OKBC 2022 Program

TIME	SPEAKER	TITLE
9:00 - 9:30	**Luca Piantanida** *In person*	*Nucleic Acid Memory: Super Resolution Microscopy enhances novel approach to DNA data storage*
9:30 - 10:00	**Seong Ho Kim** *In person*	*Improved super-resolution imaging with MB-PAINT*
10:00 - 10:30	**Lois Pollack** *Via zoom*	*From Å to nm: measuring biomolecular structural dynamics with x-rays*
10:30 - 10:45	COFFEE BREAK	
10:45 - 11:15	**Joshua Milstein** *Via zoom*	*The Role of Cell Shape in the Stochastic Dynamics of Competing Bacteria*
11:15 - 12:00	IN PERSON GRAD STUDENT PRESENTATIONS (see below)	
12:00 - 13:00	LUNCH	
13:00 - 13:30	**Pallav Kosuri** *Via zoom*	*Revealing the personalities of molecules and cells*
13:30 - 14:00	**Sarah Rauscher** *Via zoom*	*All-Atom Molecular Simulations of Disordered and Flexible Proteins*
14:00 - 14:30	**Emmanuel Osei** *In person*	*Are multicellular and multiorgan bioartificial systems to study (lung) disease pathogenesis worth it?*
14:30 - 14:45	COFFEE BREAK	
14:45 - 15:15	**John Katsaras** *Via zoom*	*Neutron Scattering and Biological Membranes*
15:15 - 16:15	**Michael Woodside** *In person*	*Probing the fundamental physics of folding by observing the microscopic dynamics of structural self-assembly in single biological molecules*

Grad Student Presentation Schedule

TIME	SPEAKER	TITLE
11:15 - 11:20	**Sakshi Phogat**	*Establishing a 3D vascularized tri-culture model of the human lung airways using a stereolithographic bio-printer.*
11:20 - 11:25	**Jason Reich**	*Pulse Sequence Design for Accelerated Sodium Magnetic Resonance Imaging*
11:25 - 11:30	**Liubov Frolova**	*New Trojan tag strategy for exosome labelling and tracking*
11:30 - 11:35	**Haris Vidimlic**	*Custom Applications: How MATLAB Can Improve Workflow*
11:35 - 11:40	**Vicente Stranger**	*Chemical tools to study molecular events at synapses*
11:40 - 11:45	**Seger Nelson**	*Investigating a Residual Neural Network to Generate Customizable Radiofrequency Pulses for Magnetic Resonance Imaging*
11:45 - 11:50	**Micah Yang**	*Characterization of Tension Gauge Tether Rupture Forces*
11:50 - 11:55	**Teddy Herriman**	*Peptide Bond Stability in Multiple Prebiotic Environments and on Mineral Surfaces*

ABSTRACTS

Nucleic Acid Memory: Super Resolution Microscopy enhances novel approach to DNA data storage

Luca Piantanida, Boise State University

The ever-present connectivity in our lives, and the data storage demands that come with it, is growing exponentially. The projected material supply for silicon-based memory technologies is unable to satisfy future demand, therefore, alternative memory materials are being explored in academia and industry. DNA is analogous to a biological hard drive. It carries and transfers information with exceptional density, stability, and energy efficiency, making it a compelling alternative to current non-volatile information storage technologies. The Nucleic Acid Memory (NAM) Institute at Boise State exploits DNA as a programmable material to engineer emerging data storage technologies. Here we present our first prototype, digital Nucleic Acid Memory (dNAM), which spatially encodes and retrieves small datasets using only DNA as the material. dNAM is made from DNA origami assembly technique, it is structurally characterized using Atomic Force Microcopy (AFM, Fig.1b) and it is read using Super Resolution Microscopy (SRM, Fig.1c). The origami structure serves as a breadboard where short dye-labelled DNA strands are the fluorescent imager probes (Fig.1a). These probes transiently hybridize with short protruding single strands periodically positioned on the origami design implementing the DNA PAINT technique on its surface. Every time a hybridization event occurs, a blinking signal is recorded. Associating the blinking signal to a “1” and no signal to a “0”, dNAM resembles a molecular version of Lite-Brite toy where distinct patterns of pegs encode different digital data. Processing the SRM reading with a custom error-correction algorithm, dNAM provides an aerial data density of 330 Gbit/cm2 and is able to use a subset of origami to retrieve the encoded message 100% of the time. Unlike other approaches to DNA-based data storage, reading dNAM does not require DNA sequencing and so, the synthesis of new custom DNA strands every time new data is encoded, reducing significantly the costs and chemical waste. As such, this research can provide a valuable path to DNA data storage applications for the next-generation of digital memory materials.

