

Queries The query window allows building complex questions to the MANTiS database. Each query is composed of one or several actions performed on one or several 'statement(s)' linked by logical operators. In each statement, four criteria can be considered in combination or isolation: a subset of user-defined genes, the type of events mapped (gains and/or losses or presence), a subset of branches, and specific functions (biological processes, molecular functions, gene expression, or tissue specificity). If the query contains more than 2 statements, the priority of each operator is also set.

Example of a complex MANTiS query "List for me the genes, among the 10,000 Entrez IDs that I provide, that: (i) are specifically expressed in the Nervous system (human EST data), (ii) are assigned to any Developmental process, (iii) were gained between the origin of vertebrates and the origin of eutherians, and (iv) are present in Human as well as in my two laboratory model species (i.e., mouse and dog)".



Reference

MANTiS: a phylogenetic framework for multi-species genome comparisons
 Athanasia C. Tzika, Raphaël Helaers, Yves Van de Peer & Michel C. Milinkovitch
Bioinformatics 2008, 24(2):151-157

MANTiS site

www.mantisdb.org

Availability

- Stand-alone versions for Windows, Macintosh, and Unix
- Online access using JAVA WebStart

Related Sites

- Laboratory of Artificial and Natural Evolution (LANE): <http://www.lanevol.org/>
- Ensembl: <http://www.ensembl.org/>
- PANTHER: <http://www.pantherdb.org/>
- HMDEG: <http://gln.ibms.sinica.edu.tw/product/HMDEG/EST/index.php>

Contact

info@mantisdb.org

MANTiS
 the missing link between multi-species full genome comparisons and functional analyses



www.mantisdb.org

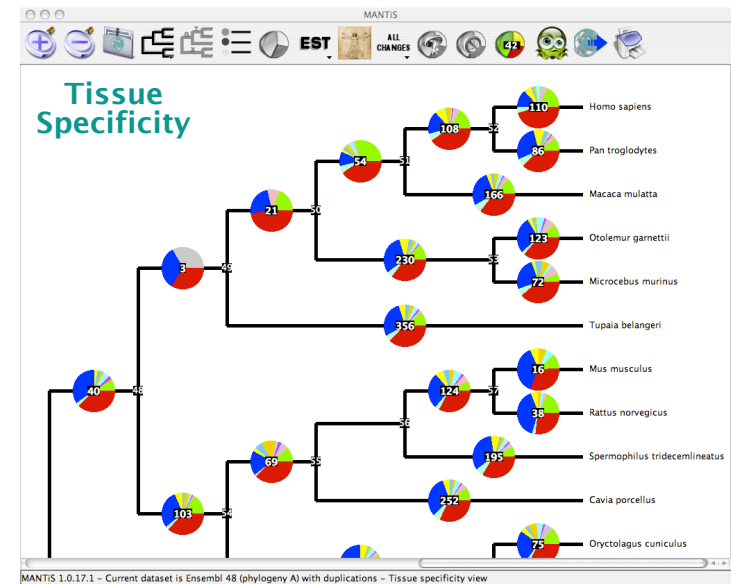
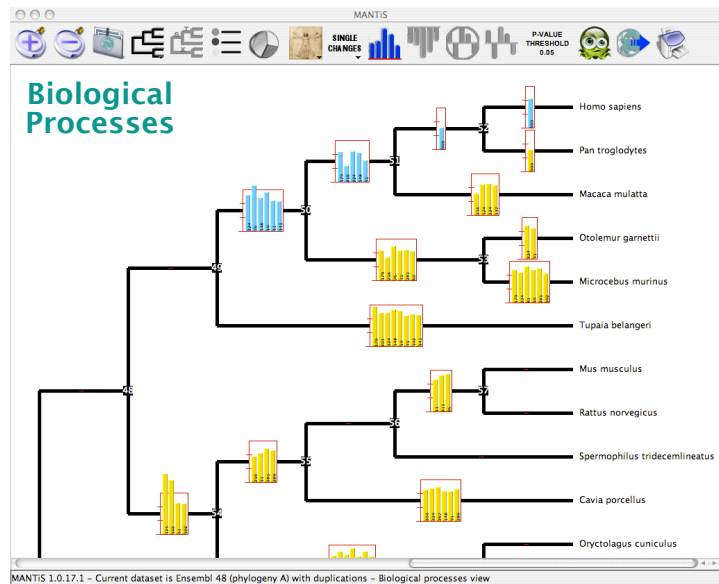
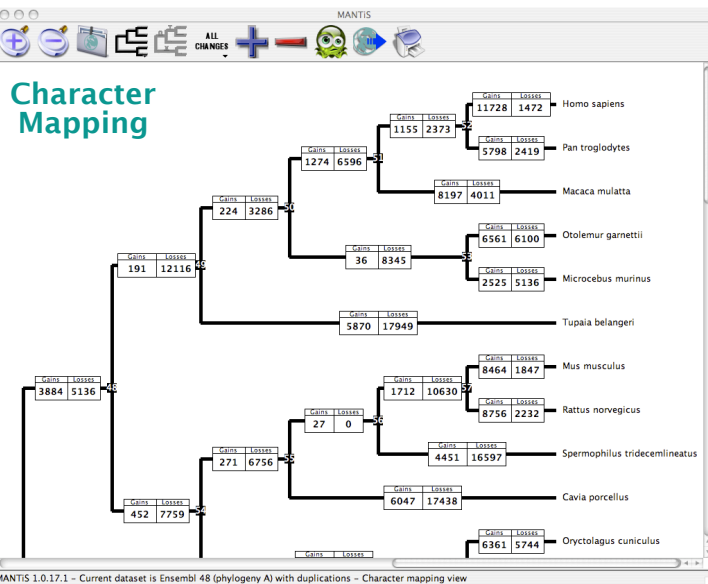
The screenshot shows the MANTiS query builder interface. It features three statements with various filters for GENE, BRANCH, and FUNCTION. Logical operators (AND, AND NOT) are used to combine statements. The results panel at the bottom shows details for the gene ENSG00000113196, including its description, orthologs, and biological processes. A green box highlights the results, stating "The result contains 5 genes".



