Yale Institute for Nanoscience and Quantum Engineering

Friday-February 16, 2018

12:00-1:00 PM

BECTON SEMINAR ROOM
Light lunch will be served at 11:45 a.m.

Benjamin Machta
Department of Physics and Systems Biology Institute, Yale University

"Bounding Dissipation in Small Thermodynamic Systems"

Abstract: Biological and engineered systems operate by coupling function to the transfer of heat and/or particles down a thermal or chemical gradient. In idealized deterministically driven systems, thermodynamic control can be exerted reversibly, with no entropy production, as long as the rate of the protocol is made slow compared to the equilibration time of the system. Here I will argue that for a complete accounting of energetic costs it is important to consider fully realizable, entropically driven systems where the control parameters themselves obey rules that are reversible and that acquire directionality in time solely through dissipation. I'll argue that in this case, when such a system moves in a directed way through thermodynamic space, it must produce entropy that is on average larger than its generalized displacement as measured by the Fisher information metric. This distance measure is sub-extensive but cannot be made small by slowing the rate of the protocol.

Kathryn Miller-Jensen
Department of Biomedical Engineering, Yale University

"Finding a Signal in the Noise: Understanding the Biological Sources and Consequences of Cell-to-Cell Heterogeneity in Gene Expression"

Mammalian gene expression is a noisy process with significant variability between cells exposed to the same environmental cues. There is evidence that gene expression noise is constrained across the genome, but how activation of gene transcription occurs within these global constraints is less clear. Here we studied transcriptional noise associated with activation by the transcription factor NF-κB, which has central roles in immunity and development. We found that NF-κB target promoters display a global mean-versus-noise relationship. We further found that within a very narrow range of mean basal transcription (1-2 transcripts per cell), transcriptional activation by NF-κB causes distinct changes in transcriptional noise for different gene targets, while remaining constrained along mean-versus-noise trend lines. Strikingly, the different modes of transcriptional noise following NF-κB activation are associated with significant differences in biological processes at the promoter, which may represent one source of global constraint. We also see evidence of phenotypic consequences: HIV promoters support gene expression that maps to the interface between these two modes of NF-κB-induced transcriptional noise, affording HIV the potential for wide phenotypic heterogeneity when coupled to viral-mediated positive feedback amplification of noise, rather than noise-controlling motifs.

Host: Professor Corey O'Hern