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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.

Photomediated Oxime Ligation as a Bioorthogonal Tool for Spatiotemporally-Controlled Hydrogel Formation and Modification

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Mary Gates Scholar, NASA Space Grant Scholar, UW Honors Program, Undergraduate Research Conference Travel Awardee, Washington Research Foundation Fellow

Mentor: Cole DeForest, Chemical Engineering & Bioengineering

Mentor: Steven Adelmund, Chemical Engineering

Water-absorbent polymer networks known as hydrogels are attractive materials from which functional tissue substitutes could be developed using patient-derived stem cells. While hydrogels demonstrate biocompatibility conducive to harboring cells, they lack mechanical and biochemical aspects of the native extracellular matrix (ECM), the intricate microenvironment about which cells function. Conventional photopolymerization-based techniques provide an avenue for incorporating these stimuli within hydrogels, but at the expense of introducing propagating free radicals that are prone to non-specific reactions with biological systems. In light of these limitations, we have developed a strategy for hydrogel formation and modification absent of propagating free radicals, proceeding through oxime ligation moderated by a photocaged alkoxyamine. Upon mild UV light exposure, the photocage is cleaved, liberating the alkoxyamine and permitting localized condensation with an aldehyde to form an oxime-based linkage. After synthesizing multi-arm crosslinkers, functionalized with either benzaldehydes or photocaged alkoxyamines, I demonstrated successful formation of oxime-based hydrogels within minutes of light exposure in the presence of live cells. Through a series of rheological studies, I found polymerization rates and final mechanical properties of these gels could be systematically tuned by varying crosslinker concentrations, light intensity, aniline catalyst concentration, and pH. Harnessing the light-driven aspect of this chemistry, I controlled hydrogel geometry and final mechanical properties by dictating the location and extent of UV exposure, respectively. I then translated photomediated oxime ligation toward the biochemical modification of hydrogels, where full-length proteins containing photocaged alkoxyamines were immobilized in user-defined regions exposed to UV light. The programmability afforded by photomediated oxime ligation can recapitulate mechanical and biochemical stimuli found throughout the ECM, which are dynamic and heterogeneous in their presentation. Consequently, photopolymerized oxime-based hydrogels will enable an enhanced understanding of cell-matrix interactions by serving as improved 3D cell culture platforms, thereby leading to advancements in tissue engineering and regenerative medicine.

Bare-Metal Robot Programming over Wifi on an ARM Cortex M4

Schuyler Quentin (Schuyler) Horky, Senior, Electrical Engineering

Mentor: Allan Ecker, Electrical Engineering

Many embedded systems employ the use of dedicated programming hardware called a programmer, or run on top of an operating system that can support many ways of accepting new programs. However, wireless programmer support is uncommon and an operating system introduces overhead. This presentation describes the design of an embedded system with wireless programming capabilities without the use of a programmer or operating system. New code is sent to an on-system wifi transceiver and then via a serial port to the microprocessor, which writes to its own flash memory and stores the program, resets, and runs. The wifi connection is also used for general communication to a host computer or other systems, depending on the application. A secure handshake method was also needed to ensure the device is never unintentionally reprogrammed by regular data packets. The wireless system was then used to control a robot platform

with a skid steer drive and motor encoders for a mobile robot that can be reprogrammed without any wired connection to a PC. This wireless programming solution enables developers to test autonomous code with quick code testing cycles, minimal overhead, and requires no conventional programmer.

The Impact of Blade Mounting Geometry on Cross-Flow Turbine Performance

Noah E (Noah) Johnson, Senior, Mechanical Engineering
UW Honors Program
Mentor: Brian Polagye, Mechanical Engineering
Mentor: Benjamin Strom, Mechanical Engineering

