PROTEIN NETWORK COMPARATIVE GENOMICS

Trey Ideker

University of California San Diego

With the appearance of large networks of protein-protein and protein-DNA interactions as a new type of biological measurement, methods are needed for constructing cellular pathway models using interaction data as the central framework. The key idea is that, by comparing the molecular interaction network with other biological data sets, it will be possible to organize the network into modules representing the repertoire of distinct functional processes in the cell. Three distinct types of network comparisons will be discussed, including those to identify:

(1) Protein interaction networks that are conserved across species

(2) Networks in control of gene expression changes

(3) Networks correlating with systematic phenotypes and synthetic lethals

Using these computational modeling and query tools, we are constructing network models to explain the physiological response of yeast to DNA damaging agents.

Relevant articles and links

1. Yeang, C.H., Mak, H.C., McCuine, S., Workman, C., Jaakkola, T., and Ideker, T. Validation and refinement of gene regulatory pathways on a network of physical interactions. *Genome Biology* **6(7):** R62 (2005).
2. Kelley, R. and Ideker, T. Systematic interpretation of genetic interactions using protein networks. *Nature Biotechnology* **23(5):**561-566 (2005).
3. Sharan, R., Suthram, S., Kelley, R. M., Kuhn, T., McCuine, S., Uetz, P., Sittler, T., Karp, R. M., and Ideker, T. Conserved patterns of protein interaction in multiple species. *Proc Natl Acad Sci U S A.* **8:102(6):** 1974-79 (2005).
4. Suthram, S., Sittler, T., and Ideker, T. The *Plasmodium* network diverges from those of other species. *Nature* **437:** (November 3, 2005).
5. http://www.pathblast.org
6. http://www.cytoscape.org

Acknowledgements