

# The *GOSim* package

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October 13, 2014

## 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,106	Character,29	Character,116	Character,3	Character,17
Term	Character,106	Character,29	Character,116	Character,3	Character,17
Definition	Character,106	Character,29	Character,116	Character,3	Character,17
IC	Numeric,106	Numeric,29	Numeric,116	Numeric,3	Numeric,17
	3169	9518	2852	26353	8614
go_id	Character,24	Character,3	Character,50	Character,3	Character,12
Term	Character,24	Character,3	Character,50	Character,3	Character,12
Definition	Character,24	Character,3	Character,50	Character,3	Character,12
IC	Numeric,24	Numeric,3	Numeric,50	Numeric,3	Numeric,12
	7494				
go_id	Character,15				
Term	Character,15				
Definition	Character,15				
IC	Numeric,15				

## 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"), m=1)
```

	GO:0007166	GO:0007267	GO:0007584	GO:0007165	GO:0007186
GO:0007166	0.2628131	0.1806383	0.1266641	0.1945233	0.2628131
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	0.2628131	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"), v=

GO:0007166 GO:0007267 GO:0007584 GO:0007165 GO:0007186
GO:0007166 0.9505312 0.5105747 0.2498911 0.7587689 0.7519293
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 0.7519293 0.4169139 0.2119568 0.5820734 0.9898931
```

Jiang and Conrath's similarity measure is defined as

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

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"), m
```

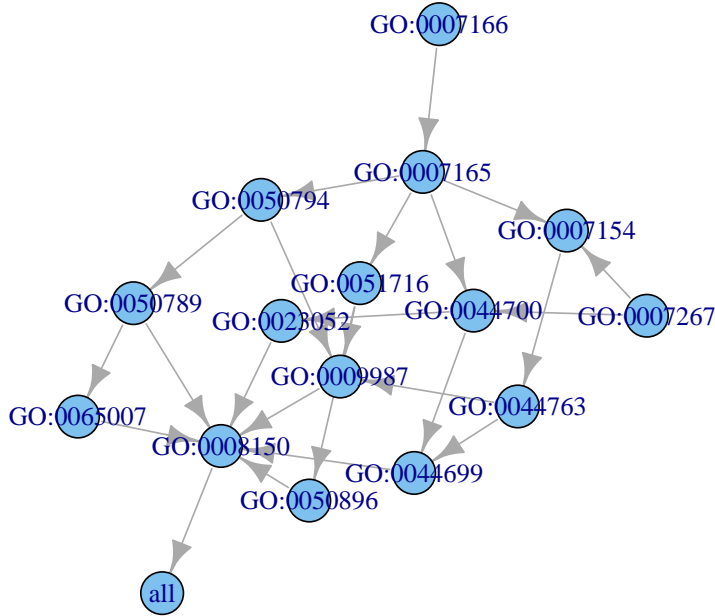
	GO:0007166	GO:0007267	GO:0007584	GO:0007165	GO:0007186
GO:0007166	1.0000000	0.5846115	0.3265762	0.8506792	0.7910622
GO:0007267	0.5846115	1.0000000	0.0000000	0.6572401	0.4773693
GO:0007584	0.3265762	0.0000000	1.0000000	0.3581018	0.2770009
GO:0007165	0.8506792	0.6572401	0.3581018	1.0000000	0.6525805
GO:0007186	0.7910622	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" "GO:0044699" "GO:0044700"
```

```
[6] "GO:0044763"
```

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", "GO:0007584", "GO:0007165", "GO:0007186"), m
```

	GO:0007166	GO:0007267	GO:0007584	GO:0007165	GO:0007186
GO:0007166	3.006413	1.507568	1.448955	1.545332	2.225221
GO:0007267	1.507568	4.062846	0.000000	1.507568	1.507568
GO:0007584	1.448955	0.000000	5.867200	1.448955	1.448955
GO:0007165	1.545332	1.507568	1.448955	2.225221	1.545332
GO:0007186	2.225221	1.507568	1.448955	1.545332	4.594539

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", "GO:0007584", "GO:0007165", "GO:0007186"), m
```

	GO:0007166	GO:0007267	GO:0007584	GO:0007165	GO:0007186
GO:0007166	9.038517	0.00000	0.00000	4.460424	3.879088
GO:0007267	0.000000	16.50672	0.00000	0.000000	0.000000
GO:0007584	0.000000	0.00000	34.42404	0.000000	0.000000
GO:0007165	4.460424	0.00000	0.00000	4.951609	0.000000
GO:0007186	3.879088	0.00000	0.00000	0.000000	21.109787

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"), m)
```

	GO:0007166	GO:0007267	GO:0007584	GO:0007165	GO:0007186
GO:0007166	0.9505312	0.5105747	0.2498911	0.7587689	0.7519293
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	0.7519293	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  $t'_{\pi i}$  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,50
Term	Character,12	Character,50
Definition	Character,12	Character,50
IC	Numeric,12	Numeric,50

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  $\pi$  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, verb
```

```
filtering out genes not mapping to the currently set GO category ... ==> list of 2
term similarity matrix:
```

	GO:0010629	GO:0046885	GO:0006874	GO:0006979	GO:0007566	GO:0030968
GO:0010629	1.0000000	0.35490465	0.19542277	0.0000000	0.0000000	0.2007658
GO:0046885	0.3549046	1.0000000	0.43030745	0.0000000	0.0000000	0.1698320
GO:0006874	0.1954228	0.43030745	1.0000000	0.0000000	0.0000000	0.1637637
GO:0006979	0.0000000	0.0000000	0.0000000	1.0000000	0.0000000	0.4414432
GO:0007566	0.0000000	0.0000000	0.0000000	0.0000000	1.0000000	0.0000000
GO:0030968	0.2007658	0.16983198	0.16376373	0.4414432	0.0000000	1.0000000
GO:0033280	0.0000000	0.0000000	0.0000000	0.2092914	0.0000000	0.4483505
GO:0040015	0.3721151	0.12218460	0.13039013	0.0000000	0.1860972	0.1368560

G0:0043434	0.0000000	0.00000000	0.00000000	0.2605260	0.0000000	0.5528910
G0:0046697	0.0000000	0.00000000	0.00000000	0.0000000	0.7783503	0.0000000
G0:0071456	0.0000000	0.05201503	0.06225648	0.4052713	0.0000000	0.5447404
G0:2001256	0.1432364	0.11414955	0.12046150	0.0000000	0.0000000	0.1268545
G0:0033280	G0:0040015	G0:0043434	G0:0046697	G0:0071456	G0:2001256	
G0:0010629	0.0000000	0.3721151	0.0000000	0.0000000	0.0000000	0.1432364
G0:0046885	0.0000000	0.1221846	0.0000000	0.0000000	0.05201503	0.1141495
G0:0006874	0.0000000	0.1303901	0.0000000	0.0000000	0.06225648	0.1204615
G0:0006979	0.2092914	0.0000000	0.2605260	0.0000000	0.40527132	0.0000000
G0:0007566	0.0000000	0.1860972	0.0000000	0.7783503	0.0000000	0.0000000
G0:0030968	0.4483505	0.1368560	0.5528910	0.0000000	0.54474045	0.1268545
G0:0033280	1.0000000	0.0000000	0.4859237	0.0000000	0.35097269	0.0000000
G0:0040015	0.0000000	1.0000000	0.0000000	0.1781009	0.0000000	0.1074404
G0:0043434	0.4859237	0.0000000	1.0000000	0.0000000	0.42580898	0.0000000
G0:0046697	0.0000000	0.1781009	0.0000000	1.0000000	0.0000000	0.0000000
G0:0071456	0.3509727	0.0000000	0.4258090	0.0000000	1.0000000	0.0000000
G0:2001256	0.0000000	0.1074404	0.0000000	0.0000000	0.0000000	1.0000000

optimal assignment:

G0:0010629	G0:0046885	G0:0006874	G0:0006979	G0:0007566	G0:0030968
G0:0010629	1	0	0	0	0
G0:0046885	0	1	0	0	0
G0:0006874	0	0	1	0	0
G0:0006979	0	0	0	1	0
G0:0007566	0	0	0	0	1
G0:0030968	0	0	0	0	0
G0:0033280	0	0	0	0	0
G0:0040015	0	0	0	0	0
G0:0043434	0	0	0	0	0
G0:0046697	0	0	0	0	0
G0:0071456	0	0	0	0	0
G0:2001256	0	0	0	0	0
G0:0033280	G0:0040015	G0:0043434	G0:0046697	G0:0071456	G0:2001256
G0:0010629	0	0	0	0	0
G0:0046885	0	0	0	0	0
G0:0006874	0	0	0	0	0
G0:0006979	0	0	0	0	0
G0:0007566	0	0	0	0	0
G0:0030968	0	0	0	0	0
G0:0033280	1	0	0	0	0
G0:0040015	0	1	0	0	0
G0:0043434	0	0	1	0	0
G0:0046697	0	0	0	1	0

G0:0071456	0	0	0	0	1	0
G0:2001256	0	0	0	0	0	1

=====

term similarity matrix:

	G0:0001934	G0:0001956	G0:0007204	G0:0008285	G0:0045909	G0:0010628
G0:0001934	1.00000000	0.31884336	0.18199644	0.25414486	0.3280870	0.9065684
G0:0001956	0.31884336	1.00000000	0.35698855	0.15779813	0.3124381	0.2918790
G0:0007204	0.18199644	0.35698855	1.00000000	0.17670495	0.4103843	0.1916341
G0:0008285	0.25414486	0.15779813	0.17670495	1.00000000	0.1596170	0.2344419
G0:0045909	0.32808696	0.31243812	0.41038426	0.15961704	1.0000000	0.3421795
G0:0010628	0.90656841	0.29187902	0.19163405	0.23444188	0.3421795	1.0000000
G0:0010629	0.88341800	0.14323644	0.18738474	0.54501949	0.1674750	0.9394387
G0:0019228	0.16972322	0.34108370	0.46126769	0.16511230	0.4431377	0.1780750
G0:0030263	0.53768169	0.03895394	0.04983805	0.05328585	0.0000000	0.5579314
G0:0030264	0.05301288	0.03821905	0.04864143	0.05192021	0.0000000	0.0000000
G0:0032024	0.39756345	0.63730945	0.43624498	0.19576113	0.3715106	0.3672641
G0:0043065	0.51862086	0.31824798	0.18151326	0.25339710	0.3273733	0.4859168
G0:0043280	0.71521907	0.14396173	0.15560831	0.21392831	0.1435905	0.7515003
G0:0043410	0.86908627	0.43346798	0.16175121	0.22317862	0.2975851	0.6463208
G0:0045599	0.19524196	0.13290279	0.13977234	0.42198544	0.1310989	0.1776742
G0:0045944	0.84089759	0.31576096	0.17950313	0.25029088	0.3243970	0.9232019
G0:0050769	0.43429381	0.28436546	0.15521828	0.21334324	0.4216132	0.4029113
G0:0051053	0.67953459	0.13918075	0.14865546	0.45113618	0.1381562	0.7122031
G0:0051055	0.65039476	0.11772184	0.14292096	0.40491955	0.1336152	0.6802600
G0:0051480	0.18368059	0.35911179	0.99180402	0.17829216	0.4131927	0.1935022
G0:0070374	0.80596426	0.41264819	0.15125169	0.20740823	0.2812671	0.5970753
G0:0071157	0.17844030	0.12489755	0.12883298	0.38649836	0.1222271	0.1617614
G0:0071333	0.15791354	0.32502484	0.68149839	0.15391441	0.3687019	0.1651188
G0:0090200	0.37850501	0.38358220	0.13720133	0.18660546	0.2588723	0.3488871
G0:2000353	0.33377457	0.23752704	0.12238158	0.16502841	0.2345299	0.3060727
G0:2001238	0.36826583	0.37641153	0.13383884	0.18167726	0.2534153	0.3390474
G0:0007186	0.26720333	0.26939824	0.18460669	0.25819191	0.1654470	0.2472380
G0:0002695	0.22007801	0.14396173	0.15560831	0.47416475	0.1435905	0.2014220
G0:0010579	0.60758037	0.22986660	0.11735835	0.15779813	0.2261048	0.5427966
G0:0014068	0.39446408	0.39451824	0.14240737	0.19427372	0.2672462	0.3642700
G0:0030518	0.22184371	0.23956576	0.15671929	0.21559634	0.1444517	0.2031207
G0:0030819	0.78464087	0.27452845	0.14800225	0.20256677	0.2761455	0.7085433
G0:0032962	0.62390673	0.23428654	0.12024546	0.16194864	0.2309581	0.5579314
G0:0043401	0.18520240	0.21218162	0.13325805	0.18082797	0.1258403	0.1681510
G0:0045742	0.37722034	0.38268923	0.13678042	0.18598749	0.2581913	0.3476513
G0:0045745	0.36650265	0.37516430	0.13325805	0.18082797	0.2524689	0.3373554
G0:0050728	0.18169213	0.12103696	0.14833294	0.42158261	0.1379022	0.1904048

