Purpose**
Cerebral aneurysms are relatively common with an overall prevalence of 2 - 5% [1, 2]. The natural risk of rupture, leading to hemorrhagic stroke, is with about 1%, however, comparatively low [3-5]. In our group, we have a large data base of patient and image data of more than 2000 aneurysms. We aim to use this data to identify hemodynamic and morphological risk factors for aneurysm rupture based on computational fluid dynamics (CFD) simulations. Aneurysm rupture risk is known to vary between aneurysm locations in the cerebral vasculature [6]. To adjust for that confounding factor, we compared hemodynamic and morphological variables between ruptured and unruptured aneurysms at each location separately. A further motivation for the analysis by location is to avoid an impact of the assumed flow conditions as input condition for the CFD simulations.

**Materials and Methods**
Patient-specific CFD simulations were performed for about 1950 aneurysms based on 3DRA images [7]. 47 hemodynamic and morphological variables were computed. The selected hemodynamic parameters describe the flow intensity, complexity and temporal stability. Aneurysm size, elongation, shape and neck size are measured by the morphological variables. Values of these parameters were compared between ruptured and unruptured aneurysms at 13 locations by univariate logistic regression.

**Results**
Overall, ruptured aneurysms had a hemodynamic environment of stronger, more complex and less stable flow. Except for minimum wall shear stress (WSS) and WSS normalized with respect to the WSS in the aneurysm parent vessel, all hemodynamic variables were larger in ruptured aneurysms. With respect to morphology, ruptured aneurysms were significantly larger, more elongated, less spherical, and had smaller necks. These relationships between rupture status and hemodynamics and morphology did not differ between locations. All variables that were significantly different were consistently larger or smaller for ruptured aneurysms for all locations. At the same time, different numbers of variables were significant at different locations, which is thought to be (partly) related to different sample sizes at different locations. These results indicate that the same hemodynamic mechanisms are related to rupture among different locations. To corroborate that finding, an interaction test was performed. No significant influence of interactions between hemodynamic variables and aneurysm locations on aneurysm rupture risk was found.

**Conclusion and Future Work**
Consistent with previous findings and the literature, it was found that ruptured aneurysms had a more adverse hemodynamic environment characterized by stronger flows and more focalized WSS [8, 9]. Moreover, they were larger and more complex in shape. It was further shown that the hemodynamic mechanisms that are associated with rupture are independent of location. Future work aims to use the large amount of data to generate a prediction model for aneurysm rupture risk based on regularized logistic regression.

Presenter(s): Devine, Megan, PhD. Research Associate;
Title: **Magnetic Hydrogel Particles for Peptide Sequestration**
Poster Location Number: 5
Keywords: Magnetic nanoparticles, hydrogels, cationic antimicrobial peptides
Abstract: Hydrogel particles are proving to be useful tools for the preferential capture and enrichment of small peptides and proteins from complex biofluids such as blood and urine. While effective, using the peptide-capture process can become cumbersome to the user as harvesting and post-harvest conditions are altered, especially at higher pH values. Additionally, the repeated centrifugation and resuspension cycles associated with traditional functionalized poly-N-isopropylacrylamide (pNiPAm)-based capture particles do not lend themselves readily to automation of the harvest process. Core-shell hydrogel particles that incorporate magnetic cores eliminate the need for centrifugal separation while retaining the harvesting capabilities of traditional pNiPAm-based harvest particles. Here we report a new strategy for generating core-shell magnetic particles for biomolecular harvesting, which involves grafting of the harvesting hydrogel polymer layer from a magnetic core particle using reversible addition-fragmentation chain-transfer (RAFT) polymerization chemistry. In this approach, the RAFT chain-transfer agent (CTA) was coupled to the surfaces of magnetic core particles, and the RAFT-ready particle was then used to “grow” the encapsulating functionalized harvesting polymer matrix. The harvesting properties of the resulting magnetic core-shell particles were evaluated, focusing on the ability of the particles to effectively harvest cationic peptides from American alligator plasma as a model system.

Presenter(s): Dhakshinamurthy, Dev, PhD in ECE, GMU; Nathalia Peixoto, Associate Professor, George Mason University
Title: Harnessing Virtual Reality in Robotic Assistive Devices
Keywords: Virtual Reality, Assistive Device
Abstract: Nearly 5.4 million people in the US suffer from some form of paralysis which causes them to lose complete or partial control of their extremities. For the majority of these people recovery from their impairment by rehabilitation is not always possible. This leads to extreme difficulties in interacting with day-to-day objects around them, and they often require some form of assistive device to improve their quality of life. However, in some cases, the user is left feeling mechanized as their interactions with such devices feel unnatural. Increasing the interaction with these devices while taking the human factors such as social stigma and acceptance into consideration is the challenge. We believe that VR headsets not only has the potential to improve the interactions but will also make the user feel more natural as it can blend realities. Our research provides an overview of leveraging vision-based VR applications in robotic assistive technology. The ability to interact with virtual objects that appear in thin air has always been fantasized in science fiction movies and novels. Movies such as the Matrix trilogy and the Thirteenth Floor popularized the possibility of computer-simulated universes where people could live in and interact with their virtual environments. With the advent of technologies such as Google Glass, PlayStation VR, and other such devices, this fantasy has become a reality. Virtual reality is enhancing the perception of users and helps to interact with the surroundings in novel ways. For example, paraplegic patients who were trained in a VR environment combined with a lower limb exoskeleton showed significant neurological improvements than traditional rehabilitation methods. We performed experiments to measure the accuracy and precision of a robotic arm controlled by the HTC VIVE™ VR headset. The experiment was repeated five times to evaluate the performance. We demonstrated that the proposed control mechanism was highly accurate and precise. The few problems we encountered in this experiment were due to the design limitations of the robotic arm. A robotic arm with a good load distribution design having highly accurate servos will increase the accuracy of the control mechanism even further. We also observed a couple of limitations of using this method. People who tried it out for long periods of time expressed feeling uncomfortable as the VR headset is a bit bulky. Eye irritation was also reported among people due to the exposure of bright lights at proximity. Another problem was that the play area for HTC VIVE™ had to be calibrated every time the experiment was started. Failing to do so often caused tracking issues when using it. We believe that the potential of VR far outweighs these limitations. They will be overcome as new technology emerges.

Presenter(s): Dubrow, Samantha, GRA; Alexis Battista, Assistant Professor, Uniformed Services University of the Health Sciences; Jill Sanko, Assistant Professor, University of Miami; Brenda Bannan, Associate Professor, George Mason University; Nathalia Peixoto, Associate Professor, George Mason University
Title: Communication in Interprofessional Multiteam Systems During Patient Handoff: A Case Study
Keywords: simulation, teams, communication, interprofessional
Abstract: Healthcare professionals emphasize the importance of non-technical skills, such as communication, in patient safety. Skills such as communication are particularly vital during patient handoff between interdependent teams. Our research team conducted a simulation in which two teams (pre-hospital and emergency department) responded to a victim in a car
accident. The purpose was to answer the research question: How do participants use verbal and nonverbal communication during information handoff between multidisciplinary teams? Our study builds on the extensive handoff literature by considering these two interdependent teams as a multiteam system (MTS). An MTS is a group of two or more teams that work closely together to reach a common goal, which each team is also responsible for completing its own short-term goals (Zaccaro, Marks, & DeChurch, 2012).

Through a descriptive, multi-method case study design, we conducted an in-depth analysis of verbal and nonverbal communication during patient handoff between a team of six pre-hospital members, and a team of nine interprofessional emergency department trauma team members. In the first phase of analysis, the simulation video was viewed multiple times, and the interdependencies between the teams were mapped. In phase two, video analysis software (Mangold INTERACT) was used to code for the frequency and duration of verbal and nonverbal communication patterns, based on an a-priori coding scheme grounded in activity theory.

Analysis of the video led us to identify a power broker (i.e., boundary spanner) who was primarily responsible for communicating information between the pre-hospital and emergency department teams (e.g., Marrone, 2010). One of the pre-hospital paramedics took on the responsibility of relaying information about the patient to the emergency trauma team.

Participants in this simulation maximized the efficiency of their verbal utterances, and there was very little overlap in people speaking. The teams exhibited efficient turn-taking in their communication (Denzin & Lincoln, 2011).

The lack of overlap in communication between the participants as well as the dearth of nonverbal communication suggests that the MTS had a shared understanding of the situation, and who was responsible for which parts of the system. Thus, we believe the MTS may have relied on a shared mental model (a mutual understanding of the situation) and a transactive memory system (shared knowledge of who holds what specific information that assisted with being able to perform at a high level despite the relative lack of communicative exchanges; Kozlowski & Ilgen, 2006). Initial findings support the notion that similar team training/education may promote the likelihood there will be formation of a shared mental model.

Next steps for this project include continued analysis of this case study as well as conducting further simulations. Through further analysis, we will align actions and technical skills with communication exchanges to identify whether communication is event-based, situation specific or associated with a task. Additionally, we plan to conduct interviews with participants to see if our conclusions about shared mental models, transactive memory systems, and similar training between the teams are correct.

Presenter(s): Fernandez, Lourdes, PhD student, English Department; Heidi Lawrence, Assistant Professor, English Department; Bonnie Stabile, Research Assistant Professor, Schar School of Policy and Government
Title: The Disappearing Accused: Media Narratives of Campus Sexual Assault
Poster Location Number: 51
Keywords: campus sexual assault, rhetoric, media

Abstract: The problem of campus sexual assault has garnered much media attention and been the focus of various contested policy initiatives in recent years. The November 2015 report, since retracted, in Rolling Stone Magazine of a brutal gang rape at the University of Virginia is among the most prominent of these stories. It is emblematic of the issue in that it precipitated calls for policy responses at both the legislative and local campus level and unleashed bitter debate about the veracity of rape allegations, the rights and culpability of the accused, and the responsibilities of individuals versus institutions in creating campus cultures that prevent, and appropriately respond to, incidents of sexual assault. To better understand this fraught policy climate, this analysis examines the rhetoric in a sample of media reports from a two-year period surrounding the publication of the Rolling Stone article. It applies a grounded theory approach to identifying prominent rhetorical themes in news coverage from The Washington Post during this time period. Findings suggest that institutions — universities, in particular — are portrayed as bearing predominant responsibility for the extent and existence of the problem, while at the same time being characterized as being inept or ill intended in addressing it. Rhetorical analysis of this coverage also reveals that students, while portrayed as engaging in aberrant or irresponsible behavior related to incidents of sexual assault, are less often assigned blame. Further, while accusers, mostly women, are prominently present in reporting of these events, with their actions often described in detail, the accused are more often noticeably absent from the narratives. Some policy implications of these findings are discussed.

Presenter(s): Fletcher, Laura, PhD Student; Samantha Dubrow, PhD student; Dr. Stephen Zaccaro, Professor; Dr. Richard Klimoski, Professor
Title: Science of Team Science at George Mason University
Poster Location Number: 31
Keywords: science teams, teamwork, leadership, team assembly, team performance
Abstract: Successful scientific research requires an understanding of how people and teams involved in a project collaborate and work together effectively. Although there is an entire discipline committed to understanding team science (i.e., the science of team science), there is limited knowledge about how science teams assemble and the nature of leadership required for multidisciplinary science initiatives to succeed. Furthermore, scientific research often occurs within multiteam systems (MTSs), which are networks of teams that are brought together to solve problems that are often too complex for any one team to successfully solve (Zaccaro, Marks, & DeChurch, 2012). Therefore, the purpose of our research was to investigate how multidisciplinary science projects begin, how leadership patterns impact the development of different team processes over the course of the project, and the frequency of MTSs in these grant projects.

Over the past two semesters, we interviewed 20 individuals who are leaders or members of projects that received one of the GMU multidisciplinary research (MDR) seed grants. Several key learnings were uncovered, the highlights of which we included here. Four leadership types emerged: idea champions, entrepreneurs, opportunity seekers, and project managers. Of these, idea champions and entrepreneurs were the most common in our interviews. Successful leaders seemed to have relatively high political skill, and relied on social capital to bring on other talented individuals or teams. In addition, successful leaders maintained social awareness of what motivated other team members based on their personal desires and gains from the project. These social skills came into play during the assembly stage so as to gain commitment to the project. For instance, during the assembly stage, it was critical for leaders to accurately predict the kinds of skills or expertise necessary to complete the project and to find the most suitable person for that role, but it was also important that they secure the talent’s commitment to the project, especially when there was no previous relationship between the leader and the talent.

