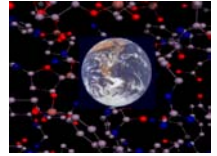




# Benchmarking ortholog identification methods using function similarity

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## Abstract

We present a strategy to test the **quality of ortholog identification methods**. This strategy is based on the assumption that orthologs have a **highly similar function**. The conservation of function between proteins in different species can be measured by using the **functional annotation** provided with the protein sequences but also with functional data like **co-expression data**, **protein interaction data** and **chromosomal position data**. These data were used within the orthology benchmarking in a direct way, looking at only one protein in each species, and in a **pairwise way**, looking at two proteins in each species having some kind of relationship (e.g. co-expressed, interacting, neighboring). The benchmarking methods were used to test a number of ortholog identification methods, both methods that identify **one-to-one** orthologous relationships and methods that identify **many-to-many** relationships.

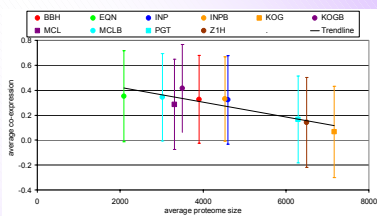
## 'Protein World' data set

For a fair comparison of all of the covered methods, the same data set was used at all time. This **'Protein World'** data set was created by **comparing** all of the currently known and predicted **proteins** (SpTrEMBL) through the **Smith-Waterman** algorithm with calculation of **Z-values**. This advanced algorithm is more precise than the more common BLAST and FASTA algorithms, which were used to build other protein relation databases. The software package used to do the calculations is called **'Biofacet'**, formerly known as 'LASSAP' ('Large Scale Sequence compARison Package'). The data set is available through the dutch bioinformatics portal site <http://www.bioasp.nl>. As for both **human** and **mouse** good expression data and other functional relationships were available, we used the orthologous relationships between these two species for our study.

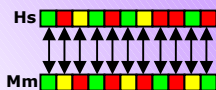
## Compared ortholog identification methods

Best Bidirectional Hit (BBH), Equal SwissProt Names (EQN), InParanoid (INP), KOG (KOG), OrthoMCL (MCL), Phylogenetic Tree (PGT) and Z>100 (Z1H)

## Direct conservation of function

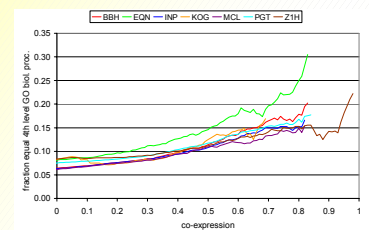
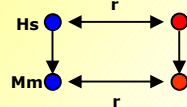


### Co-expression



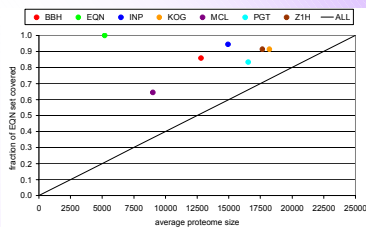
## Pairwise conservation of function

### Conservation of co-expression

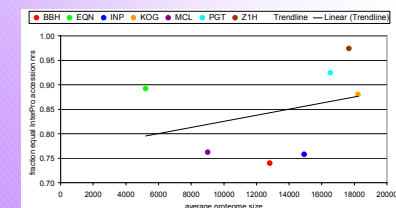
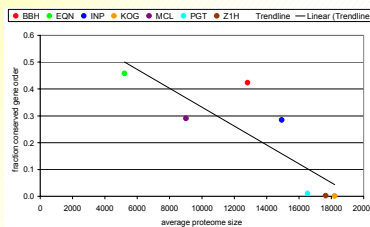
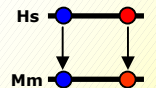


### Equal SwissProt name

ABCD\_HUMAN  
~  
ABCD\_MOUSE



### Conservation of gene order



### Equal InterPro acc. nr.

5H6\_HUMAN (IPR000276)  
~  
5H7\_HUMAN (IPR000276)

### Conservation of interaction