Cross-flow turbines are a promising approach for extracting renewable energy from tidal and river channels. These turbines consist of a set of blades rotating about an axis perpendicular to the water flow direction. While blade mounting geometry has implications for parasitic drag, lift-induced drag, and blade lift generation, which strongly influence turbine performance, little research has been published on this topic. The impact of blade mounting geometry on turbine performance was evaluated by comparing the power conversion efficiency of ten two-bladed turbines with varying mounting geometries in a recirculating water flume. Each turbine was also tested without blades to evaluate interactions between blades and mounting geometry. A servomotor rotated the test turbine at constant angular velocity and two six-axis load cells were used to measure the torque produced by the turbine rotor. Six tests were performed with connecting struts at each end of the blades. Cross sectional geometry (rectangular, rounded, and foil) and thickness were varied (chord length held equal to the blade). Three tests were also performed with solid disks of varying radii mounted to each end of the blade. Finally, one test was performed with a single foil strut mounted at the center of blade span. Complete performance curves at four Reynolds numbers were generated for each mounting geometry by varying the free stream velocity. At the highest Reynolds number, the thin foil strut performed with greatest efficiency, followed by the thin rounded strut and thick foil strut. The smallest disk, thin rectangular strut, and thick rounded strut performed similarly. Strut and disk drag was analytically modeled and compared with experimental data to characterize power loss from each mounting geometry. These results offer insight into cross-flow turbine design for optimal efficiency and encourage investigation of additional mounting geometries such as winglets or curved mounting interfaces.

FPGA-Accelerated Bloom Filter

Chih Ching (Rick) Lin, Senior, Electrical Engineering
Mentor: Scott Hauck, Electrical Engineering
Mentor: Nathaniel McVicar, Electrical Engineering

Progress in genomics research has led to increasing demands in scientific computing, especially in the field of DNA sequencing. As sequencing technologies have matured over the past decade, the rate of growth in data has outpaced the advancement of sequential processing devices such as CPU-based systems. Field-Programmable Gate Arrays (FPGAs) are reconfigurable computing devices that can be highly customized to suit specific applications, including genomic data processing. In contrast to CPU-based systems, FPGAs are parallel processing devices capable of carrying out computations more efficiently. Additionally, newly emerged memory architectures have greatly improved the random-access performance in genomics applications. One of these is the Hybrid Memory Cube (HMC), whose internal architecture incorporates fast serial communication links and efficient controllers that raise the memory bandwidth limit of the FPGA when compared to traditional DDR DRAM. In our research, we harness the high random-access rate of the HMC and the parallel computing ability of the FPGAs to establish a Bloom filter, an efficient data structure used to confirm membership in a group. The Bloom filter can be utilized to discard erroneous reads generated by normal sequencing techniques and can further relieve the need to account for false information in downstream systems. We constructed a filtering pipeline on the development board that houses a Xilinx Kintex FPGA and the HMC, using only one interface port and 2 GB storage of the HMC. The system is capable of processing 1 billion DNA segments with a maximum length of 64 base pairs. The computing ability of the FPGA along with the high random-access rate of the HMC are highly desirable when processing large amounts of genomic data.

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 nanostruc-

ture 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.

UW Medical Center - Motion Control for Fast Neutron Collimator

Joey Thai, Senior, Electrical Engineering
Marissa Kranz, Senior, Electrical Engineering
Matthew Ross (Matt) Dentinger, Senior, Electrical Engineering
Mentor: Howard Chizeck, Electrical Engineering
Mentor: Robert Emery, Radiation Oncology
Mentor: Jonathan Jacky, Radiation Oncology
Mentor: Payman Arabshahi, Electrical and Computer Engineering

The goal of this project is to design a faster and more efficient motion controller for the leaf collimator that is used to shape a neutron beam around a tumor for use in intensity modulated neutron radiation therapy. The system currently in operation was developed in the 80's and is too slow for new treatment techniques we plan to support. We started with familiarizing ourselves with the Galil motion controller and the Experimental Physics and Industrial Control System (EPICS) software to control 40 motors that will adjust the position of the collimator leaves within an accuracy of 2 mm. Because we augmented an existing system, there are some system aspects that could not change and needed to be worked into our design: the 40 motors need to be driven manually with analog feedback and the overall mechanical setup should remain mostly the same. Additionally, we rewired the system to accommodate bipolar power supplies in order to half the number of wires used in the gantry, allowing us to save on space and increase the ease of future system maintenance. This was accomplished by configuring diodes in parallel with relays that allows us to control the direction of the current, which in turn controls the rotation of the motors. Since our system's internal components are heavily exposed to radiation, we implemented the diodes on a printed circuit board to ensure that the system upkeep and component replacement is manageable. Finally, we updated the existing Extensible Display Manager (EDM) user interface so the radiation therapists and technicians can see real-time leaf locations and interact with our motion control system. The final deliverable is a complete installation of our new fully tested system inside the the gantry.

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.