CLARK UNIVERSITY
DEPARTMENT OF PHYSICS
COLLOQUIUM

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“A Mathematical Approach to Studying Gene Regulation”

ABSTRACT: Since the complete human genome was released over a decade ago, researchers have struggled to understand how 3.2 billion nucleotides in DNA encode the instructions for every biological process that takes place throughout a person’s lifetime. Accompanying the expansion in sequence data, new technologies have provided copious amounts of gene expression data, which is detected by the production of either RNA or proteins. The key challenge now is to integrate and analyze this wealth of information to reveal biological function. Mathematical modeling studies have proven to be of great value in unraveling the vast complexity in the data. In this talk, I will highlight the modeling approaches I have implemented in Drosophila melanogaster (the common fruit fly) to try to answer some of the critical questions regarding how DNA-sequences direct gene expression during embryonic development. The mathematical and computational approaches I will discuss weave together many familiar concepts from Biology, Mathematics, Physics, Chemistry, and Computer Science, and involve techniques from a broad range of areas in applied mathematics.

Wednesday, November 7, 2018, 12:30 pm, Room S-122
Sackler Sciences Center