Computational methods for understanding mammalian gene regulatory networks

Gene regulatory networks are molecular networks that control which genes must be expressed when and where in a living cell, translating the information encoded in an organism’s genome to context-specific responses. Identification of these networks is important to advance our understanding of many biological processes such as development, disease, response to stress, and evolution. Understanding mammalian regulatory networks is a major challenge because of the number of regulators, large amounts of non-coding regulatory DNA, and multiple levels of regulation including chromatin state (determining what DNA is accessible by a transcription factor), and the three-dimensional organization of the genome (how DNA is packaged in the nucleus). In this talk I will present some recent computational methods based on statistical machine learning to tackle different problems in gene regulation.

Specifically, I will talk about (a) mapping genome-scale gene regulatory networks, (b) understanding the three-dimensional organization of the genome and (c) understanding the dynamics of gene regulatory networks across short and evolutionary time scales.

Tuesday, Sept. 17, 2019
Lecture at 4:00 p.m.
Room 1610, Engineering Hall