Online Proceedings

POSTER SESSION 1

Commons West, Easel 30

11:00 AM to 1:00 PM

Family Nutrition Environments and Eating Behaviors among Low-Income Adolescents

Mia (Margaret) Strauss, Fifth Year, Nursing
UW Honors Program
Mentor: Wendy Barrington, Child, Family, and Population Health Nursing, School of Nursing

Adolescent obesity disproportionately affects lower-income and minority populations and is a strong predictor of adult obesity. Family-level eating norms (e.g. eating meals together, eating fast food, and using food as reward) and perceived neighborhood nutrition environment (e.g. access to food outlets and fast food advertising) are important predictors of obesogenic eating behaviors (e.g. intake of fast food and fruits and vegetables) among children. However, more research is needed to determine whether these factors also influence eating behaviors among adolescents. The purpose of this study is to determine which family-level environmental factors influence adolescent eating behaviors and which are most amenable to change by the adolescents themselves. Quantitative and qualitative data was collected during focus-group sessions among students at three lower-income high schools in South King County. Content analysis was performed to identify perceived barriers and facilitators to healthy eating behaviors and factors most amenable to change. Study findings will inform future youth empowerment interventions to promote obesity prevention.

POSTER SESSION 1

Commons West, Easel 35

11:00 AM to 1:00 PM

Nursing Students' Attitudes Towards Homeless Adults

Vincent S. (Vincent) Witwer, Fifth Year, Nursing
UW Honors Program
Mentor: Josephine Ensign, Psychosocial & Community Health, Nursing
Mentor: Wendy Barrington, Child, Family, and Population Health Nursing, School of Nursing

Homelessness has reached crisis levels in Seattle and King County. Poor health outcomes and limited access to culturally competent, quality medical services are significant challenges for people experiencing homelessness. Despite the need for skill-building in this area, nursing students traditionally receive limited training in caring for homeless patients, and stigma toward this population is common among clinicians. Literature indicates that service learning experiences can help prepare nursing students to offer better care to the homeless. The purpose of this study is to evaluate the impact of a quarter-long service learning course on the attitudes and behavioral intentions of nursing students toward homeless populations. This study examines data collected from 1st year Doctor of Nursing Practice (DNP) students (n=112) enrolled in NSG 552: Social Determinants of Health and Health Equity at the University of Washington during Winter 2017 quarter. Students completed a 10-item survey at the beginning of the quarter and again at the end of the quarter. Survey domains included cultural awareness, knowledge of homelessness, and self-efficacy to provide care to homeless populations. Students also completed a professional reflection related to how their service learning experience influenced their practice. The survey responses were analyzed using descriptive statistics. The written reflections were reviewed to identify common themes. This study contributes to our understanding of how a quarter-long course with a service learning component can impact nursing students' attitudes, perceptions and intentions of working with homeless populations. By better understanding the effect of the course on students, UW health sciences faculty can better tailor coursework to ensure nursing students are equipped with the knowledge and skills necessary to deliver culturally competent care to patients experiencing homelessness.

POSTER SESSION 1

MGH 241, Easel 155

11:00 AM to 1:00 PM

The Genes and Genetic Mechanisms Underlying Hereditary Spastic Paraplegia

Olga Cherepakhin, Junior, Center for Study of Capable Youth
Mentor: Wendy Raskind, School of Medicine

Hereditary Spastic Paraplegia (HSP) is a classification for a group of neurogenetic diseases that cause affected individuals to have contractions and stiffness in the limb muscles.

This group includes a wide range of disorders that vary in age of onset, rate of progression, and severity. The purpose of my project is to identify gene variants involved in HSP and their causal mechanisms. My lab acquired DNA samples from affected and unaffected members of a family with an unassigned autosomal dominant HSP. To begin my analysis, we obtained whole exome sequencing on DNA from three affected members. In a file containing all the variants (differences from a reference exome) detected in any of these three subjects, I looked for previously identified causal variants to ensure that the family did not have a known HSP subtype. Then I chose candidate variants by filtering for those that were heterozygous in all the exome sequences, and ranked them based on their absence from the Exome Aggregation Consortium database, predicted change in the protein, relevance of the gene function, absence from the UW Center for Precision Diagnostics database, and dbNSFP model predicted impact. I selected a total of 50 candidate variants and am in the process of analyzing them further. I have amplified and sequenced DNA from all the family members to determine whether certain selected candidate variants are present in all those who are affected and absent from those who are not affected, since this is the pattern expected for an autosomal dominant condition. I have currently eliminated five candidate variants and expect to soon identify the causal variant. My project will contribute to our understanding of the pathogenesis of HSP and improve clinical diagnostics for this disorder. The implications of my research could extend to other disorders if a novel mechanism was elucidated.