Successful projects also showed several characteristics during the project that are of note. For instance, the leaders or talent were in constant communication, sharing updates and maintaining organization across the project. That leads to another unique finding, which was that the quality or style of communication was established early on. People from diverse backgrounds have different ways of expressing ideas, so successful multidisciplinary teams and MTSs created a shared lexicon, or at least found ways of communicating, that would bridge disciplinary boundaries to improve communication and comprehension quality. Lastly, there was a dispersal of responsibility across deliverables and tasks such that people and teams knew the importance of each role in the project and was committed to completing their portion of the work. Sometimes this translated into people or teams taking the lead on a first-author publication or conference presentation. This dispersion of responsibility seemed to help maintain motivation and commitment to the project over the course of the grant.


Presenter(s): Gallagher, R. Isela, Lab Specialist; Julia Wulfkühle, Research Professor
Title: Protein activation mapping uncovers exploratory predictive markers for pCR in triple negative breast cancer patients treated with neratinib in the I-SPY 2 TRIAL
Poster Location Number: 33
Keywords: breast cancer; biomarkers, neratinib, reverse-phase protein microarray

Abstract: Background: In the I-SPY 2 TRIAL, the pan-ERBB inhibitor, neratinib (N) arm was open to all HR/HER2 subtypes but graduated in the HR-HER2+ signature. Exploratory analysis of protein signaling was performed to identify biomarker candidates correlated with pCR in the TN population. We evaluated 110 key signaling proteins using reverse phase protein microarray (RPPA) data from pre-treatment LCM purified tumor epithelium.

Methods: Of 59 TN patients, 49 (N: 30, concurrent controls: 19) had RPPA and pCR data. RPPA data was correlated to pCR in both the treated and untreated patients using parametric (t-test) or non-parametric (Wilcoxon) statistical analysis, depending on data distribution. Only analytes whose levels were associated with response in the N but not the control arm were selected for further analysis. Markers are analyzed individually; p-values are descriptive and were not corrected for multiple comparisons. ROC analysis identified an optimal cut point and pCR rates of biomarker positive patients were assessed using that cut point.

Results: Out of 110 analytes analyzed, only activation of HER2 Y1248, p=0.03; EGFR Y1173, p=0.009; were found to be positive predictors of pCR, and 3 proteins, TIE2 Y992, p=0.02; LC3B, p=0.02, and A-RAF S299, p=0.0008, were found to be negative predictors of pCR. pCR rates in the biomarker positive group of 62.5% (10/16), 66% (11/16), 55%(10/18), 67% (12/17). 61% (11/18) were determined for phospho-HER2, EGFR, TIE2, A-RAF and total LC3B, respectively, compared to a pCR rate of 40% for the IHC/FISH-based TN subgroup where RPPA data were available.

Conclusion: Our sample size is too small to draw definitive conclusions. However, activation of HER2-EGFR in HER2- tumors may identify patients who respond to N. Low levels of activated A-RAF and LC3B also correlated with response. The results imply that there is a subset TN patients that paradoxically exhibit HER family signaling activation and may achieve clinical benefit with N. These findings merit future consideration as we develop trials for patients with suboptimal response to neoadjuvant therapy where biomarkers could be used as the basis for treatment reassignment.
Keywords: triple-negative breast cancer, estrogen receptor, biomarkers, reverse-phase protein microarray

Abstract: Background: We have previously described that TNBC patients whose tumors have both HER2 Y1248 phosphorylation (pHER2) "high" and phospho-EGFR Y1173 (pEGFR) "high" have increased response (pCR) to neratinib in the I-SPY2 TRIAL. We hypothesize that the paradoxical finding of a response prediction signature comprised of HER2 activation in a HER2 IHC/FISH-negative population means there must be a ligand-driven biochemical event responsible for the HER2 phosphorylation because HER2 mutations were also not found to be significant. Exploratory analysis of additional cellular signaling events and protein expression levels in pre-treatment, LCM-purified tumor epithelium by reverse phase protein microarray (RPPA) included semi-quantitative measurement of total levels of estrogen receptor alpha (ERα), which has been previously shown to be able to act as a membrane non-genomic signaling molecule through direct interaction with various tyrosine kinases including EGFR and HER2. Since ERα has been previously shown to act as a ligand and co-stimulate (activate) HER2 and EGFR when present at low levels, we investigated whether or not RPPA measured ERα levels in the TNBC cohort analyzed to date were higher in tumors with both pHER2 "high" and pEGFR "high" levels and thus provide evidence explaining how HER2-EGFR activation is occurring in TNBC.

Methods: Using RPPA analysis, we measured 118 analytes in lysates of LCM tumor epithelium obtained from the pre-treatment biopsy samples of all 86 TNBC (Allred=0) patients in the I-SPY2 TRIAL analyzed to date. Cutpoints for pEGFR and pHER2 were determined previously by ROC analysis for pCR correlation in the neratinib treated TNBC population, and used here to dichotomize the pH2R and pEGFR data in the larger TNBC population. Wilcoxon Rank Sum testing was performed using the continuous variable total ERα data and comparing the TNBC that were both pHER2 and pEGFR "high" (N=39) to the rest of the TNBC population (N=47). Total ERα values were then divided into "high" and "low" groups based on the TNBC population median value in order to determine frequency/percentages within each class. Our study is exploratory with no claims for generalizability of the data, and calculations are descriptive (e.g. p-values are measures of distance with no inferential content).

Results: Total ERα values were obtained in 84/86 TNBC tumors analyzed. Total levels of ERα were higher (p< 0.006) in TNBC tumors with pHER2 and pEGFR "high" levels. 68% (26/38) of tumors in the pHER2 and pEGFR "high" group had ERα levels above the population median compared to 35% (16/46) in the rest of the TNBC population.

Conclusion: Our exploratory analysis reveals that ERα levels are significantly higher in TNBC with pHER2 and pEGFR activation and may be behaving as a direct signaling ligand in TNBC and driving HER2-EGFR signaling. This ERα-pHER2/pEGFR association was missed by current ER and HER2 clinical laboratory testing techniques, and if validated in larger independent study sets could suggest that utilization of new protein-based techniques defining ER more quantitatively could be helpful to understand tumor biology and therapeutic response prediction especially in the context of TNBC that are ostensibly ER negative.
Title: Detection of Epithelial-to-Mesenchymal Transition in Breast Cancer Cells using Endoplasmic Reticulum Stress.

Abstract: Epithelial-to-mesenchymal transition (EMT) is a complex remodeling of cell signaling pathways that activates metastatic abilities in cancer cells. Detection of EMT is essential for evaluation and management of cancer progression in patients. EMT is commonly detected using cell morphology changes and EMT markers expression, however, real-time detection of EMT in live cells is challenging. Endoplasmic reticulum (ER) stress is due to accumulation of unfolded proteins in the ER lumen, and has been related to EMT in cancer. Here, we describe the previously unknown role of ER stress in EMT in breast cancer cells, and evaluate the use of ER stress as an indicator of EMT. We have observed that induction of EMT in mammary cell lines using TGF-β1 is accompanied by a transient increase of ER stress, as measured by immunostaining of GRP78 marker. Surprisingly, specific inhibition of ER stress using 4-PBA during EMT induction does not affect early EMT marker ZEB1, however, it completely blocks the induction of late EMT markers E-cadherin and Vimentin. Considering the essential role of ER stress in EMT in mammary cells, we hypothesized that measuring the transient ER stress increase after TGF-β1 treatment would be a good indicator of EMT. Thioflavin T (ThT) is an inexpensive fluorescent compound capable of quantitatively detecting ER stress in live cells. We observed that ThT can be used conveniently to detect the transient increase of ER stress during EMT in live breast cancer cells at the single cell level. We expect that this new inexpensive and easy-to-use EMT detection method will help the investigation of EMT in breast cancer, in laboratory and clinical settings.

Title: Effects of Locomotor Training on VO2 ON-Kinetics in Persons with Incomplete Spinal Cord Injury

Abstract: Background: Incomplete spinal cord injury (iSCI) may result in gait abnormalities and prolonged oxygen uptake transitions at the onset of walking (VO2 on-kinetics). Locomotor training (LT) has been shown to improve gait performance in some individuals with iSCI but the effect of LT on the associated VO2 on-kinetics is not understood. Purpose: This pilot study investigated the effects of 15-weeks of LT on VO2 on-kinetics in adults with iSCI. We hypothesized that LT, when performed solely under volitional control and full-weight bearing, would speed VO2 on-kinetics. Methods: Three adult males with iSCI (age: 25.3±8.7 yrs; BMI: 24.0±5.7 kg/m2) completed 15-weeks of task-specific LT (two 90 minute sessions per week) which consisted of structured routines and movement drills based on components of the gait cycle. Each participant performed a 6-minute constant work-rate treadmill test at a self-selected walking speed prior to and immediately following the 15-week LT regimen. VO2 on-kinetics was determined using a mono-exponential model in which a time constant (t) was calculated during phase 2 of the biphasic kinetic response and amplitude (AMP) was measured at the end of 6 minutes of walking. The transition constant (Kt) was calculated as the AMP/t ratio. Heart rate (HR) was monitored using an electrocardiogram and averaged over the last 30-seconds of the exercise bout. Effect size was calculated using Cohen’s d (d). Results: After LT, faster VO2 on-kinetics was observed (pre: 33±7s; post: 25±7s; d=1.14), with smaller AMP (490±32 ml/min; post: 430±52 ml/min; d=1.39) and end-exercise HR response (pre: 113±6 bpm; post: 106±10 bpm; d=0.85). An increase in Kt (pre: 15.5±4.9 ml/min/sec; post: 18.1±4.3 ml/min/sec; d=0.56) was also noted. Conclusion: Completion of the LT program appeared to result in an improvement in VO2 on-kinetics during treadmill walking in these subjects with iSCI. After LT, t appeared to be similar to that typically observed in non-injured individuals during self-selected walking.

Title: Effects of a Novel Overground Locomotor Training on Muscle Oxygen Extraction in Individuals with Incomplete Spinal Cord Injury

Abstract: Background: Incomplete spinal cord injury (iSCI) may result in gait abnormalities and prolonged oxygen uptake transitions at the onset of walking (VO2 on-kinetics). Locomotor training (LT) has been shown to improve gait performance in some individuals with iSCI but the effect of LT on the associated VO2 on-kinetics is not understood. Purpose: This pilot study investigated the effects of 15-weeks of LT on VO2 on-kinetics in adults with iSCI. We hypothesized that LT, when performed solely under volitional control and full-weight bearing, would speed VO2 on-kinetics. Methods: Three adult males with iSCI (age: 25.3±8.7 yrs; BMI: 24.0±5.7 kg/m2) completed 15-weeks of task-specific LT (two 90 minute sessions per week) which consisted of structured routines and movement drills based on components of the gait cycle. Each participant performed a 6-minute constant work-rate treadmill test at a self-selected walking speed prior to and immediately following the 15-week LT regimen. VO2 on-kinetics was determined using a mono-exponential model in which a time constant (t) was calculated during phase 2 of the biphasic kinetic response and amplitude (AMP) was measured at the end of 6 minutes of walking. The transition constant (Kt) was calculated as the AMP/t ratio. Heart rate (HR) was monitored using an electrocardiogram and averaged over the last 30-seconds of the exercise bout. Effect size was calculated using Cohen’s d (d). Results: After LT, faster VO2 on-kinetics was observed (pre: 33±7s; post: 25±7s; d=1.14), with smaller AMP (490±32 ml/min; post: 430±52 ml/min; d=1.39) and end-exercise HR response (pre: 113±6 bpm; post: 106±10 bpm; d=0.85). An increase in Kt (pre: 15.5±4.9 ml/min/sec; post: 18.1±4.3 ml/min/sec; d=0.56) was also noted. Conclusion: Completion of the LT program appeared to result in an improvement in VO2 on-kinetics during treadmill walking in these subjects with iSCI. After LT, t appeared to be similar to that typically observed in non-injured individuals during self-selected walking.
Keywords: locomotor training; spinal cord injury; cardiorespiratory fitness

Abstract: Background: Locomotor training aims to enhance walking performance through practicing the activity of walking. Near-infrared spectroscopy (NIRS) has shown a reduction in skeletal muscle oxidative capacity following spinal cord injury. The reduction in skeletal muscle oxidative capacity following spinal cord injury is likely to contribute to poor work economy during walking. Given the involvement of the cardiorespiratory system during walking, locomotor training may provide an effective way to improve skeletal muscle bioenergetics.

