Undergraduate Research Symposium May 17, 2013 Mary Gates Hall

Online Proceedings

POSTER SESSION 1

Commons East, Easel 82

11:00 AM to 12:30 PM

Appliance Reader: A Smartphone Application for Blind People to Read Their Digital Displays

Antonius Denny (Denny) Harijanto, Senior, Computer Engineering
Michael Thanh Hung (Mike) Hotan, Senior, Computer Engineering
Mentor: Richard Ladner, Computer Science & Engineering
Mentor: Bryan Russell, CSE, Intel

Jane is blind and in need of a new wall oven for her apartment. As she shops for the new oven she discovers that almost all ovens have digital displays for showing the state of the oven, its temperature, and the time left on its timer. They also have buttons flush with the display panel for providing input. She knows from past experience that she can put Braille labels on the buttons and will eventually memorize which button does what, so input will not be a problem. However, how will she read the digital display? Through a friend she learns of a smartphone application called Appliance Reader, which can read digital displays for various appliances including some wall ovens. In order to implement the appliance reader, we have to utilize computer vision algorithms particularly those that match one image against another. The two images can be taken from different perspectives so geometric transformation needs to be inferred from the two images. Once the two images are matched properly, the digital data has to be interpreted to form what would be told to the user. The interpretation requires a machine learning algorithm because standard optical character recognition is not sufficient. A user interface suitable for blind users is needed to make the Appliance Reader practical. As a part of CSE Mobile Accessibility group, which develops smartphone application to aid handicapped people, the two of us have been developing Appliance Reader from the ground up. Under the guidance of Professor Ladner and our mentor, an Intel researcher, Bryan Russell, we have been researching and building Appliance Reader, which is a computer vision-based smartphone application.

POSTER SESSION 1

Commons East, Easel 80

11:00 AM to 12:30 PM

Making Public Transit Accessible via Crowdsourcing

David Kawai (David) Wong, Junior, Computer Engineering
Mentor: Richard Ladner, Computer Science & Engineering
Mentor: Shiri Azenkot, Computer Science & Engineering

Public transit plays an important role in the daily lives of blind individuals. Unable to drive, blind commuters must rely on buses, subways, and other methods of public transportation to travel from one destination to another. Although transit schedules and even real-time arrival information are now readily available and accessible, there are still barriers to overcome. For example, a blind bus rider may find it difficult to locate a designated bus stop. Prior research has shown that, given a set of information about a bus stop, blind commuters will find their bus stop with significantly greater ease and lesser time spent. Our goal is to create a database of useful and reliable information regarding every bus stop in Seattle and make that information accessible to blind individuals. In order to collect such a vast amount of data, we have turned to crowdsourcing, a process that involves dividing work amongst a large group of workers over the Internet. By providing workers with Google StreetView images (ground-level visuals on the appearance of a location) and simple, multiple-choice questions, we hope to collect accurate information to answer questions such as "How many benches are at the bus stop?" or "In what direction is the bus stop relative to the intersection?" After acquiring a sufficient set of bus stop data, we will test the usefulness of this information to blind commuters by providing them with access to our database and analyzing their feedback. We believe that our work in this field will improve the public transit experience for blind individuals by providing them with a feeling of confidence and independence during their commute. Our work in this field may lead to further research in utilizing crowdsourcing to solve accessibility issues.

POSTER SESSION 1

Commons East, Easel 81

11:00 AM to 12:30 PM

Tapulator: A Non-Visual Calculator using Natural Prefix-Free Codes

Vaspol Ruamviboonsuk, Junior, Computer Science
Mary Gates Scholar
Mentor: Richard Ladner, Computer Science & Engineering

A new non-visual method of numeric entry into a smartphone is designed, implemented, and tested. Users tap the smartphone screen with one to three fingers or swipe the screen in order to enter numbers. No buttons are used—only simple, easy-to-remember gestures. A preliminary evaluation compares the method to a standard accessible numeric keyboard with a VoiceOver-like screen reader interface. Preliminary results indicate that users can enter numbers faster and with higher accuracy when using this method. The Tapulator, a complete calculator based on this non-visual numeric entry that uses simple gestures for arithmetic operations and other calculator actions is described.

