

— Keynote Address —

Orthologous Sets of Functional Networks: Inference, Mining and Visualization

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The functions of genes and proteins in complex cellular processes, no less than the functions of words in a sentence or paragraph, cannot be understood in the absence of context. Information on correlated function of genes and proteins in different environments is being obtained by various experimental and computational methods, including ChIP assays, yeast two hybrid experiments, fusion analysis, operon analysis, phylogenetic profiling, and expression profiling. The information obtained by these and other methods has been assembled in the Predictome database, which is integrated with a powerful visual mining tool, Visant (visant.bu.edu). I will discuss the computational methods, especially phylogenetic profiling, for obtaining gene regulatory networks (interacting genes and proteins), and methods for finding hidden variables (missing links) in these nets. The utility of Predictome and Visant will be illustrated by an analysis of expression data from lung adenocarcinoma.