Yale Institute for Nanoscience and Quantum Engineering

Malone Engineering Center nano.yale.edu

Friday- September 28, 2018

12:00 -1:00 PM

BECTON SEMINAR ROOM

Light lunch will be served

Zahra Sohrabpour

Department of Chemistry, Yale University

"Characterization of Surface-active Biofilm Protein BslA Using Sum Frequency Generation (SFG) Spectroscopy"

Biofilm surface layer protein A (BslA) is a surface-active biofilm protein in a soil bacterium called, *Bascillus Subtilis*. This Biofilm adheres to surface substrates in plant roots, forms an extremely hydrophobic layer and protects the plant against external threats such as microbes. If, however it is deposited onto human tissue surfaces it can cause chronic infections. Thus, studying this biofilm's extraordinary mechanical stability and structure can help with developing new concepts for molecular design of biomaterials. In this talk results from Sum Frequency Generation (SFG) Spectroscopy, an interface-specific technique, to study BslA and its mutants at the air/water interface are reported. SFG was used to better understand which residues in this protein play a crucial role in forming such a unique biofilm structure.

Joel Rozowsky

Department of Molecular Biophysics & Biochemistry, Yale University

"Tools for the Analysis of RNA-Seq Data from the Extracellular RNA Communication Consortium"

Extracellular RNAs (exRNA) are gaining considerable interest for their potential use as biomarkers and their role in intercellular communication. Small RNA-sequencing has been widely adopted to shed light on the diversity of exRNA in biofluids, but the field faces unique technical challenges. In particular, exRNA samples are more vulnerable to contamination and artifacts from different isolation techniques, are present in lower concentrations than cellular RNA, and are occasionally of exogenous origin. To address these challenges we present the extracellular RNA processing toolkit (exceRpt), the standardized small RNA-seq analysis pipeline of the NIH Extracellular RNA Communication Consortium (ERCC) optimized for exRNA analysis. exceRpt is structured as a cascade of filters and quantifications prioritized based on the confidence of a given set of annotated RNA. The pipeline generates quality control reports and abundance estimates for RNA biotypes, and is also capable of characterizing mappings to exogenous genomes, which can be used to generate phylogenetic trees. exceRpt has uniformly processed all (currently ~2500) exRNA-seq datasets in the public exRNA atlas.

Host: Professor Corey O'Hern