Digging in the data: computational functional genomics in yeast and mammals

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Abstract

The explosion of functional genomics data, including microarrarry, proteomics, and high-throughput genetic studies, has the promise of providing us with a systems-level view of protein function, interactions, and regulation. However, these data sets are noisy, computationally diverse, and biologically heterogeneous. I will discuss our recent work in developing robust and accurate methods for analysis of these data, including a search algorithm for large microarray compendia and a Bayesian system for integration of diverse functional genomic data into interaction networks. Further, I will describe how we used an ensemble of computational data integration methods to direct quantitative laboratory experiments, leading to the discovery of 99 novel proteins involved in mitochondrial biogenesis in yeast.

References

See http://function.princeton.edu/