



BIOINFORMATICS 2014 FALL SEMINAR SERIES

Hosted by: Center for Bioinformatics and Computational Biology
Department of Computer and Information Sciences, &
Department of Electrical and Computer Engineering
<http://bioinformatics.udel.edu/seminars>

MONDAY, November 10, 2014
3:30pm
DBI Room 102

Origins and propagation of transcriptional noise in eukaryotic gene expression

Sanjay Tyagi, PhD

Professor of Medicine
Public Health Research Institute
Rutgers University
http://www.phri.org/research/res_pityagi.asp

ABSTRACT: Gene expression in individual cells deviates substantially from the average behavior of cell populations. Often referred to and analyzed as "noise", this heterogeneity amongst genetically identical cells has been documented in bacteria, yeast, and in higher eukaryotes, where it can be particularly acute. The heterogeneity arises because mRNAs are produced in bursts of synthesis that initiate and end randomly followed by RNA decay. We have explored why eukaryotic genes produce mRNAs in these episodic bursts rather than continuously. Since the transcriptional heterogeneity is so common and unavoidable, how do the fluctuations in the expression of upstream genes propagate into the expression of the downstream genes that they control? Studies of synthetic circuits in bacteria and yeast provided evidence of amplified propagation of noise in those systems. In higher eukaryotes however, that does not appear to be the case. By studying a simple naturally occurring gene regulatory pathway, we found that the downstream genes are insulated from fluctuations in the expression of upstream genes due the presence of chromatin. This work was performed using a powerful single molecule in situ mRNA imaging method.