UNIVERSITY of WASHINGTON

Undergraduate Research Symposium May 18, 2018 Mary Gates Hall

Online Proceedings

SESSION 1A

BUSINESS TOPICS RELATED TO EARNINGS, FINANCE, AND MARKETING

Session Moderator: Weili Ge, Accounting
MGH 074
12:30 PM to 2:15 PM

* Note: Titles in order of presentation.

Optimal Dynamic Pricing of Inventories with Stochastic Demand Functions for Online Fashion Retailers
Xiangjun (Aileen) Yang, Senior, Economics, Applied & Computational Mathematical Sciences (Mathematical Economics)
UW Honors Program
Mentor: Michelle Turnovsky, Economics
Mentor: Matthew Lorig, Applied Mathematics

This research deals with the specific dynamic pricing strategy of fashion products sold online. The pricing method works under the condition of a pre-determined quantity of inventory with stochastic demand functions on a limited time horizon, which is formulated as an optimization problem. To achieve the maximized profit, it is essential to balance between the extra marginal revenue earned by setting a high selling price and the cost lost from unsold items. In order to find the solution, we first develop and estimate a pricing model that captures the important characteristics of the fashion apparel market. Afterwards, we use data from a leading Taiwanese fashion retailer to examine the accuracy of our model. The final purpose of this research is to provide an insightful conclusion of the dynamic pricing policies that would generate the highest retailer revenues.

SESSION 1D

MARINE ECOLOGY AND FOOD WEBS

Session Moderator: Bonnie Becker, Environmental Science (Tacoma)
MGH 228
12:30 PM to 2:15 PM

* Note: Titles in order of presentation.

Are All Herbivores Created Equal? Linking Diet to Morphology in Phytophagous Pacus
Jonathan Michael Huie, Junior, Aquatic & Fishery Sciences
Mary Gates Scholar, UW Honors Program
Mentor: Adam Summers, Biology
Mentor: Matthew Kolmann, Friday Harbor Labs

Herbivorous fishes feed on stems, leaves, flowers, seeds, fruits, and nuts of diverse aquatic plants, as well as algae. In the Neotropics, many of these fishes have intricately tied ecologies with their prey plant's life history and facilitate seed dispersal; including the herbivorous cousins of piranhas, pacus. Most pacus experience fluctuation in their diet that reflects the changes in seasonality and plant part availability. A few species of pacus, however, exhibit a specialized feeding strategy known as phytophagy; solely consuming the plant material of *Podostemaceae* (riverweed). This trend of dietary specialization may be paralleled by a similar shift, away from general herbivory, and towards a specialized phytophage morphology. To investigate the link between diet and morphology within the greater scope of herbivory, we examined four coexisting species including: the seemingly specialized phytophage, *Ossubtus xinguense*; the generalized phytophages, *Tometes kranponhah* and *Tometes ancylorhynchus*; and a facultative phytophage, *Myloplus rhomboidalis*. We compared the gross morphology of these species with several other serrasalmids using micro-computed tomography scanning to measure functional jaw characteristics, as well as using geometric morphometrics to compare body shapes. Jaw biomechanics indicate that *O. xinguense* produces the weakest jaw leverage potentially as a result of its sub-terminal mouth. However, we also concluded that the phytophagous species as a group, do not overtly differ from the more generalized herbivorous pacus in terms of jaw mechanics (but remain distinct from the piscivorous piranhas). Body shape analyses also show little divergence among phytophage and herbivore body shapes, suggesting that many herbivores share a similar bauplan adapted for fast flowing waters. With the exception of *O. xinguense*, phytophagous pacus appear to be equipped with a general herbivory feeding morphology sufficient for a specialized diet. This suggests that phytophagy is not a particularly challenging feeding strategy, but performance may be augmented by additional morphological specialization.

SESSION 1G

TOWARDS BETTER UNDERSTANDING OF HUMAN DISEASES THROUGH MOLECULAR BIOCHEMISTRY

Session Moderator: Valerie Daggett, Bioengineering
MGH 238
12:30 PM to 2:15 PM

* Note: Titles in order of presentation.