Purpose: The purpose of this pilot study was to determine the effects of a novel overground locomotor training (OLT) program on muscle oxygen extraction in incomplete spinal cord injury (iSCI). It was hypothesized that OLT would improve gastrocnemius muscle oxygen.

Participants: Small convenience sample of ambulatory male adults with chronic cervical incomplete spinal cord injury (n=3; mean age, 21±3 years).

Methods: Constant work-rate (CWR) testing was completed on a treadmill before and following training. Each participant performed the CWR testing under volitional control and bearing full-weight. The CWR test included walking at a self-selected speed for a duration of 6-minutes from a standing rest position. Muscle oxygenation was measured by NIRS during the CWR. The tissue saturation index (TSI) and concentration changes in oxygenated [O2Hb], deoxygenated [HHb], and total [Hb] hemoglobin were measured using near-infrared spectroscopy (NIRS). The OLT intervention was structured using a part-whole practice paradigm and based on motor learning theory while incorporating principles of adaptation (i.e. progressive overload, task-specificity, movement variation). Changes in tissue saturation index (ΔTSI) were determined during reperfusion following total arterial occlusion of the gastrocnemius muscle. Concentration changes in total hemoglobin (ΔtHb)) and deoxygenated hemoglobin (ΔHHb)) during constant work rate exercise were measured before and following training. Concentration changes in ΔtHb) and ΔHHb) were normalized to changes in maximal capacity as assessed during ischemia and expressed as a percentage.

Results: Overall effect sizes were calculated using Cohen’s d (d). Training appeared to increase ΔTSI (pre 38±8.3% vs post 52±23.8%, d=0.76) and decrease normalized changes in ΔtHb) and Δ[HHb] (ΔtHb) pre 24±5.1% vs post 18±3.1%, d=1.42 and Δ[HHb] pre 49±14.5% vs post 41±7.6%, d=0.75).

Conclusions: Greater capacity for oxygen extraction was observed following this novel OLT program. The decrease in normalized ΔtHb) and Δ[HHb] suggests oxygen extraction was lower for the same exercise work bout following training and that OLT may have improved overall work economy.

Keywords: locomotor training; spinal cord injury; cardiorespiratory fitness

Abstract: Background: Exercise hyperpnea transitions toward a steady state through a feed-forward coupling of locomotor activation and a cortical irradiation pathway, which occurs prior to blood metabolite stimulation of the respiratory center. During a constant work rate (CWR) the transition curve is characterized by a sudden exponential rise in Phase I and II expired minute ventilation (VE) resolving in a Phase III steady state. However, in adults with incomplete spinal cord injuries (iSCI) efferent and afferent neural coupling is often impaired, potentially altering ventilatory control.

Purpose: This study aimed to characterize exercise hyperpnea during a rest to CWR transition and the effects of 15 weeks of task-specific locomotor training (LT) on CWR hyperpnea. Participants: Subjects were 4 adult males with iSCI (age 24.75±7.80 yrs; BMI 20.4±5.1 kg-m2) and 1 adult female (age 67) with C4-C6 lesions capable of step initiation and independent standing.

Methods: LT principles included: task specificity, practice variability, and progressive overload. Individual sessions included 5 segments: joint mobility, volitional muscle activation, task-isolation, task-integration, activity rehearsal. Training occurred 2x/week for 90 minutes focusing on developing walking efficiency through mastering the specific components of the gait cycle. All activities were weight-bearing and under volitional control. Assistance was only given when needed to ensure safety. Six minutes of CWR treadmill walking was performed before and after the LT at self-selected pace (0.5 or 0.7mph), with pulmonary gas analysis throughout the tests. VE line of best fit was predicted with linear regression and compared to actual VE observed (VEOBS - VEPred=VE variability), with VE variability assessed via an f-statistic.

Results: Suitability of linear regression was checked through visual inspection of CWR VE data. Prediction error variability decreased on average by 45.7% (p<0.001) after LT in 4 of 5 participants.

Conclusion: CWR VE from rest to work was linear throughout the transition with no phase III plateau. A significant level of VE variability was observed before LT. In 4 of the 5 participants, VE variability was reduced by 45.7% after 15 weeks of LT. In these subjects with iSCI, it appears 15 weeks of LT improves exercise hyperpnea by reducing the variability in VE.
Abstract:
It is reported that approximately 12 million people have a cerebral aneurysm in the U.S. [1]. Of this number, 3%-5% have an unruptured, asymptomatic intracranial aneurysm that they may or may not know about. In 50 people will experience a rupture, which may occur with or without obvious symptoms, equating to a rupture risk of less than 0.1% annually [2] [3]. While many risk factors for the development or rupture of a cerebral aneurysm have been identified (size, location, family history, smoking, etc.), it is difficult to assess individual risk and patients do not always understand how their instance compares to other similar cases. Currently, in the medical field, there is a lack of visual tools that would allow an individual to compare their aneurysm to others in the context of an affected patient population in both a comprehensive and meaningful manner. To combat this issue, Mapeurysm, a web application using PHP, JavaScript, and HTML, was developed. Using this application, patients can compare their cerebral aneurysm to a database of patients through statistics and visualization, manipulate a generic 3D-model of the cerebral arteries, and better understand the associated risks/dangers of their condition through comparison to known cases collected. With cross-platform capability, patients can view this information anywhere with internet connection. Mapeurysm provides patients with an intuitive visual model using a generic model with case comparison and associated statistics, allowing patients to explore their condition and facilitate communication with their clinician.

References:

Presenter(s): Hussain, Samanza, Undergraduate Student; Ms. Jenny Fotang, Undergraduate Student; Ms. Farishta Boura, Postbaccalaureate Student; Ms. Cassandra Leong, Masters Student; Mr. Rithik Binoy, Undergraduate Student; Ms. Rochelle Hopwood

Title: Activity-dependent postsynaptic signaling in hippocampal neurons is altered by transgenic expression of chimeric NMDA receptor GluN2 subunits

Abstract:
N-methyl-D-aspartate receptors (NMDARs) at excitatory synapses in the hippocampus are central players in the synaptic plasticity required for learning and memory. Two predominant signaling properties of NMDARs that have been independently linked to hippocampal plasticity are calcium conductance into the postsynaptic spine and direct intracellular protein interactions. These properties vary with the composition of the NMDAR such that, compared to NMDARs with GluN2A subunits, NMDARs with GluN2B subunits conduct calcium for a longer period after activation and display greater affinity for the obligatory synaptic plasticity protein, CaMKII. Thus, it is not possible to determine the separate influences of these NMDAR properties by switching the entire GluN2 subunit. To overcome this obstacle, GluN2 chimeras have been created and engineered into transgenic mice. While changes synaptic plasticity and behavior have been documented in these animals, direct measurement of intracellular signaling has not been performed. We generated two transgenic mouse lines, one having the amino (A)-terminus and transmembrane domains (TMDs) of GluN2A fused to the carboxy (C)-terminus of GluN2B (termed ABc) and, vice versa, the other line having the A-terminus and TMDs of GluN2B fused to the C-terminus of GluN2A (termed BAc). These chimeric GluN2 subunits were expressed in transgenic mice using the tet-off expression system with tetracycline transactivator protein (tTA) expression under transcriptional control of the CaMKII minimal promoter. tTA expression was seen in many forebrain regions, but predominantly in hippocampal pyramidal cells. To induce synaptic plasticity in the hippocampus, animals were briefly exposed to a Y-maze in a novel testing environment. We quantified intracellular signaling through immunohistochemistry and analysis of expression level and colocalization of plasticity-related proteins. Pairs of antibodies were applied (anti-pCaMKII and anti-CaMKII or anti-PSD95 and anti-calmodulin). Currently, we observe an increase in the PSD95 signal and an increase in the PSD95 to calmodulin ratio in maze-exposed animals compared to naive controls. Also, while the number of samples is low, we see no effect of maze or genotype on pCaMKII or CaMKII. These experiments will reveal which functional property of NMDARs is altered to the greatest extent in mice expressing chimeric GluN2 subunits. Findings from this study will begin to clarify how NMDARs regulate synaptic plasticity and learning and memory.
Presenter(s): Kassinger, Stephen, ; Monique van Hoek
Title: Colistin resistance in Gram-negative bacteria.
Poster Location Number: 20
Keywords: Antibacterial, Bacteria
Abstract: The discovery of penicillin ushered in a remarkable two decades where previously untreatable infection were cured with relative ease. Over time it became clear that bacteria can and do evolve to become resistant to antibiotics. Currently, an important antibiotic of last resort, colistin, is a cyclic polypeptide antibiotic of the polymyxin family, specifically polymyxin E. In addition, another polymyxin (polymyxin B) is commonly used in topical antibiotic creams in a Triple Antibiotic formulation with bacitracin and neomycin. Unfortunately, clinically important gram-negative bacterial pathogens such as Klebsiella pneumoniae, Pseudomonas aeruginosa, and Acinetobacter baumannii have developed mechanisms of surviving polymyxin treatment, thus acquiring functional resistance to polymyxins. Francisella novicida a gram-negative model organism for the respiratory pathogen Francisella tularensis. Francisella has the ability to grow in media with 100 μg/ml polymyxin B, thus this organism is highly resistant to polymyxin B. It is reported that Francisella is also resistant to colistin (polymyxin E). Sensitivity to polymyxin E, in the form of Colistin sulfate, would be advantageous as this polypeptide antibiotic is approved for clinical use and has increased shelf-stability compared to polymyxin B. We tested many Francisella strains for their resistance to polymyxins B and E by determining the MIC under CLSI conditions and the time-kill curves to each polymyxin. Preliminary data suggests that some strains of Francisella have MIC>800 μg/ml for polymyxin B. We sought to understand the mechanism of polymyxin resistance in Francisella as a model for understanding gram-negative polymyxin resistance. The literature proposes multiple “polymyxin resistance genes” in various bacteria such as plasmid mcr-1 (phosphoethanolamine transferase) and OmpA (Outer membrane protein) in Acinetobacter baumannii. In Francisella, lpxD is involved in LPS acetylation and is reported to contribute to polymyxin B resistance. We tested Francisella mutants in many of the proposed “polymyxin resistance genes” for their sensitivity to polymyxins B and E by determining the MIC under CLSI conditions. We also tested whether spontaneous resistance appears in a polymyxin-sensitive strain upon repeated exposure to sub-MIC concentrations of polymyxin. This work will contribute to our understanding of the mechanism of polymyxin resistance in important gram-negative bacteria, especially multi-drug resistant bacteria, and may enable the development of new polypeptide antibiotics that are not subject to such resistance.

