

BioMed Seminar

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The Functional-Genomics Inverse Problem

Abstract

Molecular profiling of gene expression and protein interactions on a genome-wide scale is giving rise to biological datasets of unprecedented depth and complexity. Encoded within this vast array of information is the central dogma of molecular biology – DNA makes RNA makes protein – that governs the complex regulatory cascades and metabolic pathways in organisms from yeast to humans. Unraveling the topological and causal structure of these networks based on (often incomplete) molecular data constitutes a considerable analytic challenge. In this talk, I will describe some of the physics-based, computational, and mathematical approaches that are being developed to tackle the genomic inverse problem. These methods will be illustrated with examples from the reconstruction of DNA damage-response subnetworks in yeast, and the determination of disease etiology and molecular disease subclasses in acute leukemia.

5:30 – 6:20 PM Wednesday, December 1st
Room 184, Department of Physics & Astronomy
Northeast Corner of Lomas at Yale