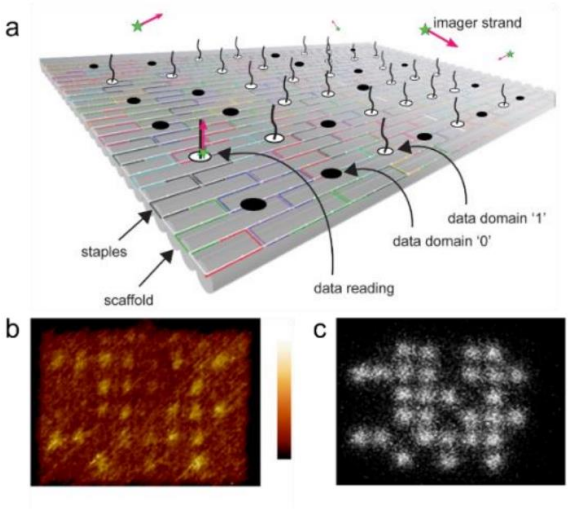

Figure 1: (a) dNAM design, (b) structure (AFM, color scale 2nm) and (c) DNA PAINT reading (SRM).

Improved super-resolution imaging with MB-PAINT

Seong Ho Kim, University of British Columbia

DNA-PAINT performance is constrained by the background from diffusion of fluorophore-labelled single-stranded DNA (ssDNA) imagers in the solution, resulting in a relatively long image acquisition time and potential artifacts. Here, we designed a fluorogenic molecular beacon (MB) as the PAINT imager. We demonstrate that MB-PAINT produces a similar localization precision to conventional linear imager DNA-PAINT. We also show that MB-PAINT is ideally suited for super-resolution imaging of molecular tension probes in living cells, eliminating the potential of artifacts from free-diffusing imagers in conventional DNA-PAINT at the cell-substrate interface.

From Å to nm: measuring biomolecular structural dynamics with x-rays

Lois Pollack, Cornell University

Proteins, DNA and RNA are among the most important macromolecules in living systems. Biologically relevant motions can occur on a variety of length scales, ranging from the flipping of a single side chain through the overall restructuring or folding of an entire macromolecule. My group has developed new techniques that exploit microfluidic mixers to trigger and monitor interesting structural dynamics on these relevant length scales, and on time scales ranging from milliseconds through minutes. I will present an overview of our experiments. Measurements with near atomic resolution are performed by coupling our mixers to x-rays from free electron laser sources (XFELs). More conventional x-ray measurements, at synchrotron sources, allow us to monitor larger scale macromolecular motions. Problems of interest include the self-assembly (folding) of RNA into functional structures and the atomic scale conformational dynamics that allow enzymes to function.

The Role of Cell Shape in the Stochastic Dynamics of Competing Bacteria

Joshua N. Milstein, University of Toronto

Bacteria constantly compete for space and resources with other microbial species. This has led them to evolve an array of active strategies, such as using quorum sensing or generating bacterial toxins, to outcompete their neighbors. One often overlooked feature that is essential to the dynamics of this spatial competition, because cells regularly push and bump into their neighbors, is the geometry of the cells involved. We have been studying the spatial population dynamics of two, ostensibly, identical populations of E. coli bacteria, with the only difference being the expression of a fluorescence reporter (GFP vs. mCherry). These mixed populations are cultured within a microfluidic monolayer device, which can support the continuous growth of the cells for extended periods of time, and imaged for up to 24 hrs by time-lapse microscopy. Competition between the two species often results in one species completely eradicating the other, which we refer to as “fixation”. However, due to their pill shaped geometry, the two populations tend to jam into an organized structure, much like the nematic phase of liquid crystals, enabling the cells to “coexist” for extended periods of time. By altering the cell shape

through modification of the actin homolog MreB, in E. coli, we can study the effects of cell morphology on the fixation vs. coexistence dynamics.