Presenter(s): Keith, Rachel, ; Matthew Keith
Title: Neuromorphological characterization of CA1 pyramidal cells in transgenic mice expressing chimeric NMDAR GluN2 subunits
Poster Location Number: 34
Keywords: CA1, Calcium Channel, CaMKII, Cognition, Cognitive, Cytoarchitecture, Dendrite, Dendrite Spines, Fluorescence, Forebrain, Gene, Gene Expression, Genetics, GluR1, GluR2, Glutamate, Glutamate Receptor, Glutamate release, Green fluorescent protein, Hippocamp
Abstract: Neural network assembly and memory formation in the central nervous system requires N-methyl-D-aspartate receptor (NMDAR) activation and persistent functional changes at glutamatergic synapses. In the mouse hippocampus, synapses continue to develop until the end of the third postnatal week, when spatial-based navigation first becomes apparent, supporting a link between the maturation of synaptic plasticity and spatial cognition. Prior to 3 weeks of age, synaptic NMDARs containing GluN2B subunits are replaced by NMDARs containing GluN2A subunits, yielding faster channel deactivation and modified intracellular signaling with increasing age. This subunit switch permits the pruning of immature excitatory synapses and the final maturation of the remaining stable synapses. Conductance regulating domains exist in the GluN2 extracellular amino (A)-terminus and transmembrane (TM) regions. Intracellular signaling domains exist in the intracellular carboxy (C) terminus. To separately examine the influence of conductance or intracellular signaling on hippocampal development, we generated two transgenic mouse lines expressing chimeric NR2 subunits having the A-terminus and TM regions of GluN2A or GluN2B fused to the C-terminus of GluN2B or GluN2A, respectively (termed ABC and BAc). These chimeric GluN2 subunits were expressed predominantly in hippocampal pyramidal cells. To examine how these genetic changes alter neuromorphological characteristics, we utilized both Golgi-Cox staining methods and Thy-1 GFP fluorescence and measured dendritic branching, the length of apical and basal dendrites, spine density, branching intervals, and terminal distances. The data indicate that ABC animals have greater spine density and more dendritic branching than BAc and WT animals, which suggest stalled development due to the greater presence of the GluN2B C-terminus. These findings advance understanding of how NMDARs regulate dendritic development by better defining the region of the GluN2B subunit that restrains hippocampal development. Further, glutamate signaling has been implicated in a wide variety of developmental disorders, such as autism and related disorders (Fragile X syndrome) and schizophrenia. By examining signaling aspects of the NMDA receptor individually with this mouse
Osteoarthritis is the most common form of arthritis and is characterized by degenerative changes in articular cartilage, bone, and associated joint tissues. Post-traumatic arthritis (PTA) is one of the etiologic subtypes of osteoarthritis, which is derived from a physical injury that leads to a change in joint mechanics. Health care costs for PTA is $7 billion annually. Therefore, there is an urgent need to develop novel therapeutic approaches for PTA post joint injury. Herein, we present our strategy for the design and synthesis of small molecule inhibitors of the heterotrimer complex formation of interleukin-1β, interleukin-1 receptor type 1, and interleukin-1 receptor accessory protein as lead compounds for the treatment of osteoarthritis.

Presenter(s): Khan, Daud, PhD Student; Nitin Agrawal, Assistant Professor
Title: Rapid Generation and Simultaneous Detection of Biomimetic Oxygen Concentration Gradients in vitro
Poster Location Number: 54
Keywords: Oxygen Concentration gradient, biomimetic, hypoxia, 3-sided coating
Abstract: Introduction: Internal oxygen concentration gradients (OCGs) regulate cellular differentiation and signaling processes. Hypoxia is a critical factor in the induction of drug resistance and angiogenesis in cancer cells. Traditionally, specialized culture chambers (e.g. O2 incubators) are utilized to maintain desired oxygen concentrations. Although convenient, such systems are only suitable for studying cellular responses at singular oxygen tensions and significantly vary from physiological conditions, where gradients of dissolved oxygen usually exist within the tissues. Advanced microfluidic devices have been made to generate OCGs in vitro, but provide only restricted spatial resolution and normally involve complex and tedious assembly. We have developed a novel and simplistic approach of reproducibly and rapidly generating stable biomimetic OCGs with high spatial resolution inside a single-compartmental microfluidic device. Passive diffusion of oxygen is achieved without the use of either gas inlets or chemical quenchers via the introduction and mixing of O2-rich (OR) and O2-depleted (OD) media within the channels.
Method: A 3-sided glass-like coating throughout the microchannels prevents multidirectional diffusion of oxygen through the PDMS substrate, thereby inhibiting possible media evaporation and facilitating the rapid production of the OCGs. Simultaneous real-time detection of DO is made possible by a layer of platinum(ii)octaethylporphyrin ketone embedded in a polystyrene matrix (PtOEPK/PS) below. A thin PDMS membrane separates the sensor-layer from the channels, preventing leeching of the dye. Computational modelling using COMSOL Multiphysics 3.5 was initially used to verify OCG formation. Characterization were performed to optimize glass thickness and calibrated to verify Stern-Volmer behavior. To test the dynamic sensing ability of the device, gaseous nitrogen and oxygen was blown into the channels periodically. Potential application of the developed approach was validated via the viability analysis of MCF-12A (immortalized epithelial breast cell-line) cells.
Results and Discussion: Heating at 800°C for 60s produced an optimal glass coating (5.68 ± 1.89 µm) throughout the device. Compared to the uncoated channels, the three-sided coated devices exhibited both superior dynamic oxygen sensing ability and linear Stern-Volmer relationship. Passive diffusive of OR and OR media yielded OCGs with high spatial and temporal resolution, which were sustained over long time periods and at various flow rates. Viability analysis of the MCF-12A cells revealed a negative correlation with hypoxia. Cell mortality increased from 0% in normal conditions to approximately 80% in hypoxic conditions (0% O2) over an 8 hour incubations period.
Conclusions: This is the first study to properly establish a means of generating and simultaneously detecting stable biomimetic OCGs in vitro. The viability analysis provided further proof-of-concept, allowing a plethora of potential studies that can be conducted in the new platform, such as migration of cells in hypoxic niches.
Acknowledgements: Funding for this project was provided by the National Science Foundation (NSF).

Presenter(s): Kim, Kyu Ah, PhD Student; Angela Dailing (Ph. D student), Lance Liotta (Professor), Alessandra Luchini (Professor), Mikell Paige (Professor)
Title: Design and Synthesis of Small Molecule Inhibitors of Interleukin-1β for the Treatment of Osteoarthritis
Poster Location Number: 55
Keywords: Osteoarthritis, inflammation, protein-protein interaction inhibition, drug design and synthesis
Abstract: Osteoarthritis is the most common form of arthritis and is characterized by degenerative changes in articular cartilage, bone, and associated joint tissues. Post-traumatic arthritis (PTA) is one of the etiologic subtypes of osteoarthritis, which is derived from a physical injury that leads to a change in joint mechanics. Health care costs for PTA is $7 billion annually. Therefore, there is an urgent need to develop novel therapeutic approaches for PTA post joint injury. Herein, we present our strategy for the design and synthesis of small molecule inhibitors of the heterotrimer complex formation of interleukin-1β, interleukin-1 receptor type 1, and interleukin-1 receptor accessory protein as lead compounds for the treatment of osteoarthritis.

Presenter(s): Krall, Jenna R., Assistant Professor; NA
Title: Estimating sources of air pollution and their impact on human health
Poster Location Number: 10
Keywords: source apportionment; pulmonary health; air pollution; traffic pollution; epidemiology; on-road exposures

Abstract: Exposure to particulate matter (PM) air pollution has been associated with increased mortality and morbidity. PM is a complex chemical mixture, and associations between PM and health vary by its chemical composition. Identifying which sources of PM, such as motor vehicles or wildfires, emit the most toxic pollution can lead to a better understanding of how PM impacts health. However, exposure to source-specific PM is not directly observed and must be estimated from PM chemical component data. Source apportionment models aim to estimate source-specific concentrations of PM and the chemical composition of PM emitted by each source. Using data from the Atlanta Commuters Exposure Studies, we estimate associations between source-specific air pollution and pulmonary response among commuters in Atlanta, GA. We found associations between secondary and crustal pollution and lung function among asthmatic commuters. We also found associations between non-tailpipe traffic pollution, such as brake wear and tire wear, and pulmonary response among non-asthmatic commuters. This study demonstrates that (1) health effects associated with air pollution exposure vary by source; (2) sources of traffic pollution can be differentiated using source apportionment models; and (3) some sources, such as brake wear, cannot be individually separated using source apportionment alone from other, correlated sources. Future work will aim to incorporate other data, such as ambient pollution monitoring data, to improve source estimates and their corresponding estimated health effects. This work indicates that sources of air pollution other than tailpipe emissions impact the health of commuters.

Presenter(s): Lee, Yi-Ching, Assistant Professor
Title: Diagnostic Driving: Real Time Driver Condition Detection Through Analysis of Driving Behavior
Poster Location Number: 11

Keywords: Informatics, human factors, driving, medical conditions, ADHD, machine learning

Abstract: The long-term goal of this research is to leverage the large amounts of health data that can be collected while driving via machine learning and context-based reasoning. Specifically, the project aims to improve the ability to monitor a medical condition, Attention-Deficit/Hyperactivity disorder (ADHD) in teenagers and young adults, and to provide preventive care via systematic monitoring of symptoms and disrupted medications. Symptoms of ADHD when uncontrolled have the potential to impact health and quality of life including motor vehicle crashes, poor academic and work performance, failed relationships, substance abuse, violence, and criminality. ADHD medication can reduce crash and injury risk among men with ADHD: injuries were 58% less likely when on-medication compared with when off. Unfortunately, a minority of drivers with ADHD are prescribed medication and among those, adherence is a continued challenge, and some may drive outside the window of time when the medications are effective. We propose to develop and test a new machine-learning-based in-vehicle behavior analysis system to automatically monitor and detect uncontrolled ADHD through the detection of unsafe driving behaviors.

Presenter(s): Lerch, Jennifer, Research Associate; Alexander Dorman, Researcher; Scott T. Walters, Professor and Chair; Faye S Taxman, Ph.D., University Professor
Title: A cross-sectional examination of criminal justice risk, multi-morbidities and determinants of health among probationers
Poster Location Number: 45

Keywords: health determinants, probation, community supervision, criminal justice risk, multi-morbidities

Abstract: This study evolves from a computerized intervention to motivate people to change. Individuals involved in the criminal justice system tend to be in worse health than the general population. These health disparities exist among multiple types of morbidities (i.e., mental health, physical health, substance abuse), as well as other determinants of health (e.g., social status, housing). Previous research with criminal justice populations has largely been limited to examining the presence of single and co-occurring morbidities, not multi-morbidities (i.e., three or more), primarily among incarcerated populations, and scarcely explores the connection of either health morbidities or determinants of health with criminal justice risk. This paper explores how single, co- and multi-morbidities and determinants of health are associated with criminal justice risk among a probation population. We found that several health disparities were related to increased odds of being high risk. Individuals with three morbidities were about three times more likely than those without any morbidities to be high risk. Individuals with lower social status, prior substance abuse treatment history, and a court-order to attend substance abuse treatment were more likely to be high risk. Furthermore, those who were current smokers, males, and older individuals were more likely to be high risk. These findings demonstrate the need for further exploration of the potential causal links between involvement in the criminal justice and health disparities. Criminal justice involvement can potentially serve as a risk factor for poorer health.
outcomes. Further understanding of this relationship can help guide criminal justice agencies to adjust policies and practices to better mitigate these risks.

Presenter(s): Leslie, Timothy, Associate Professor; Cara Frankenfeld, PhD, Associate Professor
Title: County-level socioeconomic factors and residential racial, Hispanic, poverty, and unemployment segregation associated with drug overdose deaths in the United States, 2010-2015
Poster Location Number: 13
Keywords: health, geography, social determinants
Abstract: Background: Drug overdose deaths are a critical public health concern and exhibit considerable spatial variation. The objective was to evaluate county-level drug overdose death rates in relation to socioeconomic characteristics and measures of socioeconomic residential segregation.
Methods: Overdose deaths were linked to county-level data for socioeconomic characteristics, religious adherence, and 2012 presidential voting preference. Dissimilarity and isolation segregation measures (comparing individual counties to the adjacent counties and state) and diversity were calculated for race, Hispanic, poverty, and unemployment. Ordinal logistic regression was used to compare county characteristics to quintiles of total overdose death rate, and quartiles of white, black, and Hispanic rates.
Results: Diversity and county-to-state level dissimilarity for race, Hispanic, poverty, and unemployment were positively, and isolation were inversely, associated with total overdose death rates. Associations magnitude and direction varied across total, white, black, and Hispanic overdose death rates, with dissimilarity and isolation being more similar across white and black rates than Hispanic rates; whereas, measures of diversity associations being more similar across black and Hispanic rates than white rates.
Conclusion: Residential segregation and socioeconomic characteristics have independent and race/ethnic-specific associations with overdose death rates. These results suggest that residential segregation may exert independent effects on health outcomes beyond county socioeconomic characteristics, and effects differ across race and ethnic groups.

