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***Learning Models of cis-Regulatory
Modules from Sequence Data***

Abstract:

The process of genetic transcription is controlled by systems of transcription factors called cis-regulatory modules (CRMs), which bind to specific patterns of binding sites in the transcriptional control regions of genes. The discovery of such binding sites from sequence data is an important open problem in computational biology. I will discuss our approach in training a CRM model which is capable of capturing several structural aspects of a CRM, such as the relative orientation and distance between binding sites. I will also discuss current and future work learning CRM binding site motifs in the context of a CRM.

**Tuesday, November 8th
4:00 p.m.**

Auditorium (Room 1111)
Genetics/ Biotechnology Center
425 Henry Mall