CPLC/Biophysics Graduate Student/Postdoc Spring Symposium 2014

8:30 AM – 9:00 AM Breakfast

9:00 AM – 9:15 AM

Jingyi Fei **–** Ha Lab

Imaging and Analysis of small RNA-based Regulation in Bacteria

We present a new approach for characterization and quantification of small regulatory RNA (sRNAs), target mRNA and sRNA-mRNA complex at single-cell level. The quantitative analysis and localization information allow us to establish a kinetic model to describe the sRNA-induced target mRNA degradation in the cell.

9:15 AM – 9:30 AM

Boon Chong Goh – Schulten Lab

Molecular Modeling of the Immature Retroviral Lattice

We present a new approach for characterization and quantification of small regulatory RNA (sRNAs), target mRNA and sRNA-mRNA complex at single-cell level. The quantitative analysis and localization information allow us to establish a kinetic model to describe the sRNA-induced target mRNA degradation in the cell.

9:30 AM – 9:45 AM

Joseph Courtney – Rienstra Lab

COMPASS: Protein Structure Determination with a Single, Unassigned NMR Spectrum

Manual data analysis is a major bottleneck for traditional NMR-based protein structure determination. Here we present the Comparative, Objective Measurement of Protein Architectures by Scoring Shifts (COMPASS), an algorithm that determines a protein model by numerical comparison of homology models with a single, unassigned 2D 13C-13C NMR spectrum.

9:45 AM – 10:00 AM

Pei-Chen Peng – Sinha Lab

Quantitative modeling of gene expression from sequence and DNA accessibility

Thermodynamics-based models that map an enhancers sequence to its expression readout have provided a quantitative framework to test our understanding of the cis-regulatory ‘code’. We will present a model, called GEMSTAT-A, that has been demonstrated successfully model segmentation enhancers in Drosophila when integrating chromatin state data such as DNA accessibility.

10:00 AM – 10:15 AM

Isaac Li – Ha Lab & Chemla Lab

Single molecule mechano-memory

Here, we introduce a new class of molecular force sensors that remembers cellular adhesion events at the single-molecule level. We are applying this to study leukocyte rolling adhesion, a unique mode of adhesion critical to the body's immune system.

10:15 AM – 10:30 AM - Coffee

10:30 AM – 10:45 AM

Shu-Han Chao – Gruebele Lab & Aksimentiev Lab

Two structural scenarios for protein stabilization by PEG

Recent studies suggest that stabilization of a protein by a covalent-attached PEG oligomer on the protein surface is sequence-dependent. Here, by experimentally and computationally studying a full mutant cycle at two positions of human Pin1 WW domain, we connect PEG-aided stabilization directly to the structural dynamics of the protein and the PEG.

10:45 AM – 11:00 AM

Nitesh Shashikanth – Leckband Lab

Allosteric Modulation of Cadherin Activity by p120 catenin mediated inside-out signaling

Using Micropipette Aspiration adhesion frequency measurements, we show direct (and one of the first) evidence for allosteric modulation of cadherin (transmembrane adhesion protein) activity by inside out signaling through the membrane. The phosphorylation status of p120 catenin which binds to the cadherin cytoplasmic domain modulates the activity of cadherin ectodomain.

11:00 AM – 11:15 AM

Tao Jiang – Tajkhorshid Lab

Characterization of Anion Binding and Proton Coupling in CLC Cl-/H+ Transporter

The CLC superfamily is a ubiquitous membrane protein family that mediates selective Cl- conductance. Our simulations on a bacterial CLC transporter, ClC-ec1, characterize the various binding properties of uncoupled anions compared to the physiological transport Cl- ion, and explain the differential proton coupling of different anions by revealing their effects on water wire formation.

11:15 AM – 11:30 AM

Michael Martini – Goldenfeld Lab

Observation of fluctuation-induced Turing instability in a forward-engineered biofilm.

Turing instabilities are thought to be a major source of pattern formation in biology, but they have been very hard to rigorously document. In ecology, Turing patterns arise but are modified due to demographic fluctuations. This work is exciting because it is the first time that fluctuation-induced Turing patterns have been observed.

11:30 AM – 11:45 AM

Yupeng Qiu – Myong Lab

Differential mechanism of unwinding trinucleotide repeat by yeast Srs2 and Sgs1

Trinucleotide repeat (TNR) expansion causes many neurodegenerative diseases in human. Expansion arises from replication defects when the TNR sequences form hairpins and lengthens. Using single molecule fluorescence, we investigated the mechanisms by which yeast Srs2 and Sgs1 can resolve TNR hairpins for the prevention of DNA expansion during replication.

11:45 AM – 12:45 PM Lunch