POSTER SESSION 1

Balcony, Easel 102

11:00 AM to 1:00 PM

Design of a Photo-switchable Protein Using Bacterial FimH

Brianna Mc Intosh, Senior, Bioengineering
Mary Gates Scholar, UW Honors Program
Mentor: Wendy Thomas, Bioengineering

Antibodies play a crucial role in both therapeutics and diagnostics due to their high target specificity. However, a characteristic that accompanies this high specificity is the reluctance to release the bound target. This presents challenges when either the protein or target needs to purified and analyzed or the protein needs to be removed from a site of interest. Current methods to reverse binding are often toxic and require large environmental changes that are not always feasible. These environmental changes can negatively affect the ligand structure, thus hampering analysis to characterize the target ligand. Therefore, a need exists for a protein whose binding can be externally controlled in a nontoxic manner. The Thomas Lab proposes using a light-activated azobenzene linker to create a crosslinked protein whose binding affinity can be controlled by light. The protein of interest is the bacterial adhesion protein, FimH, which has two known conformations that are regulated by force. The goal is to replicate the two conformations in the absence of force by using the linker. FimH has been mutated to have two free cysteines across the two domains for crosslinking. An assay has been developed to differentiate between crosslinked and non-crosslinked proteins to determine whether the linker has bound to the free cysteines. The azobenzene linker has been crosslinked to the mutated FimH and the change in binding to the target under UV light has been characterized. If a change in binding is detected, the design of a crosslinked protein whose binding can be externally controlled by light will be successful.

POSTER SESSION 1

Balcony, Easel 101

11:00 AM to 1:00 PM

A Computational Model for a Global Health Anesthetic Vaporizer

Ross J Boitano, Senior, Bioengineering
Mentor: Wendy Thomas, Bioengineering

Providing quality surgical care and anesthesia in low-resource communities has proven to be quite challenging, as many anesthetic devices are either too expensive or require electricity. Anesthetic vaporizers work by evaporating a liquid anesthetic into an air flow, which is then delivered to the patient. As the liquid anesthetic is evaporated, the temperature decreases, leading to a decrease in delivered anesthetic, which is problematic if not addressed. Current devices address this issue by encompassing the vaporizer in a large steel heat sink, but this makes the device unsuitable for transport long distances. A low-cost anesthetic vaporizer has been proposed and developed by Bioengineers Without Borders that will utilize phase change material to hold the vaporizer temperature constant, and they are seeking a predictive tool to guide design choices. A computational model of this vaporizer has been previously built utilizing laminar flow dynamics. However, this model did not sufficiently predict the dynamics of the vaporizer under various operating conditions. The model has now been converted to utilize turbulent flow dynamics, and is undergoing validation steps through comparisons with the experimental measurements of concentration output and halothane surface temperature. Additional adjustments have also been made to the laminar flow model, resulting in a more accurate model. Currently, both the turbulent and laminar models predict a decreasing temperature over time, resulting in decreasing amounts of anesthetic being delivered. Both models perform very well at high flow rates, but constantly overestimate deliveries at low flow rates. Upon validation, this model will give Bioengineers Without Borders the ability to computationally test possible design modifications to the vaporizer prior to production, saving time and resources.

SESSION 1K

MOLECULAR BASIS FOR HUMAN DISEASE

Session Moderator: Caroline Harwood, Microbiology
MGH 271
12:30 PM to 2:15 PM

* Note: Titles in order of presentation.

