



**DEPARTMENT OF GENETICS
&
HUMAN GENETICS INSTITUTE OF NEW JERSEY**

RESEARCH SEMINAR



**“Systems Biology in Single
Cells: A Tale of Two Viruses”**

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Newark, DE**

In the noisy cellular environment, expression of genes has been shown to be stochastic across organisms ranging from prokaryotic to human cells. Stochastic expression manifests as cell-to-cell variability in the levels of RNAs/proteins, in spite of the fact that cells are genetically identical and are exposed to the same environment. Development of computationally tractable frameworks for modeling stochastic fluctuations in gene product levels is essential to understand how noise at the cellular level affects biological function and phenotype. I will introduce state-of-the-art computational tools for stochastic modeling, analysis and inferences of biomolecular circuits. Mathematical methods will be combined with experiments to study infection dynamics of two viral systems in single cells. First, I will show how stochastic expression of proteins results in intercellular lysis time and viral burst size variations in the bacterial virus, lambda phage. Next, I will describe our efforts in stochastic analysis of the Human Immunodeficiency Virus (HIV) genetic circuitry. Our results show that HIV encodes a noisy promoter and stochastic expression of key viral regulatory proteins can drive HIV into latency, a drug-resistant state of the virus.

**Noon, Monday, April 1, 2019
Auditorium, Life Sciences Building,
145 Bevier Road, Busch Campus, Piscataway, New Jersey
Host: Premal Shah, Phone: 415-374-9664, Email: premal.shah@rutgers.edu**