

Prediction of Protein-Protein Interactions Using Random Decision Forest Framework

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Motivation: Protein interactions are of biological interest because they orchestrate a number of cellular processes such as metabolic pathways and immunological recognition. Domains are the building blocks of proteins; therefore, proteins are assumed to interact as a result of their interacting domains. Many domain based models for protein interaction prediction have been developed, and preliminary results have demonstrated their feasibility. Most of the existing domain-based methods, however, consider only single domain pairs (one domain from one protein) and assume independence between domain-domain interactions. Results: In this poster, we introduce a domain based Random Forest of Decision Trees to infer protein interactions. Our proposed method is capable of exploring all possible domain interactions and making predictions based on all the protein domains. Experimental results on *Saccharomyces Cerevisiae* dataset demonstrate that our approach can predict protein-protein interactions with higher sensitivity (79.78%) and specificity (64.38%) compared to the Maximum Likelihood approach. Furthermore, our model can be used to infer interactions not only for single domain pairs but also for multiple domain pairs.