Design of an Alpha-Sheet Peptide for the Inhibition of Aggregation in AL Amyloidosis
Lauren Nicole Martini, Senior, Computer Engineering, Bioengineering
Mary Gates Scholar
Mentor: Valerie Daggett, Bioengineering
Mentor: Matthew Childers, Bioengineering

The misfolding and aggregation of free light-chains into amyloid fibrils is the hallmark of antibody light-chain (AL) amyloidosis, a fatal disease associated with the accumulation of amyloid species in tissues throughout the body, including the heart and kidneys. Current treatment options, including chemotherapy and bone marrow transplant, do not address the causes of aggregation on a molecular level. Molecular dynamics (MD) simulations were used to investigate misfolding pathways in the aggregation of two light chain monomers, Jto and Wil. These simulations showed that under amyloidogenic conditions, conversion from beta-sheet to alpha-sheet secondary structure was observed in both Jto and Wil. Misfolded conformations, obtained from the MD simulations, were used to guide the design of alpha-sheet peptides, which have been used previously to inhibit amyloid formation in diverse systems. The designed peptides were evaluated computationally by docking them against misfolded conformations of Wil, and the best performing peptide was chosen for future experimental work to explore its potential to limit aggregation.

SESSION 1L

SOUND TO MOUNTAINS: WATER, LIFE, AND CLIMATE IN THE SALISH SEA

Session Moderator: Peter Selkin, School of Interdisciplinary Arts & Sciences
MGH 271
12:30 PM to 2:15 PM

* Note: Titles in order of presentation.

Risk Assessment of *Phytophthora alni* in Washington State
Brandon E. Voelker, Junior, Environmental Science, UW Tacoma
Mentor: Matthew Kelley, Urban Studies

Phytophthora alni is a species complex of pathogenic oomycetes (water molds) that can cause lethal disease in alder trees, *Alnus* spp. One variant, *P. alni* subsp. *alni*, is widespread across Europe, devastating stands of alder since the 1990s. One less lethal member of the species complex, *P. alni* subsp. *uniformis*, has already been found in the wild in Alaska and Oregon, but not in Washington State. Recently, it has been detected in potted alders in nurseries in Pierce County. It is currently unknown whether any member of the *P. alni* species complex is in the wild in Washington, either naturally or through introduction from nursery plants. To begin efforts to detect *Phytophthora alni* in Washington State, a risk assessment map will be created using Geographic Information System (GIS) techniques. The spatial analysis will involve examining the environmental factors that increase infection susceptibility, such as slope, soil grain size, and flooding, and correlating with the distribution of alders. Important questions that could be revealed are whether high risk areas are upstream, where infection could spread, or downstream, and whether high risk areas correlate with urban or agricultural land use. The risk assessment will provide a starting point for choosing sampling sites, which is the next step in detecting the existence of *P. alni*. Additionally, the final analysis will inform forest management practices, as the highest risk areas could be inspected for symptomatic alders and mitigation measures could be enacted if any are found. The assessment will also have implications for restoration sites, where native trees such as alder are planted from nursery stock.

SESSION 1M

LIFE AND DEATH IN THE OCEAN

Session Moderator: Virginia Armbrust, Oceanography
MGH 284
12:30 PM to 2:15 PM

* Note: Titles in order of presentation.

Use It or Lose It: Three Ways That Snailfishes (Liparidae) Reduce Their Skeleton in the Deep
Abigail Andrea (Abby) Von Hagel, Senior, Biology (Molecular, Cellular & Developmental), Neurobiology
Mary Gates Scholar, UW Honors Program
Mentor: Adam Summers, Biology
Mentor: Stacy Farina, Friday Harbor Laboratories
Mentor: Mackenzie Gerringer, Friday Harbor Labs
Mentor: Matthew Kolmann, Friday Harbor Labs

