



HAPPI: A Bioinformatics Database Platform Enabling Network Biology Studies

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HAPPI: A Bioinformatics Database Platform Enabling Network Biology Studies

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Abstract:

The publication of the draft human genome consisting of 30,000 genes is merely the beginning of genome biology. A new way to understand the complexity and richness of molecular and cellular function of proteins in biological processes is through understanding of biological networks. These networks include protein-protein interaction networks, gene regulatory networks, and metabolic networks. In this thesis, we focus on human protein-protein interaction networks using informatics techniques. First, we performed a thorough literature survey to document different experimental methods to detect and collect protein interactions, current public databases that store these interactions, computational software to predict, validate and interpret protein networks. Then, we developed the Human Annotated Protein-Protein Interaction (HAPPI) database to manage a wealth of integrated information related to protein functions, protein-protein functional links, and protein-protein interactions. Approximately 12900 proteins from Swissprot, 57900 proteins from Trembl, 52186 protein-domains from Swisspfam, 4084 gene-pathways from KEGG, 2403190 interactions from STRING and 51207 interactions from OPHID public databases were integrated into a single relational database platform using Oracle 10g on an IU Supercomputing grid. We further assigned a confidence score to each protein interaction pair to help assess the quality and reliability of protein-protein interaction. We hosted the database on the Discovery Informatics and Computing web site, which is now publicly accessible. HAPPI database differs from other protein interaction databases in these following aspects: 1) It focuses on human protein interactions and contains approximately 860000 high-confidence protein interaction records—one of the most complete and reliable sources of human protein interaction today; 2) It includes thorough protein domain, gene and pathway information of interacting proteins, therefore providing a whole view of

protein functional information; 3) It contains a consistent ranking score that can be used to gauge the confidence of protein interactions. To show the benefits of HAPPI database, we performed a case study using Insulin Signaling pathway in collaboration with a biology team on campus. We began by taking two sets of proteins that were previously well studied as separate processes, set A and set B. We queried these proteins against the HAPPI database, and derived high-confidence protein interaction data sets annotated with known KEGG pathways. We then organized these protein interactions on a network diagram. The end result shows many novel hub proteins that connect set A or B proteins. Some hub proteins are even novel members outside of any annotated pathway, making them interesting targets to validate for subsequent biological studies.

Description:

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