G0:0051281	0.36463635	0.51408245	0.82201990	0.37356134	0.3474814	0.3355652
G0:0070474	0.30304961	0.21392453	0.12552444	0.14770597	0.5371171	0.3150341
G0:0071356	0.06965070	0.04617023	0.06229511	0.06777665	0.0000000	0.0000000
G0:0071375	0.07934080	0.05023743	0.06993437	0.07691810	0.0000000	0.0000000
G0:0071392	0.05871209	0.04109495	0.05339731	0.05737480	0.0000000	0.0000000
G0:0090004	0.31837899	0.48644738	0.13128821	0.17795176	0.2492503	0.3316331
G0:0008284	0.52148479	0.31932412	0.18238716	0.83460599	0.3286635	0.4887648
G0:0030335	0.47047325	0.45733181	0.16663498	0.23058080	0.3050573	0.4383232
G0:0006954	0.00000000	0.00000000	0.00000000	0.00000000	0.0000000	0.0000000
G0:0007049	0.10125241	0.05821424	0.08641867	0.09733977	0.0000000	0.0000000
G0:0045087	0.00000000	0.00000000	0.00000000	0.00000000	0.0000000	0.0000000
	G0:0010629	G0:0019228	G0:0030263	G0:0030264	G0:0032024	G0:0043065
G0:0001934	0.8834180	0.16972322	0.53768169	0.05301288	0.39756345	0.51862086
G0:0001956	0.1432364	0.34108370	0.03895394	0.03821905	0.63730945	0.31824798
G0:0007204	0.1873847	0.46126769	0.04983805	0.04864143	0.43624498	0.18151326
G0:0008285	0.5450195	0.16511230	0.05328585	0.05192021	0.19576113	0.25339710
G0:0045909	0.1674750	0.44313769	0.00000000	0.00000000	0.37151057	0.32737331
G0:0010628	0.9394387	0.17807498	0.55793145	0.00000000	0.36726410	0.48591680
G0:0010629	1.0000000	0.17439994	0.54907611	0.00000000	0.17951462	0.23603440
G0:0019228	0.1743999	1.00000000	0.04756549	0.04647432	0.41272661	0.16930293
G0:0030263	0.5490761	0.04756549	1.00000000	0.76892582	0.04558657	0.46346781
G0:0030264	0.0000000	0.04647432	0.76892582	1.00000000	0.04458335	0.45136246
G0:0032024	0.1795146	0.41272661	0.04558657	0.04458335	1.00000000	0.39663822
G0:0043065	0.2360344	0.16930293	0.46346781	0.45136246	0.39663822	1.00000000
G0:0043280	0.7355225	0.14654752	0.47905404	0.40405208	0.17490633	0.70063704
G0:0043410	0.4286789	0.31693087	0.15798112	0.04872672	0.52991020	0.45370543
G0:0045599	0.4155298	0.13241834	0.04469363	0.04372891	0.15884735	0.19480035
G0:0045944	0.8691041	0.16755285	0.71394167	0.05250039	0.39278254	0.51051478
G0:0050769	0.1965692	0.23780115	0.04841018	0.04728037	0.34535312	0.43318996
G0:0051053	0.6978366	0.14036472	0.62064129	0.04579454	0.16789912	0.20859120
G0:0051055	0.6671415	0.13524100	0.44907452	0.00000000	0.14116889	0.17391886
G0:0051480	0.1891706	0.46481870	0.05014181	0.04893073	0.43941984	0.18318844
G0:0070374	0.3966884	0.29752466	0.15021535	0.04638634	0.49912439	0.42083403
G0:0071157	0.3789525	0.12255922	0.04194583	0.04109495	0.14754447	0.17807135
G0:0071333	0.1619543	0.40926308	0.04527597	0.04428622	0.38944335	0.15754964
G0:0090200	0.1706975	0.27131524	0.37580949	0.36781069	0.45721814	0.60911953
G0:2000353	0.1500891	0.11670658	0.34357588	0.33687814	0.27862662	0.64427772
G0:2001238	0.1659695	0.26500167	0.36863425	0.36093485	0.44706654	0.59267736
G0:0007186	0.2408168	0.35865295	0.05499861	0.05354497	0.33674516	0.26637688
G0:0002695	0.4698884	0.14654752	0.04850166	0.04736763	0.17490633	0.21951705
G0:0010579	0.5344116	0.23382403	0.51599856	0.03821905	0.26814434	0.31824798
G0:0014068	0.1780793	0.28105884	0.04534089	0.04434833	0.47284146	0.39355320

G0:0030518	0.1987664	0.30764941	0.04876162	0.04761553	0.29138827	0.22127373
G0:0030819	0.6943227	0.13978220	0.61856523	0.04564481	0.33095101	0.41076798
G0:0032962	0.5490761	0.11476240	0.39229369	0.03895394	0.27417819	0.32678326
G0:0043401	0.1651560	0.26390952	0.04306930	0.04217273	0.25185292	0.18480499
G0:0045742	0.1701040	0.27052578	0.04395192	0.04301861	0.45594997	0.37638727
G0:0045745	0.1651560	0.26390952	0.04306930	0.04217273	0.44530823	0.36571620
G0:0050728	0.4447040	0.14007714	0.00000000	0.00000000	0.14596298	0.18125313
G0:0051281	0.3916027	0.38328136	0.04291406	0.04202387	0.60979728	0.36385788
G0:0070474	0.1544103	0.41376788	0.00000000	0.00000000	0.25180640	0.30244062
G0:0071356	0.0000000	0.05878453	0.04724700	0.04617023	0.05579138	0.06947992
G0:0071375	0.0000000	0.06554035	0.05151490	0.05023743	0.06184133	0.07911928
G0:0071392	0.0000000	0.05079703	0.04194583	0.04109495	0.04854645	0.05859069
G0:0090004	0.1624036	0.12477909	0.26105619	1.02058130	0.57617755	0.31770691
G0:0008284	0.2373824	0.17006297	0.05452169	0.05309282	0.39831119	0.51989403
G0:0030335	0.2134480	0.15628727	0.05104167	0.04978728	0.56180407	0.46917809
G0:0006954	0.0000000	0.00000000	0.00000000	0.00000000	0.00000000	0.00000000
G0:0007049	0.0000000	0.07980700	0.05993654	0.05821424	0.07438889	0.10089191
G0:0045087	0.0000000	0.00000000	0.00000000	0.00000000	0.00000000	0.00000000
G0:0043280	G0:0043410	G0:0045599	G0:0045944	G0:0050769	G0:0051053	
G0:0001934	0.71521907	0.86908627	0.19524196	0.84089759	0.43429381	0.67953459
G0:0001956	0.14396173	0.43346798	0.13290279	0.31576096	0.28436546	0.13918075
G0:0007204	0.15560831	0.16175121	0.13977234	0.17950313	0.15521828	0.14865546
G0:0008285	0.21392831	0.22317862	0.42198544	0.25029088	0.21334324	0.45113618
G0:0045909	0.14359053	0.29758509	0.13109895	0.32439701	0.42161318	0.13815619
G0:0010628	0.75150029	0.64632075	0.17767416	0.92320189	0.40291129	0.71220309
G0:0010629	0.73552249	0.42867890	0.41552981	0.86910408	0.19656919	0.69783664
G0:0019228	0.14654752	0.31693087	0.13241834	0.16755285	0.23780115	0.14036472
G0:0030263	0.47905404	0.15798112	0.04469363	0.71394167	0.04841018	0.62064129
G0:0030264	0.40405208	0.04872672	0.04372891	0.05250039	0.04728037	0.04579454
G0:0032024	0.17490633	0.52991020	0.15884735	0.39278254	0.34535312	0.16789912
G0:0043065	0.70063704	0.45370543	0.19480035	0.51051478	0.43318996	0.20859120
G0:0043280	1.00000000	0.35581504	0.17060336	0.70580784	0.18880885	0.58851010
G0:0043410	0.35581504	1.00000000	0.17643524	0.62095697	0.38782674	0.36528020
G0:0045599	0.17060336	0.17643524	1.00000000	0.19295940	0.56398485	0.36334547
G0:0045944	0.70580784	0.62095697	0.19295940	1.00000000	0.42859502	0.89993969
G0:0050769	0.18880885	0.38782674	0.56398485	0.42859502	1.00000000	0.18066935
G0:0051053	0.58851010	0.36528020	0.36334547	0.89993969	0.18066935	1.00000000
G0:0051055	0.56652778	0.32674210	0.32879640	0.64260292	0.15150587	0.54390365
G0:0051480	0.15683783	0.16308014	0.14076355	0.18114125	0.15644163	0.14977717
G0:0070374	0.33349222	0.93494170	0.16643102	0.57643178	0.36355289	0.34332811
G0:0071157	0.15763386	0.16259985	0.32021425	0.17653177	0.15731597	0.33672475
G0:0071333	0.13765840	0.28112917	0.12511796	0.15603302	0.13735308	0.13218892

