

The *GOSim* package

Holger Fröhlich

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1 Introduction

The Gene Ontology (GO) has become one of the most widespread systems for systematically annotating gene products within the bioinformatics community and is developed by the Gene Ontology Consortium (The Gene Ontology Consortium, 2004). It is specifically intended for describing gene products with a controlled and structured vocabulary. GO terms are part of a Directed Acyclic Graph (DAG), covering three orthogonal taxonomies or "aspects": *molecular function*, *biological process* and *cellular component*. Two different kinds of relationship between GO terms exist: the "is-a" relationship and the "part-of" relationship. Providing a standard vocabulary across any biological resources, the GO enables researchers to use this information for automated data analysis.

The *GOSim* package (Fröhlich et al., 2007) provides the researcher with various information theoretic similarity concepts for GO terms (Resnik, 1995, 1999; Lin, 1998; Jiang and Conrath, 1998; Lord et al., 2003; Couto et al., 2003, 2005). Moreover, since version 1.1.5 *GOSim* contains several new similarity concepts, which are based on so-called diffusion kernel techniques (Lerman and Shakhnovich, 2007). Additionally *GOSim* implements different methods for computing functional similarities between gene products based on the similarities between the associated GO terms (Speer et al., 2005; Fröhlich et al., 2006; Schlicker et al., 2006; Lerman and Shakhnovich, 2007; del Pozo et al., 2008). This can, for instances, be used for clustering genes according to their biological function (Speer et al., 2005; Fröhlich et al., 2006) and thus may help to get a better understanding of the biological aspects covered by a set of genes.

Since version 1.1 *GOSim* additionally offers the possibility of a GO enrichment analysis using the topGO package (Alexa et al., 2006). Hence, *GOSim* acts now as an umbrella for different analysis methods employing the GO structure.

2 Usage of *GOSim*

To elucidate the usage of *GOSim* we show an example workflow and explain the employed similarity concepts. We create a character vector of Entrez gene IDs, which we assume to be from human:

```
> library(GOSim)
> genes=c("207", "208", "596", "901", "780", "3169", "9518", "2852", "26353", "8614", "7494")
```

Next we investigate the GO annotation within the current ontology (which is *biological process* by default):

```
> getGOInfo(genes)
```

	207	208	596	901	780
go_id	character,131	character,33	character,130	character,3	character,24
Term	character,131	character,33	character,130	character,3	character,24
Definition	character,131	character,33	character,130	character,3	character,24
IC	numeric,131	numeric,33	numeric,130	numeric,3	numeric,24
	3169	9518	2852	26353	8614
go_id	character,33	character,12	character,54	character,2	character,12
Term	character,33	character,12	character,54	character,2	character,12
Definition	character,33	character,12	character,54	character,2	character,12
IC	numeric,33	numeric,12	numeric,54	numeric,2	numeric,12
	7494				
go_id	character,50				
Term	character,50				
Definition	character,50				
IC	numeric,50				

2.1 Term Similarities

Let us examine the similarity of the GO terms for genes "8614" and "2852" in greater detail:

```
> getTermSim(c("GO:0007166", "GO:0007267", "GO:0007584", "GO:0007165", "GO:0007186"),met
```

	GO:0007166	GO:0007267	GO:0007584	GO:0007165	GO:0007186
GO:0007166	0.2628131	0.1806383	0.1266641	0.1945233	0.1945233
GO:0007267	0.1806383	0.3551639	0.0000000	0.1806383	0.1806383
GO:0007584	0.1266641	0.0000000	0.5128961	0.1266641	0.1266641
GO:0007165	0.1945233	0.1806383	0.1266641	0.1945233	0.1945233
GO:0007186	0.1945233	0.1806383	0.1266641	0.1945233	0.4016432

This calculates Resnik's pairwise similarity between GO terms (Resnik, 1995, 1999):

$$sim(t, t') = IC_{ms}(t, t') := \max_{\hat{t} \in Pa(t, t')} IC(\hat{t}) \quad (1)$$

