

Applied and Computational Mathematics and Statistics Colloquium

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Will give a lecture entitled:

Geometric Interpretation of Gene Coexpression Network Analysis

Monday, November 1st, 2010

4:00 PM

Location: 127 Hayes-Healy Hall

Abstract:

The merging of network theory and microarray data analysis techniques has spawned a new field: gene coexpression network analysis. While network methods are increasingly used in biology, the network vocabulary of computational biologists tends to be far more limited than that of, say, social network theorists. Here we review and propose several potentially useful network concepts. We take advantage of the relationship between network theory and the field of microarray data analysis to clarify the meaning of and the relationship among network concepts in gene coexpression networks. Network theory offers a wealth of intuitive concepts for describing the pairwise relationships among genes, which are depicted in cluster trees and heat maps. Conversely, microarray data analysis techniques (singular value decomposition, tests of differential expression) can also be used to address difficult problems in network theory. We describe conditions when a close relationship exists between network analysis and microarray data analysis techniques, and provide a rough dictionary for translating between the two fields. Using the angular interpretation of correlations, we provide a geometric interpretation of network theoretic concepts and derive unexpected relationships among them. We use the singular value decomposition of module expression data to characterize approximately factorizable gene coexpression networks, i.e., adjacency matrices that factor into node specific contributions. High and low level views of coexpression networks allow us to study the relationships among modules and among module genes, respectively. We characterize coexpression networks where hub genes are significant with respect to a microarray sample trait and show that the network concept of intramodular connectivity can be interpreted as a fuzzy measure of module membership. We illustrate our results using human, mouse, and yeast microarray gene expression data. The unification of coexpression network methods with traditional data mining methods can inform the application and development of systems biologic methods.

This talk builds on results presented in Horvath S, Dong J (2008) PLoS Comput Biol 4(8): e1000117.