G0:0090200	0.53480750	0.50690915	0.15276537	0.37416899	0.33088061	0.16111904
G0:2000353	0.47861622	0.30563127	0.13799483	0.33039825	0.29618227	0.14477534
G0:2001238	0.52209060	0.60771187	0.14944663	0.36415995	0.32302924	0.15743179
G0:0007186	0.22310634	0.41569542	0.19762166	0.26294644	0.22247007	0.21182945
G0:0002695	0.18926695	0.19647155	0.37813650	0.21718211	0.18880885	0.40137701
G0:0010579	0.49791837	0.55845669	0.13290279	0.95475829	0.28436546	0.60661177
G0:0014068	0.17371799	0.64670116	0.15786659	0.38975697	0.34301195	0.16680380
G0:0030518	0.19057139	0.35275172	0.17166251	0.21890146	0.19010697	0.18228255
G0:0030819	0.58600894	0.70460010	0.16329917	1.22952914	0.35601605	0.75349131
G0:0032962	0.47905404	0.57221986	0.13583481	0.53234541	0.29116065	0.46277665
G0:0043401	0.16288774	0.29983881	0.14887147	0.18314731	0.16254833	0.15679366
G0:0045742	0.16706246	0.62109575	0.15235096	0.37291353	0.32989845	0.16065814
G0:0045745	0.16288774	0.60506945	0.14887147	0.36243577	0.32167182	0.15679366
G0:0050728	0.15740531	0.44032289	0.33969886	0.17942456	0.15704152	0.35967194
G0:0051281	0.16215778	0.33130786	0.30781487	0.36061057	0.32023328	0.32412456
G0:0070474	0.13387850	0.27683954	0.12295528	0.29989865	0.39315259	0.12914229
G0:0071356	0.06022107	0.29730203	0.05445975	0.06876871	0.06008011	0.05770114
G0:0071375	0.06733108	0.33385218	0.06020947	0.07819834	0.06715492	0.06419648
G0:0071392	0.05186616	0.25475572	0.04753508	0.05808412	0.05176156	0.04998602
G0:0090004	0.16055023	0.28957626	0.14691652	0.31490302	0.27999240	0.15462663
G0:0008284	0.22053153	0.45589577	0.19559881	0.51328965	0.43518626	0.20950699
G0:0030335	0.20218546	0.41642345	0.18102954	0.46379271	0.39907660	0.19288020
G0:0006954	0.00000000	0.25898413	0.00000000	0.00000000	0.00000000	0.00000000
G0:0007049	0.08247807	0.08668825	0.07204021	0.09939915	0.08221389	0.07782324
G0:0045087	0.00000000	0.27943082	0.00000000	0.00000000	0.00000000	0.00000000
	G0:0051055	G0:0051480	G0:0070374	G0:0071157	G0:0071333	G0:0090200
G0:0001934	0.6503948	0.18368059	0.80596426	0.17844030	0.15791354	0.37850501
G0:0001956	0.1177218	0.35911179	0.41264819	0.12489755	0.32502484	0.38358220
G0:0007204	0.1429210	0.99180402	0.15125169	0.12883298	0.68149839	0.13720133
G0:0008285	0.4049195	0.17829216	0.20740823	0.38649836	0.15391441	0.18660546
G0:0045909	0.1336152	0.41319265	0.28126713	0.12222713	0.36870189	0.25887232
G0:0010628	0.6802600	0.19350221	0.59707526	0.16176141	0.16511880	0.34888709
G0:0010629	0.6671415	0.18917058	0.39668841	0.37895249	0.16195433	0.17069751
G0:0019228	0.1352410	0.46481870	0.29752466	0.12255922	0.40926308	0.27131524
G0:0030263	0.4490745	0.05014181	0.15021535	0.04194583	0.04527597	0.37580949
G0:0030264	0.00000000	0.04893073	0.04638634	0.04109495	0.04428622	0.36781069
G0:0032024	0.1411689	0.43941984	0.49912439	0.14754447	0.38944335	0.45721814
G0:0043065	0.1739189	0.18318844	0.42083403	0.17807135	0.15754964	0.60911953
G0:0043280	0.5665278	0.15683783	0.33349222	0.15763386	0.13765840	0.53480750
G0:0043410	0.3267421	0.16308014	0.93494170	0.16259985	0.28112917	0.50690915
G0:0045599	0.3287964	0.14076355	0.16643102	0.32021425	0.12511796	0.15276537
G0:0045944	0.6426029	0.18114125	0.57643178	0.17653177	0.15603302	0.37416899

G0:0050769	0.1515059	0.15644163	0.36355289	0.15731597	0.13735308	0.33088061
G0:0051053	0.5439037	0.14977717	0.34332811	0.33672475	0.13218892	0.16111904
G0:0051055	1.0000000	0.14395750	0.30782116	0.30546637	0.12763502	0.13565846
G0:0051480	0.1439575	1.00000000	0.15241308	0.12967464	0.68641384	0.13815629
G0:0070374	0.3078212	0.15241308	1.00000000	0.15406515	0.26493336	0.47866667
G0:0071157	0.3054664	0.12967464	0.15406515	1.00000000	0.11627969	0.14228290
G0:0071333	0.1276350	0.68641384	0.26493336	0.11627969	1.00000000	0.24286041
G0:0090200	0.1356585	0.13815629	0.47866667	0.14228290	0.24286041	1.00000000
G0:2000353	0.1223115	0.12314081	0.29035356	0.12938428	0.11099850	0.43406582
G0:2001238	0.1326552	0.13474741	0.57463937	0.13939968	0.23750866	0.89191211
G0:0007186	0.1765016	0.18633973	0.38510107	0.18042597	0.31553102	0.34503835
G0:0002695	0.3619262	0.15683783	0.18414548	0.34939005	0.13765840	0.16756089
G0:0010579	0.4392172	0.11805636	0.53163360	0.12489755	0.21088121	0.25933705
G0:0014068	0.1402797	0.14343645	0.60937914	0.14669795	0.25109319	0.45444183
G0:0030518	0.1528078	0.15796651	0.33047271	0.15853767	0.27339872	0.30052807
G0:0030819	0.5417666	0.14911409	0.66243137	0.15137765	0.13167215	0.31763715
G0:0032962	0.4490745	0.12097834	0.54409166	0.12748357	0.10923842	0.26497687
G0:0043401	0.1321350	0.13415872	0.28358829	0.13889913	0.46301278	0.26125033
G0:0045742	0.1352833	0.13772950	0.58659183	0.14192334	0.24219195	0.43881764
G0:0045745	0.1321350	0.13415872	0.57227618	0.13889913	0.23658152	0.42895194
G0:0050728	0.3467988	0.14944977	0.41391508	0.31485445	0.19291606	0.37813697
G0:0051281	0.3136332	0.81409510	0.31343039	0.28727435	0.57233839	0.28884138
G0:0070474	0.1251660	0.12632329	0.26266324	0.11511849	0.11357774	0.24302958
G0:0071356	0.0000000	0.06277042	0.27924902	0.05043397	0.51560532	0.25483610
G0:0071375	0.0000000	0.07053395	0.31125615	0.05532686	0.57100148	0.28122706
G0:0071392	0.0000000	0.05374615	0.24138385	0.04443888	0.44913575	0.22292384
G0:0090004	0.1303673	0.13216236	0.27410197	0.13719582	0.11827606	0.58609898
G0:0008284	0.1746496	0.18407858	0.42271783	0.17873833	0.15820761	0.37918272
G0:0030335	0.1613393	0.16804573	0.38856648	0.16649391	0.14621792	0.35147299
G0:0006954	0.0000000	0.00000000	0.24068887	0.00000000	0.22499621	0.21655431
G0:0007049	0.0000000	0.08733608	0.07954792	0.53371824	0.07356535	0.07039971
G0:0045087	0.0000000	0.00000000	0.25825085	0.00000000	0.24027013	0.23066763
	G0:2000353	G0:2001238	G0:0007186	G0:0002695	G0:0010579	G0:0014068
G0:0001934	0.33377457	0.36826583	0.26720333	0.22007801	0.60758037	0.39446408
G0:0001956	0.23752704	0.37641153	0.26939824	0.14396173	0.22986660	0.39451824
G0:0007204	0.12238158	0.13383884	0.18460669	0.15560831	0.11735835	0.14240737
G0:0008285	0.16502841	0.18167726	0.25819191	0.47416475	0.15779813	0.19427372
G0:0045909	0.23452986	0.25341533	0.16544703	0.14359053	0.22610477	0.26724622
G0:0010628	0.30607267	0.33904743	0.24723804	0.20142197	0.54279659	0.36427001
G0:0010629	0.15008907	0.16596950	0.24081684	0.46988842	0.53441156	0.17807925
G0:0019228	0.11670658	0.26500167	0.35865295	0.14654752	0.23382403	0.28105884
G0:0030263	0.34357588	0.36863425	0.05499861	0.04850166	0.51599856	0.04534089

G0:0030264	0.33687814	0.36093485	0.05354497	0.04736763	0.03821905	0.04434833
G0:0032024	0.27862662	0.44706654	0.33674516	0.17490633	0.26814434	0.47284146
G0:0043065	0.64427772	0.59267736	0.26637688	0.21951705	0.31824798	0.39355320
G0:0043280	0.47861622	0.52209060	0.22310634	0.18926695	0.49791837	0.17371799
G0:0043410	0.30563127	0.60771187	0.41569542	0.19647155	0.55845669	0.64670116
G0:0045599	0.13799483	0.14944663	0.19762166	0.37813650	0.13290279	0.15786659
G0:0045944	0.33039825	0.36415995	0.26294644	0.21718211	0.95475829	0.38975697
G0:0050769	0.29618227	0.32302924	0.22247007	0.18880885	0.28436546	0.34301195
G0:0051053	0.14477534	0.15743179	0.21182945	0.40137701	0.60661177	0.16680380
G0:0051055	0.12231148	0.13265519	0.17650161	0.36192617	0.43921721	0.14027972
G0:0051480	0.12314081	0.13474741	0.18633973	0.15683783	0.11805636	0.14343645
G0:0070374	0.29035356	0.57463937	0.38510107	0.18414548	0.53163360	0.60937914
G0:0071157	0.12938428	0.13939968	0.18042597	0.34939005	0.12489755	0.14669795
G0:0071333	0.11099850	0.23750866	0.31553102	0.13765840	0.21088121	0.25109319
G0:0090200	0.43406582	0.89191211	0.34503835	0.16756089	0.25933705	0.45444183
G0:2000353	1.00000000	0.42565095	0.17043710	0.14995556	0.23752704	0.27710074
G0:2001238	0.42565095	1.00000000	0.45341130	0.16357655	0.30973233	0.54619932
G0:0007186	0.17043710	0.45341130	1.00000000	0.22310634	0.59899810	0.35976742
G0:0002695	0.14995556	0.16357655	0.22310634	1.00000000	0.14396173	0.17371799
G0:0010579	0.23752704	0.30973233	0.59899810	0.14396173	1.00000000	0.26673083
G0:0014068	0.27710074	0.54619932	0.35976742	0.17371799	0.26673083	1.00000000
G0:0030518	0.15077324	0.29333945	0.40096172	0.19057139	0.25798039	0.31164093
G0:0030819	0.28552603	0.31039482	0.21077711	0.18031913	0.80570540	0.32880043
G0:0032962	0.24224950	0.25991773	0.16715416	0.14740834	0.51185417	0.27270051
G0:0043401	0.13290279	0.25580092	0.33397079	0.16288774	0.22849132	0.26960781
G0:0045742	0.26847935	0.52782094	0.46456731	0.16706246	0.31489797	0.55698685
G0:0045745	0.26300535	0.51620176	0.68956821	0.16288774	0.47177884	0.54406382
G0:0050728	0.12589407	0.36949901	0.24528662	0.37518069	0.16129923	0.39145296
G0:0051281	0.26204290	0.28284025	0.18637737	0.33666581	0.25275048	0.29804305
G0:0070474	0.22145124	0.23821386	0.15268474	0.13387850	0.21392453	0.25039531
G0:0071356	0.04804196	0.24894993	0.33604865	0.06022107	0.21985244	0.26391601
G0:0071375	0.05246140	0.27407573	0.38350699	0.06733108	0.23921956	0.29232594
G0:0071392	0.04257122	0.21840651	0.28268505	0.05186616	0.19568509	0.22984118
G0:0090004	0.22952691	0.24758423	0.18425690	0.16055023	0.22145124	0.26076939
G0:0008284	0.33430145	0.36890733	0.26787217	0.22053153	0.31932412	0.39520019
G0:0030335	0.31257520	0.34262700	0.24127903	0.20218546	0.29944313	0.36519261
G0:0006954	0.00000000	0.21083661	0.29960026	0.00000000	0.18313090	0.22545089
G0:0007049	0.06122166	0.06827613	0.10321131	0.08247807	0.05821424	0.07373689
G0:0045087	0.00000000	0.22419151	0.32730614	0.53979486	0.19312334	0.24078871
	G0:0030518	G0:0030819	G0:0032962	G0:0043401	G0:0045742	G0:0045745
G0:0001934	0.22184371	0.78464087	0.62390673	0.18520240	0.37722034	0.36650265
G0:0001956	0.23956576	0.27452845	0.23428654	0.21218162	0.38268923	0.37516430