Here $Pa(t, t')$ denotes the set of all common ancestors of GO terms t and t' , while $IC(t)$ denotes the information content of term t . It is defined as (e.g. Lord et al. (2003))

$$IC(\hat{t}) = -\log P(\hat{t}) \quad (2)$$

i.e. as the negative logarithm of the probability of observing \hat{t} . The information content of each GO term is already precomputed for each ontology based on the empirical observation, how many times a specific GO term or any of its direct or indirect offsprings appear in the annotation of the GO with gene products. GOSim provides a normalized version of Resnik's similarity measure, which divides the information content of the minimum subsumer by the maximum information content of all GO terms, hence obtaining a number between 0 and 1.

```
> data("ICsBPhumanall")
> IC[c("GO:0007166", "GO:0007267", "GO:0007584", "GO:0007165", "GO:0007186")]
```

```
GO:0007166 GO:0007267 GO:0007584 GO:0007165 GO:0007186
  3.006413   4.062846   5.867200   2.225221   4.594539
```

This loads the information contents of all GO terms within "biological process". Likewise, the data files ICsMFhumanall and ICsCChumanall contain the information contents of all GO terms within "molecular function" and "cellular component" for human. Since GOSim version 1.1.4.0 the information content of GO terms relies on the mapping of primary gene IDs (mainly Entrez) to GO terms provided by the libraries org.Dm.eg.db (fly), org.Hs.eg.db (human), org.Mm.eg.db (mouse), etc. Additionally, it is possible to pass a user provided mapping via the function `setEvidenceLevel`. Please refer to the manual pages for details. If only GO terms having certain evidence codes should be considered, one must explicitly calculate the corresponding information contents in the function `calcICs`. Again, more information on this function can be found in the manual pages.

To continue our example from above, let us also calculate Jiang and Conrath's pairwise similarity between GO terms, which is the default, for comparison reasons (Jiang and Conrath, 1998):

```
> getTermSim(c("GO:0007166", "GO:0007267", "GO:0007584", "GO:0007165", "GO:0007186"), ver
```

```

      GO:0007166 GO:0007267 GO:0007584 GO:0007165 GO:0007186
GO:0007166  0.9505312  0.5105747  0.2498911  0.7587689  0.5222505
GO:0007267  0.5105747  0.9828000  0.0000000  0.5740054  0.4169139
GO:0007584  0.2498911  0.0000000  0.9971692  0.2740140  0.2119568
GO:0007165  0.7587689  0.5740054  0.2740140  0.8919565  0.5820734
GO:0007186  0.5222505  0.4169139  0.2119568  0.5820734  0.9898931
```

Jiang and Conrath's similarity measure is defined as

$$\text{sim}(t, t') = 1 - \min(1, IC(t) - 2IC_{ms}(t, t') + IC(t')) \quad (3)$$

i.e. the similarity between t and t' is 0, if their normalized distance is at least 1.

Likewise, we can also compute Lin's pairwise similarity between GO terms (Lin, 1998):

```
> getTermSim(c("GO:0007166", "GO:0007267", "GO:0007584", "GO:0007165", "GO:0007186"), met
```