Presenter(s): Leslie, Timothy, Associate Professor, Department of Geography and Geoinformation Science; Paul L. Delamater, Assistant Professor, Department of Geography and Geoinformation Science; Kathryn H. Jacobsen, Professor, Department of Global and Community Health; Y. Tony Yang, Associate Professor, Department of Health Administration and Policy; Erica
Title: Vaccine-preventable disease outbreaks and community-level vaccination coverage
Poster Location Number: 14
Keywords: Vaccines, Vaccination, Disease, Public health, Geography, GIS
Abstract: This research project examined the relationships among vaccination coverage, herd immunity, and risk of vaccine-preventable infectious disease outbreaks. Childhood vaccination programs have been one of the most successful public health interventions, saving countless lives worldwide. Despite the demonstrated success of vaccination programs, concerns over vaccine safety have led to increases in refusal and/or delay of vaccination in many places throughout the US. In the United States, 48 of 51 jurisdictions (50 states and Washington DC) allow non-medical exemptions (NMEs) from childhood vaccination requirements based on personal or philosophical grounds or religious beliefs. Vaccine- and exemption-related behavior has been shown to be highly spatially variable at local scales within states or larger geographic regions. Importantly, when a community has a high rate of vaccine coverage, they achieve the “herd immunity” effect, shielding susceptible members of the population from contracting vaccine-preventable diseases (VPDs) via a decreased likelihood of a transmission occurring between infectious and susceptible individuals. In some regions, the increased use of NMEs has yielded dangerously low levels of vaccination coverage, which has compromised herd immunity and resulted in vaccine-preventable disease outbreaks.
We report the results from research supported by a 2015-16 GMU Provost Multidisciplinary Research Initiatives Grant. The first study presents an approach to estimate community-level vaccination coverage, using school-level data and integrating population mobility information. A case study from California is presented, which demonstrates the high spatial variation in vaccination coverage throughout the state, including many regions where herd immunity is threatened. The second study details and explains eight common misconceptions regarding the basic reproduction number (R0), an epidemiological metric commonly used to calculate the herd immunity threshold and to define disease transmissibility. The third study examines the availability childhood vaccination data for all US states, finding that both the level of spatial aggregation and characteristics provided are highly variable, impeding cross-state research regarding vaccine- and exemption-related behavior. The final study presented asks the question, “who is the herd in herd immunity?” and evaluates how the identification of at-risk populations can vary depending on how the populations are grouped into herds. The results show that the potentially at-risk population
Inhibitors constitute the starting point for a new class of small molecule inhibitors for cancer immunotherapy. Molecules that block the interaction in molecular and immune recognition cellular assays. We have used protein painting to identify hot spots of interaction at the interface and we have made candidates for blocking the tumor cell. Thus a critical strategy for cancer immunotherapy is to block by displaying PD-1R with the anti-inflammatory effects of the novel inhibitors will be tested in vivo, in a well-established equine model of osteoarthritis. Furthermore, we will analyze joint fluid inflammatory markers (IL-1β, IL-33, PGE2, TNF-α, IL-6, IL-10, IL-1ra and TSG-6) in human patients with osteoarthritis to determine the baseline value for future response monitoring.

Protein Painting is also revealing new treatment strategies for cancer immunotherapy. Tumor cells evade immune recognition by displaying PD-L1 on their surface. PD-L1 binds to a receptor, PD-1, on immune cells and suppresses the immune cell from killing the tumor cell. Thus a critical strategy for cancer immunotherapy is to block the interaction of PD-L1 with PD-1 on the cell surface. We have used protein painting to identify hot spots of interaction at the interface and we have made candidate molecules that block the interaction in molecular and in immune recognition cellular assay. Protein painting data and the novel inhibitors constitute the starting point for a new class of small molecule inhibitors for cancer immunotherapy.
Title: **Nanotrap-enhanced mass spectrometry: direct detection of pathogen antigens in body fluids of animal models and human patients affected by tick borne diseases**

Keywords: Hydrogel nanoparticles, Nanotrap, Lyme disease, Tick-borne diseases

Abstract:Ixodes ticks can harbor multiple pathogens that can be simultaneously transmitted to humans by a single tick bite. Lyme disease (LD) is the most common tick-borne infection worldwide, but other diseases have been increasingly reported. Co-infections are often associated with stronger and prolonged symptoms and the diagnosis is often challenging. LD diagnosis is currently based on clinical detection of erythema migrans (EM) coupled with serological testing. Babesiosis is diagnosed by the identification of Babesia microti in blood smears coupled with serological testing. Anaplasma phagocytophilum is detected through blood smears examination and PCR. Unfortunately these tests often lack sensitivity and specificity and no reliable direct antigen test is available.

An antigen test for the simultaneous detection of proteins of tick-borne pathogens would be ideal. Unfortunately, pathogen antigens, because of their low concentration, lability, and presence of resident, high abundant proteins, are below the detection limit of mass-spectrometry and clinical grade immunoassays. In order to overcome these physiological and technical barriers, we employed the Nanotraps, a nanotechnology based concentration and preservation method. Nanotraps are polymeric networks functionalized with affinity reactive baits that are able in one step to capture, concentrate and preserve disease antigens in body fluids.

In this study we optimized a protocol for the capture and concentration of tick-borne pathogen antigens in red blood cells, plasma and urine using Nanotrap enhanced mass spectrometry analysis. Detection sensitivity was proven to be as low as 5pg/mL for multiple Borrelia antigens. We then analyzed plasma and red blood cell lysate from hamsters infected with Babesia microti (n=7 and n=2 respectively), and urine samples from patients under treatment for Post-Treatment Lyme disease Syndrome (PTLDS) (n=12). 502 proteins from Babesia microti were identified in red blood cell lysate of hamsters during acute infection (parasitemia 28%) while no protein was identified after treatment (parasitemia 0%). 9 proteins from Babesia were also found in plasma form hamster infected by B. microti (parasitemia 30-57%) thus supporting the evidence of shed antigens in the plasma. In patient samples suspected of PTLDS we identified proteins from Borrelia burgdorferi and other pathogens responsible for Lyme disease co-infections. Proteins derived from 3 or more pathogens were detected in 9 of the 12 patients treated for PTLDS.

Our data for the first time demonstrates evidence of shed Babesia antigens in plasma and urine of animal models and humans. Our results also prove that a direct antigen detection assay via nanotechnology enhanced mass spectrometry can reach the required analytical sensitivity for the identification of Borrelia as well as other tick-borne pathogen antigens in urine of patients under treatment for PTLDS. The clinical consequences are very relevant. A single, highly specific, and highly sensitive antigen test for the diagnosis of multiple tick-borne infections would help physicians to unravel the complexity of tick-borne infections and design targeted combination therapies.
Calcium Channel (LCC) varied in a mutation specific manner, and indicate an increase in stability of CAM:LCC binding underlie in the beating heart. The interna used to predict the impact of sequence variation on structural dynamics specific to CAMs role in regulating cellular contract simulations provide a more evolutionary pressure to maintain high sequence identity through finely tuned functional interactions. Molecular dynamics rather than mutagenesis of multiple CAM structures reveals most mutations are predicted to be stabilizing, regardless of where they occur reveal associated with multiple arrhythmic cardiac disease phenotypes with a range of severity. Computational structural analysis the severity of a particular mutation. The CAM mutations occur at similar locations in the protein structure, but have been recently identified mutations in the ubiquitous calcium sensing protein calmodulin (CAM) illustrate the challenges in predicting disease phenotype can be studied on multiple scales to provide missing context that is often lacking in statistical associ...
the phenotypic changes seen in mutant individuals. The resulting influence on LCC regulation, specifically the rate of CAM dependent inactivation immediately following the action potential, was simulated using a physiologically based cell model of the cardiac myocyte. A small change in CAM regulatory function will severely impact the emergent properties of the cardiac myocyte, and examination of the underlying mechanism provides evidence how multiple arrhythmic disease phenotypes can arise from deficiencies in a single underlying molecular function.

Presenter(s): McDowell, Ben, Undergraduate Student; Adissa Silue, PHD Student; Nathalia Peixoto, Associate Professor
Title: Electrochemical Sensing of Dopamine with Chitosan – Catechol Modified Electrodes
Poster Location Number: 23
Keywords: dopamine, modified electrodes, biosensor, neurotransmitter, electrochemistry
Abstract: Chitosan – catechol chemically modified electrodes provide an alternative biosensor platform to the commonly used carbon fiber electrode. These biosensors have potential use in monitoring of various neurotransmitters, which may be associated with neurological disorders at abnormal concentrations. Abnormalities in dopamine concentration have been noted in literature for both Parkinson’s and Huntington’s disease, two commonly studied neurological disorders. Chitosan – catechol electrodes are sensitive to dopamine concentrations through the application of cyclic voltammetry (CV), where the oxidative peak in current due to dopamine is proportional to the concentration of dopamine in solution. In this study, ten gold electrodes were modified with chitosan – catechol and subsequently tested in five concentrations of dopamine, ranging from 10-9 M to 10-5 M. The aging of these modified electrodes was also examined, in order to determine the consistency of measurements made over time. These exhibited sensitivity as high as 0.277 +/- 0.087 A/M and limit of detection as low as 965 nM. This compares to an average sensitivity of 0.101 +/- 0.059 A/M and an average limit of detection of 19.7 mM for the unmodified gold electrodes. Although the consistency with which the electrodes perform shows room for improvement, the increase in the limit of detection and sensitivity after the modification supports the use of chitosan – catechol modified electrodes as potential biosensors for dopamine.
(1) Cepeda, C., Murphy, K. P., Parent, M., & Levine, M. S. (2014). The Role of Dopamine in Huntington’s Disease.

Presenter(s): Meyer, Shaun, Undergraduate Student; Lynn Gerber, Siddhartha Sikdar, Hussain Allawi, Zobair Younossi
Title: Quantitative Ultrasound Techniques used in the Detection of Fatty Liver
Poster Location Number: 35
Keywords: NAFLD, Quantitative Ultrasound, Fatty Liver Detection
Abstract: Introduction: The objective of our work is the noninvasive detection of early stage Non-alcoholic fatty liver disease (NAFLD) using raw radio frequency (RF) data from ultrasound (US) scans of the liver. NAFLD affects roughly 25-35% of the Western civilization, and there are few reliable biochemical markers. Most diagnoses occur later in the progression of NAFLD. Additionally, studies have shown that NAFLD can be linked to insulin resistance, metabolic syndrome, type II diabetes, obesity, and CVD/CAD [1]. This study implemented an objective, non-invasive, QUS method to delineate fatty liver from normal liver tested against current clinical diagnoses for patients at risk for CAD.
Materials and Methods: RF US data were acquired using a Terson3000®, using a curved SC2A transducer (3.5 MHz center frequency) following procedures approved by our IRB. This initial study tested 26 subject’s US scans which had a radiologist US based reading for hepatic steatosis. Using Matlab®, a manual ROI on a B-mode US scan was indicated, making sure to avoid large hepatic vessels and image artifacts. Next, the power spectra with respect to frequency, within a rectangular sub-ROI, were computed by a fast Fourier transform (FFT) algorithm. Next, the power spectral estimates were averaged within the sub-ROI and expressed in dB. The same steps are applied to a normal liver tissue reference phantom at each of the same locales; then linear regression is performed on the sample power spectra calibrated by the reference power spectra. For each sub-ROI a local estimate of the spectral slope (dB/MHz) and the midband-fit (MBF) is calculated from the regression line. Spectral slope and MBF parametric images are produced and then overlaid atop the B-mode images (figure 1).
Results and Discussion: Table 1 shows the T-test results of 7 statistical measures for Slope and MBF images within the ROI. The null hypothesis that normal liver images and abnormal liver images are significantly similar was rejected for 5 statistical features with the best p-value from the mean slope test feature. Additional ROC validation is needed, and we have parametric images produced for 70 additional subjects that will also be tested against subjective clinical diagnoses.
Conclusion: QUS features such as mean Spectral slope and mean MBF can accurately diagnose hepatic steatosis (early stage NAFLD); however, current literature shows that Back Scatter Coefficient compensated for Attenuation does a better job of delineation between healthy and unhealthy liver as well as quantifying severity of hepatic steatosis [2]. Future research to produce BSC measurements and parametric imaging is recommended.
Developing a Text Messaging Intervention for Smoking Cessation Among Chinese and Korean Immigrants: Findings from Message Pretesting

Abstract: Smoking cessation has many challenges that exist in many immigrants. In this study, we developed a tailored mHealth application for smoking cessation support, which integrates the WHO guidelines with established health behavior theories, cutting-edge technology, and user-centered design to provide an easy-to-use, culturally-tailored mHealth application for psychosocial support of mothers with microcephaly in deprived areas. The online platform defined serves as an information tool for mothers with microcephaly. By employing user-centric design techniques, we develop an innovative mHealth solution that combines a mobile application with an online portal, where medical practitioners, including physical therapists and nurses, upload validated multimodal contents for the caregivers to access it. The application facilitates access to updated, validated, medical information to improve the quality of care and stimuli given to the patients, in a low-cost, personalized, timely and scalable approach.

