UNIVERSITY of WASHINGTON

Undergraduate Research Symposium May 17, 2019 Mary Gates Hall

Online Proceedings

POSTER SESSION 1

Balcony, Easel 122

11:00 AM to 1:00 PM

Identifying Species Divergence in the Endemic *Caecidotea* Cave Populations

Justin Harris, Senior, Molecular Biology, East Central Coll
McNair Scholar
Mentor: Alisha Howard, Department of Biology, East Central University
Mentor: Kevin Blackwood, Earth Science, East Central University

The Arbuckle karst system consists of caves, microfractures, and hydrogeologic barriers. Isopods in the genus *Caecidotea* inhabit the pools of water within the groundwater system. Young *Caecidoteas* travel through microfractures, and small populations move from one cave system to the next. Over the time these fractures close, causing the populations of *Caecidotea* to be isolated and potentially drift genetically. The sampled distinct populations have become morphologically distinct, but it is yet to be determined if they also have become genetically distinct species. Genetic classification may also provide a more timely identification of fracture closing. DNA Barcoding using the Cytochrome Oxidase subunit 1 (COX1) gene will provide the percent of divergence in the samples obtained from different populations/locations; however, the chitin-heavy exoskeleton of isopoda could make it difficult to have DNA extractions that are "clean" (without protein) and decent yield. An extraction method was used proteinaseK (protK) and high salt to release the DNA followed by ethanol precipitation to concentrate the extract. For DNA Barcoding, the COX1 gene sequences need a PCR protocol with the robust primers is crucial. We plan to explore various primer sets for the optimal amplification.

SESSION 1Q

BIOLOGICAL STRUCTURE AND FUNCTION

Session Moderator: Matt Kaeberlein, Pathology

JHN 022

12:30 PM to 2:15 PM

* Note: Titles in order of presentation.

Improvement and Validation of Dotted Traction Force Microscopy Platform

Robin Zhexuan Yan, Senior, Mechanical Engineering
Mary Gates Scholar
Mentor: Nathan Sniadecki, Mechanical Engineering
Mentor: Kevin Beussman

Human induced pluripotent stem cell-derived cardiomyocytes (hiPSC-CM) have great potentials in biomedical research and can be used extensively in drug screening and heart simulations. To understand the cardiomyocytes, we need to perform functional analysis on these muscle cells. Therefore, we need a simple, controllable, yet biocompatible and high throughput tool to measure the cellular traction force. At the Sniadecki Lab, we are developing a new technique to measure the force generation of hiPSC-CM: dotted traction force microscopy platform. To create the platform, fluorescent proteins were first absorbed to a dotted polydimethylsiloxane (PDMS) negative and stamped onto a polyvinyl alcohol film. The film was then transferred to a soft PDMS substrate and subsequently dissolved using phosphate buffered saline solution while the patterned fluorescent proteins stained the substrate. Since the stiffness of the soft PDMS substrate is known, the force generation of the cardiomyocytes can be calculated in real time by optically tracking the deformation of the fluorescent dots. Currently, we are able to manufacture the platform with high fidelity and uniform alignment with a production time of less than 2 hours. Moreover, the cardiomyocytes can fully spread out to their in vivo state on the substrate which ensures the force measurement is valid and accurate. Potentially, this method is not limited to cardiomyocyte research and can be applied to study the interaction between force generation and cell performance of other cells. We are also exploring the possibility of automated manufacture and integration with 96-well to enable mass production.

SESSION 1R

COMPUTER SECURITY, PRIVACY, ACCESSIBILITY, AND GRAPHICS

Session Moderator: Franziska Roesner, Computer Science and Engineering

JHN 026

12:30 PM to 2:15 PM

* Note: Titles in order of presentation.

