Prediction of Regulatory Networks for Non-Model Organisms

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Determination of regulatory pathways from available data is one of the major challenges in bioinformatics research. The functions of genes in any genome are regulated (inhibited or activated) by other genes or a combination of other genes. These regulatory relationships between the genes and the complete regulatory network for a genome, often including feedback loops, is of great interest to the biologists. Some organisms such as yeast, *Arabidopsis thaliana* and fruit fly are being investigated very thoroughly by biologists as model organisms. Similar genes in different genomes tend to have similar regulatory relationships and to be involved in similar network motifs in a regulatory network. These similarities can be useful for inferring regulatory pathways for a non-model organism using a model organism. The goal of this work is to predict the regulatory relationships of a non-model organism using information about the regulatory relationships of a model organism.