Keywords: smoking cessation, text messaging, intervention, immigrants

Poster Location Number: 21
Abstract: Background: Tobacco use is the leading cause of preventable morbidity and mortality in the United States. The public health burden caused by tobacco is particularly heavy among first-generation Chinese and Korean immigrants whose home countries have significantly higher smoking rates than the United States. This study is part of a larger effort to pilot a tobacco cessation intervention using mobile phone technologies targeting these immigrant populations.

Objective: Based on the Extended Parallel Process Model (EPPM), we pilot test several types of threat and efficacy messages. The three main categories of threat messages presented in the focus groups included (a) graphic warning messages proposed by the FDA for use in the United States, (b) more vivid graphic tobacco warnings from other countries, and (c) a series of culturally-tailored graphics and messages developed by the research team. The efficacy messages tested consisted of varied “tips to quit” adapted from a national database (SmokefreeTXT) as well as newly developed messages directing participants to an Asian-specific Quitline. Testing focuses primarily on message comprehension, congruency between text and graphics, message relatability, and cultural sensitivity.

Methods: We conducted 9 focus group interviews (5 in Chinese and 4 in Korean) with 32 Chinese and 13 Korean immigrants. Participants were recruited from local Chinese and Korean communities in the Metropolitan DC area in 2016.

Results: Participants were on average 39.5 years old, with nearly 10 years of living in the US. Most Participants had a smart phone (95.6%). Overall, messages that focused on impact of smoking on family and loved ones were better received. Quitting tips were preferred over Quitline information. There were mixed opinions about whether texting is a better choice than social media platforms. Participants had relatively low English proficiency, averaging 2.6 on a rating scale ranging from 1 (very well) to 4 (not at all). This suggests that graphics are an important means of communication with this population. Recruiting participants for this research has been challenging potentially due to increasing awareness of the stigmatization of smoking and the rigid work hours of working class immigrants.

Discussion: Chinese and Korean (and other East Asian) immigrants are a unique vulnerable population for tobacco control. Graphic text messaging hold promise as an intervention method. Our findings suggest that culturally tailored and enriched message systems are needed to address tobacco-related disparities faced by this population.

Keywords: Neuroscience Education, Medical Education

Abstract: The knowledge divide that separates non-scientists, health-care professionals, and private investigators has caused inadequate patient education within the medical field. Often, the only materials that patients receive are relatively complex medical packets that are only understood by professionals. A new model of educational quality improvement must be developed to help patients understand their diseases and conditions. These new models can introduce patient-control and educated decision-making through user-friendly learning-materials. The introduction of more effective medical education tools could raise awareness of the importance of a mutual understanding between healthcare professionals and patients. In this study, we are investigating the quality of education in Traumatic Brain Injury subjects to determine the role that the healthcare system had in educating these patients on biological and neuroscience concepts. We attempt to provide patient-centered education through innovative teaching strategies and redefine the meaning of personalized medicine. Throughout the course of this study, we use engaging lesson plans on the central and peripheral nervous system, the regenerative properties of the nervous system, and the biological properties of Traumatic Brain Injury. We intend to determine the quality and the extent of education before and after patients experienced the study. We intend to collect data points through interviews, surveys, and quizzes; these data points will be useful for quantitative and qualitative data. We intend to demonstrate the importance of medical educators within hospitals and doctor offices. As a patient becomes an expert regarding their condition, respective decisions can be made on clinical trials. This research is significant because patients can be valuable resources for describing symptoms that are undetectable by technologies. If patients and healthcare professionals work together, there is a higher probability of discovering a cure. The expected result of this project is to raise awareness of the severity of Traumatic Brain Injuries while improving the quality of educational tools for patients.

Keywords: LOPAC; Spectrum Collection; Burkholderia; anti-virulence; biofilm

Abstract: Burkhodleria pseudomallei, the causative agent of melioidosis, displays widespread resistance to several antimicrobial compounds. Some Burkhodleria isolates have even displayed resistance against the primary therapeutic agent, ceftazidime. A promising alternative to traditional antibiotics involves selecting compounds that are active in biofilm dispersal.
Abstract: Background: The introduction of molecular profiling has opened new opportunities for personalized treatment. While genomic alterations are central players in tumor onset and progression, proteins that are the targets for precision therapy. The degree by which “actionable” genomic alterations translate into activated/altered protein and pathway activation is still under investigation. Using a multi-OMIC approach from the SideOut 2 metastatic breast cancer (MBC) trial, this study explored the concordance between selected “actionable” genomic alterations and protein expression/activation.

Methods: Snap frozen biopsies from 29 MBC patients enrolled in a prospective phase II trial were used for this analysis. Exome (WES) and RNAseq data was processed using an in-house developed pipeline and identified amplification of CCND1 (6/29 patients), amplification of FGFR1 (4/29 patients), and FGF 3, 4, 5, and 19 (4/29 patients) as some of most frequent “actionable” genomic alterations in our MBC cohort. Signaling analysis of the 29 cases was performed using Reverse Phase Protein Microarray coupled with Laser Capture Microdissection to procure purified tumor cell populations. Protein expression/activation (phosphorylation) were measured in a continuous scale and classified based on quartile distribution. This allowed for the correlation between genomic alterations and impact on protein/phosphoprotein and signaling. Concordance between CCND1 amplification and Cyclin D1 expression along with the activation/phosphorylation of FOXM1 (T600) and Rb (S780) was performed. Amplification of the FGFR1 locus or its ligands was correlated with the level of activation/phosphorylation of FGFR1 Y653/654.

Results: While Cyclin D1 protein expression was greater than the population mean for 4/6 (67%) patients with CCND1 amplification, only 2/6 (33%) of the patients with CCND1 amplification had Cyclin D1 expression within the top quartile of the population (N=29). FOXM1 (T600) activation was independent from CCND1 amplification, with high levels of activation of FOXM1 (T600) predominantly in the CCND1 wild-type population. Only 1/6 (17%) patients with CCND1 amplification had FOXM1 T600 level similar to the top quartile of the population while a second patients was above the population median. Activation of Rb (S780), a major downstream substrate of the CCND1/CDK4 complex, was above the population median, but below the top quartile, in 2/6 (33%) CCND1 amplified patients. Similarly, none of the patient with activation of FGFR Y653/654 equal to the top quartile harbored a FGFR1 amplification. Only 1/4 (25%) patients carrying a FGFR1 amplification had activation level of FGFR Y653/654 above the population median. Similarly, 1/4 (25%) patients with FGF ligand amplification showed FGFR Y653/654 level within the top quartile. The remaining three patients (75%) had FGFR Y653/654 activation below the population median. No significant results were found between protein expression/activation (below/above the median) and genomic characteristics by Fisher test (p>0.05).

Discussion: Molecular genotyping of “actionable” cancer targets alone may be insufficient in predicting whether or not the actual drug target protein is expressed and/or activated in any given patient’s tumor. Although these results need further validation, the combination of genomic and proteomic data may represent a more informative approach for identifying real molecular drivers of individual lesions as well as identifying “actionable” protein/phosphoprotein driven results in the absence of genomic events. Multi-OMIC approaches like the one utilized herein the SideOut 2 Trial may lead to more effective stratification in precision medicine trials.

Presenter(s): Pierobon, Mariaelena, Research Associate Professor, Center for Applied Proteomics and Molecular Medicine;
Title: A multi-OMIC analysis to explore the impact of “actionable” genomic alterations on protein pathway activation: clinical implication for precision medicine in metastatic breast cancer
Poster Location Number: 8
Keywords:
Abstract:

By preventing adherence and biofilm formation, colonization can be prevented without selecting for antibiotic resistance. In order to identify potentially novel antibiofilm agents, we investigated the Library of Pharmacologically Active Compounds (LOPAC), a repository of 1,280 small molecules that target various eukaryotic signaling pathways as well as drugs and drug targets. We also screened the Spectrum Collection, a repository of 2,000 compounds similarly comprising cell signaling and drug targets. A static biofilm inhibition assay protocol was developed in order to screen both libraries of compounds, accounting for inhibition of growth and biofilm formation. Two (2) compounds displayed antimicrobial activity against Burkholderia thailandensis, the model organism for B. pseudomallei. Five (5) different compounds displayed significant inhibitory activity on B. thailandensis biofilm formation. Additionally, the lead compound dispersed pre-formed B. thailandensis biofilms, and the mechanism of action is discussed. Although Burkholderia species are naturally antibiotic resistant, these results demonstrate that existing compounds targeting biofilm formation may provide novel avenues of treatment for melioidosis.

Presenter(s): Pinto, Daniel, Msc. / PhD Student
Title: Crossing anatomical and cellular barriers: A novel approach for activating latent HIV-1 and host cell death using low level irradiation
Poster Location Number: 58
Keywords: HIV, radiation, apoptosis, genomics, virology, CNS, therapeutics, FDA approved Drugs.

Abstract: The highly active antiretroviral therapy reduces HIV-1 RNA in plasma to undetectable levels. However, the virus continues to persist in the long-lived resting CD4(+) T cells, macrophages and astrocytes which form a viral reservoir in infected individuals. Reactivation of viral transcription is critical since the host immune response in combination with antiretroviral therapy may eradicate the virus. Using the chronically HIV-1 infected T lymphoblastoid and monocyctic cell lines, primary quiescent CD4(+) T cells and humanized mice infected with dual-tropic HIV-1 89.6, we examined the effect of various X-ray irradiation (IR) doses (used for HIV-related lymphoma treatment and lower doses) on HIV-1 transcription and viability of infected cells. Treatment of both T cells and monocytes with IR, a well-defined stress signal, led to increase of HIV-1 transcription, as evidenced by the presence of RNA polymerase II and reduction of HDAC1 and methyl transferase SUV39H1 on the HIV-1 promoter. This correlated with the increased GFP signal and elevated level of intracellular HIV-1 RNA in the IR-treated quiescent CD4(+) T cells infected with GFP-encoding HIV-1. Exposition of latently HIV-1 infected monocytes treated with PKC agonist bryostatin 1 to IR enhanced transcription activation effect of this latency-reversing agent. Increased HIV-1 replication after IR correlated with higher cell death: the level of phosphorylated Ser46 in p53, responsible for apoptosis induction, was markedly higher in the HIV-1 infected cells following IR treatment. Exposure of HIV-1 infected humanized mice with undetectable viral RNA level to IR resulted in a significant increase of HIV-1 RNA in plasma, lung and brain tissues. Collectively, these data point to the use of low to moderate dose of IR alone or in combination with HIV-1 transcription activators as a potential application for the "Shock and Kill" strategy for latently HIV-1 infected cells.

Presenter(s): Pleet, Michelle, M.S.
Title: Ebola VP40 in exosomes can cause immune cell dysfunction
Poster Location Number: 37
Keywords: Ebola virus, exosomes, ESCRT, pathogenesis

Abstract: Ebola virus can result in severe hemorrhagic fever with up to 80-90% mortality; however, long-lasting persistence and recurrence in survivors has been documented, potentially leading to further transmission of the virus. Additionally, massive cell death of uninfected bystander T-cells occurs during infection by an unknown mechanism in a phenomenon known as bystander lymphocyte apoptosis, which allows for un-checked viral replication. We have previously shown that exosomes from cells infected with HIV, HTLV and RVFV are able to transfer viral proteins and noncoding RNAs to naïve recipient cells, resulting in altered cellular activity. Here, we examined the effect of Ebola structural proteins VP40, GP, and NP on recipient immune cells, as well as the effect of exosomes containing these proteins on naïve immune cells. We found that VP40-transfected cells packaged VP40 into exosomes which were then capable of inducing apoptosis in recipient immune cells. Additionally, we show that VP40 within parental cells or in exosomes delivered to naïve cells could regulate host RNai machinery, which may contribute to the induction of cell death. Exosome biogenesis was regulated by VP40 in transfected cells by increasing levels of ESCRT-I protein TSG101, ESCRT-II proteins EAP20 and EAP45, and exosomal markers CD63 and Alix. VP40 was phosphorylated at Serine 233 by Cdk2/Cyclin A/E complexes, which could be reversed with r-Roscovitine treatment. Additionally, we used novel nanoparticles to capture VP40 from human samples spiked with Ebola VLPs using SDS/reducing agents, minimizing the need for BSL-4 conditions for downstream assays. Collectively, our data indicates that VP40 is packaged into exosomes which may be responsible for the deregulation and eventual destruction of the T-cell and myeloid arms of the immune system, allowing for the virus to replicate to high titers in the immunocompromised host.