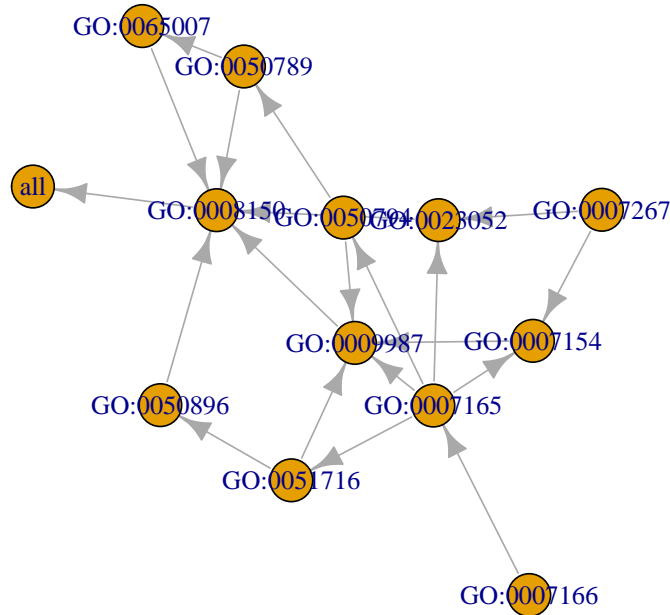
	GO:0007166	GO:0007267	GO:0007584	GO:0007165	GO:0007186
GO:0007166	1.0000000	0.5846115	0.3265762	0.8506792	0.5855112
GO:0007267	0.5846115	1.0000000	0.0000000	0.6572401	0.4773693
GO:0007584	0.3265762	0.0000000	1.0000000	0.3581018	0.2770009
GO:0007165	0.8506792	0.6572401	0.3581018	1.0000000	0.6525805
GO:0007186	0.5855112	0.4773693	0.2770009	0.6525805	1.0000000

It is defined as:

$$sim(t, t') = \frac{2IC_{ms}(t, t')}{IC(t) + IC(t')} \quad (4)$$

Resnik's, Jiang-Conraths's and Lin's term similarities all refer to $IC_{ms}(t, t')$, the information content of the minimum subsumer of t and t' , i.e. of the lowest common ancestor in the hierarchy. For illustration let us plot the GO graph with leaves GO:0007166 and GO:0007267 and let us compute their minimum subsumer (see Fig. ??):

```
> library(igraph)
> G = getGOGraph(c("GO:0007166", "GO:0007267"))
> G2 = igraph.from.graphNEL(G)
> plot(G2, vertex.label=V(G2)$name)
```



```
> getMinimumSubsumer("GO:0007166", "GO:0007267")
```

```
[1] "GO:0023052"
```

In contrast to the above defined similarity measures Couto et al. (Couto et al., 2005) introduced a concept, which is not based on the minimum subsumer, but on the set of all disjunctive common ancestors. Roughly speaking, the idea is not to consider the common ancestor having the highest information content only, but also others, if they are somehow "separate" from each other, i.e. there exists a path to t or to t' not passing any other of the disjunctive common ancestors.

```
> getDisjCommAnc("GO:0007166", "GO:0007267")
```

```
[1] "GO:0007154" "GO:0009987" "GO:0023052"
```

In this case the set of disjunctive common ancestors consists of the minimum subsumer, GO:0007154, and its parent, GO:0009987, because from both there exists a path to GO:0007166 not passing any other disjunctive common ancestor(see Fig. ??).

Based on the notion of disjunctive common ancestors Resnik's similarity concept can be extended by defining:

$$sim(t, t') = IC_{share}(t, t') = \frac{1}{|DisjCommAnc|} \sum_{t \in DisjCommAnc} IC(t) \quad (5)$$

Likewise, Jiang-Conraths's and Lin's measures can be extended as well by replacing $IC_{ms}(t, t')$ by $IC_{share}(t, t')$.

```
> getTermSim(c("GO:0007166", "GO:0007267"), method="CoutoResnik", verbose=FALSE)
```

```
GO:0007166 GO:0007267
GO:0007166 3.006413 1.507568
GO:0007267 1.507568 4.062846
```

Finally, it should be mentioned that also the depth and density enriched term similarity by Couto et al. (Couto et al., 2003) has been integrated into *GOSim*:

```
> setEnrichmentFactors(alpha=0.5, beta=0.3)
> getTermSim(c("GO:0007166", "GO:0007267"), method="CoutoEnriched", verbose=FALSE)
```

```
GO:0007166 GO:0007267
GO:0007166 9.038517 0.000000
GO:0007267 0.000000 16.50672
```

Since version 1.1.5 *GOSim* contains several new similarity concepts, which are based on so-called diffusion kernel techniques (Lerman and Shakhnovich, 2007) rather than on the information theoretic ideas presented before. For using these similarity measures it is necessary to pre-compute a diffusion kernel on the Gene Ontology graph via `calc.diffusion.kernel`. This will take some time and result in a kernel/similarity matrix that is stored in a file called e.g. 'diffKernelpowerBPhumanall.rda' (meaning matrix power diffusion kernel for ontology BP in human using all evidence codes) in the current working directory. Once the kernel is created, it has to be loaded into the environment first `load.diffusion.kernel`. Afterwards GO term similarities can be computed via function `getTermSim`. Please check the manual pages for details.