Greedy Face Meshing: An Efficient Meshing Algorithm for Polygon Rendering in Computer Graphics

Ryan Raghav Pachauri, Senior, Computer Science
Mentor: Kevin Zatloukal, Computer Science and Engineering, Allen School

In computer graphics, a voxel (volume element) is a point in a 3D world coordinate system (i.e. the coordinate system of a virtual world). In games like Toca Blocks or Minecraft, voxels are used to store the texture of a particular terrain. Sometimes, voxels next to each other have the same texture. When voxels of homogeneous textures form polygons, rendering systems will optimize memory storage by storing the polygons' vertices rather than every single voxel in the polygon. The process of choosing polygons that cover the voxels is known as meshing. We refer to these polygons as quads and the collection of quads as a mesh. Current methods for polygon meshing require too much data storage or require a drastic change in the mesh after a small change in the world coordinate system. We propose the Greedy Face Meshing (GFM) Algorithm, a linear time algorithm for meshing voxels into quads. We prove that our algorithm is within a constant factor of the optimal solution (in terms of number of quads) and can update in constant time for a single-voxel change in the world coordinate system. We also show how the GFM Algorithm can be implemented using the Segment Tree data structure. Rendering systems can use the GFM algorithm to mesh polygons since its storage is no worse than any existing algorithm and its updates take constant time.

POSTER SESSION 2

MGH 241, Easel 152

1:00 PM to 2:30 PM

Automated Methods of Classifying Rat Ultrasonic Vocalizations into Discrete Categories

Rachel Shi, Freshman, Center for Study of Capable Youth
Mentor: John Neumaier, Psychiatry
Mentor: Kevin Coffey, Psychiatry and Behavioral Science

Rats produce ultrasonic vocalizations (USVs) in a range from 20-kHz to 95-kHz that vary in frequency and shape across social and motivational contexts and can correspond to the affective state of the animal. To assess these USVs accurately and efficiently, our lab created DeepSqueak, a novel machine learning software package that expedites the detection and analysis of rat USVs by using neural networks to differentiate them from noise. DeepSqueak also allows for automatic and unbiased classification of USVs into discrete categories using call parameters such as shape, frequency and duration. Prior to this unbiased categorization method, identified 14 subjective categories in 50-kHz rat vocalizations that could be manually identified by a trained experimenter. These categories have received some limited study, but the excessive labor and time needed for manual classification restricted broad adoption. We aim to use neural networks to quickly and automatically classify USVs into these categories to promote broad adoption and better our understanding of the relationship between USVs and behavior. The process of training our neural network to differentiate between vocalizations was approached in two ways. Audio files were converted to sonograms through DeepSqueak and manually labeled. Thousands of these labeled calls were then inputted as training data for the neural network. This method allowed the network to learn using a large set of labeled vocalization data. The second method is based around the manual selection of an optimal call for each subtype using DeepSqueak's "call clusters" function; the neural network was then trained around how closely vocalizations matched the optimal calls. We now plan to compare DeepSqueak's automated calls and clustering to manual scoring in order to develop the best possible system that reliably categorizes USVs, thus allowing for more specific analyses of USV categories and behavior.

POSTER SESSION 2

MGH 241, Easel 153

1:00 PM to 2:30 PM

Inhibition of FKBP51 in the Dorsal Raphe Using SAFit2 Has Antidepressant Effects

Emily K Vo, Senior, Biochemistry
UW Honors Program
Mentor: John Neumaier, Psychiatry
Mentor: Kevin Coffey, Psychiatry and Behavioral Science
Mentor: Russell Marx

Polymorphisms in the gene, FKBP5, and its resulting protein, FKBP51, are associated with stress-related disorders. Although FKBP51 inhibitors may have antidepressant-like effects, the relevant brain regions mediating this effect are still unknown. We found that FKBP51 expression is elevated in serotonin neurons of the mouse dorsal raphe nucleus (DRN) after stress, so we tested whether FKBP51 inhibition in the DRN by the novel FKBP51 antagonist, SAFit2, has antidepressant-like effects. First, we implanted guide cannulas into the DRN of wildtype mice stereotaxically, then

we habituated the mice to 2.5% sucrose-containing bottles in their home cages overnight. On the following two days, the mice were stressed through repeated forced swims after receiving either SAFit2 (n=8) or a vehicle (n=7) to the DRN via the cannulas, prior to each swim session. That evening, the mice underwent a sucrose preference test to assess motivation by quantifying sucrose versus water preference using lickometers. On the next day, the mice were tested in a three-chambered social interaction test, where one chamber contained a wired cup enclosing another mouse of the same sex and the other chamber had an empty wired cup. Our results show that the SAFit2 and vehicle mice had the same immobility time during the forced swim stress, signifying that SAFit2 did not interfere with our immediate stressor. The SAFit2 mice demonstrated an increased preference for sucrose after stress compared to the vehicle mice, indicating greater motivation to consume a pleasurable liquid. However, there was no significant difference in the time spent interacting with the same sex during the social interaction test. This suggests that SAFit2 may have blocked stress-induced anhedonia by inhibiting FKBP51 activity in serotonergic neurons, as measured by the sucrose preference test. Further studies of FKBP51 inhibition in the DRN can lead to potential therapeutic treatments of neuropsychiatric disorders.