Microfluidic Flow Chamber Array to Study Viridans Group Streptococci
Christian Matthews, Senior, Bioengineering
Mary Gates Scholar, NASA Space Grant Scholar, UW Honors Program
Mentor: Wendy Thomas, Bioengineering

Bacterial endocarditis is a life-threatening disease that occurs when bacteria bind to the inner surface of cardiovascular tissue. One group of bacteria in particular, the viridans group Streptococci, cause a high percentage of cases of endocarditis. It is known that adhesion is mediated by specialized proteins on the surface of bacteria capable of binding to specific glycans expressed outside of host cells, and that binding is also dependent on shear stress from flow through allosteric regulation of the binding site. However, the exact mechanisms and resulting rates of binding are not sufficiently understood. If adhesion of the viridans group Streptococci can be experimentally tested and characterized, it could lead to the development of anti-adhesive therapies to treat or prevent diseases such as endocarditis. Current methods of testing bacterial adhesion utilize a parallel plate flow chamber to test the binding of one species of bacteria to a single glycan under one flow rate. Significant progress could be made through the construction of a microfluidic flow chamber compatible with a glycan array capable of testing bacterial adhesion to various glycans under a range of shear stresses in a single run. I have designed such a device using CAD and COMSOL fluid modeling software, and will construct it through the process of 3D stereolithography and laser-cutting. Additionally, I have conducted experiments to identify conditions that minimize non-specific adhesion, maximizing specificity for the device. Bacteria were fluorescently tagged, run through the flow chamber and across the glycan array, and then adhesion was analyzed using a microarray scanner. Data gathered from this device will help collaborators develop treatments to treat and prevent this type bacterial endocarditis. The flow chamber is also now accessible to others in the field to be used to study other clinically relevant types of bacterial adhesion.

SESSION 1S

NEW DIAGNOSTIC TOOLS FOR SEEING AND SENSING DISEASE

Session Moderator: Benjamin Freedman, Medicine/Nephrology
JHN 175
12:30 PM to 2:15 PM

* Note: Titles in order of presentation.

Design of Activatable Recognition Proteins for Improved *In Vitro* Diagnostics
William (Bill) Koski, Senior, Bioengineering
UW Honors Program
Mentor: Wendy Thomas, Bioengineering

Biological recognition proteins are widely used for a variety of biomedical applications, including *in vitro* diagnostics (IVD). IVD tests that use antibodies as recognition proteins, such as rapid antigen tests, are one of the fastest methods for providing point-of-care diagnosis of infectious diseases. However, many current applications of antibody-based molecular diagnostics are restricted by poor sensitivity in a sample with low target antigen concentration. One method which has shown promise for improving the sensitivity of rapid antigen tests is to pre-concentrate a target sample. We are using selection from a random library of *Escherichia coli* bacteria expressing the adhesion protein, FimH, to develop an activatable recognition protein for capture-and-release preconcentration of a target antigen. FimH is a two-domain bacterial adhesion protein that exhibits conformation-dependent binding to mannose. We predict that mutations in the CDR2 and CDR3 loops of the FimH binding pocket can be used to design a protein with binding specificity for a diagnostic target while maintaining conformation-dependent affinity. In previous work, random mutations of the amino acid residues in the FimH binding pocket produced a library of FimH variants with variable binding specificity. Our results suggest that using a biomagnetic selection assay to screen this library of FimH mutants against the small molecule targets digoxigenin and cortisol enriches FimH variants with target binding specificity. Currently, we are designing and optimizing an assay, iterating on the wash conditions, conjugation strategy, and other parameters, to screen the library against protein targets such as the viral antigens influenza hemagglutinin and dengue NS1. In future work, we seek to demonstrate that a variant with binding specificity for a diagnostic target has distinct conformation-dependent affinity which can be actively regulated to capture and release a target antigen.

SESSION 2B

CHEMISTRY, BIOCHEMISTRY, AND MATERIALS SCIENCE

Session Moderator: Sharona Gordon, Physiology and Biophysics

MGH 228

3:30 PM to 5:15 PM

* Note: Titles in order of presentation.

Correcting for Mass Transport Effects in Bacterial Adhesion Studies

Kayla Marie (Kayla) Hogan, Senior, Bioengineering
Mary Gates Scholar, NASA Space Grant Scholar
Mentor: Wendy Thomas, Bioengineering