Skeletal reduction is a common feature among deep-sea

fishes that have diversified from shallow-water relatives, such as snailfishes. These skeletal reductions may be an adaptation to environmental conditions of high pressures, low temperatures, declining luminosity and limited food availability. Snailfishes (family Liparidae) are found across a large bathymetric range (0 –>8,000 m), with intertidal ancestors giving rise to a large clade of deep-sea species. We used microcomputed tomography (micro-CT) to estimate average bone mineral density and examine jaw, pectoral girdle, and neurocranium morphology. Our results suggest at least three mechanisms of skeletal reduction: (1) reduction of bone size, (2) reduction of bone density, and (3) loss of skeletal elements. First, using phylogenetic generalized least squares (PGLS) analysis, we found that the change in cranial dimensions with depth was not uniform. While the size of the maxilla, dentary, and pectoral girdle decreased with greater depth, length of the upper premaxilla and the neurocranium did not vary with collection depth. Second, average density of the lower jaw decreased with increasing depth. Lastly, the ventral suction disc has been lost multiple times within the deep sea lineage. While all three methods are seen in snailfishes, other groups may use some or all of these mechanisms to different extents. Some mechanisms of skeletal reduction may be more advantageous than others. The extent to which a structure is retained in deep-dwelling fishes may indicate its functional importance. Variable skeletal reduction in the family Liparidae provides insights into the physiological adaptations that allow fishes to survive in deep-water environments. We conclude that some skeletal elements are maintained at the expense of others as fishes balance the functional demands of life in the deep sea.

SESSION 1P

MCNAIR SESSION - SCIENCE AND TECHNOLOGY FROM CELLS TO OUTER SPACE

Session Moderator: Laura Pina, Human Centered Design and Engineering

MGH 295

12:30 PM to 2:15 PM

* Note: Titles in order of presentation.

Stimulation of Neuronal Toll-like Receptor 7 on C-fibers Increases Nerve Growth *in vitro*

Karol Wai, Senior, Biology, Portland State University
McNair Scholar
Mentor: Matthew Drake
Mentor: Becky Proskocil

Viral infection is associated with asthma exacerbations. Normally, viral presence is detected by Toll-like receptor 7 (TLR7)—an innate immune receptor in airway epithelium that responds to single-stranded RNA viruses (like influenza) and triggers an immune response to infection. TLR7 is also expressed on airway sensory nerves, but its specific role is unknown. Here, I tested the role of TLR7 on sensory nerves and identified which sensory nerve populations express TLR7 using nerves isolated from dorsal root ganglia from female Hartley guinea pigs (˜400 g). Ganglia were isolated, plated onto matrigel, and treated with a TLR7 agonist R837 (0.1-100 microM) for 16 hours. Neurite number per cell was not changed by stimulating TLR7, but neurite length, and the number of branch points were significantly increased. Separate experiments measured which types of sensory nerves expressed TLR7. Vagal and dorsal root ganglia were isolated and fixed in zinc formalin. Nerves were immunolabeled with antibodies against TLR7 and either neurofilament-1 (NF-H) to identify A???? fiber sensory nerves or transient receptor potential V1 (TRPV1) to identify C-fiber sensory nerves. I found that airway sensory nerves originating in the vagal and dorsal root ganglia expressed TLR7. However, TLR7 was expressed predominantly on small TRPV1-expressing C-fiber neurons, but not on large NF-H-positive A???? neurons. In conclusion, TLR7 is highly expressed by airway sensory C-fibers nerves, and its activation stimulates neurite growth. These findings suggest TLR7 may increase airway C-fibers supplying the lungs which may enhance airway reactivity and be a mechanism for virus induced exacerbations of asthma.

