Presentation title: Inference and application of gene regulatory networks

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Abstract:
Gene regulatory networks are 'circuit diagrams' showing putative co-expression and in some cases directional cause-and-effect relationships between RNA species. In a gene regulatory network, RNA transcripts are represented as nodes in a graph, each node corresponding to one or more RNAs. Links between nodes are represented as edges on the graph, which indicate putative relationships between RNAs, where the abundance of one RNA can affect the abundance of a second RNA. In this session, I will review different methods of inferring gene networks and explain how they might be useful; describe some new tools and ideas developed to make better use of gene expression data; and show some of the most exciting results from my group's work and that of other groups.