# Completion of the yeast transcriptional regulation network by protein-protein interactions

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http://www.genoscope.cns.fr/biopathways/bib



### From Structural Topological properties of the heterogeneous network .....

#### **Cooperativity of Networks into Distance**



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To assess how PPI and TRI complement each other we shuffled the interface between the two networks and build a 'shuffled network' on which statistical properties can be compared with the real network. Thus, in both networks topological properties of each subnetwork are kept the same.

From one protein, directed distance is computed to other proteins. Compared to the real network, in the shuffled network, distance are shorter.



## **7** Structure in Layers Upstream of Regulation

A protein is linked to about 8 other proteins in mean We observe an non trivial repartition of links between layers of Transcriptional Factors, putative CoRegulators, and putative Co-coregulators



To validate the structure in layers, we add protein localisation data for each layer.



#### .. To local dynamical properties and dynamical motifs •••••



#### **4** Galactose, new dynamical properties

due to the slow interaction.

This is an example of a dynamical study of a miss understood heterogeneous loop found, from which new biological knowledge can be suggested.



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Time

without delay