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PATH WEIGHTS, NETWORKED PARTIAL CORRELATIONS AND THEIR APPLICATION TO THE ANALYSIS OF GENETIC INTERACTIONS

Abstract: Genetic interactions confer robustness on cells in response to genetic perturbations. This often occurs through molecular buffering mechanisms that can be predicted using, among other features, the degree of coexpression between genes, commonly estimated through marginal measures of association such as Pearson or Spearman correlation coefficients. However, marginal correlations are sensitive to indirect effects and often partial correlations are used instead. Yet, partial correlations convey no information about the (linear) influence of the coexpressed genes on the entire multivariate system, which may be crucial to discriminate functional associations from genetic interactions. To address these two shortcomings, here we propose to use the edge weight derived from the covariance decomposition over the paths of the associated gene network. We call this new quantity the networked partial correlation and use it to analyze genetic interactions in yeast. More concretely, in its well-characterized leucine biosynthesis pathway and on a previously published data set of genome-wide quantitative genetic interaction profiles. In both cases, networked partial correlations substantially improve the identification of genetic interactions over classical coexpression measures.

This talk is based on a joint work with Robert Castelo, University Pompeu Fabra, Spain