G0:0007204	0.15671929	0.14800225	0.12024546	0.13325805	0.13678042	0.13325805
G0:0008285	0.21559634	0.20256677	0.16194864	0.18082797	0.18598749	0.18082797
G0:0045909	0.14445173	0.27614547	0.23095808	0.12584030	0.25819131	0.25246887
G0:0010628	0.20312066	0.70854332	0.55793145	0.16815105	0.34765126	0.33735540
G0:0010629	0.19876643	0.69432266	0.54907611	0.16515597	0.17010395	0.16515597
G0:0019228	0.30764941	0.13978220	0.11476240	0.26390952	0.27052578	0.26390952
G0:0030263	0.04876162	0.61856523	0.39229369	0.04306930	0.04395192	0.04306930
G0:0030264	0.04761553	0.04564481	0.03895394	0.04217273	0.04301861	0.04217273
G0:0032024	0.29138827	0.33095101	0.27417819	0.25185292	0.45594997	0.44530823
G0:0043065	0.22127373	0.41076798	0.32678326	0.18480499	0.37638727	0.36571620
G0:0043280	0.19057139	0.58600894	0.47905404	0.16288774	0.16706246	0.16288774
G0:0043410	0.35275172	0.70460010	0.57221986	0.29983881	0.62109575	0.60506945
G0:0045599	0.17166251	0.16329917	0.13583481	0.14887147	0.15235096	0.14887147
G0:0045944	0.21890146	1.22952914	0.53234541	0.18314731	0.37291353	0.36243577
G0:0050769	0.19010697	0.35601605	0.29116065	0.16254833	0.32989845	0.32167182
G0:0051053	0.18228255	0.75349131	0.46277665	0.15679366	0.16065814	0.15679366
G0:0051055	0.15280782	0.54176659	0.44907452	0.13213497	0.13528330	0.13213497
G0:0051480	0.15796651	0.14911409	0.12097834	0.13415872	0.13772950	0.13415872
G0:0070374	0.33047271	0.66243137	0.54409166	0.28358829	0.58659183	0.57227618
G0:0071157	0.15853767	0.15137765	0.12748357	0.13889913	0.14192334	0.13889913
G0:0071333	0.27339872	0.13167215	0.10923842	0.46301278	0.24219195	0.23658152
G0:0090200	0.30052807	0.31763715	0.26497687	0.26125033	0.43881764	0.42895194
G0:2000353	0.15077324	0.28552603	0.24224950	0.13290279	0.26847935	0.26300535
G0:2001238	0.29333945	0.31039482	0.25991773	0.25580092	0.52782094	0.51620176
G0:0007186	0.40096172	0.21077711	0.16715416	0.33397079	0.46456731	0.68956821
G0:0002695	0.19057139	0.18031913	0.14740834	0.16288774	0.16706246	0.16288774
G0:0010579	0.25798039	0.80570540	0.51185417	0.22849132	0.31489797	0.47177884
G0:0014068	0.31164093	0.32880043	0.27270051	0.26960781	0.55698685	0.54406382
G0:0030518	1.00000000	0.18150277	0.14819840	0.29209690	0.29962867	0.29209690
G0:0030819	0.18150277	1.00000000	0.61359704	0.15621637	0.31673193	0.30914130
G0:0032962	0.14819840	0.61359704	1.00000000	0.13089808	0.26434662	0.25903819
G0:0043401	0.29209690	0.15621637	0.13089808	1.00000000	0.26057039	0.25485553
G0:0045742	0.29962867	0.31673193	0.26434662	0.26057039	1.00000000	0.52582647
G0:0045745	0.29209690	0.30914130	0.25903819	0.25485553	0.52582647	1.00000000
G0:0050728	0.21114524	0.15028506	0.12383164	0.18167408	0.37705728	0.36800401
G0:0051281	0.16311437	0.30781242	0.25810450	0.14239968	0.28809266	0.28179904
G0:0070474	0.13462683	0.25819131	0.21826401	0.11831811	0.24242927	0.23737736
G0:0071356	0.28867021	0.05746362	0.04724700	0.48522580	0.25410019	0.24793151
G0:0071375	0.32300623	0.06390262	0.05151490	0.72478273	0.28033111	0.27284186
G0:0071392	0.24839124	0.04980768	0.04194583	0.88052109	0.22236050	0.21762227
G0:0090004	0.16148789	0.26923567	0.22610477	0.14115851	0.25214097	0.24668075
G0:0008284	0.22230455	0.41256254	0.32791800	0.18552347	0.37789345	0.36713802

G0:0030335	0.20367476	0.37996912	0.30698758	0.17236599	0.35036498	0.34110028
G0:0006954	0.25018801	0.00000000	0.00000000	0.20985126	0.21583735	0.20985126
G0:0007049	0.08323263	0.07739180	0.05993654	0.06791182	0.07013252	0.06791182
G0:0045087	0.26921835	0.00000000	0.00000000	0.22307771	0.22985434	0.22307771
	G0:0050728	G0:0051281	G0:0070474	G0:0071356	G0:0071375	G0:0071392
G0:0001934	0.1816921	0.36463635	0.3030496	0.06965070	0.07934080	0.05871209
G0:0001956	0.1210370	0.51408245	0.2139245	0.04617023	0.05023743	0.04109495
G0:0007204	0.1483329	0.82201990	0.1255244	0.06229511	0.06993437	0.05339731
G0:0008285	0.4215826	0.37356134	0.1477060	0.06777665	0.07691810	0.05737480
G0:0045909	0.1379022	0.34748145	0.5371171	0.00000000	0.00000000	0.00000000
G0:0010628	0.1904048	0.33556516	0.3150341	0.00000000	0.00000000	0.00000000
G0:0010629	0.4447040	0.39160266	0.1544103	0.00000000	0.00000000	0.00000000
G0:0019228	0.1400771	0.38328136	0.4137679	0.05878453	0.06554035	0.05079703
G0:0030263	0.00000000	0.04291406	0.00000000	0.04724700	0.05151490	0.04194583
G0:0030264	0.00000000	0.04202387	0.00000000	0.04617023	0.05023743	0.04109495
G0:0032024	0.1459630	0.60979728	0.2518064	0.05579138	0.06184133	0.04854645
G0:0043065	0.1812531	0.36385788	0.3024406	0.06947992	0.07911928	0.05859069
G0:0043280	0.1574053	0.16215778	0.1338785	0.06022107	0.06733108	0.05186616
G0:0043410	0.4403229	0.33130786	0.2768395	0.29730203	0.33385218	0.25475572
G0:0045599	0.3396989	0.30781487	0.1229553	0.05445975	0.06020947	0.04753508
G0:0045944	0.1794246	0.36061057	0.2998986	0.06876871	0.07819834	0.05808412
G0:0050769	0.1570415	0.32023328	0.3931526	0.06008011	0.06715492	0.05176156
G0:0051053	0.3596719	0.32412456	0.1291423	0.05770114	0.06419648	0.04998602
G0:0051055	0.3467988	0.31363316	0.1251660	0.00000000	0.00000000	0.00000000
G0:0051480	0.1494498	0.81409510	0.1263233	0.06277042	0.07053395	0.05374615
G0:0070374	0.4139151	0.31343039	0.2626632	0.27924902	0.31125615	0.24138385
G0:0071157	0.3148544	0.28727435	0.1151185	0.05043397	0.05532686	0.04443888
G0:0071333	0.1929161	0.57233839	0.1135777	0.51560532	0.57100148	0.44913575
G0:0090200	0.3781370	0.28884138	0.2430296	0.25483610	0.28122706	0.22292384
G0:2000353	0.1258941	0.26204290	0.2214512	0.04804196	0.05246140	0.04257122
G0:2001238	0.3694990	0.28284025	0.2382139	0.24894993	0.27407573	0.21840651
G0:0007186	0.2452866	0.18637737	0.1526847	0.33604865	0.38350699	0.28268505
G0:0002695	0.3751807	0.33666581	0.1338785	0.06022107	0.06733108	0.05186616
G0:0010579	0.1612992	0.25275048	0.2139245	0.21985244	0.23921956	0.19568509
G0:0014068	0.3914530	0.29804305	0.2503953	0.26391601	0.29232594	0.22984118
G0:0030518	0.2111452	0.16311437	0.1346268	0.28867021	0.32300623	0.24839124
G0:0030819	0.1502851	0.30781242	0.2581913	0.05746362	0.06390262	0.04980768
G0:0032962	0.1238316	0.25810450	0.2182640	0.04724700	0.05151490	0.04194583
G0:0043401	0.1816741	0.14239968	0.1183181	0.48522580	0.72478273	0.88052109
G0:0045742	0.3770573	0.28809266	0.2424293	0.25410019	0.28033111	0.22236050
G0:0045745	0.3680040	0.28179904	0.2373774	0.24793151	0.27284186	0.21762227
G0:0050728	1.0000000	0.32353808	0.1289204	0.20315185	0.22596869	0.17603662

G0:0051281	0.3235381	1.00000000	0.2364896	0.05184028	0.05702387	0.04552712
G0:0070474	0.1289204	0.23648960	1.00000000	0.00000000	0.00000000	0.00000000
G0:0071356	0.2031519	0.05184028	0.00000000	1.00000000	0.60516659	0.47000721
G0:0071375	0.2259687	0.05702387	0.00000000	0.60516659	1.00000000	0.69984532
G0:0071392	0.1760366	0.04552712	0.00000000	0.47000721	0.69984532	1.00000000
G0:0090004	0.1344452	0.53976174	0.2345299	0.05134081	0.05642010	0.04514144
G0:0008284	0.1820470	0.36526526	0.3035415	0.06978875	0.07951998	0.05881015
G0:0030335	0.1676317	0.51848390	0.2832949	0.06418704	0.07232767	0.05478137
G0:0006954	0.8258406	0.00000000	0.00000000	0.23904322	0.27127403	0.20236550
G0:0007049	0.00000000	0.06752665	0.00000000	0.07891447	0.09158813	0.06515992
G0:0045087	0.6405987	0.00000000	0.00000000	0.25635723	0.29379169	0.21463757
G0:0090004 G0:0008284 G0:0030335 G0:0006954 G0:0007049 G0:0045087						
G0:0001934	0.31837899	0.52148479	0.47047325	0.00000000	0.10125241	0.00000000
G0:0001956	0.48644738	0.31932412	0.45733181	0.00000000	0.05821424	0.00000000
G0:0007204	0.13128821	0.18238716	0.16663498	0.00000000	0.08641867	0.00000000
G0:0008285	0.17795176	0.83460599	0.23058080	0.00000000	0.09733977	0.00000000
G0:0045909	0.24925026	0.32866354	0.30505729	0.00000000	0.00000000	0.00000000
G0:0010628	0.33163309	0.48876477	0.43832321	0.00000000	0.00000000	0.00000000
G0:0010629	0.16240362	0.23738239	0.21344797	0.00000000	0.00000000	0.00000000
G0:0019228	0.12477909	0.17006297	0.15628727	0.00000000	0.07980700	0.00000000
G0:0030263	0.26105619	0.05452169	0.05104167	0.00000000	0.05993654	0.00000000
G0:0030264	1.02058130	0.05309282	0.04978728	0.00000000	0.05821424	0.00000000
G0:0032024	0.57617755	0.39831119	0.56180407	0.00000000	0.07438889	0.00000000
G0:0043065	0.31770691	0.51989403	0.46917809	0.00000000	0.10089191	0.00000000
G0:0043280	0.16055023	0.22053153	0.20218546	0.00000000	0.08247807	0.00000000
G0:0043410	0.28957626	0.45589577	0.41642345	0.2589841	0.08668825	0.2794308
G0:0045599	0.14691652	0.19559881	0.18102954	0.00000000	0.07204021	0.00000000
G0:0045944	0.31490302	0.51328965	0.46379271	0.00000000	0.09939915	0.00000000
G0:0050769	0.27999240	0.43518626	0.39907660	0.00000000	0.08221389	0.00000000
G0:0051053	0.15462663	0.20950699	0.19288020	0.00000000	0.07782324	0.00000000
G0:0051055	0.13036730	0.17464963	0.16133926	0.00000000	0.00000000	0.00000000
G0:0051480	0.13216236	0.18407858	0.16804573	0.00000000	0.08733608	0.00000000
G0:0070374	0.27410197	0.42271783	0.38856648	0.2406889	0.07954792	0.2582508
G0:0071157	0.13719582	0.17873833	0.16649391	0.00000000	0.53371824	0.00000000
G0:0071333	0.11827606	0.15820761	0.14621792	0.2249962	0.07356535	0.2402701
G0:0090200	0.58609898	0.37918272	0.35147299	0.2165543	0.07039971	0.2306676
G0:2000353	0.22952691	0.33430145	0.31257520	0.00000000	0.06122166	0.00000000
G0:2001238	0.24758423	0.36890733	0.34262700	0.2108366	0.06827613	0.2241915
G0:0007186	0.18425690	0.26787217	0.24127903	0.2996003	0.10321131	0.3273061
G0:0002695	0.16055023	0.22053153	0.20218546	0.00000000	0.08247807	0.5397949
G0:0010579	0.22145124	0.31932412	0.29944313	0.1831309	0.05821424	0.1931233
G0:0014068	0.26076939	0.39520019	0.36519261	0.2254509	0.07373689	0.2407887

