Topic Gene regulatory networks

Gene regulatory networks

Gene regulatory networks attempt to model the regulatory relationship between genes. The genes are depicted as nodes and the regulatory as edges. GRNs can be directed or undirected, the edges can be weighted or unweighted. An example for such a regulatory relationship would be transcription factors (TFs) whose expression can lead to an increase in the expression of a gene, called activation; or the reduction of the expression of certain genes, called repression. There are a plethora of tools and algoritithms attempting to reconstruct GRNs from gene expression data (Genie3, GRNBoost, WCGNA, …), but not many take into account the presence or absence of splice isoforms.
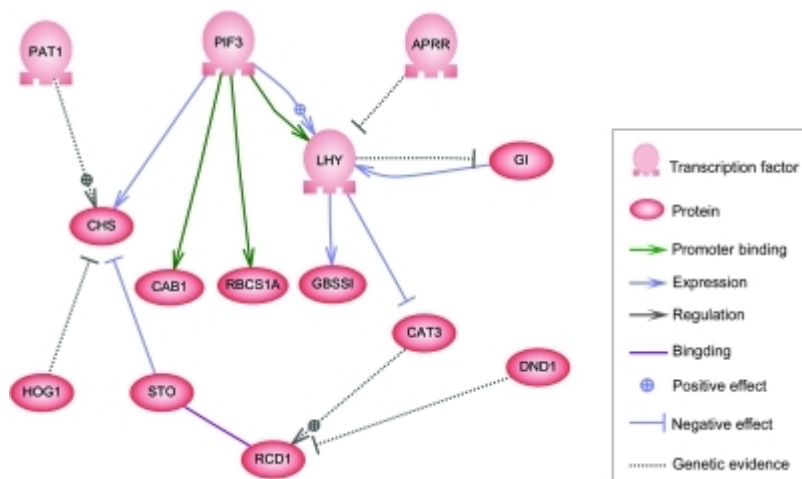

Figure 1. Example gene regulatory network, source:
https://en.wikipedia.org/wiki/Gene_regulatory_network#/media/File:DG_Network_in_Hybrid_Rice.png

The number of available tools make it difficult for biologists to know which tools to use, and how to interpret the output. For this there are several topics of interest. Firstly, investigating the usage of network inference tools by biologists and bioinformaticians. Secondly, develop appealing and interpretable ways of visualising the networks. Other topics include the use and interpretation of predicted edges in the GRNs for downstream analyses.