

DEgenes Hunter - Functional analysis report

December 1, 2016

1 General description of the analysis workflow

The functional analysis script is based on the gene ID of the DEGs provided for a model organism. BiomaRt package has been included to get the annotations to perform a gene enrichment analysis of molecular functions, biological processes and cellular components with package topGO and a pathway enrichment study with KEGGREST and web service call to the KEGG database.

Results provided from the functional analysis script are gene enrichment graphs of (i) the complete DEG set and its (ii) overexpressed and (iii) sub-expressed candidates separately. Moreover, it provides the significant KEGG pathway maps as an interactive html file.

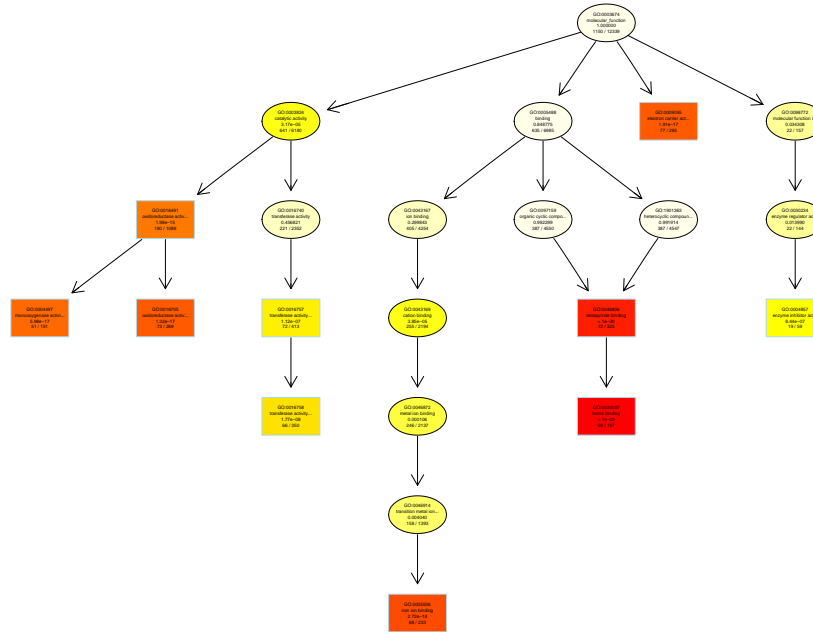
In DEgenes Hunter, genes are labeled according the following considerations:

- **Prevalent DEGs:** Differentially expressed genes considered by all packages employed but one.
- **All possible DEGs:** Differentially expressed genes considered by at least one of the R-packages but not enough of them to be considered as "prevalent DEGs".

2 GO graphs of all possible DEGs: Molecular Functions (MF)

2.1 General GOgraph of all possible DEGs

This is the GO graph provided by the topGO package (Image extracted from "GOgraph.allpos.MF.pdf" file):



2.3 GOgraph showing ONLY underexpressed functions from all possible DEGs

This is the GO graph concerning the underexpressed DEGs from the all possible DEGs (Image extracted from "GOgraph.allpos_underex.MF.pdf" file):