Revealing the personalities of molecules and cells

Pallav Kosuri, Salk Institute

Mechanical movements of DNA are integral to human biology: Polymerases pry apart the double-stranded helix to transcribe or replicate DNA; chromatin factors bend DNA to restrict or allow access to specific regions of the genome. Collectively, dynamic reactions like these shape the physical organization of our genome and determine the fate of every cell. To investigate protein-DNA interactions, we are developing Origami Movement Microscopy (OMM), a new technology that enables direct observation of DNA movements. Our technology works by structurally amplifying DNA movements with the help of lever-arm-like DNA origami devices. We have designed a set of OMM devices where each device amplifies a specific mode of DNA movement and makes this movement visible in a standard fluorescence microscope. Using our new approach, we can now observe protein-DNA movements at a resolution of single base pairs, revealing the mechanics of protein-DNA interactions in rich detail. We envision OMM to become a standard method in our pursuit to illuminate the largely unexplored universe of protein-DNA interaction dynamics.

All-Atom Molecular Simulations of Disordered and Flexible Proteins

Sarah Rauscher, University of Toronto

Molecular dynamics (MD) simulations are a useful tool to investigate the structure and dynamics of proteins because they can provide an all-atom view of their complex conformational landscapes. Using MD simulations, we are able to identify conformational states and their populations. I will present recent and ongoing simulation studies of disordered and flexible proteins. I will also present our recent efforts to track ordered waters in simulation using a new local alignment based approach.

Are multicellular and multiorgan bioartificial systems to study (lung) disease pathogenesis worth it?

Emmanuel Osei, University of British Columbia

In recent years, it has been suggested that a crosstalk between lung structural cells as well as the gut and lungs may play a role in lung diseases. This talk will provide a summary on how different lung 3D co-culture, organoid and bioartificial models are built using isolated human cells to assess these multicellular and multiorgan interactions. Examples to be looked at will include 3D epithelial-fibroblast co-cultures, organoids, bioprinted systems, fibroblast-embedded collagen gels, multi-organ-systems etc. The talk will also briefly evaluate whether these bioartificial models are worth the ‘hype’ of replacing current preclinical models in basic science and translational research.

Neutron Scattering and Biological Membranes

John Katsaras, Oak Ridge National Laboratory

In 1932 James Chadwick discovered the neutron using a polonium source and a beryllium target. Where it concerns hydrogen-rich biological materials, the neutron's differential sensitivity for hydrogen and its isotope deuterium make it a powerful tool for understanding the static and dynamic structures of biological membranes, supramolecular assemblies of lipids and proteins that separate a cell's interior from its external environment. In this seminar I will describe the approach of neutron contrast variation used to detect nanoscopic lipid domains populating model membranes.

Probing the fundamental physics of folding by observing the microscopic dynamics of structural self-assembly in single biological molecules

Michael T. Woodside, University of Alberta

Biological molecules like proteins, DNA, and RNA must self-assemble into complex structures in order to carry out their function. This 'folding' process typically occurs spontaneously, and involves searching through a huge number of possibilities to find the correct structure. Physically, it is described in terms of a diffusive search over an energy landscape describing the energy of the molecule as a function of its structure, where the landscape features barriers separating the potential wells defining the folded and unfolded states. In recent years it has become possible to watch single molecules in the act of folding, as they travel along the 'transition paths' that take them over the energy barrier. I will discuss studies of individual transition paths in DNA hairpins, as a model system for understanding folding. By observing transition paths directly, we can determine how long it takes a molecule to cross the barrier, probe the local velocity along the paths, characterize the shapes of the paths through the landscape, and even detect brief pauses within high-energy states that reflect the microscopic motions of base pairs as they search for the correct structure. We use these measurements to test fundamental physical theories of folding reactions, finding that they agree well on all time scales that can be observed.