Online Proceedings

SESSION 2R

EXPLORING PROTEIN FUNCTION AT SCALES FROM WHOLE TISSUES TO SINGLE ATOMS

Session Moderator: Celeste Berg, Genome Sciences
JHN 111
3:30 PM to 5:15 PM
* Note: Titles in order of presentation.

Computational Design of Symmetric Fc-Binding Homooligomers
Vanessa Thuy Anh Nguyen, Senior, Bioen: Nanoscience & Molecular Engr
Mary Gates Scholar
Mentor: Franziska Seeger

Protein homooligomers, multibodied assemblies built from identical polypeptide chains, comprise a large fraction of known cellular proteins. Homooligomers prove to be particularly amenable for many biological applications; they hold the potential as oligomerization domains, often have enzymatic functionality as a byproduct of their oligomeric configuration, and can serve as structural scaffolds for bionanomaterials. While there exists a multitude of protein homooligomers in the Protein Data Bank, the finite number of existing homooligomers limits the potential for custom applications. Our current work involves designing novel cyclic protein homooligomers from a set of de novo designed repeat proteins that bind the Fc region of antibodies. Using the Rosetta software suite, we generated a set of de novo homooligomer models by designing the oligomeric interface to direct self-assembly into a target configuration with three to six identical chains. After a round of refinement, we expressed the designs in *Escherichia coli* and purified them by immobilized metal affinity chromatography. Their oligomerization state was validated by measuring the molecular weight in solution by size exclusion chromatography paired with multi-angled light scattering and comparing it to the predicted molecular weight of the design. Designs that exhibited the desired molecular weight were submitted to collaborators for small angle X-ray scattering data and X-ray crystallography. The exclusive use of de novo proteins in homooligomer design granted a greater control over the shape and stability by nature of the repeats, thus making one successful interface design useful for a multitude of shapes and sizes. This variability opens up a wide scope of scaffolds for using these homooligomers for near atomic scale structural characterization by cryo-EM.

SESSION 2S

HOT TOPICS: ROBOTS, AR, CV, AI

Session Moderator: Kurtis Heimerl, Computer Science and Engineering
JHN 175
3:30 PM to 5:15 PM
* Note: Titles in order of presentation.

Designing for Security and Privacy in Multi-User Augmented Reality Interactions
Kimberly Christine Ruth, Junior, Computer Engineering, Mathematics
Mary Gates Scholar, UW Honors Program, Washington Research Foundation Fellow
Mentor: Franziska Roesner, Computer Science and Engineering
Mentor: Tadayoshi Kohno, Computer Science and Engineering

Augmented reality (AR), which overlays virtual content on top of the user's perception of the real world, is now beginning to enter the consumer market. Besides smartphone platforms, early-stage head-mounted displays such as the Microsoft HoloLens are being actively developed. Many of the most compelling uses of these AR technologies are multi-user: for instance, in-person collaborative tools, multiplayer gaming, and telepresence. Although AR technologies enable new forms of interaction, new security and privacy challenges will also arise when users can augment each other's reality, and it is imperative that these challenges be addressed while the technology is still new and highly malleable. In this work, I explore these emerging challenges in secure and private content sharing for multi-user AR. I systematize design goals for security and functionality that an AR content sharing framework should support, and I design and prototype a framework for the HoloLens that meets these goals. By evaluating my framework against representative application case studies, I show that it meets desired security and functionality goals

flexibly across a range of use cases. Preliminary investigations into developer effort suggest that applications' content sharing needs can be achieved in relatively few lines of code. I plan to convert my research prototype into an open-source toolkit so developers can address these challenges in practice. This work opens up directions for future research in how these underlying paradigms should manifest to users in the form of an application's user interface. By building foundations for secure multi-user AR content sharing, my work takes steps toward allowing AR to securely reach its full potential.

POSTER SESSION 3

Commons East, Easel 54

2:30 PM to 4:00 PM

Using Programming by Demonstration to Reduce Errors in Smart Home End-User Programming

Mitali Vishwesh Palekar, Senior, Computer Science
UW Honors Program
Mentor: Earlence Fernandes, CSE
Mentor: Franziska Roesner, Computer Science and Engineering

Over the past few years, the presence of smart homes has increased rapidly. Previous research has observed that people make errors in smart home programming with their mental models differing from their actual programming implementation which can cause serious security and safety concerns. The most common errors include missing half-rules and the incorrect use of conjunctions in triggers. For example, if users desire to program a rule for turning on the light when they are at home, they might program a rule such as "when I come home, turn on the lights", forgetting to program the rule for "when I leave home, turn off the lights". Our research focuses on reducing user errors in end-user programming by using programming by demonstration. Our hypothesis is that when users physically demonstrate a trigger-action rule, they are less likely to commit the trigger-action programming errors explained above. We compare the number and types of errors made within the IFTTT (if-this-then-that) interface that does not implement programming by demonstration and two interfaces that we built that implement programming by demonstration: a web interface and an augmented reality based interface within the Microsoft HoloLens. If our hypothesis holds true, we might observe that programming by demonstration significantly reduces programming errors in end-user programming in the case of both missing half rules and incorrect trigger conjunctions. We postulate that there might not be a difference in the case of error reduction between both the web and augmented reality interface; however, the augmented reality interface might provide for a broader range of programming by demonstration interfaces such as those related to temperature, humidity etc. Moreover, if our hypothesis holds, we might further suggest that smart home providers incorporate programming by demonstration models in their programming processes for end users within smart homes.

POSTER SESSION 4

Balcony, Easel 106

4:00 PM to 6:00 PM

Computational Design of IL-17A Cytokine Binders

Lauren Marie Miller, Senior, Biology (Molecular, Cellular & Developmental)
Mentor: David Baker, Biochemistry
Mentor: Franziska Seeger

Autoimmune diseases are characterized by one's own immune system attacking healthy cells in the body. Current treatments for autoimmune diseases require regular intravenous injections. The objective of this project is to develop a new generation of oral protein therapeutics. As a proof of concept, we computationally designed inhibitors against the inflammatory cytokine IL-17 in order to inhibit its activity in autoimmune conditions. IL-17 elicits its effect by triggering a signal cascade through heterodimerization of its cognate receptors. Our goal is to selectively occlude this dimerization to prevent the progression of disease. We have designed our inhibitors to bind in the same location as the native receptor, preventing downstream signaling that leads to autoimmune diseases. Historically, binders have been created by using existing protein interfaces grafted onto native protein shapes. However, we succeeded in designing IL-17 binders without using any prior protein interface information through de novo protein scaffolds. This project could revolutionize the way protein therapeutics are developed. Our goal is to analyze the biophysical characterization of our binders. In order to create a new standard in protein design our binders should have accurate size and folding in relation to the designed model which we are analyzing through mass spectrometry and circular dichroism spectroscopy. In order to become an effective drug candidate the binders must have successful binding to the IL-17 target which we are analyzing using octet binding analysis. In the end we hope to test our successful IL-17 binders in mouse models of multiple sclerosis, eventually transitioning to human clinical trials.