The result contains 5 genes



UNIVERSITÉ DE GENÈVE
 FACULTÉ DES SCIENCES
 Département de zoologie et biologie animale



MANTiS: a phylogenetic framework for multi-species genome comparisons

MANTiS overview

MANTiS is an application system that builds a relational database integrating, in a phylogenetic framework, all *Ensembl* genes, corresponding *PANTHER* molecular functions and biological processes, as well as *GNF*, *eGenetics*, and *HMDEG* expression data; makes extensive use of the *Ensembl* ortholog/paralog prediction pipeline for identifying gene duplication events; and implements a dynamical programming approach for the mapping of gene gains, duplications, and losses on the phylogenetic tree.

Through a user-friendly interface, MANTiS allows the user to identify

1. gains and losses on specific branches of the tree,
2. genome content of ancestral species,
3. statistically over- or under-represented molecular functions, biological processes and anatomical systems (expression data), and
4. tissue specificity of gained, duplicated, and lost genes.

Finally, the entire set of information available in MANTiS can be exploited further using an advanced system of queries by which gene identity, mapping, and function parameters can be combined using logical operators.

Character Mapping Two types of MANTiS characters are generated: (i) one new character is created for each tree representing a protein family (i.e., these correspond to *de novo* gains, and not to duplication events) and (ii) one new character is created for each duplication event (i.e., each protein family may include one to many duplication events).

Gains and losses of characters are then mapped by MANTiS on the 'true' species-tree, i.e., the best-supported tree on the basis of the available literature. Gains are assigned to the branch leading to the most-recent-common ancestor of all species exhibiting the character. Based on a recursive function, a maximum-likelihood approach is used to identify the branches where gene losses occurred.

Genome Content MANTiS builds the genome content of each ancestral species (i.e., at each internal node) by (starting from the root) adding all gained and subtracting all lost characters along the branches leading to the node of interest.

Biological Processes and Molecular Functions MANTiS is not limited to providing lists of Gene Ontology terms for each gene, but goes further by plotting the over- or under-representation of each category associated with gains or losses on each branch of the species tree.

Gene Expression and Tissue Specificity

Three sources of gene expression data are used in MANTiS: *eGenetics* and *HMDEG*, two databases of Expressed Sequence Tags, and *GNF*, which is using microarray expression data.

Main Functionalities Besides basic functionalities, such as zoom in/out, the user can easily switch among datasets, change the tree type to a phylogram or a chronogram, export all 'View' data, or just print the current window. Furthermore, a simple double-click on the histograms or pie-charts provides not only an enlarged view but also all information necessary to build these graphs.

Biological processes (All changes with over-rep)

88 - Vitamin/cofactor transport
 Category contains 36 genes
 Current branch has 64 gains
 0.0708 genes are expected
 1 gene are observed
 p-Value : 2.3545E-3
 Fractional difference : 1.3132E1

Branch Euarchonta - Present

ENSG00000000938
 ENSG00000000971
 ENSG0000001036
 ENSG00000000971
 Species : Homo sapiens
 View it on Ensembl 48

Description :
 Complement factor H precursor (H factor 1).
 [Source:UniProt/SwissProt;Acc:P08063]

Orthologs :
 Main gene (Homo sapiens) :
 ENSG00000000971
 Orthologs :
 Pan troglodytes : ENSPTRG00000001799
 Ootolemur garnettii : ENSOCAC00000002008
 Mus musculus : ENSMUSG00000026365
 Rattus norvegicus : ENSRNORG00000030715
 Spermophilus tridecemlineatus : ENSSTOG00000015522
 Canis familiaris : ENSCAF00000010290
 Sorex araneus : ENSSARG00000009221
 Echinops telfairi : ENSETEG0000004065

Character origin and duplications path :
 Found in Homo sapiens biological processes :
 Immunity and defense
 Complement-mediated immunity
 Found in Homo sapiens molecular functions :