Since version 1.2 *GOSim* also contains Schlicker et al.'s GO term similarity measure (Schlicker et al., 2006), which is an adaption of Lin's similarity measure. Moreover, the graph information content similarity by Pesquita et al. has been implemented (Pesquita et al., 2007).

```
> getTermSim(c("GO:0007166", "GO:0007267", "GO:0007584", "GO:0007165", "GO:0007186"), met
```

```
GO:0007166 GO:0007267 GO:0007584 GO:0007165 GO:0007186
GO:0007166 0.9505312 0.5105747 0.2498911 0.7587689 0.5222505
GO:0007267 0.5105747 0.9828000 0.0000000 0.5740054 0.4169139
GO:0007584 0.2498911 0.0000000 0.9971692 0.2740140 0.2119568
GO:0007165 0.7587689 0.5740054 0.2740140 0.8919565 0.5820734
GO:0007186 0.5222505 0.4169139 0.2119568 0.5820734 0.9898931
```

2.2 Functional Gene Similarities

The special strength of *GOSim* lies in the possibility not only to calculate similarities for individual GO terms, but also for genes based on their complete GO annotation. Since *GOSim* version 1.1.5 for this purpose the following ideas have been implemented:

1. Maximum (Couto et al., 2003) and average pairwise GO term similarity
2. Average of best matching GO term similarities (Schlicker et al., 2006).
3. Computation of a so-called *optimal assignment* of terms from one gene to those of another one (Fröhlich et al., 2006).
4. Similarity derived from Hausdorff distances between sets (del Pozo et al., 2008).
5. Embedding of each gene into a feature space: (Speer et al., 2005; Fröhlich et al., 2006) proposed to define feature vectors by a gene's maximum GO term similarity to certain prototype genes. More simple (but probably also less accurate), (Mistry and Pavlidis, 2008) recently proposed to represent each gene by a feature vector describing the presence/absence of all GO terms. The absence of each GO term is additionally weighted by its information content. Within a feature space gene functional similarities naturally arise as dot products between feature vectors. These dot products can be understood as so-called *kernel functions* (Schölkopf and Smola, 2002), as used in e.g. Support Vector Machines (Cortes and Vapnik, 1995). Depending on the choice of later normalization (see below) one can arrive at the cosine similarity (Eq. 6), at the Tanimoto coefficient (Eq. 7) or at a measure similar to Lin's one (Eq. 8, Eq. 4).

2.2.1 Normalization of Similarities

Often, people want to normalize similarities, e.g. on the interval $[0, 1]$, for better interpretation. To do so, we can perform the transformation

$$sim_{gene}(g, g') \leftarrow \frac{sim_{gene}(g, g')}{\sqrt{sim_{gene}(g, g)sim_{gene}(g', g')}} \quad (6)$$

Provided $sim_{gene} \geq 0$, the consequence will be a similarity of 1 for g with itself and between 0 and 1 for g with any other gene. In case of a feature space embedding this transformation is equivalent to computing the cosine similarity between two feature vectors.

Another possibility is to use Lin's normalization (see Eq. 4):

$$sim_{gene}(g, g') \leftarrow \frac{2sim_{gene}(g, g')}{sim_{gene}(g, g) + sim_{gene}(g', g')} \quad (7)$$

Furthermore, one can use a normalization in the spirit of the Tanimoto coefficient:

$$sim_{gene}(g, g') \leftarrow \frac{sim_{gene}(g, g')}{sim_{gene}(g, g) + sim_{gene}(g', g') - sim_{gene}(g, g')} \quad (8)$$

In case of a feature space embedding the transformation corresponds exactly to the Tanimoto coefficient between two feature vectors.

