



Emerging Topics in Biological Networks and Systems Biology

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Networks as a Service: Bringing Added Value and Functional Insights to Experimental Biologists

Abstract:

The functional interactions among molecules in cells are difficult to capture fully, and remain a “moving target” depending on cellular context and external conditions. Nevertheless, they constitute a powerful framework with which to interpret experimental results and genetic observations, and they provide the basis for the description of pathways and modules.

From a database perspective, a number of challenges arise in terms of how to discretize noisy and context-dependent networks, and how to present them to users in a maximally intuitive and useful way. I will present our ongoing efforts to address these challenges, in terms of the STRING database dedicated to all known and predictable interactions between proteins. Apart from collecting and reassessing available experimental data on protein–protein interactions, and importing known pathways and protein complexes from curated databases, interaction predictions in STRING are derived from the following sources: (i) systematic co-expression analysis, (ii) detection of shared selective signals across genomes, (iii) automated text-mining of the scientific literature and (iv) computational transfer of interaction knowledge between organisms based on gene orthology. I will describe the STRING system and some of its use cases, and discuss network-based approaches of detecting functional enrichments in user-provided gene lists.

About:

Christian von Mering originally studied Biochemistry at Free University of Berlin. After a Ph.D. in Developmental Biology, working with *Drosophila* in the lab of Prof. Konrad Basler in Zurich, he became a PostDoc and later Staff Scientist in the group of Peer Bork at EMBL Heidelberg. While at EMBL, he began studying protein networks, and initiated the STRING database of protein-protein interactions. Since 2006, he is Professor for Computational Biology at the University of Zurich, continuing his work on protein networks and expanding his interests to microbiology (environmental DNA sequencing) and proteomics (protein abundance quantification).