Assembling the Yeast Interactome

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Motivation

How is the yeast proteome wired? This important question is still unanswered in spite of the abundance of protein interaction data obtained using high-throughput approaches and made available to the scientific community. Unfortunately, such large-scale studies show remarkable discrepancies in their results and coverage so combining them is not a trivial task: information on interactomes, or networks of interacting proteins, produced with diverse experimental techniques,each with their own inherent experimental errors, must be evaluated to construct a trustworthy protein interaction network.

Methods

Although the task of integrating different data sources has already been undertaken by different groups, the recent availability of the results of two new large scale studies has motivated a fresh approach to the problem. We examine different algorithms and approaches to the problem and introduce our own model for building a trustworthy network of protein interactions.

Results

We present a draft of the yeast interactome taking advantage of various heterogeneous sources of data: tandem-affinity-purification coupled to mass spectrometry (TAP-MS) data, large-scale yeast two-hybrid studies, and literature data stored in dedicated databases of protein-protein interactions. We compare our interactome with others available and we evaluate it for biological consistency. A trustworthy interactome is the starting point of other kinds of analyses: it can be used in simulation studies (cell automata) aimed at discovering the dynamic and evolutionary properties of molecular networks, and it can be useful for pathway analysis and network reconstruction studies. Ultimately, it can be used in machine learning approaches to predict or evaluate new protein interactions.

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