We now give a more detailed overview over the different similarity concepts mentioned above.

2.2.2 Maximum and Average Pairwise GO Term Similarity

The idea of the maximum pairwise GO term similarity is straight forward. Given two genes g and g' annotated with GO terms t_1, \dots, t_n and t'_1, \dots, t'_m we define the functional similarity between g and g' as

$$sim_{gene}(g, g') = \max_{\substack{i=1, \dots, n \\ j=1, \dots, m}} sim(t_i, t'_j) \quad (9)$$

where sim is some similarity measure to compare GO terms t_i and t'_j . This idea is, for instance, realized in FuSSiMeg (Couto et al., 2003). Instead of computing the maximum pairwise GO term similarity one may also take the average here.

2.2.3 Average of Best Matching GO Term Similarities

The idea of this approach (Schlicker et al., 2006) is to assign each GO term t_i occurring in gene g to its best matching partner t'_{π_i} in gene g' . Hence multiple GO terms from gene g can be assigned to one GO term from gene g' . A similarity score is computed by taking the average similarity of assigned GO terms. Since, however, genes can have an unequal number of GO terms the result depends on whether GO terms of gene g are assigned to those of gene g' or vice versa. Hence, in Schlicker et al. (2006) it was proposed to either take the maximum or the average of both similarity scores. Both strategies are implemented in *GOSim*.

2.2.4 Optimal Assignment Gene Similarities

To elucidate the idea of the optimal assignment (Fröhlich et al., 2006), consider the GO terms associated with gene "8614" on one hand and gene "2852" on the other hand:

```
> getGOInfo(c("8614", "2852"))
```

	8614	2852
go_id	character,12	character,54
Term	character,12	character,54
Definition	character,12	character,54
IC	numeric,12	numeric,54

Given a similarity concept *sim* to compare individual GO terms, the idea is now to assign each term of the gene having fewer annotation to exactly one term of the other gene such that the overall similarity is maximized. More formally the optimal assignment problem can be stated as follows: Let π be some permutation of either an n -subset of natural numbers $\{1, \dots, m\}$ or an m -subset of natural numbers $\{1, \dots, n\}$ (this will be clear from context). Then we are looking for the quantity

$$sim_{gene}(g, g') = \begin{cases} \max_{\pi} \sum_{i=1}^n sim(t_i, t'_{\pi(i)}) & \text{if } m > n \\ \max_{\pi} \sum_{j=1}^m sim(t_{\pi(j)}, t'_j) & \text{otherwise} \end{cases} \quad (10)$$

The computation of (10) corresponds to the solution of the classical maximum weighted bipartite matching (optimal assignment) problem in graph theory and can be carried out in $O(\max(n, m)^3)$ time (Mehlhorn and Näher, 1999). To prevent that larger lists of terms automatically achieve a higher similarity we may further sim_{gene} divide 10 by $\max(m, n)$.

In our example, using Lin's GO term similarity measure the following assignments yielding a corresponding similarity matrix are found:

```
> getGeneSim(c("8614", "2852"), similarity="OA", similarityTerm="Lin", avg=FALSE, verbose=FALSE)

filtering out genes not mapping to the currently set GO category ... ==> list of 2
      8614      2852
8614 1.0000000 0.3265955
2852 0.3265955 1.0000000
```

Note the difference to a gene similarity that is just based on the maximum GO term similarity and to a gene similarity that is based on the average of best matching GO terms:

```
> getGeneSim(c("8614", "2852"), similarity="max", similarityTerm="Lin", verbose=FALSE)

filtering out genes not mapping to the currently set GO category ... ==> list of 2
      8614      2852
8614 1.0000000 0.9340789
2852 0.9340789 1.0000000
```

```
> getGeneSim(c("8614", "2852"), similarity="funSimMax", similarityTerm="Lin", verbose=FALSE)

filtering out genes not mapping to the currently set GO category ... ==> list of 2
      8614      2852
8614 1.0000000 0.6865975
2852 0.6865975 1.0000000
```