POSTER SESSION 2

Commons West, Easel 21

1:00 PM to 2:30 PM

Using Linguistic Knowledge to Resolve Ambiguity in Speech Perception When Hearing is Degraded

Siuho Gong, Senior, Speech and Hearing Sci (Com Disorders)
Mentor: Matthew Winn, Speech & Hearing Sciences
Mentor: Steven Gianakas

Sometimes speech sounds (phonemes) can be ambiguous, and people have a tendency to interpret the ambiguous phoneme differently in different contexts so that they perceive a real word, as opposed to a non-word. This effect is called ”lexical bias.” For example, when there is ambiguity between whether /m/ or /n/ is heard, /m/ is more likely to be perceived if it is followed by ”uch,” because ”much” is a word, but ”nuch” is not (and vice versa if the context is ”udge”). We hypothesized that for people who have hearing loss or use a cochlear implant, there will be additional ambiguity in hearing speech, and that the lexical bias effect would be stronger. We simulated degraded hearing using vocoded speech played to listeners with normal hearing. Participants heard speech continua that gradually morphed from /m/ to /n/ in the ”uch” and ”udge” contexts, and either had a clear

spectral quality or a degraded spectral quality. Results suggest that the lexical bias is stronger when the speech signal quality is less clear, which is consistent with the hypothesis because of the increased phonemic ambiguity in these conditions. By understanding how signal degradation impacts the perception of phonemes, audiological tests for speech reception can be improved to separately acknowledge the effects of hearing from the adjustments that the listener makes to maintain lexical biases in speech perception.

SESSION 2B

ENHANCING IMMUNE RESPONSES TARGETING INFECTION, INJURY AND CANCER

Session Moderator: Kristin Anderson, Immunology
MGH 228
3:30 PM to 5:15 PM
* Note: Titles in order of presentation.

T-Bet Mediated Control of Effector T Cell Phenotypes
Leonard Daniel Chen, Senior, Bioengineering
Mary Gates Scholar
Mentor: Hao Yuan Kueh, Bioengineering
Mentor: Matthew Wither, Bioengineering

T cells of the immune system protect humans from most threats because they can recognize and eliminate foreign targets, as well as protect from reinfections. However, the persistence of an infection in the body leads to chronic stimulation of T cells, causing them to lose their effector function and enter a state known as "exhaustion". Exhausted T cells are defined by increased expression of inhibitory receptors, loss of immune cell regulation, and most importantly, loss of cytotoxicity and effector function. Studies have shown that the transcription factors, T-bet and Eomes, play crucial roles in regulating T cell differentiation, with T-bet being highly associated with effector T cell differentiation. T-bet expression is dampened in exhausted T cells, and therefore, I hypothesize that controlled induction of T-bet expression can reverse the exhausted phenotype in antigen-experienced T cells. I constructed a T-bet overexpression vector containing T-bet cDNA fused to a fluorescent protein and destabilizing domain. The destabilizing domain, or degron, facilitates degradation of the constitutively expressed T-bet transgene in the absence of the ligand, Shield-1, which when added at varying concentrations allows for a range of protein stability. This method of overexpression confers faster control kinetics compared to commonly used transcriptional approaches, such as inducible promoters. I have characterized the range of the T-bet transgene in Jurkat cells by titrating Shield-1 to provide a working range of 5-60% overexpression of T-bet compared to endogenous levels. Validating these parameters in primary T cells will allow me to apply this T-bet overexpression vector in a mouse model of T cell exhaustion. This tool has significant implications for improving immunotherapy strategies, such as TIL and CAR-T therapies, where exhaustion of the therapeutic T cells has led to reduced efficacy of the treatment.

POSTER SESSION 3

Commons East, Easel 82
2:30 PM to 4:00 PM

What Can the James Webb Space Telescope Tell Us about the Dark Matter Halos of the First Galaxies?
Eden Faith Harris, Junior, Environmental Science & Resource Management
Mentor: Matthew McQuinn, Astronomy

