

A Combined Experimental and Inferring Interactomes

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Abstract

With the significant growth of protein interaction data, the difficulty of the task of using simple graphs to describe the complicated biological network is obvious. Therefore, a clear and integrated platform for protein network (interactome) presentation becomes more essential than ever. The work starts with constructing a protein interaction database from both high-quality experimental dataset and inferred dataset. We will use human gastric pathogen *Helicobacter pylori* as an example. We first adopt the *H. pylori* interaction data from high-throughput two-hybrid experiments to build a prediction matrix based on the theory of domain-domain interactions. A protein interaction database of *H. pylori* is then built by combining the inferred associations and experimental data. A comprehensive and interactive graphical interface for visualization and integrated annotation is also developed.

The benefit of this system combines the convenience of the user-friendly, web-based interactive interface and the efficiency of system performance with high referencing value of statistics on the possibility of protein interaction based on the configurations of their sequence-signatures, domains. Through visualized presentation with integrated annotations in web-based interface, it will be easy to add the readability of the graph and get the whole picture of protein interactions network of *H. pylori*. For example, we unscramble the network of urease, the most abundant complex proteins in *H. pylori*, based on the combination of experimental and inferring interactions. The interacting partners can also annotate the ORFs. And this database can provide proper candidates to narrow down the scale of further high-throughput screening and validating experiments for drug targets.

Key words: interactome, protein interaction, inferring, domain, web database, network visualization

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