Computational methods towards understanding gene regulation

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Abstract

This talk will survey some of the current techniques for understanding gene regulation via gene expression studies (e.g., microarrays, SAGE), localization data (e.g., Chip on Chip experiments), motif finding (e.g., weight matrices, co-occurrence), and phylogenetic footprinting. We will examine some of the properties of each of these types of data and describe some of the computational strategies that are currently being used. We will also focus on the integration of these heterogeneous types of data via a Bayesian network. Special attention will be given to describing current computational strategies for searching the tremendously large search-spaces induced by these models.