POSTER SESSION 2

Balcony, Easel 113

1:00 PM to 2:30 PM

Characterizing the Role of Chlamydia Inclusion Protein CT147 in Inclusion Formation and Pathogenesis

Forrest Michael Kwong, Senior, Biology (Molecular, Cellular & Developmental)
Mary Gates Scholar, UW Honors Program
Mentor: Kevin Hybiske, Medicine

Chlamydia trachomatis is a human urogenital pathogen and the leading cause of bacterial sexually transmitted infection worldwide. A major aim of the Hybiske Lab is to develop a functional genetic understanding for *Chlamydia*. I am studying a set of newly generated *C. trachomatis* chimeric mutants that were generated from interspecies lateral gene transfer between *C. trachomatis* and the mouse adapted species *C. muridarum.* This series of recombinant strains contain a differing extent of genetic exchange surrounding the predicted inclusion membrane protein (Inc) CT147. CT147 is predicted to be secreted into the *Chlamydia*-containing vacuole (inclusion) membrane by type III secretion and subsequently mediate molecular interactions with host proteins. In cultured cells, strains lacking CT147 prematurely rupture inclusions at 24 hours post infection, in stark contrast to wild-type *C. trachomatis* or control recombinant strains that grow normally inside host cells and do not exhibit inclusion lysis at any stage of infection. We therefore hypothesized that the *C. muridarum* ortholog of CT147 is incompatible with the series of ˜30 Inc proteins normally secreted by *C. trachomatis*, in such a way that inclusion integrity is not properly maintained during this strain's developmental growth. I have used quantitative RT-PCR to evaluate transcript levels early and late in each strain's life cycle to determine if the diversion in phenotypes is due to an alteration in the Inc's promoter. I have expressed in trans CT147 in the chimeric strain lacking the Inc and analyze if CT147 can rescue the premature rupturing phenotype. Similarly, I expressed the *C. muridarum* ortholog TC0424 into wild type *C. trachomatis* to determine if the phenotype is dominant. Overall, we anticipate that a molecular and functional characterization of this novel Inc protein will reveal new insight into the mechanisms by which *Chlamydia* manipulate host cell function to facilitate their infection.

POSTER SESSION 4

MGH 241, Easel 132

4:00 PM to 6:00 PM

The Effects of Aspirin on Platelet Mechanics of Males and Females

Kenia Diaz, Senior, Biology (Physiology), English
Mary Gates Scholar
Mentor: Nathan Sniadecki, Mechanical Engineering
Mentor: Molly Mollica, Bioengineering
Mentor: Kevin Beussman

Platelets seal wounds in blood vessels in order to prevent blood loss. When there is an exposed vascular matrix, platelets bind at the wound site through the glycoprotein (GP) Ib-IX-V complex. Glycoprotein receptors allow platelets to initiate homeostasis by forming attachments to the damaged tissue. Platelets use their glycoprotein receptors to form bridges between other platelets and the surrounding proteins that form the clot within the blood vessel. Aspirin, a common household medication, produces its effects through inhibition of thromboxane production which prevents the formation of these blood clots by meddling with platelet aggregation. Standard doses of aspirin for an adult are 81mg, 325mg, and 500mg. However, there could be differences between male and female platelets, indicating that there may be different amounts of glycoprotein receptors between males and females. Here, we evaluated the force of single platelets without aspirin in males and females and single platelets with aspirin in males and females by using a reference-free traction force microscopy (TFM) platform. This TFM platform contained a grid of a fluorescent protein at known locations and was coated with von Willebrand Factor (VWF) to mediate platelet binding. Immunofluorescent staining and fluorescent imaging was conducted to visualize to platelet f-actin, a cytoskeletal component, and GPIb. Platelet binding, spreading, and contraction is observed on these substrates. By placing the platelets on the substrate, we are able to measure the de-

flection of the grid and determine the force a single platelet generates. In the future, we hope to measure the force of platelets at 0mg, 81mg, 325mg, and 500mg between men and women and hope to elucidate how GPIb expression, platelet mechanics, and response to aspirin varies in males and females.