

Computational Identification of Signalling Pathways in Protein Interaction Networks

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Abstract : The knowledge of signaling pathways is central to understanding the biological mechanisms of organisms since it has been identified that in eukaryotic organisms, the number of signaling pathways determines the number of ways the organism will react to external stimuli. Signaling pathways are studied using protein interaction networks constructed from protein-protein interaction data obtained using high throughput experimental procedures. However, these high throughput methods are known to produce very high rates of false positive and negative interactions. In order to construct a useful protein interaction network from this noisy data, computational methods are applied to validate the protein-protein interactions. In this study, a computational technique to identify signaling pathways from a protein interaction network constructed using validated protein-protein interaction data was designed. A weighted interaction graph of the *Saccharomyces cerevisiae* (Baker's Yeast) organism using the proteins as the nodes and interactions between them as edges was constructed. The weights were obtained using Bayesian probabilistic network to estimate the posterior probability of interaction between two proteins given the gene expression measurement as biological evidence. Only interactions above a threshold were accepted for the network model. A pathway was formalized as a simple path in the interaction network from a starting protein and an ending protein of interest. We were able to identify some pathway segments, one of which is a segment of the pathway that signals the start of the process of meiosis in *S. cerevisiae*.

Keywords : Bayesian networks, protein interaction networks, *Saccharomyces cerevisiae*, signalling pathways

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