Analysis of transcription regulatory associations in *Saccharomyces cerevisiae* using the YEASTRACT database.

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The YEASTRACT (Yeast Search for Transcriptional Regulators And Consensus Tracking; www.yeastract.com) database is a tool for the analysis of transcription regulatory associations in *Saccharomyces cerevisiae*. Last updated in January 2007, this database contains over 27800 regulatory associations between transcription factors (TF) and target genes and includes 281 specific DNA binding sites for more than 100 characterized TF. Computational tools are also provided to facilitate the exploitation of the gathered data when solving a number of biological questions. They are particularly interesting in the analysis of global gene expression results. YEASTRACT was presented and described in a paper published in the 2006 Database Issue of Nucleic Acids Research [1]. During 2006, researchers from more than 300 different groups from 60 different countries have performed over 100.000 queries per month using YEASTRACT.

YEASTRACT will shortly include DISCOVERER, a set of computational tools that can be used to identify complex motifs over-represented in the promoter regions of co-regulated genes. DISCOVERER is based on MUSA [2] and RISO [3] algorithms. These algorithms take as input a list of genes (for example those coming out from microarray experiments) and identify over-represented motifs. These motifs can be compared with known transcription factor binding sites described in the YEASTRACT database. A demonstration of the use of these new tools will be presented.


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