

SEMINAR

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“Computational Methods for Gene Regulatory Network Discovery”

Environmental changes induce various types of abiotic stresses. Characterization of regulatory mechanisms by which plants sense and respond to such stresses at the molecular level is crucial to understanding the responses of organisms to environmental changes. Traditionally, abiotic stress studies are carried out by perturbing the optimal growth conditions and inferring a gene's function from the observed changes in gene expression. With high-throughput technologies, it is now feasible and essential to develop new and effective methods for systematic characterization of regulatory networks for plants in response to abiotic stresses. We show how multiple sources of information including gene expression, DNA sequences and literature, can be integrated to identify such networks. In particular, we show how DNA sequence information can be used to improve dependencies networks constructed from gene expression data alone. This process involves identifying transcription factors in a dependency network and transcription factor binding sites (TFBS) upstream of potentially regulated genes. Dependency networks are combined with the TFBS information to determine potential gene regulatory networks of interest. The resulting networks are validated based on available knowledge in biological literature.

Date: Monday, July 14

Time: 1:10 - 2:00pm

Location: 1652 Gilman

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