Presenter(s): Poon, Jennifer, M.A.; James Thompson, Ph.D., Associate Professor of Psychology; Tara Chaplin, Ph.D., Assistant Professor of Psychology
Title: Adolescents’ Reward-Related Neural Activation: Links to Thoughts of Non-Suicidal Self-Injury
Poster Location Number: 59
Keywords: reward, adolescence, fMRI, self-injury

Abstract: Adolescence is a critical developmental period marked by an increase in risk behaviors, including non-suicidal self-injury (NSSI), which refers to behaviors such as cutting or carving one’s skin and bruising one’s self (Favaazza, 1998). Heightened reward-related brain activation, coupled with relatively limited recruitment of prefrontal regions, may contribute to the initiation of risky behaviors (perhaps including NSSI) during this developmental period (Steinberg, 2010). However, despite many studies documenting both increases in reward-related brain activation (e.g., Galvan et al., 2006, 2010) and increases in NSSI during adolescence (e.g., Nock et al., 2006), there is little research examining whether reward-related brain activation is associated with adolescents’ thoughts of NSSI. The current study seeks to fill a gap in the literature by examining how early adolescents’ brain activation in response to the receipt of a monetary reward is associated with thoughts of self-injury. We hypothesized that altered activation in reward-related regions of interest (ROIs: caudate, putamen, nucleus accumbens [NAcc], ventromedial prefrontal cortex [vmPFC]) would be associated with early adolescents’ thoughts of NSSI.
Seventy-one adolescents ages 12-14 (M = 12.52; 38 boys; 74.6% White) were recruited from a larger study of emotion to participate in an fMRI session. In the MRI session, adolescents' neural responses were assessed during a monetary reward task (Forbes et al., 2009). The task was a single run, event-related design comprising 24 trials, 12 of which were potential win trials (with 6 win outcome, 6 neutral outcome) (Figure 1). In a separate session, adolescents reported on their past and future thoughts of NSSI via two items on the Self-Injurious Thoughts and Behaviors Interview (Nock et al., 2007). Thoughts of NSSI were used as a proxy for NSSI behavior in these young adolescents, as research has shown that NSSI thoughts are correlated with future behaviors (Nock et al., 2009). For analyses, we created a dichotomous variable for past and future thoughts (yes/no). We extracted mean contrasts of parameter estimates (COPE) values for the win outcome and neutral outcome trials from the ROIs, with regions defined by the Harvard-Oxford and AAL atlases. Win–neutral outcome scores were calculated. Results showed that early adolescents who endorsed thoughts of NSSI showed significantly higher r NAcc and bilateral putamen activation to win (minus neutral) trials. Furthermore, those who endorsed thoughts of NSSI showed increased L caudate and R vmPFC activation at a trend level (Table 1).

Findings suggest that, compared to those who have never considered self-injury, adolescents who have endorsed thoughts of NSSI evidenced heightened activation in reward-related brain regions in response to a monetary reward. Congruent with functional theories of NSSI (Nock & Prinstein, 2004), it is possible that early adolescents considering NSSI believe this behavior will generate a desirable, ostensibly rewarding sensation. It is also possible that they are at risk for NSSI due to a general biological vulnerability towards reward-seeking (e.g., Galvan et al., 2006). This study contributes to the understudied role of positive affect in the etiology of adolescent NSSI and may inform both psychological and pharmacological interventions for self-injury.

Presenter(s): Roberts, Steven; Nitin Agrawal, Assistant Professor
Title: Advanced Nanocarriers: Rapid Production, Purification, and Concentration of Small Drug Loaded Liposomes
Poster Location Number: 47
Keywords: Liposomes, Drug delivery, Cancer, Vesicles, Nanoparticles
Abstract: Liposomes are one of the most studied nano-delivery systems. However, only a handful of formulations have received FDA approval. Existing liposome synthesis protocols are complex and require specialized facilities to produce populations of monodisperse small unilamellar liposomes. This poses a major impediment in the design and implementation of liposome delivery systems, both as point of care and mass produced therapeutics. Here, we demonstrate a unique approach for rapid and efficient production, purification, and concentration of small drug loaded liposomes using common benchtop equipment. Small unilamellar liposomes, with mean diameter of 80 nm and polydispersity of 0.13 were synthesized without any secondary post processing techniques, using a customized injection method. Encapsulation of a wide range of dextran (300 to 20,000 Da), representing small and large molecule drug formulations, was demonstrated without affecting the liposome characteristics. High purification efficiencies were achieved and 99.9% of the unencapsulated molecules were removed using a novel filter centrifugation technique, largely eliminating the need for tedious ultracentrifugation protocols currently employed in nano-research facilities. Finally, the functional efficacy of loaded liposomes as drug delivery vehicles was validated by encapsulating a fluorescent cell tracker (CMFDA) and observing the liposomal release and subsequent uptake of dye by metastatic breast cancer cells (MDA-MB-231) in vitro. Thus, our simplified technique addresses the existing challenges associated with liposome preparation in resource limited settings and offers significant potential for advances in translational pharmaceutical development, both in basic research and point-of-care formulations.

Presenter(s): Schulte, Erin, Student; Zepher Begnell, Omar Sangid, Kostyantyn Scherbina, Connor Stapp
Title: Touch Screen Application in a Stroke Rehabilitation Setting
Poster Location Number: 60
Keywords: Bioengineering technology designed to aid in the stroke rehabilitation process
Abstract: Stroke rehabilitation is a field populated by technologies that focus primarily on hand dexterity exercises, or fail to mimic real-world movement patterns and are thus inefficient. The absence of technology allowing for training of reaching exercises in a simple, inexpensive way has resulted in a niche that we have filled, through an adjustable touchscreen table and python-based user interface. Our custom system uses motion tracking algorithms as well as adjustable equipment to allow patient-specific training paradigms to be implemented. The technology currently tracks response, reaction, and movement times of each patient over multiple trials and training periods. The software also records the trajectory of the patient's limb, allowing for further data analysis and tracking of progress, while providing visual feedback to the patient. The system is portable and relatively inexpensive, making it easy to implement at multiple locations, including potentially in patients' homes. The versatility of our Python and OpenCV based software will allow for external objects to be implemented, as well as customized training experiences for individual patients.
Consenting participants completed the assessment methods in random order. Survey and interview results were cross-

and older were recruited as they exited a single dining hall during lunch service hours during one week in Spring 2016.

Abstract:

Keywords: Electrochemistry, electrochemical sensor, sensors, neurotransmitter, dopamine

Poster Location Number: 61

Title: Overview: Electrochemical Sensors for Dopamine

Presenter(s): Silue, Tjerignimin Adissa, PhD Student; Ben McDowell, Undergraduate student; Nathalia

Abstract: Dopamine (DA) is a neurotransmitter located in the ventral tegmental area of the midbrain, the substantia nigra pars compacta, and the arcuate nucleus of the hypothalamus of the human brain [1]. It is a critical puzzle piece in understanding neural behavior and in developing therapeutic intervention technologies for neurological disorders. Monitoring of extracellular DA concentration can serve as a clinically relevant biomarker for specific diseases states as well as a gateway to monitor treatment efficacy. Raman and flow injections are some examples of analytical techniques that have been reported in the literature [2,3] for the detection of neurotransmitters. Although they offer good selectivity and low limits of detection, they require complex steps and expensive instrumentation. Electrochemical sensors, on the other hand, provide an inexpensive, easy, sensitive, rapid, and selective tool for detection of biomarkers of several diseases and can be easily embedded into portable, more efficient devices for targeted applications in both the clinical and diagnostic fields. In Parkinson’s disease for example, such sensors can be integrated with therapeutic interventions such as deep brain stimulation systems. A wide range of sensors have been recently developed to detect different neurotransmitters in addition to DA, such as norepinephrine, serotonin in the presence of uric acid (UA) and ascorbic acid (AA) at an improved limit of detection, close to the physiologically relevant concentrations [4,5]. Some of the electrochemical sensors used in the detection of DA include carbon electrodes coated with Nafion, electrodes coated with non-conducting polymers, gold electrodes modified on self-assembled monolayers, and nanoparticles-based electrodes. In recent years, nanoparticles-based electrodes have received attention due to their inherent electrocatalytic nature to accelerate the rate of electrons transfer between specific molecules and the electrode, and thus improving the selectivity of the sensor towards neurotransmitters in the presence of UA and AA. The improvement of electrode materials with the power of electroanalysis techniques resulted in the improved detection of DA at nanomolar levels. This improved sensing performance has been achieved using techniques such as cyclic voltammetry, differential pulse voltammetry, square wave voltammetry, and fast-scan cyclic voltammetry, and by using electrodes under physiological conditions, in the presence of abundant interfering molecules such as UA and AA [7]. In all these techniques, the main shortcoming of electrochemical sensors is their lifetime. In order to truly offer a solution for long-term implants and neurotransmitter detection, the main bottleneck will be to design sensors that can reliably detect neurotransmitters for years.


Presenter(s): Slavin, Magaret, Assistant Professor, Nutrition & Food Studies; Amy Best, Professor and Chair, Sociology & Anthropology; Alexandra Hauver, Nutrition MS alumna, Nutrition & Food Studies; Katie Brennan, Nutrition MS alumna, Nutrition & Food Studies; Cara Frankenfeld, Associate Professor, Global & Community Health

Title: Validation of a self-administered electronic exit survey for single meal dietary assessment in Mason undergraduates in an all-you-care-to-eat dining hall

Poster Location Number: 42

Abstract: The lack of reliable, unobtrusive, economical dietary assessment methods in all-you-care-to-eat dining settings poses a challenge to assessing the nutritional intake of University undergraduates. New methods which streamline accurate dietary data collection in University dining halls would facilitate identification of interventions designed to improve nutrient intake in this group of emerging adults. The objective of this study was to compare nutrient intake data of university undergraduate students from a single visit to an all-you-care-to-eat campus dining hall, collected by two methods. A multiple-pass, structured dietary recall interview conducted by a trained interviewer served as the reference method for comparison of a novel, self-administered survey. The electronic tablet-based exit survey listed all available menu items at that service, and included drop-down menus for students to self-report their portion size consumed. Undergraduate students (n=42) ages 18 and older were recruited as they exited a single dining hall during lunch service hours during one week in Spring 2016. Consenting participants completed the assessment methods in random order. Survey and interview results were cross-
Poster Location Number:

Title: How Point Mutations of Calsequestrin Contribute to Arrhythmias and Sudden Cardiac Death

Presenter(s): Ullah, Aman, Research Assistant Professor.; Professor. M. Saleet Jafri, Professor. W. Jonathan Lederer, Dr. Tuan M. Hoang-Trong

Title: Associations between Parent Emotional Arousal and Regulation and Adolescent Affective Brain Response

Poster Location Number: 39

Keywords: parenting, emotion, adolescence, fMRI

Abstract: Parent emotional functioning represents a central mechanism in the caregiving environment's influence on adolescent affective brain function (Bariola et al., 2011). However, a paucity of research has examined links between parental emotional arousal and regulation and adolescents' affective brain function. Thus, the present study examined direct and interactive effects of parents' self-rated negative emotion and emotion regulation difficulties on adolescent brain responsivity to negative emotional stimuli.

