Stochastic modeling of biological networks and its implications for HIV latency

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Abstract:

Many protein and mRNA species occur at low molecular counts within cells, and hence are subject to large stochastic fluctuations in copy numbers over time. In the first part of my talk, I will introduce state-of-art computational tools for stochastic modeling, analysis and parameter identification of subcellular biological networks. In the second part of my talk, I will describe current efforts in combining the above computational techniques with experimental data for quantitatively characterizing Human immunodeficiency virus (HIV) genetic circuit. In particular, our joint computational-experimental approach reveals that HIV encodes a noisy promoter where mRNAs are made in stochastic bursts. Processing of these transcriptional bursts by downstream feedback circuitry is sufficient to drive a viral cell-fate decision between active replication (lysis) and proviral latency (a dormant state of the virus analogous to phage lysogeny) in single cells.