POSTER SESSION 2

Balcony, Easel 113

12:45 PM to 2:15 PM

Aqueous Dispersions of Composite Nanoparticles for Polymer Solar Cell Applications

Curtis Liam (Curtis) Whittle, Senior, Chemical Engr: Nanosci & Molecular Engr
Mentor: Lilo Pozzo, Chemical Engineering
Mentor: Jeffrey Richards, Department of Chemical Engineergin

Poly(3-hexylthiophene) (P3HT) and 6,6-phenyl-C60 butyric acid methyl ester (PCBM) are model materials used to study and understand the performance of polymer solar cells. A critical design parameter in improving device performance is the structural morphology of the active layer. Traditional processing of organic solar cells involves the deposition of a P3HT/PCBM composite film from a common solvent and then post-processing treatments (i.e. annealing) to influence the extent of phase segregation and improve the percolation of electron and hole transport pathways throughout the film volume. Therefore, the electronic properties of the resulting solar cells are inherently tied to how the film is processed (e.g. choice of solvent, annealing temperature, film thickness). While process optimization has led to improvements in laboratory performance, it is challenging to extend the same principles to improve the performance of large scale roll-to-roll processes because deposition conditions vary significantly. Increasingly, researchers recognize the need for methods that decouple film processing from active layer structure and device performance. My research involves the synthesis of P3HT/PCBM composite nanoparticles (CNPs) in aqueous dispersion as a means to circumvent the dependence of active layer structure on the specific mode of deposition of the P3HT/PCBM film. I have synthesized CNPs with variable content of P3HT/PCBM and different preparation procedures while also controlling particle size. The characterization of these particles focuses on spectroscopy, small angle X-ray scattering (SAXS), dynamic light scattering and the performance evaluation of devices produced with CNP active layers. This project will tie device performance to CNP structure regardless of active layer processing, and assist in identifying CNPs with optimized morphology without the need for annealing or post-processing.

POSTER SESSION 2

Commons East, Easel 45

12:45 PM to 2:15 PM

Engineering a Survival-Based Protein-Fragment Complementation Assay to Detect Ubiquitination in *Escherichia coli*

Anupam Kumar (Anupam) Garg, Senior, Bioen: Nanoscience & Molecular Engr
Mary Gates Scholar
Mentor: Richard Gardner, Pharmacology
Mentor: Michelle Oeser, Pharmacology/Molecular & Cellular Biology

Ubiquitin is a protein modifier that is essential for many eukaryotic cellular processes. Attachment of ubiquitin to substrate proteins (ubiquitination) occurs in a three-step cascade that involves a ubiquitin activase, ubiquitin conjugase, and ubiquitin ligase; it is the ligase that targets substrate proteins. One challenge for the ubiquitin field is identification of substrate cohorts for ubiquitin ligases. Although ubiquitination only occurs naturally in eukaryotic organisms, we previously demonstrated that it is possible to reconstitute the ubiqutination cascade in *E. coli*, allowing for analysis of ubiquitination outside of its natural environment. Our project consists of the construction of a protein complementation assay, using two fragments of dihydrofolate reductase (DHFR) to detect the ubiquitination of proteins in *E. coli*, outside of the natural eukaryotic environment of ubiquitin. To perform the assay, I transformed all of the essential components of the ubiquitination pathway, including individual fragments of DHFR fused to ubiquitin and a substrate protein of interest, into *E. coli* cells. The assay tests for the covalent attachment of ubiquitin to the substrate protein through growth on selective medium, which is possible only through the combination of the separated fragments of DHFR. After construction and transformation of vectors using a known yeast ubiquitin ligase and substrate partner, I have found that ubiquitin fused to a fragment of DHFR functionally attaches to other proteins via a known ubiquitin ligase. Transformation of entire cDNA libraries into the bacterial cell in place of a ubiquitin ligase will allow for high throughput screening of ligases with homologous function as well as discovery of new ubiquitin ligase substrates. As no functional screening mechanisms presently exist, our system to efficiently screen for ubiquitin ligases and substrates provides a novel tool to address a significant challenge faced by the ubiquitin field.

SESSION 2J

INFECTIOUS DISEASES

Session Moderator: James Mullins, Microbiology
254 MGH
3:45 PM to 5:15 PM
* Note: Titles in order of presentation.

