Poster G-16

Evaluation of predicted human protein networks

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Short Abstract: We used recently published experimental datasets for the human interactome to assess the reliability of previously predicted protein-protein interactions and to compare prediction methods. In our comprehensive analysis, we found significant differences between the experimental and predicted human networks regarding prediction accuracy, functional consistency, information contents, and network topology.

Long Abstract:
Novel high-throughput techniques have generated enormous amounts of protein-protein interaction data for different species (Sharan and Ideker, 2006). These data can now be mined for new information on the functions and interrelationships of proteins (Bork et al., 2004). In particular, different bioinformatics methods, mainly based on the homology of protein sequences, have supported the large-scale prediction of human protein networks (Huang et al., 2004; Lehner and Fraser, 2004; Brown and Jurisica, 2005; McDermott et al., 2005; Persico et al., 2005; Rhodes et al., 2005). In addition, manually curated literature data and two large yeast-2-hybrid maps have recently become available for the human interactome (Rual et al., 2005; Stelzl et al., 2005; Gandhi et al., 2006). However, the experimental coverage of the human interactome is still low in contrast to predicted data.

Therefore, we used the recent experimental data to assess the reliability of previous predicted interactions. Such an evaluation and comparison of prediction methods is not only important for further methodological improvements, but also for gaining confidence into functional hypotheses derived from predictions, for instance, when studying disease-associated proteins and potential drug targets. Indeed, in our comprehensive analysis, we found significant differences between the experimental and predicted human networks regarding prediction accuracy, functional consistency, information contents, and network topology. For this work, we built a sophisticated database to integrate diverse biological information on protein interactions and implemented a useful Cytoscape plugin named NetworkAnalyzer to compute topological network parameters.

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