2.2.5 Gene Similarities In the Spirit of Hausdorff Metrics

Hausdorff metrics are a general concept for measuring distances between compact subsets of a metric space. Let X and Y be the two sets of GO terms associated to genes g and g' , and let $d(t, t')$ denote the distance between GO terms t and t' . Then the Hausdorff distance X and Y is defined as

$$d_{Hausdorff}(X, Y) = \max\{\sup_{t \in X} \inf_{t' \in Y} d(t, t'), \sup_{t' \in Y} \inf_{t \in X} d(t, t')\} \quad (11)$$

Using Hausdorff metrics for measuring gene functional distances was proposed in del Pozo et al. (2008). We translate the idea to define a similarity measure between g and g' (see the difference to previous GOSim versions):

$$sim_{gene}(g, g') = \exp(-d_{Hausdorff}(g, g')) \quad (12)$$

```
> getGeneSim(c("8614", "2852"), similarity="hausdorff", similarityTerm="Lin", verbose=FALSE)
filtering out genes not mapping to the currently set GO category ... ==> list of 2
      8614 2852
8614    1    1
2852    1    1
```

2.2.6 Feature Space Embedding of Gene Products

The Simple Approach Mistry and Pavlidis (2008) proposed to represent each gene by a feature vector describing the presence/absence of all GO terms. The absence of each GO term is additionally weighted by its information content. In the feature space similarities arise as dot products. Hence, the similarity between two GO terms t and t' is implicitly defined as the product of their information content values, hence ignoring the exact DAG structure of the Gene Ontology as employed by the GO term similarity measures explained in the beginning of this document.

```
> getGeneSim(c("8614", "2852"), similarity="dot", method="Tanimoto", verbose=FALSE)
filtering out genes not mapping to the currently set GO category ... ==> list of 2
      8614 2852
8614    1  NaN
2852  NaN    1
```

This will calculate the Tanimoto coefficient between feature vectors as a similarity measure. It is possible to retrieve the feature vectors via:

```
> features = getGeneFeatures(c("8614", "2852"))
filtering out genes not mapping to the currently set GO category ... ==> list of 2
```

Embeddings via GO Term Similarities to Prototype Genes This approach is due to Speer et al. (2005); Fröhlich et al. (2006). The idea is to define a feature vector for each gene by its pairwise GO term similarity to certain prototype genes, i.e. the prototype genes form a (nonorthogonal) basis, and each gene is defined relative to this basis. The prototype genes can either be defined a priori or one can use one of the heuristics implemented in the function `selectPrototypes`. The default behavior is to select the 250 best annotated genes, i.e. which have been annotated with GO terms most often, but here we just use 3 for computational reasons:

```
> proto = selectPrototypes(n=3, verbose=FALSE)
```

We now calculate for each gene g feature vectors $\phi(g)$ by using their similarity to all prototypes p_1, \dots, p_n :

$$\phi(g) = (\text{sim}'(g, p_1), \dots, \text{sim}'(g, p_n))^T \quad (13)$$

Here sim' by default is the maximum pairwise GO term similarity. Alternatively, one can use other similarity measures for sim' as well. These similarity measures can by itself again be combined with arbitrary GO term similarity concepts. The default is the Jiang-Conrath term similarity.

Because the feature vectors are very high-dimensional we usually perform a principal component analysis (PCA) to project the data into a lower dimensional subspace. The results are not shown here due to long computation time.

```
> PHI = getGeneFeaturesPrototypes(genes, prototypes=proto, verbose=FALSE)
```

This uses the above define prototypes to calculate feature vectors and performs a PCA afterwards. The number of principal components is chosen such that at least 95% of the total variance in feature space can be explained (this is a relatively conservative criterion).