The formation of the universe's first galaxies is currently not well understood; with the launch of the James Webb Space Telescope (JWST) in the near future, however, it may soon be possible to uncover critical details about how and when the first galaxies formed. In this project, we examine whether it will be possible to discern the clustering of high-mass, high-redshift dark matter halos from background noise when looking at data from the JWST. The ability to detect these halos, which are believed to play a key role in galaxy formation, through their clustering could lead to further breakthroughs in the study of the early universe. An initial test of the effects of projection was run using data from the Illustris simulation at redshifts z=6 and z=10. Halo positions were analyzed in both 3D and 2D at each redshift in order to determine how much projection altered our ability to detect halo clustering. When viewing 2D projections of halo positions, it became evident that projection was significantly reducing our ability to detect clustering. When we made use of the third dimension to eliminate the projection effect, the clustering of high-mass, high-redshift halos become apparent at both redshifts. In reality, it will not be possible to replicate this 3D case; exact measurements for the depths of high-redshift galaxies are not obtainable using the JWST. Going forward, we will work to refine our results by applying real JWST data specifications in order to determine the feasibility of using JWST data to detect early halo clustering. Making use of information such as limits on the detectability of galaxies based on their star formation rates and the uncertainty of JWST spectroscopic measurements will allow us to better determine whether the idea of studying halo clustering at high redshifts using JWST data is worth pursuing.

POSTER SESSION 3

Commons East, Easel 83
2:30 PM to 4:00 PM

Cross-Correlations between Lyman Alpha and Lyman Beta from the XQ-100 Legacy Survey

Bayu Jarod Wilson, Senior, Physics: Comprehensive Physics, Astronomy
Mary Gates Scholar
Mentor: Matthew McQuinn, Astronomy
Mentor: Vid Irsic, Department of Astronomy

Radiation emitted from supermassive black holes in the early universe (quasars) is absorbed by hydrogen in the intergalactic medium. Hydrogen absorbs light at certain resonant frequencies in the spectra of quasars. Statistics of Lyman-alpha absorption (the most studied resonant frequency of hydrogen) probes the cosmological parameters governing the universe (e.g. mass of dark matter) and the temperature of intergalactic gas (which constrains how the universe was heated). To further improve these constraints, I will be using another Lyman series transition (Lyman-beta). Due to the smaller absorption cross-section of Lyman-beta, we may probe higher densities than measured with the Lyman-alpha transition therefore increasing the number of data points to analyze. By including the Lyman-beta transition, our analysis allows for a better understanding of intergalactic gas which provides for more robust cosmological constraints.

POSTER SESSION 4

MGH 241, Easel 146

4:00 PM to 6:00 PM

Cell Cycle Control Mechanism Against Fatal Genomic Missegregations in Aging Yeast

Mung Gi (David) Hong, Senior, Public Health-Global Health
Joslyn Goings, Senior, Biology (Physiology)
Mentor: Matthew Crane, Pathology

Cell divisions require proper replication and distribution of genetic materials between mother and daughter cells, and mistakes made during the process may result in aneuploidy (abnormal number of chromosomes in a cell) and possible carcinogenesis. Thus, checkpoints exist along the cell cycle to ensure that cellular errors are corrected. Likewise, during the mitotic processes of budding yeast, *Saccaromyces cerevisiae*, numerous checkpoint mechanisms evolved to prevent catastrophic genomic missegregations. By observing the replicative life span of aging yeasts fluorescently tagged with histone 2B through single cell imaging, we identified a new mechanism that is needed in aging cells for correcting nuclear missegregation. This Retrograde Transport Nuclear (RETRN) pathway fixes genomic missegregation by delaying the incorrect mitotic division and returning the genetic material from the daughter to the mother cell. Following the correction, mother cells could continue to divide and produce healthy daughter cells. In our research, we generated new strains of mutant yeasts that underwent incorrect mitotic divisions to further observe the activation of the RETRN mechanism. Each mutant strain had different non-essential genes relevant to the cell cycle deleted. We confirmed the genetic makeup of each mutant strain through replica plating and PCR. Then, we imaged mother cells from verified mutant strains and observed the budding events throughout their lifespans. This allowed us to see specific points along the lifespan where mitotic divisions occurred, and whether the deletions affected the RETRN pathway. We have speculated that this mechanism is a result of cellular damage due to increasing genomic instability in aging cells, and thus is rarely observed in young, healthy cells. The RETRN pathway could be part of many new pathways needed when cells age and become genomically unstable. Since mammalian cells also become genomically unstable with age, similar mechanisms may be necessary for age-associated genomic instability in multicellular eukaryotes.