Determining Reservoirs of HIV-1
Cameron Riley (Cameron) Adams, Senior, Biochemistry
Initiative for Maximizing Student Development Scholar
Mentor: James Mullins, Microbiology
Mentor: Richard Fox, Microbiology

Administration of Anti-Retroviral Therapy (ART) slows disease progression and reduces HIV-1 viremia to near undetectable levels. Poor adherence or withdrawal of therapy often results in rapid rebound of viremia with the potential for the establishment of drug resistant variants. HIV is known to establish latency in long-lived central memory T-cells (CM) and is often referred to as "the reservoir". However, we now understand that there is both latent and actively replicating HIV-1 that comprises reservoir sites. Using sequence information and computational tools we can define reservoirs as cells or tissues harboring HIV-1 with genotypic features of reduced temporal structure, high diversity within the population, and low divergence from their most recent common ancestor (MRCA). This is because reservoirs are populated with virus seeded at both early and late periods of infection. If a reservoir is established in a site with reduced drug penetrance, "drug-sanctuaries", continued viral replication and diversification could occur. This may result in the accumulation of drug resistant variants that lead to therapy failure. Here we hypothesize that tissue and cellular sites with phenotypes reflective of reservoirs may also be drug restricted providing a boundary for unrestricted viral replication. To test this hypothesis we sequenced single genome template derived amplicons (SGA) of env and pol regions of HIV-1. Presented is data from the autopsy of subject S104. S104 presented with multi-drug resistant genotypes in all tissues sampled. Bioinformatical analysis measuring viral genetic diversity within and divergence from the MRCA of the viral population of S104 demonstrated reservoir phenotypes in tissue virus isolated from lung. We continue to expand our characterization of reservoirs and compartments to clearly define sites that must be targeted to eradicate HIV-1 in the host.

SESSION 2T

EVOLUTION, GENETICS, AND BIOCHEMISTRY OF PLANTS, ALGAE, AND FUNGI

Session Moderator: Richard Olmstead, Biology, Burke Museum
111 JHN
3:45 PM to 5:15 PM
* Note: Titles in order of presentation.

Primer Development for the Pentatricopeptide Repeat Gene Family for use in the Large Plant Group Lamiales
Benjamin Paul (Ben) Meersman, Junior, Biology (Ecology, Evolution & Conservation)
Mentor: Richard Olmstead, Biology, Burke Museum
Mentor: Patricia Lu-Irving, Biology

Phylogenetics is the study of evolutionary relationships and in order to infer these relationships in plants, various loci that are phylogenetically useful in nuclear as well as chloroplast DNAs should be utilized. Presently, the use of chloroplast loci is widespread in phylogenetic studies whereas the nuclear genome is still somewhat under-utilized. The pentatricopeptide repeat (PPR) gene family is a large group of protein coding nuclear genes that has been shown to be highly informative in the inference of evolutionary relationships among closely related species. There are multiple reasons that make these genes useful to these types of studies. The PPR gene family is very large which offers researchers multiple loci that are available for phylogenetic analyses. This is important because having multiple loci is imperative to answering important phylogenetic questions. A large portion of PPR genes are intronless making it possible to sequence and align data with little or no difficulty. They also have a high rate of evolution, and are single-copy in most plant genomes. 127 of these loci have been identified as phylogenetically useful but of these only 5 have been developed. This research looks to develop 10 more loci that will specifically target the Lamiales. To do this, 10 primer sets were tested using a sampling of species across the Lamiales. The primers were used to amplify these loci in order to ascertain their usefulness for a wide range of species and to obtain sequence data for each species. The sequences obtained were aligned and the alignments were used to design new primers. These new primer sets will allow for new data to be more easily collected that has been either difficult to obtain or previously unavailable and will increase the number of nuclear loci available for phylogenetic studies.

