

# Identifying cooperative transcription factors in yeast using multiple data sources

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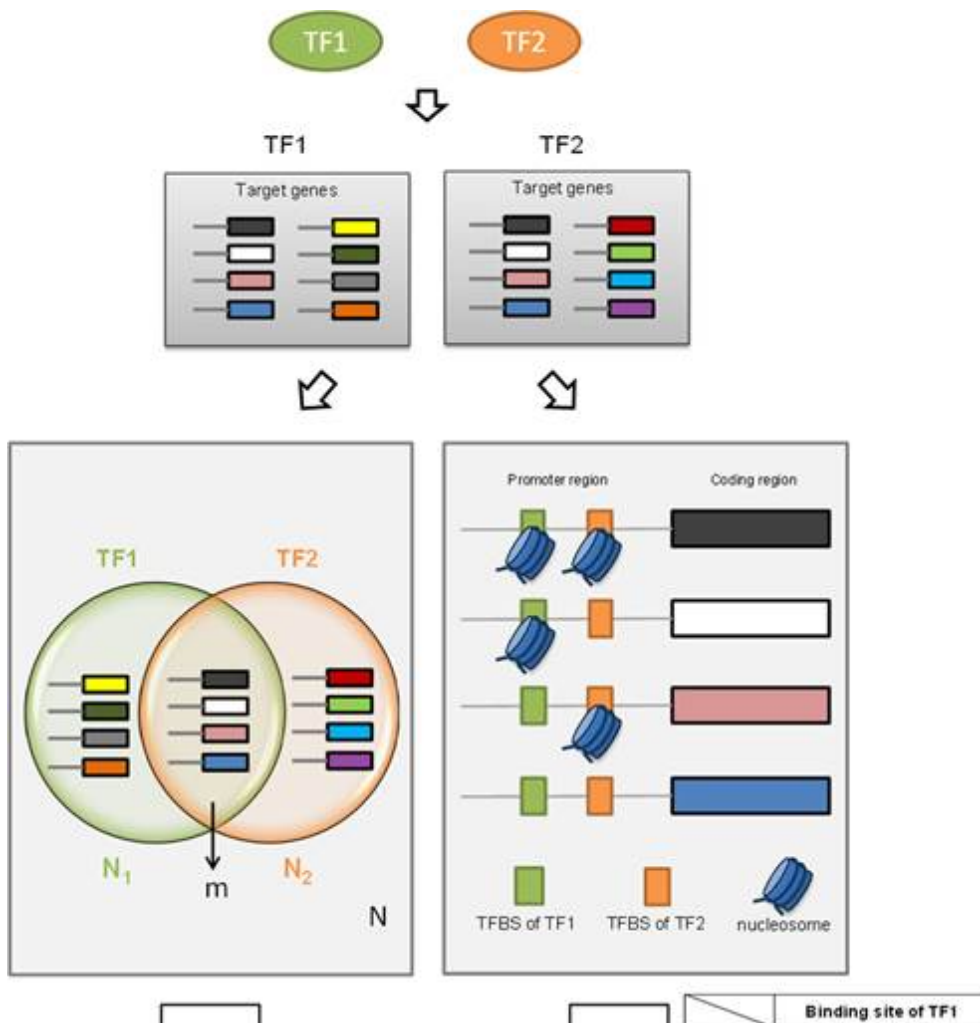
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**T**ranscriptional regulation of gene expression is usually accomplished by multiple cooperative transcription factors (TFs). Therefore, it is important to understand the precise cooperativity among TFs. Various kinds of experimental data have been used to identify cooperative TF pairs in existing methods. The nucleosome occupancy data is not yet used for this research topic despite that several experimental studies have revealed the association between nucleosomes and TF binding sites (TFBSs). Here we developed a novel method to infer the cooperativity between two TFs by integrating the TF-gene documented regulation, TFBS and nucleosome occupancy data. We show that our method performs better than 11 existing methods in identifying cooperative TF pairs in yeast. Moreover, the cooperative TF network constructed from our predicted cooperative TF pairs shows that our method has the power to find cooperative TF pairs of different biological processes.



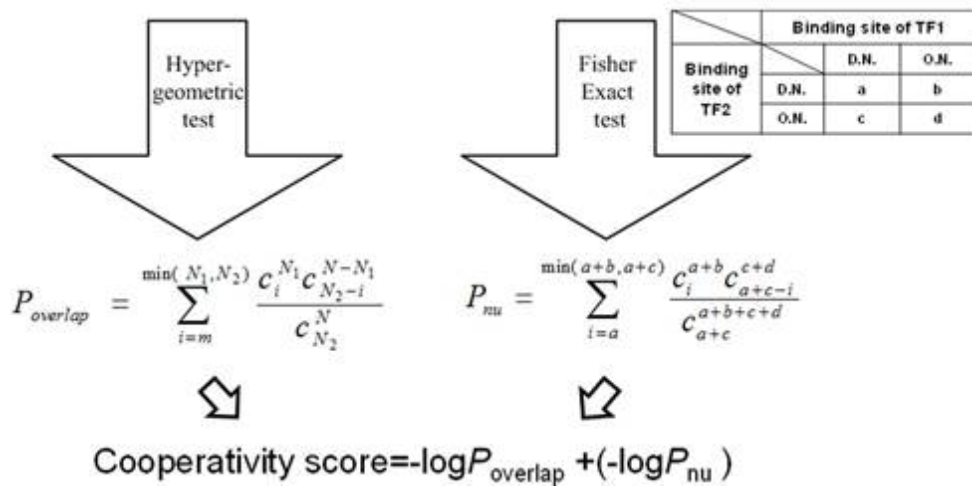


Figure 1. Flowchart of our method.

