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A regulatory similarity measure using the location information of transcription factor binding sites in *Saccharomyces cerevisiae*

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Abstract

Background

Defining a measure for regulatory similarity (RS) of two genes is an important step toward identifying co-regulated genes. To date, transcription factor binding sites (TFBSs) have been widely used to measure the RS of two genes because transcription factors (TFs) binding to TFBSs in promoters is the most crucial and well understood step in gene regulation. However, existing TFBS-based RS measures consider the relation of a TFBS to a gene as a Boolean (either 'presence' or 'absence') without utilizing the information of TFBS locations in promoters.

Results

Functional TFBSs of many TFs in yeast are known to have a strong positional preference to occur in a small region in the promoters. This biological knowledge prompts us to develop a novel RS measure that exploits the TFBS location information. The performances of different RS measures are evaluated by the fraction of gene pairs that are co-regulated (validated by literature evidence) by at least one common TF under different RS scores. The experimental results show that the proposed RS measure is the best co-regulation indicator among the six compared RS measures. In addition, the co-regulated genes identified by the proposed RS measure are also shown to be able to benefit three co-regulation-based applications: detecting gene co-function, gene co-expression and protein-protein interactions.

Conclusions

The proposed RS measure provides a good indicator for gene co-regulation. Besides, its good performance reveals the importance of the location information in TFBS-based RS measures.