Genecentric: uncovering graph-theoretic structure in high-throughput epistasis data

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New technology has resulted in high-throughput screens for pairwise genetic interactions in yeast and other model organisms. For each pair in a collection of non-essential genes, an epistasis score is obtained, representing how much sicker (or healthier) the double-knockout organism will be compared to what would be expected from the sickness of the component single knockouts. Our recent algorithmic work has identified graph-theoretic patterns in this data that can indicate functional modules, and even sets of genes that may occur in compensatory pathways, such as a BPM-type schema first introduced by Kelley and Ideker. We introduce Genecentric, an easy-to-use software package that can find BPMs in epistasis data.

This is joint work with Andrew Gallant, Max Leiserson, Maxim Kachalov, and Ben Hescott