POSTER SESSION 3

Balcony, Easel 88

2:30 PM to 4:00 PM

The Multi Dimensions of Blackness: Cultural Hegemony in the U.S. and Hispaniola

Marcus Johnson, Senior, Global Studies (Bothell)
Mary Gates Scholar
Mentor: Benjamin Gardner, Interdisciplinary Arts & Sciences

Since the French and Spanish occupation of Hispaniola and specifically the US occupation from 1915-1934, Dominicans and Haitians have lived in a borderlands of blackness. However, these imaginary boundaries have been entwined with the African American response to the US occupation in Haiti. There have been many studies on the relationship between Dominicans and Haitians, but few have complicated how the relationship of African Americans living in Hispaniola played a fundamental role in shaping the multiple dimensions of blackness. By drawing upon Antonio Gramsci's theory of cultural hegemony, Stuart Hall's concept of cultural identity and diasporas in the Caribbean, in conjunction with Michael Omi and Howard Winant's work on racial formation in the United States, my research aims to draw the connections between these three groups and determine how these understandings have transformed preexisting definitions of blackness on the island. This paper is significant for comprehending the complexity of Dominican and Haitian identity, as well as locating the mechanisms of Western power, privilege and discourse. My research contributes to scholarship on the cultural production of blackness and race in the Caribbean and the United States.

POSTER SESSION 3

Commons East, Easel 76

2:30 PM to 4:00 PM

Characterizing a New Pathway in Nuclear Quality Control

Joshua (Joseph) Sanchez, Recent Graduate, Psychology, University of Washington
Mentor: Richard Gardner, Pharmacology

Proteins typically adopt a three dimensional (3D) structure that allows for their specific activity and function. While proteins' 3D structures are usually stable, they can be damaged by physical and/or chemical stresses. Such damage results in loss of structure, more commonly known as misfolding, which is often accompanied by exposure of hydrophobic residues normally buried in the interior of the protein. Exposed hydrophobicity can lead to the aggregation of misfolded proteins, and protein aggregation is associated with many prominent neurodegenerative diseases such as Alzheimer's and Parkinson's disease. To avoid these deleterious consequences, cells have evolved protein quality control (PQC) systems that degrade misfolded proteins. In eukaryotes, PQC utilizes ubiquitin ligases to flag proteins for proteosome degradation. How these PQC ligases recognize their misfolded substrates remains an open question. We have been addressing this question by studying the yeast PQC ubiquitin San1, which destroys misfolded proteins in the nucleus. We discovered that San1 recognizes exposed hydrophobicity minimally equal to 5 contiguous hydrophobic residues. Interestingly, we found that there is another PQC degradation system that recognizes exposed hydrophobicity at a lower threshold than San1. In this study we are trying to understand the mechanism by which this new pathway functions. By using degradation assays and western blots, we will take multiple constructs of varying degrees of hydrophocity to define how broad the pathway is. This allows us to determine whether the constructs are San1 dependent or independent, and if the San1-independent pathway is in fact a ubiquitin ligase. We know that a couple of the constructs are San1 independent, although they possess the hydrophibicity threshold required for San1 degradation. By exploring the mechanisms that ensure misfolded protein degradation, we hope to gain a better understanding of the PQC degradation systems within the cell and how they prevent severe pathologies caused by protein aggregation.

POSTER SESSION 3

Balcony, Easel 95

2:30 PM to 4:00 PM

Reflections of the Repressed: Filmic Representations of French Collaboration During World War II

Kathleen (Katey) Houck, Senior, International Studies, French
Mentor: Richard Watts, French & Italian Studies
Mentor: Deborah Porter, International Studies

French films about World War II tend to fall into either the category of heritage film, which promotes a narrative of reconciliation in relation to the collaboration, or another group of films that serves to implicitly or explicitly question that narrative of reconciliation. Films of the latter category have probed the memory of the Vichy collaboration since the end of the war despite Charles de Gaulle's efforts to repress narratives that challenged the idea of a country united against Germany. In the 1980's, however, heritage film became the prevalent genre and offered a Gaullist view of World War II in France. This thesis asks, why, given the plethora of films dealing with the realities of the French role in World War II dating from the late 1940's, a rubric of heritage film emerged as one way of classifying filmic discourse on the Vichy collaboration. I hypothesize that the heritage cinema rubric, specifically the Vichy cinema rubric, asserts a legibility of French identity,

which was compromised by France's collaboration with Nazi Germany, and attempts to thwart filmic narratives of identity loss. Through tropes of the uncanny and characters that experience repressed trauma and blocked mourning, films such as *Le Silence de la Mer* (1949), *Lacombe, Lucien* (1974), *Mr. Klein* (1976), and *Le Dernier Metro* (1980) reflect the French collective experience of loss during and in the aftermath of the collaboration. WWII films produced in the decades leading up to the emergence of this genre in essence dramatize a troubling disappearance of French cultural identity, which the heritage rubric sought to control.