Participants included 66 12-14 year-old adolescents (39 females) and their female primary caregivers (mostly mothers). Adolescents completed an emotion-processing task during an fMRI scanning session. The emotion-processing task was comprised of viewing 27 negative, 27 neutral, and 27 positive International Affective Picture System (IAPS) images presented in an event-related design in a pseudo-randomized order across three 6.5-minute runs (analyses focus on negative-neutral contrasts). In a separate session, caregivers reported on their subjective negative emotion experience using the Differential Emotions Scale-Revised short form (DES-R, Izard, 1972) and on their emotion regulation difficulties using the Difficulties in Emotion Regulation Scale (DERS, Gratz & Roemer, 2004).

Region of interest (ROI) analyses of a priori regions were conducted using the Automated Anatomical Atlas (AAL, Tzourio-Mazoyer et al., 2002), including bilateral amygdala, anterior ACC, and vmPFC. Linear regressions testing the main effects of parent negative emotion and emotion regulation difficulties and the parent negative emotion X emotion regulation interaction on each ROI were performed. For all analyses, the predictor and moderator were mean-centered, and gender was covaried. False discovery rate procedures were used to adjust interaction coefficient p-values for multiple comparisons (Benjamini & Hochberg, 1995; Benjamini & Yekutieli, 2001).

First, results of linear regressions showed that greater parent negative emotion was related to adolescent BOLD responses in the negative-neutral contrast, including higher left amygdala, left and right anterior ACC, and left and right vmPFC. Second, linear regressions showed significant parent negative emotion X ER difficulties interactions for bilateral amygdala, left anterior ACC, and bilateral vmPFC. Significant simple slopes suggested that for parents with high ER difficulties (+1 SD), high negative emotion was associated with adolescents’ greater amygdala (L: B = 1.58, p < .001; R: B = 0.95, p < .05), left anterior ACC (L: B =2.71, p < .001), and vmPFC responsivity (L: B = 2.71, p < .001; R: B = 1.59, p < .001). Simple slopes for parents with low emotion regulation difficulties (-1 SD) were nonsignificant for all regions.

Altogether, high levels of parent negative emotional arousal were associated with adolescents’ greater emotion-related brain responsivity, particularly when parents also had difficulties regulating emotions. These findings suggest that adolescents may attune to their caregiving affective environment at a neurobiological level, underscoring the importance of caregiver emotionality and regulation in the development of youth’s emotional competencies. Furthermore, these findings suggest that family prevention and intervention efforts should focus on improving parent’s emotional arousal and emotion regulation in order to affect youth’s emotional development, even at the neurobiological level.

Poster Location Number: 41

Presenter(s): Turpyn, Caitlin, Doctoral Student in Psychology; Jennifer Poon, M.A., Doctoral Student in Psychology; Corynne Ross, B.S., Post-baccalaureate Researcher; James Thompson, Ph.D., Associate Professor of Psychology; Tara Chaplin, Ph.D., Assistant Professor of Psychology

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Keywords:
Abstract: Point mutations in the Ca2+ cycling proteins, calsequestrin 2 (CASQ2), have been found to underlie the arrhythmic cause of sudden cardiac death (SCD) known as catecholaminergic polymorphic ventricular tachycardia (CPVT-2). Understanding the subcellular mechanisms of CPVT is experimentally challenging because the arrhythmias are rare and the development of SCD are even rarer. For example, an episode of SCD may not occur in an affected individual for many decades if at all. To gain insight into the nature of this rare but potentially lethal class of arrhythmias we developed a multiscale model of cardiac electrical excitation and Ca2+ dynamics in heart cells and tissue with features that would include stochastic gating of channels and subcellular Ca2+ signaling. Models of the genetic mutant forms CASQ2 based on experimental data are incorporated into our models and enables us to explore how the mutations give rise to arrhythmia under conditions of beta adrenergic stimulation. Increased sensitivity to SR lumenal Ca2+ of RyR2, located in the junctional sarcoplasmic reticulum (jSR), leads to reductions in SR calcium content in CPVT-2 as a required by pump-leak balance of Ca2+ in the SR. Furthermore, increased SR Ca2+ content via enhanced SERCA Ca2+ pumping after treatment with catecholamines is attenuated due to the increased SR Ca2+ leak and does not lead to arrhythmia. Instead, in CPVT-2 additional changes (specifically the increased SR volume and decreased SR Ca2+ buffer) are sufficient to destabilize Ca2+ signaling. Therefore the increased SR lumenal Ca2+ sensitivity, increased SR volume and decreased buffering all are important elements in the model to produce cellular Ca2+ signaling alternans at high stimulation rates with simultaneous catecholamine treatment. The cellular Ca2+ instability underlies the multicellular development of extra-systoles.

Presenter(s): Valibeigi, Nazanin, Undergraduate Student; Daniel McHail, PhD Student; Afua Agyeman-Andoh, Postbac Research Assistant; Jennifer Chen, Research Assistant; Carmen Kimball, PhD Student; Nicholas Costello, Undergraduate Research Assistant
Title: A Barnes maze for juvenile rats delineates the emergence of spatial navigation ability
Poster Location Number: 24
Keywords: learning and memory, spatial navigation, hippocampus
Abstract: The neurobiology of postnatal hippocampal development in rodents is receiving increased attention as a means to address neurodevelopmental questions and to better understand the neural code(s) for spatial navigation in adulthood. Prior research has documented a robust improvement in spatial learning and memory tasks at three weeks of age. We showed that the developmental increase in spontaneous alternation (SA) in a Y-maze was related to changes in fast glutamatergic synaptic transmission in the hippocampus and to increases in network oscillation power at frequency bands known to support learning and memory in adults. However, there are no discrete learning and memory phases during free exploration in the Y-maze and the gold standard for assessing hippocampal integrity, the MWM, is not compatible with in vivo electrophysiological recording. Thus, a dry maze with minimal training would greatly benefit the field. We have adapted the Barnes maze for use with juvenile rats. Following a platform exposure in dim light (to encourage exploration), animals are trained for two days in bright light to find a hidden escape box and then undergo a memory test 24 hours later. We found that rats just under and over three weeks of age similarly explored the platform in dim light. During escape training under bright lighting, the older animals learn the task in one day, while the younger animals require two days. Long-term memory performance was superior in the older animals. Thus, we have demonstrated that the Barnes maze can be performed at this developmental stage and is able to separate differences in cognitive abilities in animals younger and older than three weeks. This work sets the stage for in vivo recording of local field potentials and single units to determine the neural network properties that are responsible for the emergence of spatial learning and memory.

Presenter(s): Waisenen, Cody, ; Monique van Hoek
Title: Francisella resistance to Aztreonam and Carbapenems is dependent on the beta-lactamase genes
Poster Location Number: 12
Keywords: Antibacterial, Bacteria, Multi-drug resistance
Abstract: Francisella species are generally resistant to the antimicrobial activity of beta-lactam antibiotics such as penicillin through the activity of beta-lactamase enzyme. Francisella species are also reported to have varying resistance to aztreonam and carbapenems, two modern antibiotics. We sought to identify the genes involved in Francisella’s resistance to these antibiotics. Aztreonam is a synthetic monocyclic beta-lactam antibiotic (monobactam), which was developed to treat gram-negative bacterial infections. Aztreonam is cleaved by (and thus resistance conferred by) extended-spectrum beta-lactamases, and this inhibition is relieved by Clavulanic acid. Carbapenems are an important new class of antibiotics for gram-negative bacterial infections, which can also be inactivated by some beta-lactamases, especially metallo-beta lactamase genes. It has recently been reported that some Francisella strains express different beta-lactamases and carbapenemases, thus we wondered if we could observe a difference in their sensitivity to the antibiotic Aztreonam as well as some carbapenems. We will
examine the resistance of different strains of Francisella to Aztreonam and Carbapenems. We will test if this resistance can be attributed to the beta-lactamase gene (BlaA) or the Extended spectrum beta-lactamase gene in Francisella.

Presenter(s): Wheeler, Diek W., Research Assistant Professor; Giorgio A. Ascoli, Professor
Title: Hippocampome.org v1.1 and beyond: increasing open-access knowledge of neuron types and their properties for the rodent hippocampus
Poster Location Number: 25
Keywords: neuroinformatics
Abstract: Hippocampome.org is an open-access knowledge base of rodent hippocampal neurons types, each defined by the patterns of axonal and dendritic presence across the parcels of the hippocampal formation. In addition to this morphological knowledge, Hippocampome.org also includes information on biomarker expression, electrophysiological properties, and connectivity for all types. The new v1.1 release constitutes a multi-dimensional expansion of this knowledge base. Since the official 2015 launch, continued literature mining has yielded the addition of 20 new neuron types, bringing the total number to 141. Notable new content includes splitting CA1 Pyramidal cells into Superficial and Deep types, due to converging evidence of multiple distinct molecular biomarkers and electrophysiological properties, and the inclusion of Adult-Born Immature Granule cells. We also track several new properties. Neuron types are now characterized by their firing patterns, and we have identified over 20 unique firing patterns. Moreover, we have developed spiking computational models for many of the neuron types contained in the knowledge base. In the biochemical dimension, we have increased molecular-expression pieces of knowledge by 75%, by leveraging inferential evidence, which is based upon experimental observations of systematic if-then logical relationships between the presence or absence of biomarkers. Further gene expression information is derived by mining Allen Brain Atlas in situ hybridization mouse data. Additionally, we have refined the connectivity information between neuron types by expanding the evidence for known synapses (or the lack thereof) in order to confirm or, in rare cases, refute our morphologically-derived potential connectivity calculations, which are based on histological and electrophysiological evidence. Finally, we have made numerous modifications to the web portal to enhance the experience of the user, including an interactive connectivity navigator and a neuron term portal offering definitions of neuron types and properties.

Presenter(s): Yusuf, Sameen, bioengineering undergraduate student; Marissa Howard, bioengineering student; Sara Sharif, bioengineering student; Rohit Madhu, bioengineering student
Title: Application of Hydrogel Nanoparticles for a Latent Tuberculosis Rapid Diagnostic Test
Poster Location Number: 62
Keywords: Diagnostics, global health development, immunology, medical devices
Abstract: BACKGROUND: The diagnostic test available to most people in the world where tuberculosis (TB) is a major health problem is essentially the same as that available to Robert Koch, who discovered the bacteria in the latter 19th century. According to the World Health Organization (WHO), there is an urgent need for a highly sensitive, rapid point of care diagnostic test for TB. The diagnostic tests available to people where TB is a leading cause of death are indirect, invasive, time consuming and expensive. In the past a rapid urine test for (non HIV+) TB patients has not been feasible because it has been impossible to achieve the required analytical sensitivity.
SPECIFICATIONS: Our device must achieve 80% specificity, 95% sensitivity, and a 1 ng/mL analytical sensitivity for detecting ESAT-6 (the protein associated with tuberculosis) from the urine. The test must also produce a result in less than 30 minutes, be as easy to use as an at home pregnancy test, and be portable.
METHODS & RESULTS: We are developing an electrical, paper-based immunoassay using high affinity capture hydrogel nanoparticles (NP) and amperometric sensors to provide a sensitive, specific, and quantitative method for TB diagnostics from urine samples. To capture the TB biomarker, ESAT-6, we are using NPs that have an open mesh network of polymers with high affinity chemical baits internally immobilized. They exhibit strong protein degradation protection and amplification of target biomarkers. They can be electrically detected at the capture antibody line. To enhance the signal generated by the NPs at the capture antibody line, we have functionalized the internal volume of the NPs with the enzyme Horseradish Peroxidase (HRP). When HRP is in the presence of hydrogen peroxide, generated by the redox reaction of glucose by glucose oxidase, the HRP further generates free electrons. Coupling an Arduino Pro Mini microcontroller board with the NPs, amperometric sensor, and enzymatic reactions allows for a more sensitive and analytical diagnostic test. The Reactive Blue 221 dyed NPs demonstrated a consistent threshold for differentiating between the test and control line, and using 230,000,000 nanoparticles/mL concentration effectively leads to 1 nanogram per milliliter detection of ESAT-6.
CONCLUSION: Current approaches lack objective sensitivity or are too expensive to implement in developing countries where TB is most prevalent. Thus, our approach of utilizing NPs in a LFI allows for our amperometric sensor to detect the current change and ultimately achieve the high sensitivity required.