Yale Institute for Nanoscience and Quantum Engineering

Malone Engineering Center nano.yale.edu

Friday- February 22, 2018

12:00 -1:00 PM

Mann Student Center-Room 107
10 Hillhouse Ave/ Dunham Lab
Light lunch will be served

Marcos Latorre

Department of Biomedical Engineering, Yale University

"Mechanobiological Stability of Biological Soft Tissues"

Like all other materials, biological soft tissues are subject to general laws of physics, including those governing mechanical equilibrium and stability. In addition, however, these tissues are able to respond actively to changes in their mechanical and chemical environment. There is, therefore, a pressing need to understand such processes theoretically. In this talk, we present a new rate-based constrained mixture formulation suitable for studying mechanobiological equilibrium and stability of soft tissues exposed to transient or sustained changes in material composition or applied loading. These concepts are illustrated for canonical problems in arterial mechanics, which distinguish possible stable versus unstable mechanobiological responses. Such analyses promise to yield insight into biological processes that govern both health and disease progression.

Sabyasachi Sutradhar

Department of Molecular Biophysics & Biochemistry, Yale University

"Deciphering the Dendritic Tip Dynamics of Drosophila Class IV Sensory Neuron in Light

of a Three-State Model"

Individual neurons form highly intricate dendritic structures that receive synaptic input from other neurons or sensory input from the outside world. The precise dendritic morphology is crucial for the proper connectivity and information processing of neural circuits. However, little is known how the dendrites form and grow. We observed that the dendrites of our model system, Drosophila class IV neuron, are highly dynamic. Using an automated tip tracking 'MATLAB' software, we characterized the dynamics of the dendritic tips and observed that the tip traces can be segmented into regions of growth (G), shrinkage (S) and paused (P) states. We were able to identify these regions by fitting a piecewise linear function to the traces. We also calculated the transition rates among these different states.Using the above-mentioned dynamic parameters (growth and shrink velocities and transition rates) we will be able to simulate an *in-silico* model to quantitatively compare whether the morphologies predicted by the model captures the complexities of the morphologies observed during development.

Host: Professor Corey O'Hern