G0:0030518	0.16148789	0.22230455	0.20367476	0.2501880	0.08323263	0.2692184
G0:0030819	0.26923567	0.41256254	0.37996912	0.0000000	0.07739180	0.0000000
G0:0032962	0.22610477	0.32791800	0.30698758	0.0000000	0.05993654	0.0000000
G0:0043401	0.14115851	0.18552347	0.17236599	0.2098513	0.06791182	0.2230777
G0:0045742	0.25214097	0.37789345	0.35036498	0.2158373	0.07013252	0.2298543
G0:0045745	0.24668075	0.36713802	0.34110028	0.2098513	0.06791182	0.2230777
G0:0050728	0.13444522	0.18204697	0.16763172	0.8258406	0.00000000	0.6405987
G0:0051281	0.53976174	0.36526526	0.51848390	0.0000000	0.06752665	0.0000000
G0:0070474	0.23452986	0.30354148	0.28329493	0.0000000	0.00000000	0.0000000
G0:0071356	0.05134081	0.06978875	0.06418704	0.2390432	0.07891447	0.2563572
G0:0071375	0.05642010	0.07951998	0.07232767	0.2712740	0.09158813	0.2937917
G0:0071392	0.04514144	0.05881015	0.05478137	0.2023655	0.06515992	0.2146376
G0:0090004	1.00000000	0.31892193	0.51304937	0.0000000	0.06668164	0.0000000
G0:0008284	0.31892193	1.00000000	0.47152076	0.0000000	0.10154441	0.0000000
G0:0030335	0.51304937	0.47152076	1.00000000	0.0000000	0.09010291	0.0000000
G0:0006954	0.00000000	0.00000000	0.00000000	1.0000000	0.00000000	0.7875390
G0:0007049	0.06668164	0.10154441	0.09010291	0.0000000	1.00000000	0.0000000
G0:0045087	0.00000000	0.00000000	0.00000000	0.7875390	0.00000000	1.0000000

optimal assignment:

	G0:0001934	G0:0001956	G0:0007204	G0:0008285	G0:0045909	G0:0010628
G0:0001934	1	0	0	0	0	0
G0:0001956	0	1	0	0	0	0
G0:0007204	0	0	1	0	0	0
G0:0008285	0	0	0	1	0	0
G0:0045909	0	0	0	0	1	0
G0:0010628	0	0	0	0	0	1
G0:0010629	0	0	0	0	0	0
G0:0019228	0	0	0	0	0	0
G0:0030263	0	0	0	0	0	0
G0:0030264	0	0	0	0	0	0
G0:0032024	0	0	0	0	0	0
G0:0043065	0	0	0	0	0	0
G0:0043280	0	0	0	0	0	0
G0:0043410	0	0	0	0	0	0
G0:0045599	0	0	0	0	0	0
G0:0045944	0	0	0	0	0	0
G0:0050769	0	0	0	0	0	0
G0:0051053	0	0	0	0	0	0
G0:0051055	0	0	0	0	0	0
G0:0051480	0	0	0	0	0	0
G0:0070374	0	0	0	0	0	0
G0:0071157	0	0	0	0	0	0

G0:0071333	0	0	0	0	0	0
G0:0090200	0	0	0	0	0	0
G0:2000353	0	0	0	0	0	0
G0:2001238	0	0	0	0	0	0
G0:0007186	0	0	0	0	0	0
G0:0002695	0	0	0	0	0	0
G0:0010579	0	0	0	0	0	0
G0:0014068	0	0	0	0	0	0
G0:0030518	0	0	0	0	0	0
G0:0030819	0	0	0	0	0	0
G0:0032962	0	0	0	0	0	0
G0:0043401	0	0	0	0	0	0
G0:0045742	0	0	0	0	0	0
G0:0045745	0	0	0	0	0	0
G0:0050728	0	0	0	0	0	0
G0:0051281	0	0	0	0	0	0
G0:0070474	0	0	0	0	0	0
G0:0071356	0	0	0	0	0	0
G0:0071375	0	0	0	0	0	0
G0:0071392	0	0	0	0	0	0
G0:0090004	0	0	0	0	0	0
G0:0008284	0	0	0	0	0	0
G0:0030335	0	0	0	0	0	0
G0:0006954	0	0	0	0	0	0
G0:0007049	0	0	0	0	0	0
G0:0045087	0	0	0	0	0	0
G0:0010629	G0:0019228	G0:0030263	G0:0030264	G0:0032024	G0:0043065	
G0:0001934	0	0	0	0	0	0
G0:0001956	0	0	0	0	0	0
G0:0007204	0	0	0	0	0	0
G0:0008285	0	0	0	0	0	0
G0:0045909	0	0	0	0	0	0
G0:0010628	0	0	0	0	0	0
G0:0010629	1	0	0	0	0	0
G0:0019228	0	1	0	0	0	0
G0:0030263	0	0	1	0	0	0
G0:0030264	0	0	0	0	0	0
G0:0032024	0	0	0	0	1	0
G0:0043065	0	0	0	0	0	1
G0:0043280	0	0	0	0	0	0
G0:0043410	0	0	0	0	0	0
G0:0045599	0	0	0	0	0	0

G0:0045944	0	0	0	0	0	0
G0:0050769	0	0	0	0	0	0
G0:0051053	0	0	0	0	0	0
G0:0051055	0	0	0	0	0	0
G0:0051480	0	0	0	0	0	0
G0:0070374	0	0	0	0	0	0
G0:0071157	0	0	0	0	0	0
G0:0071333	0	0	0	0	0	0
G0:0090200	0	0	0	0	0	0
G0:2000353	0	0	0	0	0	0
G0:2001238	0	0	0	0	0	0
G0:0007186	0	0	0	0	0	0
G0:0002695	0	0	0	0	0	0
G0:0010579	0	0	0	0	0	0
G0:0014068	0	0	0	0	0	0
G0:0030518	0	0	0	0	0	0
G0:0030819	0	0	0	0	0	0
G0:0032962	0	0	0	0	0	0
G0:0043401	0	0	0	0	0	0
G0:0045742	0	0	0	0	0	0
G0:0045745	0	0	0	0	0	0
G0:0050728	0	0	0	0	0	0
G0:0051281	0	0	0	0	0	0
G0:0070474	0	0	0	0	0	0
G0:0071356	0	0	0	0	0	0
G0:0071375	0	0	0	0	0	0
G0:0071392	0	0	0	0	0	0
G0:0090004	0	0	0	1	0	0
G0:0008284	0	0	0	0	0	0
G0:0030335	0	0	0	0	0	0
G0:0006954	0	0	0	0	0	0
G0:0007049	0	0	0	0	0	0
G0:0045087	0	0	0	0	0	0
G0:0043280	G0:0043410	G0:0045599	G0:0045944	G0:0050769	G0:0051053	
G0:0001934	0	0	0	0	0	0
G0:0001956	0	0	0	0	0	0
G0:0007204	0	0	0	0	0	0
G0:0008285	0	0	0	0	0	0
G0:0045909	0	0	0	0	0	0
G0:0010628	0	0	0	0	0	0
G0:0010629	0	0	0	0	0	0
G0:0019228	0	0	0	0	0	0

G0:0030263	0	0	0	0	0	0
G0:0030264	0	0	0	0	0	0
G0:0032024	0	0	0	0	0	0
G0:0043065	0	0	0	0	0	0
G0:0043280	1	0	0	0	0	0
G0:0043410	0	1	0	0	0	0
G0:0045599	0	0	1	0	0	0
G0:0045944	0	0	0	0	0	0
G0:0050769	0	0	0	0	1	0
G0:0051053	0	0	0	0	0	1
G0:0051055	0	0	0	0	0	0
G0:0051480	0	0	0	0	0	0
G0:0070374	0	0	0	0	0	0
G0:0071157	0	0	0	0	0	0
G0:0071333	0	0	0	0	0	0
G0:0090200	0	0	0	0	0	0
G0:2000353	0	0	0	0	0	0
G0:2001238	0	0	0	0	0	0
G0:0007186	0	0	0	0	0	0
G0:0002695	0	0	0	0	0	0
G0:0010579	0	0	0	0	0	0
G0:0014068	0	0	0	0	0	0
G0:0030518	0	0	0	0	0	0
G0:0030819	0	0	0	1	0	0
G0:0032962	0	0	0	0	0	0
G0:0043401	0	0	0	0	0	0
G0:0045742	0	0	0	0	0	0
G0:0045745	0	0	0	0	0	0
G0:0050728	0	0	0	0	0	0
G0:0051281	0	0	0	0	0	0
G0:0070474	0	0	0	0	0	0
G0:0071356	0	0	0	0	0	0
G0:0071375	0	0	0	0	0	0
G0:0071392	0	0	0	0	0	0
G0:0090004	0	0	0	0	0	0
G0:0008284	0	0	0	0	0	0
G0:0030335	0	0	0	0	0	0
G0:0006954	0	0	0	0	0	0
G0:0007049	0	0	0	0	0	0
G0:0045087	0	0	0	0	0	0
G0:0001934	0	0	0	0	0	0
G0:0051055						
G0:0051480						
G0:0070374						
G0:0071157						
G0:0071333						
G0:0090200						

G0:0001956	0	0	0	0	0	0
G0:0007204	0	0	0	0	0	0
G0:0008285	0	0	0	0	0	0
G0:0045909	0	0	0	0	0	0
G0:0010628	0	0	0	0	0	0
G0:0010629	0	0	0	0	0	0
G0:0019228	0	0	0	0	0	0
G0:0030263	0	0	0	0	0	0
G0:0030264	0	0	0	0	0	0
G0:0032024	0	0	0	0	0	0
G0:0043065	0	0	0	0	0	0
G0:0043280	0	0	0	0	0	0
G0:0043410	0	0	0	0	0	0
G0:0045599	0	0	0	0	0	0
G0:0045944	0	0	0	0	0	0
G0:0050769	0	0	0	0	0	0
G0:0051053	0	0	0	0	0	0
G0:0051055	1	0	0	0	0	0
G0:0051480	0	1	0	0	0	0
G0:0070374	0	0	1	0	0	0
G0:0071157	0	0	0	1	0	0
G0:0071333	0	0	0	0	1	0
G0:0090200	0	0	0	0	0	1
G0:2000353	0	0	0	0	0	0
G0:2001238	0	0	0	0	0	0
G0:0007186	0	0	0	0	0	0
G0:0002695	0	0	0	0	0	0
G0:0010579	0	0	0	0	0	0
G0:0014068	0	0	0	0	0	0
G0:0030518	0	0	0	0	0	0
G0:0030819	0	0	0	0	0	0
G0:0032962	0	0	0	0	0	0
G0:0043401	0	0	0	0	0	0
G0:0045742	0	0	0	0	0	0
G0:0045745	0	0	0	0	0	0
G0:0050728	0	0	0	0	0	0
G0:0051281	0	0	0	0	0	0
G0:0070474	0	0	0	0	0	0
G0:0071356	0	0	0	0	0	0
G0:0071375	0	0	0	0	0	0
G0:0071392	0	0	0	0	0	0
G0:0090004	0	0	0	0	0	0



