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Systems genetics is an emerging biological approach that exploits natural genetic variation to examine biological networks across levels of scale, time and space. Genetic reference populations (GRPs) contain lines of genetically identical individuals, which allow cumulative data aggregation. Biological characteristics measured in GRPs can be used to generate large correlation matrices of biological traits, from molecular phenotypes such as microarrays to those representing more global complex functions. A high-pass filter can be used to transform a correlation matrix into an unweighted graph. Interpretation of this entire correlation matrix is obtained by analysis of the properties of this graph. Clique and a related algorithm we term “paraclique” are used to decompose the large graph into dense subgraphs, vertex coverage analysis allows examination of the relation of these subgraphs to higher-order biological phenotypes and the genetic polymorphisms responsible for trait covariance. Evaluating adjacency of subgraph members refines the genetic regulatory path. Our goal is unbiased extraction of testable biological networks.

This talk is based in part on:

Baldwin NE et al, J. Biomed Biotechnol. 2005;2005:172-80. Chesler EJ et al, Nat Genet. 2005;37:233-42. (Received August 22, 2005)