

## MADIBA: MicroArray Data Interface for Biological Annotation

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Many algorithms and software have been developed for analyzing gene expression. However, the extraction of relevant information from experimental data requires significant time and skill, as operating and post-processing these algorithms is still a substantial challenge. We are currently developing MADIBA, a tool designed to facilitate the assignment of biological meaning to gene expression patterns by automating the post processing stage.

A user of MADIBA is able to: identify the biological processes, the molecular functions and the cellular components represented by each cluster; identify the DNA binding sites to the genes in each cluster and examine the characteristics of the regulons inferred by the use of Bayesian networks; examine the visualizations of the metabolic pathways and the genomic localizations represented by each cluster; and also highlight specific information for the pathogen organisms that can be helpful for drug target identification.

This tool consists of a database with data from PlasmoDB, KEGG Orthology and also precalculated data with enzyme predictions from PRIAM, the promoters, the homologues, and Plasmodium-specific protein inserts. The results of the different analyses are visualized with a PHP interface (GO annotation, metabolic pathway, chromosomal localization, results of Bayesian networks and Plasmodium characteristics). Some analyses consist of links with other web tools (for searching of known and *ab initio* transcription factor motifs and for comparative genomic searches of transcription factor motifs). MADIBA thus allow the researcher to quickly identify potentially new biological discoveries.