G0:0008284	0	0	0	0	0	0
G0:0030335	0	0	0	0	0	0
G0:0006954	0	0	0	0	0	0
G0:0007049	0	0	0	0	0	0
G0:0045087	0	0	0	0	0	0
G0:2000353	G0:2001238	G0:0007186	G0:0002695	G0:0010579	G0:0014068	
G0:0001934	0	0	0	0	0	0
G0:0001956	0	0	0	0	0	0
G0:0007204	0	0	0	0	0	0
G0:0008285	0	0	0	0	0	0
G0:0045909	0	0	0	0	0	0
G0:0010628	0	0	0	0	0	0
G0:0010629	0	0	0	0	0	0
G0:0019228	0	0	0	0	0	0
G0:0030263	0	0	0	0	0	0
G0:0030264	0	0	0	0	0	0
G0:0032024	0	0	0	0	0	0
G0:0043065	0	0	0	0	0	0
G0:0043280	0	0	0	0	0	0
G0:0043410	0	0	0	0	0	0
G0:0045599	0	0	0	0	0	0
G0:0045944	0	0	0	0	0	0
G0:0050769	0	0	0	0	0	0
G0:0051053	0	0	0	0	0	0
G0:0051055	0	0	0	0	0	0
G0:0051480	0	0	0	0	0	0
G0:0070374	0	0	0	0	0	0
G0:0071157	0	0	0	0	0	0
G0:0071333	0	0	0	0	0	0
G0:0090200	0	0	0	0	0	0
G0:2000353	1	0	0	0	0	0
G0:2001238	0	1	0	0	0	0
G0:0007186	0	0	1	0	0	0
G0:0002695	0	0	0	1	0	0
G0:0010579	0	0	0	0	1	0
G0:0014068	0	0	0	0	0	1
G0:0030518	0	0	0	0	0	0
G0:0030819	0	0	0	0	0	0
G0:0032962	0	0	0	0	0	0
G0:0043401	0	0	0	0	0	0
G0:0045742	0	0	0	0	0	0
G0:0045745	0	0	0	0	0	0

G0:0050728	0	0	0	0	0	0
G0:0051281	0	0	0	0	0	0
G0:0070474	0	0	0	0	0	0
G0:0071356	0	0	0	0	0	0
G0:0071375	0	0	0	0	0	0
G0:0071392	0	0	0	0	0	0
G0:0090004	0	0	0	0	0	0
G0:0008284	0	0	0	0	0	0
G0:0030335	0	0	0	0	0	0
G0:0006954	0	0	0	0	0	0
G0:0007049	0	0	0	0	0	0
G0:0045087	0	0	0	0	0	0
G0:0030518	G0:0030819	G0:0032962	G0:0043401	G0:0045742	G0:0045745	
G0:0001934	0	0	0	0	0	0
G0:0001956	0	0	0	0	0	0
G0:0007204	0	0	0	0	0	0
G0:0008285	0	0	0	0	0	0
G0:0045909	0	0	0	0	0	0
G0:0010628	0	0	0	0	0	0
G0:0010629	0	0	0	0	0	0
G0:0019228	0	0	0	0	0	0
G0:0030263	0	0	0	0	0	0
G0:0030264	0	0	0	0	0	0
G0:0032024	0	0	0	0	0	0
G0:0043065	0	0	0	0	0	0
G0:0043280	0	0	0	0	0	0
G0:0043410	0	0	0	0	0	0
G0:0045599	0	0	0	0	0	0
G0:0045944	0	1	0	0	0	0
G0:0050769	0	0	0	0	0	0
G0:0051053	0	0	0	0	0	0
G0:0051055	0	0	0	0	0	0
G0:0051480	0	0	0	0	0	0
G0:0070374	0	0	0	0	0	0
G0:0071157	0	0	0	0	0	0
G0:0071333	0	0	0	0	0	0
G0:0090200	0	0	0	0	0	0
G0:2000353	0	0	0	0	0	0
G0:2001238	0	0	0	0	0	0
G0:0007186	0	0	0	0	0	0
G0:0002695	0	0	0	0	0	0
G0:0010579	0	0	0	0	0	0

G0:0014068	0	0	0	0	0	0
G0:0030518	1	0	0	0	0	0
G0:0030819	0	0	0	0	0	0
G0:0032962	0	0	1	0	0	0
G0:0043401	0	0	0	1	0	0
G0:0045742	0	0	0	0	1	0
G0:0045745	0	0	0	0	0	1
G0:0050728	0	0	0	0	0	0
G0:0051281	0	0	0	0	0	0
G0:0070474	0	0	0	0	0	0
G0:0071356	0	0	0	0	0	0
G0:0071375	0	0	0	0	0	0
G0:0071392	0	0	0	0	0	0
G0:0090004	0	0	0	0	0	0
G0:0008284	0	0	0	0	0	0
G0:0030335	0	0	0	0	0	0
G0:0006954	0	0	0	0	0	0
G0:0007049	0	0	0	0	0	0
G0:0045087	0	0	0	0	0	0
G0:0050728 G0:0051281 G0:0070474 G0:0071356 G0:0071375 G0:0071392						
G0:0001934	0	0	0	0	0	0
G0:0001956	0	0	0	0	0	0
G0:0007204	0	0	0	0	0	0
G0:0008285	0	0	0	0	0	0
G0:0045909	0	0	0	0	0	0
G0:0010628	0	0	0	0	0	0
G0:0010629	0	0	0	0	0	0
G0:0019228	0	0	0	0	0	0
G0:0030263	0	0	0	0	0	0
G0:0030264	0	0	0	0	0	0
G0:0032024	0	0	0	0	0	0
G0:0043065	0	0	0	0	0	0
G0:0043280	0	0	0	0	0	0
G0:0043410	0	0	0	0	0	0
G0:0045599	0	0	0	0	0	0
G0:0045944	0	0	0	0	0	0
G0:0050769	0	0	0	0	0	0
G0:0051053	0	0	0	0	0	0
G0:0051055	0	0	0	0	0	0
G0:0051480	0	0	0	0	0	0
G0:0070374	0	0	0	0	0	0
G0:0071157	0	0	0	0	0	0

G0:0071333	0	0	0	0	0	0
G0:0090200	0	0	0	0	0	0
G0:2000353	0	0	0	0	0	0
G0:2001238	0	0	0	0	0	0
G0:0007186	0	0	0	0	0	0
G0:0002695	0	0	0	0	0	0
G0:0010579	0	0	0	0	0	0
G0:0014068	0	0	0	0	0	0
G0:0030518	0	0	0	0	0	0
G0:0030819	0	0	0	0	0	0
G0:0032962	0	0	0	0	0	0
G0:0043401	0	0	0	0	0	0
G0:0045742	0	0	0	0	0	0
G0:0045745	0	0	0	0	0	0
G0:0050728	1	0	0	0	0	0
G0:0051281	0	1	0	0	0	0
G0:0070474	0	0	1	0	0	0
G0:0071356	0	0	0	1	0	0
G0:0071375	0	0	0	0	1	0
G0:0071392	0	0	0	0	0	1
G0:0090004	0	0	0	0	0	0
G0:0008284	0	0	0	0	0	0
G0:0030335	0	0	0	0	0	0
G0:0006954	0	0	0	0	0	0
G0:0007049	0	0	0	0	0	0
G0:0045087	0	0	0	0	0	0
G0:0090004	G0:0008284	G0:0030335	G0:0006954	G0:0007049	G0:0045087	
G0:0001934	0	0	0	0	0	0
G0:0001956	0	0	0	0	0	0
G0:0007204	0	0	0	0	0	0
G0:0008285	0	0	0	0	0	0
G0:0045909	0	0	0	0	0	0
G0:0010628	0	0	0	0	0	0
G0:0010629	0	0	0	0	0	0
G0:0019228	0	0	0	0	0	0
G0:0030263	0	0	0	0	0	0
G0:0030264	1	0	0	0	0	0
G0:0032024	0	0	0	0	0	0
G0:0043065	0	0	0	0	0	0
G0:0043280	0	0	0	0	0	0
G0:0043410	0	0	0	0	0	0
G0:0045599	0	0	0	0	0	0

G0:0045944	0	0	0	0	0	0
G0:0050769	0	0	0	0	0	0
G0:0051053	0	0	0	0	0	0
G0:0051055	0	0	0	0	0	0
G0:0051480	0	0	0	0	0	0
G0:0070374	0	0	0	0	0	0
G0:0071157	0	0	0	0	0	0
G0:0071333	0	0	0	0	0	0
G0:0090200	0	0	0	0	0	0
G0:2000353	0	0	0	0	0	0
G0:2001238	0	0	0	0	0	0
G0:0007186	0	0	0	0	0	0
G0:0002695	0	0	0	0	0	0
G0:0010579	0	0	0	0	0	0
G0:0014068	0	0	0	0	0	0
G0:0030518	0	0	0	0	0	0
G0:0030819	0	0	0	0	0	0
G0:0032962	0	0	0	0	0	0
G0:0043401	0	0	0	0	0	0
G0:0045742	0	0	0	0	0	0
G0:0045745	0	0	0	0	0	0
G0:0050728	0	0	0	0	0	0
G0:0051281	0	0	0	0	0	0
G0:0070474	0	0	0	0	0	0
G0:0071356	0	0	0	0	0	0
G0:0071375	0	0	0	0	0	0
G0:0071392	0	0	0	0	0	0
G0:0090004	0	0	0	0	0	0
G0:0008284	0	1	0	0	0	0
G0:0030335	0	0	1	0	0	0
G0:0006954	0	0	0	1	0	0
G0:0007049	0	0	0	0	1	0
G0:0045087	0	0	0	0	0	1

=====

term similarity matrix:

	G0:0001934	G0:0001956	G0:0007204	G0:0008285	G0:0045909	G0:0010628
G0:0010629	0.88341800	0.14323644	0.18738474	0.54501949	0.1674750	0.9394387
G0:0046885	0.37227565	0.31645835	0.41734827	0.18660546	0.3577173	0.3615608
G0:0006874	0.18956951	0.36642792	0.96327998	0.18383542	0.4229081	0.2000490
G0:0006979	0.00000000	0.00000000	0.00000000	0.00000000	0.0000000	0.0000000
G0:0007566	0.00000000	0.00000000	0.00000000	0.00000000	0.1968291	0.0000000
G0:0030968	0.22401252	0.24108839	0.15808124	0.21764415	0.1455048	0.2052091