We can now plot our genes in the space spanned by the first 2 principal components to get an impression of the relative "position" of the genes to each other in the feature space (see Fig. ??). The feature vectors are normalized to Euclidian norm 1 by default:

```
> x=seq(min(PHI$features[,1]),max(PHI$features[,1]),length.out=100)
> y=seq(min(PHI$features[,2]),max(PHI$features[,2]),length.out=100)
> plot(x,y,xlab="principal component 1",ylab="principal component 2",type="n")
> text(PHI$features[,1],PHI$features[,2],labels=genes)
```

Finally, we can directly calculate the similarities of the genes to each other, this time using the Resnik's GO term similarity concept. These similarities may then be used to cluster genes with respect to their function:

```
> sim = getGeneSimPrototypes(genes[1:3], prototypes=proto, similarityTerm="Resnik", verbose=FALSE)
> h=hclust(as.dist(1-sim$similarity), "average")
> plot(h, xlab="")
```

This produces a hierarchical clustering of all genes using average linkage clustering (see Fig. 2).

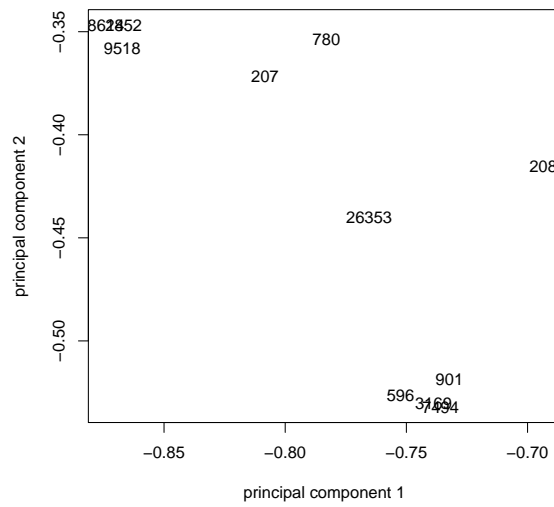


Figure 1: Embedding of genes into feature space spanned by the first 2 principal components

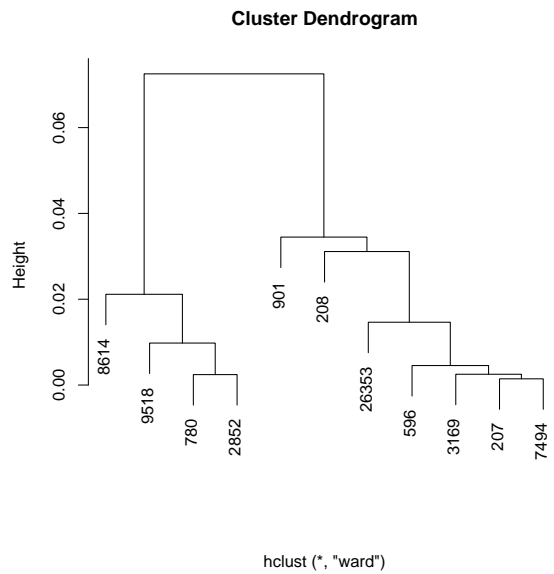


Figure 2: Possible functional clustering of the genes using Ward's method.



Figure 3: Silhouette plot of a possible given grouping of genes.

2.2.7 Combination of Similarities from Different Ontologies

It should be mentioned that up to now all similarity computations were performed within the ontology "biological process". One could imagine to combine functional similarities between gene products with regard to different taxonomies. An obvious way for doing so would be to consider the sum of the respective similarities:

$$sim_{total}(g, g') = sim_{Ontology1}(g, g') + sim_{Ontology2}(g, g') \quad (14)$$

Of course, one could also use a weighted averaging scheme here, if desired.

2.3 Cluster Evaluations

GOSim has the possibility to evaluate a given clustering of genes or terms by means of their GO similarities. Supposed, based on other experiments (e.g. microarray), we have decided to put genes "8614", "9518", "780", "2852" in one group, genes "3169", "207", "7494", "596" in a second and the rest in a third group. Then we can ask ourselves, how similar these groups are with respect to their GO annotations:

```
> ev = evaluateClustering(c(2,3,2,3,1,2,1,1,3,1,2), sim$similarity)
> plot(ev$clustersil, main="")
```

A good indication of the clustering quality can be obtained by looking at the cluster silhouettes (Rousseeuw, 1987) (see Fig. 3). This shows that clusters 1 and 2 are relatively homogenous with respect to the functional similarity of the genes contained in it, while the genes in cluster 3 are more dissimilar.

