Interaction prediction using conserved network motifs in protein-protein interaction networks

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High-throughput protein interaction detection methods are strongly affected by false positive and false negative results. Focused experiments are needed to complement the large-scale methods by validating previously detected interactions but it is often difficult to decide which proteins to probe as interaction partners. Developing reliable computational methods assisting this decision process is a pressing need in bioinformatics. This talk will describe the recent developments in analyzing and understanding protein interaction networks, then present a method that uses the conserved properties of the protein network to identify and validate interaction candidates. We apply a number of machine learning algorithms to the protein connectivity information and achieve a surprisingly good overall performance in predicting interacting proteins. Using a "leave-one-ou approach we find average success rates between 20-50% for predicting the correct interaction partner of a protein. We demonstrate that the success of these methods is based on the presence of conserved interaction motifs within the network. A reference implementation and a table with candidate interacting partners for each yeast protein are available at http://www.protsuggest.org