Weighted Correlation Network Analysis: learning about cancer and evolution from a million correlations

Peter Langfelder
University of California, Los Angeles

Abstract

In this talk I present an overview of Weighted Correlation Network Analysis (also known as Weighted Gene Co-expression Network Analysis, WGCNA). WGCNA methods have successfully been used to analyze gene expression, proteomics and functional MRI data and can be applied to any situation in which one is faced with the task of studying relationships among thousands of variables for which one has relatively few (tens or hundreds of) observations.

In the first part of the talk I introduce the basic steps of WGCNA: definition of a weighted network from expression data, identification of network modules (groups of highly co-expressed genes), relating the identified gene modules to external traits (such as body weight, disease status etc), and identifying genes that may play a central role in each module.

In the second part I illustrate applications of WGCNA to microarray gene expression data. I describe an application in which network analysis identified a module related to survival time in glioblastoma (brain cancer) patients, and within that module identified a novel cancer gene. I then describe an application of WGCNA to studying the similarities and differences between human and chimpanzee brains.

Thursday July 15 at 1:30 pm
Millikan 134, Pomona College
After the talk, meet Prof. Langfelder, Harry’s Room (ML 209)