With the rising prevalence of drug resistant bacteria, there is a pressing need to develop novel approaches which do not rely upon antibiotics. Anti-adhesive therapies target the ability of bacteria to adhere to tissue via adhesin receptor interactions. Yet, commonly used methods for characterizing these interactions involve parallel plate flow chambers (PPFCs), and are consistently done without consideration of mass transport effects. Here, we demonstrate that measurements of adhered bacteria taken within a large adhesive spot can vary significantly based upon the location measured. A computational model of a PPFC experiment is developed and validated in order to use partial differential equations to determine how various parameters influence spatial variation in adhesion. Use of a computational model allows investigation into a wide range of parameter values which would be impractical to experimentally test. Based upon these results, analytic models are established to accurately predict how transport conditions affect adhesion measurements. Interestingly, the measurement which best demonstrates a spot's affinity for a bacterial ligand is the difference between the concentration of bound bacteria at the start of the spot and the consistent concentration reached well into the spot, according to these models. This is validated through PPFC experiments. Additionally, we demonstrate that within a multispot array, the adhesion in the spot of interest is highly affected by the preceding spot. It is vital that experimenters recognize this issue while interpreting their data. Guidelines to help experimenters set up and interpret their data in a manner that accounts for mass transport effects are described. Ultimately these guidelines could help reduce or negate the systematic error which mass transport introduces to adhesion experiments, and lead to better anti-adhesive therapies.

SESSION 2E

ADVANCED TECHNOLOGIES FOR HEALTHCARE AND OTHER APPLICATIONS

Session Moderator: Daniel Kirschen, Electrical Engineering

MGH 238

3:30 PM to 5:15 PM

* Note: Titles in order of presentation.

Creating a Template for Spacing Single Molecules for Force Measurements

Amy Stegmann, Junior, Materials Science & Engineering
Mary Gates Scholar, NASA Space Grant Scholar
Mentor: Wendy Thomas, Bioengineering
Mentor: Molly Mollica, Bioengineering

Characterizing fundamental mechanical properties of individual molecules is essential to understanding and treating disease, because proteins have diverse responses to stimulus. The ability to predict a response enables targeted treatments. Although atomic force microscopy (AFM) and magnetic tweezers are able to measure the response of single molecules to mechanical force, it is challenging to ensure single molecules are being measured. In this project, structural DNA nanotechnology (DNA origami) is used to create a template which spaces molecules for single molecule force measurements. DNA is an excellent nanoscale building material due to its self-assembly properties, nanoscale structural precision, and the capability for precise control over placement of functionalization. By attaching functionalized DNA at specific sites and polymerizing the structure, a repeated precise interval is created for molecules of interest. This nanostructure was designed using caDNAno and canDo. Nanostructure folding time, temperature, and salt conditions were optimized using agarose gel electrophoresis. Nanostructures were imaged with transmission electron microscopy to confirm correct formation of the structure. Polymerization will be imaged using AFM, and force characteristics of the structure will be measured via AFM, to establish a base point for measuring the molecules of interest.

SESSION 2E

ADVANCED TECHNOLOGIES FOR HEALTHCARE AND OTHER APPLICATIONS

Session Moderator: Daniel Kirschen, Electrical Engineering

MGH 238

3:30 PM to 5:15 PM

* Note: Titles in order of presentation.

Computational Modeling of Hydrodynamic Lift Effects on Initial Bacterial Adhesion under Different Flow Conditions

Uyen Phan Khanh (Uyen) Tran, Senior, Bioengineering
Mary Gates Scholar
Mentor: Wendy Thomas, Bioengineering

As antibiotic resistance becomes a growing problem, there is a need to research alternative bacterial infection treatments without relying on antibiotics. Anti-adhesive therapy, which prevents bacteria from adhering to tissue, is an alternative solution to the antibiotic resistance problem. Flow rate (or shear stress) is one of the factors that affect bacterial adhesion in solution. Bacteria adhere to tissue in vivo where shear stress can go up to 8 Pascal, but they are unable to adhere in vitro in shear stresses above 1 Pascal. Hydrodynamic lift is the force known to push microparticles away in high flow and prevent the particles from getting close to a surface. However, there is no tool that describes how lift affects bacterial adhesion. This project aims to determine whether lift pushes the bacteria away from the wall and prevents bacteria from initiating binding in continuous flow in vitro as opposed to pulsatile flow in vivo. To do this, we developed a computational model which uses discrete finite element method to determine how lift affects initial adhesion. The model showed bacterial concentration depletes by the wall but concentrates where lift and gravity are balanced. The flow rate or wall shear stress affected where the bacteria accumulates thus influenced their adhesion. Moreover, this model has improved the mass loss problem, which the previous model faced. We validated the model by existing parallel plate flow chamber experiments with different bacteria. The validation experiments also gave some understanding regarding how lift affects the binding of different bacterial species under multiple continuous and pulsatile flow conditions. The results of this project will help researchers make informative decisions to design bacterial binding experiments by providing a tool to understand how lift and gravity affect initial bacterial adhesion.