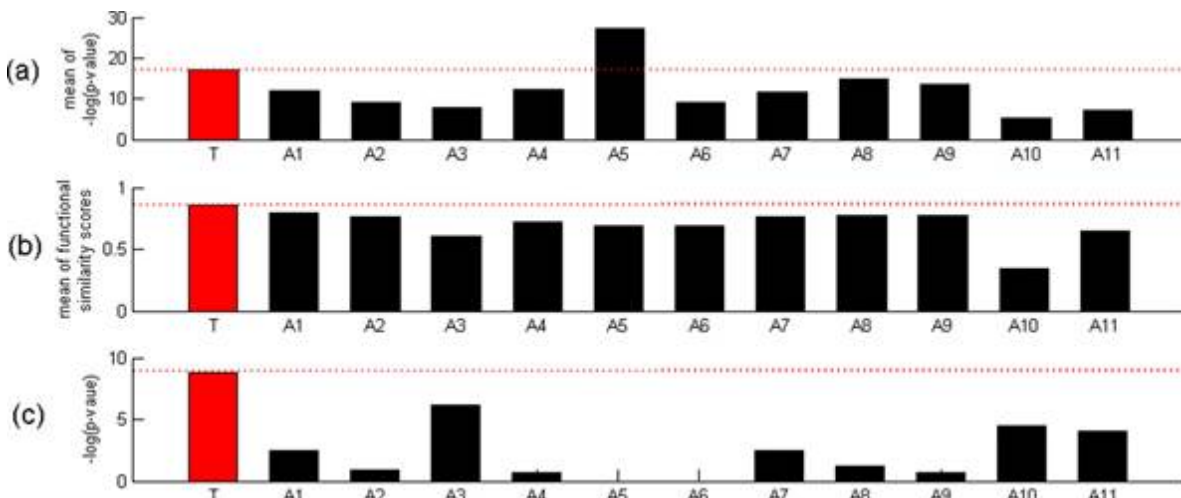


Figure 2. Comparison of our method with 11 existing methods based on three performance indices.

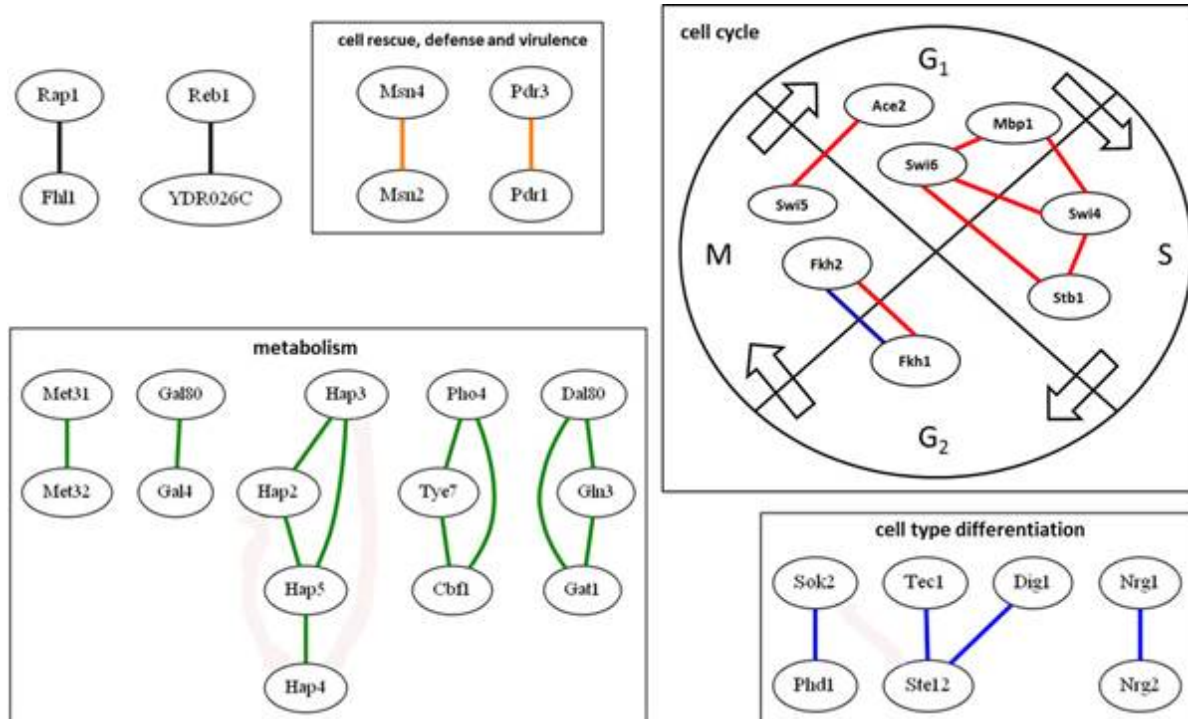


Figure 3. A TF cooperativity network.

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