POSTER SESSION 4

MGH 206, Easel 176

4:00 PM to 6:00 PM

Development and Testing of WRANGLER for Design and Modeling of Peptides and Proteins with Interactive Visual Analytics

Jennifer Ann (Jenny) Ferina, Senior, Bioengineering
UW Honors Program
Mentor: Valerie Daggett, Bioengineering
Mentor: Matthew Childers, Bioengineering

Computational simulations of protein dynamics provide an efficient way of predicting protein behavior and are increasingly being applied to peptide and protein design. However, design tools and software focus on static structures. Incorporation of dynamics directly or through design libraries derived from dynamics simulations allows the user to focus on optimization of the native dynamics of the protein for a specific purpose. Critical libraries for design, such as side chain rotamer libraries and amino acid propensities are typically derived from static structures, which do not reflect behavior in dynamic conditions. Therefore, including rotamers and conformational propensities derived from behavior during protein simulations in molecular modeling and design software should improve the design process and outcome, particularly for peptides. Additionally, current software does not allow the user to adjust the main chain dihedral angles of the backbone according to Ramachandran plots reflecting the unique free energy landscape of each residue. The WRANGLER software was designed in order to include dynamic data to better model and design against and for dynamic systems. A number of libraries derived from dynamics simulations of all known protein folds have been incorporated. In addition, the software is interactive with a graphical interface to easily

change and visualize geometries and analyze peptide/protein properties. WRANGLER was evaluated based on ability to facilitate design of several amyloid peptide aggregation inhibitors. Resulting designs were evaluated through molecular dynamics simulations for their secondary structure retention and physical properties. Control amyloid peptide aggregation inhibitors were included that have already been designed, synthesized and tested experimentally in lab. Several peptides designed in WRANGLER appear to be better than the controls by a variety of metrics. The next step is to synthesize these new designs and test them against the amyloid-beta peptide associated with Alzheimer's Disease to see if they outperform our current compounds.

POSTER SESSION 4

MGH 258, Easel 187

4:00 PM to 6:00 PM

Novelty Not Disparity - Body Shape Evolution in Marine and Freshwater Needlefishes

Justin Yi Kai Ng, Senior, Aquatic & Fishery Sciences
Mary Gates Scholar
Mentor: Matthew Kolmann, Friday Harbor Labs

The Neotropics hold the greatest diversity of fishes, with South America alone hosting around 25% of global fish biodiversity. Despite presumably fierce competition with entrenched primary freshwater fishes like otophysans, South America is also home to a conspicuously high number of marine-derived lineages (MDLs), freshwater taxa which have evolved from marine ancestors. Transitions from marine to freshwater may have catalyzed ecological opportunity and are apt systems for examining whether habitat transitions prompt ecomorphological diversification. Body-shape and size correlate with many aspects of ecology and life history: foraging through locomotion and feeding morphology, reproduction by predicting offspring size and number, and more generally, larger fishes generally occupy higher trophic niches. We examined how such an ecological transition has affected the body-shape diversity of tropical needlefishes and sauries (Beloniformes). Using micro-computed tomographic (μCT) scanning, geometric morphometrics, and phylogenetic comparative methods we examined body-shape evolution in 33 species of belonids and two scomberesocids. We examined the evolutionary pattern and tempo of body-shape evolution in Asian and South American beloniforms using a published molecular phylogeny,. The primary axis of body shape variation is elongation/truncation, driven by lengthening/shortening of either the rostral or trunk regions. We also find that freshwater taxa are generally smaller than their marine counterparts, and become reduced in size either through miniaturization (skeletal reduction) or dwarfism (skeletal loss). Despite morphological novelty in freshwater belonids, our results show similar levels of body shape diversity between marine and freshwater taxa. Despite similar disparity between marine and freshwater taxa, freshwater belonids occupy a surprisingly large region of morphospace considering their relatively low species richness.