G0:0033280	0.00000000	0.00000000	0.00000000	0.00000000	0.00000000	0.00000000
G0:0040015	0.15268665	0.10744042	0.12676207	0.35578731	0.3546344	0.1587928
G0:0043434	0.00000000	0.00000000	0.00000000	0.00000000	0.00000000	0.00000000
G0:0046697	0.00000000	0.00000000	0.00000000	0.00000000	0.1879061	0.00000000
G0:0071456	0.06712798	0.04504801	0.06026934	0.06538553	0.00000000	0.00000000
G0:2001256	0.14034178	0.38899661	0.11735835	0.13744912	0.1126994	0.1454839
	G0:0010629	G0:0019228	G0:0030263	G0:0030264	G0:0032024	G0:0043065
G0:0010629	1.00000000	0.17439994	0.54907611	0.00000000	0.17951462	0.23603440
G0:0046885	0.3549046	0.39577287	0.13940443	0.04311900	0.64144684	0.19084364
G0:0006874	0.1954228	0.47714979	0.05118915	0.04992759	0.45042420	0.18904533
G0:0006979	0.00000000	0.00000000	0.00000000	0.00000000	0.00000000	0.00000000
G0:0007566	0.00000000	0.21844329	0.00000000	0.00000000	0.00000000	0.00000000
G0:0030968	0.2007658	0.31016500	0.04907904	0.04791817	0.29364399	0.22343135
G0:0033280	0.00000000	0.00000000	0.00000000	0.00000000	0.00000000	0.00000000
G0:0040015	0.3721151	0.19629550	0.00000000	0.00000000	0.12663682	0.15237651
G0:0043434	0.00000000	0.00000000	0.00000000	0.00000000	0.00000000	0.00000000
G0:0046697	0.00000000	0.20750745	0.00000000	0.00000000	0.00000000	0.00000000
G0:0071456	0.00000000	0.05697733	0.04607250	0.04504801	0.05416098	0.06696934
G0:2001256	0.1432364	0.11212971	0.00000000	0.00000000	0.45377292	0.14007972
	G0:0043280	G0:0043410	G0:0045599	G0:0045944	G0:0050769	G0:0051053
G0:0010629	0.73552249	0.4286789	0.41552981	0.86910408	0.19656919	0.69783664
G0:0046885	0.30345710	0.3370771	0.15276537	0.43221174	0.16720175	0.31359590
G0:0006874	0.16111130	0.1677056	0.14419635	0.18686592	0.16069324	0.15366975
G0:0006979	0.00000000	0.2424541	0.00000000	0.00000000	0.00000000	0.00000000
G0:0007566	0.00000000	0.00000000	0.23259552	0.00000000	0.28241049	0.00000000
G0:0030968	0.19216964	0.3558245	0.17295825	0.22101285	0.19169741	0.18374426
G0:0033280	0.00000000	0.2052803	0.00000000	0.00000000	0.00000000	0.00000000
G0:0040015	0.13516123	0.1393507	0.29564479	0.15108208	0.39691205	0.31065885
G0:0043434	0.00000000	0.2543398	0.00000000	0.00000000	0.00000000	0.00000000
G0:0046697	0.00000000	0.00000000	0.22172749	0.00000000	0.29190372	0.00000000
G0:0071456	0.05832589	0.2876131	0.05290517	0.06630835	0.05819365	0.05595895
G0:2001256	0.12539701	0.1289950	0.11576418	0.13898504	0.12516602	0.12123256
	G0:0051055	G0:0051480	G0:0070374	G0:0071157	G0:0071333	G0:0090200
G0:0010629	0.6671415	0.18917058	0.3966884	0.37895249	0.1619543	0.1706975
G0:0046885	0.3532486	0.42025312	0.3182968	0.14228290	0.3743134	0.1503213
G0:0006874	0.1475498	0.97146738	0.1564457	0.13258230	0.7034463	0.1414616
G0:0006979	0.00000000	0.00000000	0.2263471	0.00000000	0.2124147	0.2048747
G0:0007566	0.00000000	0.00000000	0.00000000	0.00000000	0.00000000	0.00000000
G0:0030968	0.1539868	0.15935032	0.3331681	0.15964221	0.5391736	0.3027555
G0:0033280	0.00000000	0.00000000	0.1936150	0.00000000	0.4084756	0.1776853
G0:0040015	0.3010081	0.12757680	0.1321480	0.27664626	0.1145900	0.1221846
G0:0043434	0.00000000	0.00000000	0.2366725	0.00000000	0.4934850	0.2132975

GD:0046697	0.0000000	0.00000000	0.00000000	0.00000000	0.00000000	0.00000000
GD:0071456	0.0000000	0.06071413	0.2706841	0.04909791	0.4573328	0.2476841
GD:2001256	0.1177218	0.11805636	0.1227992	0.10879127	0.1068504	0.1141495
GD:2000353	GD:2001238	GD:0007186	GD:0002695	GD:0010579	GD:0014068	
GD:0010629	0.1500891	0.1659695	0.2408168	0.46988842	0.5344116	0.1780793
GD:0046885	0.1359974	0.1471068	0.1935507	0.16756089	0.2995666	0.1552580
GD:0006874	0.1257599	0.1378898	0.1924032	0.16111130	0.1204615	0.1470025
GD:0006979	0.0000000	0.1997499	0.2776981	0.00000000	0.1747083	0.2128199
GD:0007566	0.0000000	0.0000000	0.00000000	0.00000000	0.0000000	0.0000000
GD:0030968	0.1517719	0.2954612	0.4049366	0.19216964	0.2596200	0.3140368
GD:0033280	0.0000000	0.1738176	0.2299946	0.00000000	0.1545423	0.1836310
GD:0040015	0.1112504	0.1197429	0.1543554	0.32216121	0.1074404	0.1259208
GD:0043434	0.0000000	0.2077483	0.2934024	0.00000000	0.1807964	0.2219232
GD:0046697	0.0000000	0.0000000	0.00000000	0.00000000	0.0000000	0.0000000
GD:0071456	0.0468281	0.2421200	0.3237220	0.05832589	0.2145087	0.2562529
GD:2001256	0.1045497	0.1120156	0.1417504	0.12539701	0.1011779	0.1174040
GD:0030518	GD:0030819	GD:0032962	GD:0043401	GD:0045742	GD:0045745	
GD:0010629	0.1987664	0.69432266	0.5490761	0.1651560	0.1701040	0.1651560
GD:0046885	0.1685825	0.36691042	0.3060813	0.1465495	0.1499200	0.1465495
GD:0006874	0.1623026	0.15297184	0.1235053	0.1372734	0.1410142	0.1372734
GD:0006979	0.2347282	0.00000000	0.00000000	0.1988652	0.2042329	0.1988652
GD:0007566	0.0000000	0.00000000	0.00000000	0.0000000	0.0000000	0.0000000
GD:0030968	0.3449739	0.18295194	0.1491631	0.5060426	0.3018427	0.2942007
GD:0033280	0.1997148	0.00000000	0.00000000	0.8463625	0.1772024	0.1731474
GD:0040015	0.1359240	0.12987743	0.1096368	0.1193189	0.1218802	0.1193189
GD:0043434	0.2458512	0.00000000	0.00000000	0.6434940	0.2126020	0.2067916
GD:0046697	0.0000000	0.00000000	0.00000000	0.0000000	0.0000000	0.0000000
GD:0071456	0.2795270	0.05573554	0.0460725	0.4311230	0.2469888	0.2411566
GD:2001256	0.1260533	0.12083618	0.1031233	0.1116445	0.1138838	0.1116445
GD:0050728	GD:0051281	GD:0070474	GD:0071356	GD:0071375	GD:0071392	
GD:0010629	0.4447040	0.39160266	0.1544103	0.00000000	0.00000000	0.00000000
GD:0046885	0.1400797	0.35246126	0.1211354	0.05351699	0.05905924	0.04681524
GD:0006874	0.1533251	0.78669393	0.1290810	0.06442044	0.07262417	0.05495129
GD:0006979	0.4135955	0.00000000	0.00000000	0.22489114	0.25319268	0.19213013
GD:0007566	0.0000000	0.00000000	0.1844556	0.00000000	0.00000000	0.00000000
GD:0030968	0.3967368	0.16428383	0.1355411	0.56953487	0.63789352	0.48951240
GD:0033280	0.5165396	0.00000000	0.00000000	0.42901743	0.47442112	0.82129547
GD:0040015	0.3101200	0.28332785	0.3342800	0.00000000	0.00000000	0.00000000
GD:0043434	0.2317917	0.00000000	0.00000000	0.52378374	0.97040777	0.62086240
GD:0046697	0.0000000	0.00000000	0.1765969	0.00000000	0.00000000	0.00000000
GD:0071456	0.3672759	0.05042972	0.00000000	0.48115018	0.53408293	0.41795952
GD:2001256	0.1210370	0.63522824	0.1066283	0.00000000	0.00000000	0.00000000

	G0:0090004	G0:0008284	G0:0030335	G0:0006954	G0:0007049	G0:0045087
G0:0010629	0.16240362	0.2373824	0.21344797	0.0000000	0.0000000	0.0000000
G0:0046885	0.14465464	0.1916099	0.17760756	0.0000000	0.07039971	0.0000000
G0:0006874	0.13518396	0.1899935	0.17296137	0.0000000	0.09056352	0.0000000
G0:0006979	0.0000000	0.0000000	0.0000000	0.4947236	0.0000000	0.5348280
G0:0007566	0.0000000	0.0000000	0.0000000	0.0000000	0.0000000	0.0000000
G0:0030968	0.16263407	0.2244824	0.20550140	0.4707938	0.08416176	0.5069705
G0:0033280	0.0000000	0.0000000	0.0000000	0.2214949	0.0000000	0.2362815
G0:0040015	0.11787561	0.1529372	0.14263294	0.0000000	0.0000000	0.0000000
G0:0043434	0.0000000	0.0000000	0.0000000	0.2797096	0.0000000	0.3037114
G0:0046697	0.0000000	0.0000000	0.0000000	0.0000000	0.0000000	0.0000000
G0:0071456	0.04995693	0.0672562	0.06203847	0.4298750	0.07569159	0.4598363
G0:2001256	0.38299885	0.1405534	0.45733181	0.0000000	0.0000000	0.0000000

optimal assignment:

	G0:0010629	G0:0046885	G0:0006874	G0:0006979	G0:0007566	G0:0030968
G0:0001934	0	0	0	0	0	0
G0:0001956	0	0	0	0	0	0
G0:0007204	0	0	0	0	0	0
G0:0008285	0	0	0	0	0	0
G0:0045909	0	0	0	0	0	0
G0:0010628	0	0	0	0	0	0
G0:0010629	0	0	0	0	0	0
G0:0019228	0	0	0	1	0	0
G0:0030263	0	0	0	0	0	0
G0:0030264	0	0	0	0	0	0
G0:0032024	0	0	0	0	0	0
G0:0043065	0	0	0	0	0	0
G0:0043280	0	0	0	0	0	0
G0:0043410	0	0	0	0	0	0
G0:0045599	0	0	0	0	0	0
G0:0045944	0	0	0	0	0	0
G0:0050769	0	0	0	0	0	0
G0:0051053	0	0	0	0	0	0
G0:0051055	0	0	0	0	0	0
G0:0051480	0	0	0	0	0	0
G0:0070374	0	0	0	0	0	0
G0:0071157	0	0	0	0	0	0
G0:0071333	0	0	0	0	0	0
G0:0090200	0	0	0	0	0	0
G0:2000353	0	0	0	0	0	0
G0:2001238	0	1	0	0	0	0
G0:0007186	0	0	0	0	0	0



G0:0002695	0	0	0	0	0	0
G0:0010579	0	0	0	0	0	0
G0:0014068	0	0	0	0	0	0
G0:0030518	0	0	0	0	0	0
G0:0030819	0	0	0	0	0	0
G0:0032962	0	0	0	0	0	0
G0:0043401	0	0	0	0	0	0
G0:0045742	0	0	0	0	1	0
G0:0045745	0	0	0	0	0	0
G0:0050728	0	0	0	0	0	0
G0:0051281	0	0	0	0	0	0
G0:0070474	0	0	0	0	0	0
G0:0071356	0	0	0	0	0	0
G0:0071375	0	0	0	0	0	0
G0:0071392	0	0	0	0	0	0
G0:0090004	0	0	0	0	0	0
G0:0008284	0	0	0	0	0	0
G0:0030335	0	0	0	0	0	0
G0:0006954	1	0	0	0	0	0
G0:0007049	0	0	0	0	0	1
G0:0045087	0	0	1	0	0	0
G0:0033280 G0:0040015 G0:0043434 G0:0046697 G0:0071456 G0:2001256						
G0:0001934	1	0	0	0	0	0
G0:0001956	0	0	0	0	1	0
G0:0007204	0	0	0	0	0	0
G0:0008285	0	0	0	0	0	0
G0:0045909	0	0	0	0	0	0
G0:0010628	0	0	0	0	0	0
G0:0010629	0	0	0	0	0	0
G0:0019228	0	0	0	0	0	0
G0:0030263	0	0	0	0	0	0
G0:0030264	0	0	0	0	0	0
G0:0032024	0	0	0	0	0	0
G0:0043065	0	0	0	0	0	0
G0:0043280	0	0	0	0	0	0
G0:0043410	0	0	0	0	0	0
G0:0045599	0	0	0	1	0	0
G0:0045944	0	0	0	0	0	1
G0:0050769	0	0	0	0	0	0
G0:0051053	0	0	0	0	0	0
G0:0051055	0	0	0	0	0	0
G0:0051480	0	0	0	0	0	0

