



Emerging Topics in Biological Networks and Systems Biology

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The Semantics of Transcription Factor Network Maps and the Limitations of Experimental Data

Abstract:

A transcription factor (TF) network map is a directed graph in which the nodes represent genes and the proteins they encode. The edges point from TFs to their direct, functional targets -- the genes they regulate by physically binding to their cis-regulatory DNA. Since there are high-throughput experimental methods for measuring both which genes a TF regulates and which genes it binds, one might hope that taking the intersection of the bound and regulated targets would identify the direct functional targets and hence the TF network map. In this talk, I will demonstrate mathematically that carrying out this intersection procedure with existing high throughput data on yeast and other eukaryotes produces a TF network map of very low accuracy. This might be because the existing experimental data are of poor quality or it might be because the simple model of transcriptional regulation underlying the intersection procedure is incorrect, or both. I will briefly explore each of these possibilities and their implications for the future of TF network mapping.

About:

Michael Brent received his BS in Mathematics and Ph.D. in Computer Science from MIT. Next, he served as Assistant and then Associate Professor of Cognitive Science at Johns Hopkins University, where his research focused on modeling how children learn their native languages. In 1999, Brent moved to Washington University in Saint Louis, where he transitioned his research to computational genomics. In the early 2000s his group produced the TWINSKAN and N-SCAN algorithms for gene structure prediction and participated in the initial analyses of many genome sequences. Around 2009, Prof. Brent shifted his focus again, to mapping and modeling transcriptional regulatory networks. Since then, his group has produced NetProphet and NetProphet 2, for mapping transcriptional regulatory networks, PhenoProphet, for predicting which gene deletions will produce a phenotype of interest, and NetSurgeon, for transcriptome engineering. Dr. Brent is the Henry Edwin Sever Professor of Engineering and a fellow of the American Association for the Advancement of Science.