2.4 GO Enrichment Analysis

Since version 1.1 *GOSim* also offers the possibility of a GO enrichment analysis. Suppose, we may now want to get a clearer picture of the genes involved in cluster 1. For this purpose we use the topGO tool (Alexa et al., 2006).

```
> library(org.Hs.eg.db)
> library(topGO)
> allgenes = union(c("8614", "9518", "780", "2852"), sample(keys(org.Hs.egGO), 1000))
> GGOenrichment(c("8614", "9518", "780", "2852"), allgenes) # print out what cluster
```

\$GOTerms

	go_id
14681	GO:0006468
15743	GO:0006874
16312	GO:0007169
16996	GO:0007566
23940	GO:0014068
32386	GO:0022411
36102	GO:0031667
47519	GO:0040015
48270	GO:0042327
68330	GO:0051130
70608	GO:0051896
70716	GO:0051924
78326	GO:0071375

	Term
14681	protein phosphorylation
15743	intracellular calcium ion homeostasis
16312	transmembrane receptor protein tyrosine kinase signaling pathway
16996	embryo implantation
23940	positive regulation of phosphatidylinositol 3-kinase signaling
32386	cellular component disassembly
36102	response to nutrient levels
47519	negative regulation of multicellular organism growth
48270	positive regulation of phosphorylation
68330	positive regulation of cellular component organization
70608	regulation of protein kinase B signaling
70716	regulation of calcium ion transport
78326	cellular response to peptide hormone stimulus

14681
15743

16312 The series of molecu
 16996
 23940
 32386
 36102 Any p
 47519
 48270
 68330 Any process that activates or increases the fre
 70608
 70716
 78326 Any process that results in a change in state or activity of a cell (in terms

\$p.values

G0:0051924	G0:0007566	G0:0040015	G0:0007169	G0:0031667	G0:0042327
0.0018320747	0.0006166495	0.0006166495	0.0004867702	0.0006166495	0.0024160424
G0:0051130	G0:0051896	G0:0006874	G0:0071375	G0:0022411	G0:0006468
0.0018692576	0.0059887349	0.0036285973	0.0059887349	0.0088952006	0.0056113608
G0:0014068					
0.0036285973					

\$genes

\$genes\$`G0:0051924`

[1] "2852" "5170" "8614"

\$genes\$`G0:0007566`

[1] "780" "8614"

\$genes\$`G0:0040015`

[1] "8614" "9518"

\$genes\$`G0:0007169`

[1] "2852" "3630" "367" "5170" "53834" "780" "79801" "9518"

\$genes\$`G0:0031667`

[1] "8614" "9518"

\$genes\$`G0:0042327`

[1]	"2852"	"3263"	"3320"	"3630"	"367"	"3670"	"4057"	"406915"
[9]	"4296"	"5170"	"6366"	"780"	"9518"			

\$genes\$`G0:0051130`

[1] "10435" "154664" "2150" "2852" "3320" "3630" "367" "4204"

```

[9] "6366"      "780"      "9518"      "9555"

$genes$`G0:0051896`
[1] "2852" "3320" "3630" "6366" "9518"

$genes$`G0:0006874`
[1] "2852" "5170" "6366" "8614"

$genes$`G0:0071375`
[1] "142"  "2852" "3630" "5170" "9518"

$genes$`G0:0022411`
[1] "2150" "2852" "56893" "57602" "6601"  "780"

$genes$`G0:0006468`
[1] "2852" "29941" "3263" "3320" "3630" "3670" "4057" "406915"
[9] "4296" "5170" "5577" "6366" "780" "79007" "8711" "9518"
[17] "9555"

$genes$`G0:0014068`
[1] "2150" "2852" "3630" "780"

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