GO:0070374	0	0	0	0	0	0
GO:0071157	0	0	0	0	0	0
GO:0071333	0	0	0	0	0	0
GO:0090200	0	0	0	0	0	0
GO:2000353	0	0	0	0	0	0
GO:2001238	0	0	0	0	0	0
GO:0007186	0	0	0	0	0	0
GO:0002695	0	0	0	0	0	0
GO:0010579	0	0	0	0	0	0
GO:0014068	0	0	0	0	0	0
GO:0030518	0	0	0	0	0	0
GO:0030819	0	1	0	0	0	0
GO:0032962	0	0	0	0	0	0
GO:0043401	0	0	0	0	0	0
GO:0045742	0	0	0	0	0	0
GO:0045745	0	0	1	0	0	0
GO:0050728	0	0	0	0	0	0
GO:0051281	0	0	0	0	0	0
GO:0070474	0	0	0	0	0	0
GO:0071356	0	0	0	0	0	0
GO:0071375	0	0	0	0	0	0
GO:0071392	0	0	0	0	0	0
GO:0090004	0	0	0	0	0	0
GO:0008284	0	0	0	0	0	0
GO:0030335	0	0	0	0	0	0
GO:0006954	0	0	0	0	0	0
GO:0007049	0	0	0	0	0	0
GO:0045087	0	0	0	0	0	0

=====

	8614	2852
8614	1.0000000	0.3111701
2852	0.3111701	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	0.9018423
2852	0.9018423	1.0000000

```
> getGeneSim(c("8614", "2852"), similarity="funSimMax", similarityTerm="Lin", verbose=1)
filtering out genes not mapping to the currently set GO category ... ==> list of 2
      8614      2852
8614 1.0000000 0.6419092
2852 0.6419092 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=1)
filtering out genes not mapping to the currently set GO category ... ==> list of 2
      8614      2852
8614 1.0000000 0.9873622
2852 0.9873622 1.0000000
```

### 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 5 for computational reasons:

```
> proto = selectPrototypes(n=5,verbose=FALSE)
```

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

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

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:

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

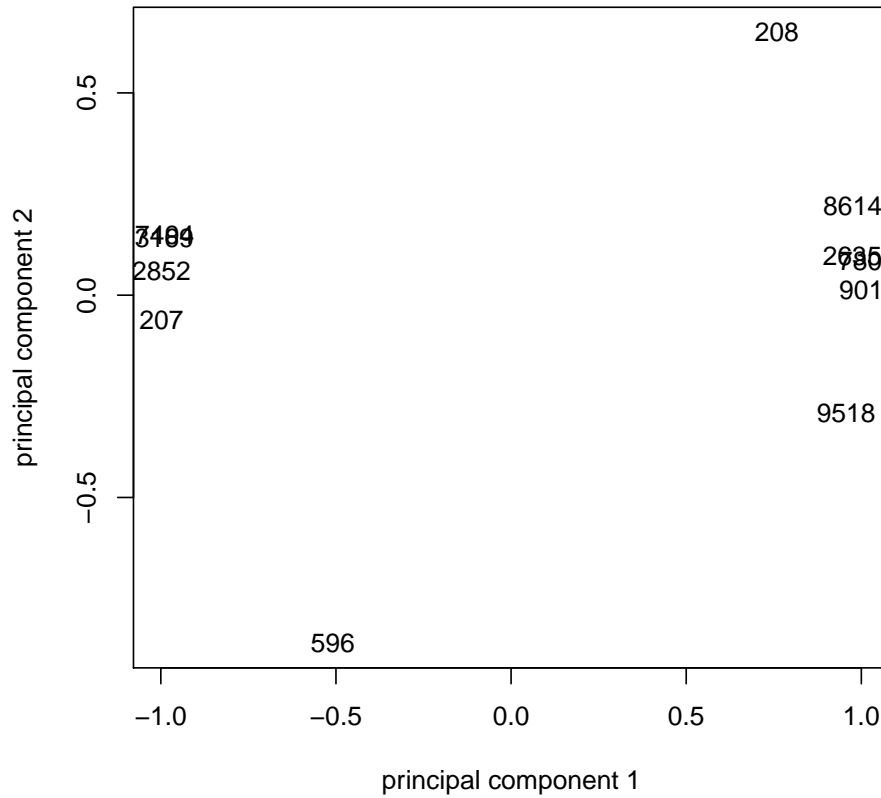
filtering out genes not mapping to the currently set GO category ... ==> list of 1

filtering out genes not mapping to the currently set GO category ... ==> list of 5

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,prototypes=proto,similarityTerm="Resnik",verbose=TRUE)
> h=hclust(as.dist(1-sim$similarity),"ward")
> plot(h,xlab="")
```

This produces a hierarchical clustering of all genes using Ward's method (see Fig. 1).

### 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:

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

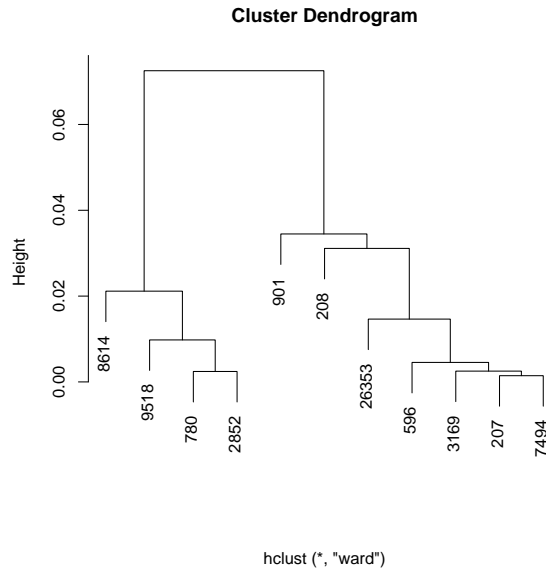


Figure 1: Possible functional clustering of the genes using Ward's method.

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. 2). 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).

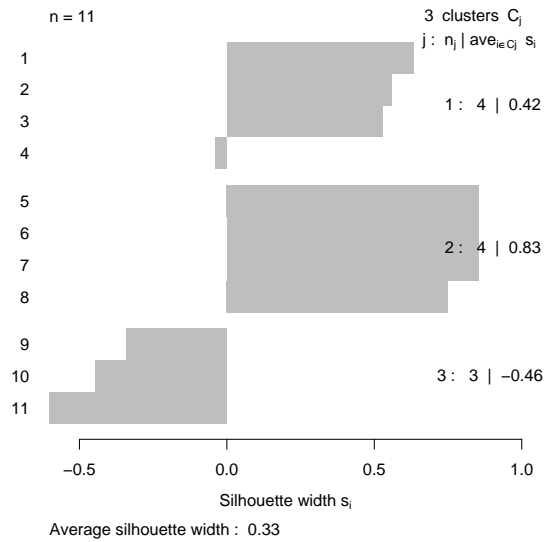


Figure 2: Silhouette plot of a possible given grouping of genes.

```
> library(org.Hs.eg.db)
> library(topGO)

groupGOTerms:          GOBPterm, GOMFterm, GOCCTerm environments built.

> allgenes = union(c("8614", "9518", "780", "2852"), sample(keys(org.Hs.egGO), 1000))
> GOenrichment(c("8614", "9518", "780", "2852"), allgenes) # print out what clusters

Building most specific GOs .....      ( 1317 GO terms found. )

Build GO DAG topology .....          ( 3639 GO terms and 7953 relations. )

Annotating nodes .....                ( 363 genes annotated to the GO terms. )

-- Elim Algorithm --

the algorithm is scoring 683 nontrivial nodes
parameters:
  test statistic: fisher
  cutOff: 0.01

Level 16:          2 nodes to be scored      (0 eliminated genes)
```

Level 15:	4 nodes to be scored	(0 eliminated genes)
Level 14:	4 nodes to be scored	(0 eliminated genes)
Level 13:	5 nodes to be scored	(0 eliminated genes)
Level 12:	13 nodes to be scored	(0 eliminated genes)
Level 11:	29 nodes to be scored	(0 eliminated genes)
Level 10:	42 nodes to be scored	(5 eliminated genes)
Level 9:	56 nodes to be scored	(9 eliminated genes)
Level 8:	73 nodes to be scored	(9 eliminated genes)
Level 7:	102 nodes to be scored	(16 eliminated genes)
Level 6:	113 nodes to be scored	(19 eliminated genes)
Level 5:	115 nodes to be scored	(27 eliminated genes)
Level 4:	72 nodes to be scored	(57 eliminated genes)
Level 3:	35 nodes to be scored	(79 eliminated genes)
Level 2:	17 nodes to be scored	(79 eliminated genes)
Level 1:	1 nodes to be scored	(79 eliminated genes)

\$GOTerms

go\_id

13036 GO:0007169  
 16520 GO:0006874  
 17677 GO:0007566  
 18479 GO:0008285  
 24496 GO:0010817  
 24907 GO:0014070  
 33256 GO:0022411  
 47876 GO:0040008  
 51441 GO:0043434  
 65340 GO:0048609  
 71984 GO:0051924



79394 GO:0071310  
83873 GO:0097305

	Term
13036	transmembrane receptor protein tyrosine kinase signaling pathway
16520	cellular calcium ion homeostasis
17677	embryo implantation
18479	negative regulation of cell proliferation
24496	regulation of hormone levels
24907	response to organic cyclic compound
33256	cellular component disassembly
47876	regulation of growth
51441	response to peptide hormone
65340	multicellular organismal reproductive process
71984	regulation of calcium ion transport
79394	cellular response to organic substance
83873	response to alcohol

13036		A seri
16520		
17677		
18479		
24496	Any process that modulates the levels of hormone within an organism	
24907		
33256		
47876		
51441	Any process that results in a change in state or activity of a cell or an orga	
65340		
71984		
79394		
83873		

#### \$p.values

GO:0097305	GO:0071310	GO:0007566	GO:0051924	GO:0007169	GO:0022411
0.0009031028	0.0036526115	0.0005438770	0.0009031028	0.0025005920	0.0018824532
GO:0014070	GO:0048609	GO:0043434	GO:0040008	GO:0010817	GO:0008285
0.0068365860	0.0068365860	0.0025005920	0.0068365860	0.0048570367	0.0068365860
GO:0006874					
0.0025005920					

#### \$genes

\$genes\$`GO:0097305`

[1] "1026" "2852" "3688" "84676" "8614"

```

$genes$`G0:0071310`
[1] "1026" "1053" "10859" "11031" "1869" "1911" "2649" "2852" "3444"
[10] "3577" "3688" "4052" "4053" "4306" "51606" "529" "54106" "5495"
[19] "5754" "6376" "64102" "64581" "6755" "7293" "7410" "7415" "7466"
[28] "84676" "8614" "8882" "8986" "91319" "9315" "948" "949" "9518"
[37] "9631"

$genes$`G0:0007566`
[1] "126206" "780" "8614" "91"

$genes$`G0:0051924`
[1] "10859" "2852" "56704" "7466" "8614"

$genes$`G0:0007169`
[1] "1026" "2852" "51606" "529" "54106" "7410" "780" "920"

$genes$`G0:0022411`
[1] "1303" "2852" "3909" "6191" "780" "9313" "9631"

$genes$`G0:0014070`
[1] "1026" "163732" "2267" "23180" "2649" "2852" "3444" "3688"
[9] "4306" "4821" "84676" "8614" "948"

$genes$`G0:0048609`
[1] "124783" "132625" "1869" "2176" "26108" "2649" "286234" "3688"
[9] "50487" "780" "84953" "8614" "8890"

$genes$`G0:0043434`
[1] "11031" "1605" "2852" "51606" "529" "54106" "8614" "8890"

$genes$`G0:0040008`
[1] "1026" "147040" "4666" "4722" "5716" "7466" "780" "85004"
[9] "8614" "8882" "91" "948" "978"

$genes$`G0:0010817`
[1] "223" "25924" "2852" "54097" "6294" "6755" "79644" "8614" "8622"
[10] "8630" "949"

$genes$`G0:0008285`
[1] "1026" "10859" "147040" "2765" "2852" "3688" "50514" "64102"
[9] "6755" "780" "80762" "8493" "85004"

```

\$genes\$`GO:0006874`

[1] "1760" "2852" "3688" "4987" "56704" "63933" "7466" "8614"

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