

Disease Ontology Semantic and Enrichment analysis

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1 Introduction

Disease Ontology (DO) provides an open source ontology for the integration of biomedical data that is associated with human disease. DO analysis can lead to interesting discoveries that deserve further clinical investigation.

DOSE was designed for semantic similarity measure and enrichment analysis.

Four information content (IC)-based methods, proposed by Resnik [Philip, 1999], Jiang [Jiang and Conrath, 1997], Lin [Lin, 1998] and Schlicker [Schlicker et al., 2006], and one graph structure-based method, proposed by Wang [Wang et al., 2007], were implemented. These methods were also implemented in our *GOSemSim* [Yu et al., 2010] package for measuring GO-term semantic similarities. Hypergeometric test [Boyle et al., 2004] was implemented for enrichment analysis.

To start with *DOSE* package, type following code below:

```
> library(DOSE)
> help(DOSE)
```

2 Semantic Similarity Measurement

The *DOSE* package contains functions to estimate semantic similarity of DO terms based on Resnik's, Lin's, Jiang and Conrath's, Rel's and Wang's method. Details about Resnik's, Lin's, and Jiang and Conrath's methods can be seen in [Lord et al., 2003], details about Rel's method can be seen in [Schlicker et al., 2006], and details about Wang's method can be seen in [Wang et al., 2007].

IC-based method depend on the frequencies of two DO terms involved and that of their closest common ancestor term in a specific corpus of DO annotations. Information content is defined as frequency of each term occurs in the corpus.

As DO allow multiple parents for each concept, two terms can share parents by multiple paths. We take the minimum $p(t)$, where there is more than one shared parents. The p_{ms} is defined as:

$$p_{ms}(t1, t2) = \min_{t \in S(t1, t2)} \{p(t)\}$$

Where $S(t1, t2)$ is the set of parent terms shared by $t1$ and $t2$.

- Resnik’s method is defined as:

$$sim(t1, t2) = -\ln p_{ms}(t1, t2)$$

- Lin’s method is defined as:

$$sim(t1, t2) = \frac{2 \times \ln(p_{ms}(t1, t2))}{\ln p(t1) + \ln p(t2)}$$

- Schlicker’s method, which combine Resnik’s and Lin’s method, is defined as:

$$sim(t1, t2) = \frac{2 \times \ln p_{ms}(t1, t2)}{\ln p(t1) + \ln p(t2)} \times (1 - p_{ms}(t1, t2))$$

- Jiang and Conrath’s method is defined as:

$$sim(t1, t2) = 1 - \min(1, d(t1, t2))$$

where

$$d(t1, t2) = \ln p(t1) + \ln p(t2) - 2 \times \ln p_{ms}(t1, t2)$$

Graph-based methods using the topology of DO graph structure to compute semantic similarity. Formally, a DO term A can be represented as $DAG_A = (A, T_A, E_A)$ where T_A is the set of DO terms in DAG_A , including term A and all of its ancestor terms in the DO graph, and E_A is the set of edges connecting the DO terms in DAG_A .

- Wang’s method

To encode the semantic of a DO term in a measurable format to enable a quantitative comparison, Wang firstly defined the semantic value of term A as the aggregate contribution of all terms in DAG_A to the semantics of term A , terms closer to term A in DAG_A contribute more to its semantics. Thus, defined the contribution of a DO term t to the semantics of DO term A as the S-value of DO term t related to term A . For any of term t in DAG_A , its S-value related to term A . $S_A(t)$ is defined as:

$$\begin{cases} S_A(A) = 1 \\ S_A(t) = \max\{w_e \times S_A(t') | t' \in \text{childrenof}(t)\} \text{ if } t \neq A \end{cases}$$

where w_e is the semantic contribution factor for edge $e \in E_A$ linking term t with its child term t' . Wang defined term A contributes to its own as one. After obtaining the S-values for all terms in DAG_A , the semantic value of GO term A, $SV(A)$, is calculated as:

$$SV(A) = \sum_{t \in T_A} S_A(t)$$

Thus, given two DO terms A and B, the semantic similarity between these two terms, $DO_{A,B}$, is defined as:

$$sim_{Wang}(A, B) = \frac{\sum_{t \in T_A \cap T_B} S_A(t) + S_B(t)}{SV(A) + SV(B)}$$

where $S_A(t)$ is the S-value of DO term t related to term A and $S_B(t)$ is the S-value of DO term t related to term B.

This method proposed by Wang [Wang et al., 2007] determines the semantic similarity of two DO terms based on both the locations of these terms in the DO graph and their relations with their ancestor terms.

3 Enrichment Analysis

Enrichment analysis is a widely used approach to identify biological themes. Here we implement hypergeometric model to assess whether the number of selected genes associated with disease is larger than expected. We also implement a bar plot and gene-category-network for visualization.

- Calculation of Statistical Significance

To determine whether any DO terms annotate a specified list of genes at frequency greater than that would be expected by chance, *DOSE* calculates a p-value using the hypergeometric distribution:

$$p = 1 - \sum_{i=0}^{k-1} \frac{\binom{M}{i} \binom{N-M}{n-i}}{\binom{N}{n}}$$

In this equation, N is the total number of genes in the background distribution, M is the number of genes within that distribution that are annotated (either directly or indirectly) to the node of interest, n is the size of the list of genes of interest and k is the number of genes within that list which are annotated to the node. The background distribution by default is all the genes that have DO annotation.

4 Example

The following lines provide a quick and simple example on the use of *DOSE*.

- Calculate DO terms Similarity

```
> data(DO2EG)
> set.seed(123)
> terms <- list(a=sample(names(DO2EG), 5), b= sample(names(DO2EG), 6))
> terms

$a
[1] "DOID:1474" "DOID:6432" "DOID:2571" "DOID:8622"
[5] "DOID:9206"

$b
[1] "DOID:10591" "DOID:332" "DOID:8689" "DOID:3458"
[5] "DOID:2893" "DOID:9346"

> ## Setting Parameters...
> params <- new("DOParams", IDs=terms, type="DOID", method="Wang")
> ## Calculating Semantic Similarities...
> sim(params)

          DOID:10591 DOID:332 DOID:8689 DOID:3458 DOID:2893
DOID:1474      0.100   0.078   0.041   0.026   0.026
DOID:6432      0.660   0.116   0.057   0.041   0.041
DOID:2571      0.139   0.116   0.057   0.041   0.041
DOID:8622      0.093   0.082   0.093   0.075   0.075
DOID:9206      0.173   0.149   0.071   0.055   0.055
          DOID:9346
DOID:1474      0.100
DOID:6432      0.139
DOID:2571      0.139
DOID:8622      0.093
DOID:9206      0.173
```

Four combine methods which called *max*, *average*, *rcmax* and *BMA*, were implemented to combine semantic similarity scores of multiple DO terms.

```
> params <- new("DOParams",
+             IDs=terms,
+             type="DOID",
+             method="Wang",
+             combine="BMA")
> sim(params)

[1] 0.217
```

- Calculate Gene products Similarity

```
> geneid <- list(a=c("5320", "338"),
+               b= c("341", "581", "885"))
> params <- new("DOParams",
+              IDs=geneid,
+              type="GeneID",
+              method="Wang",
+              combine="BMA")
> x <- sim(params)
> x
```

```
      341  581  885
5320 0.886 0.687 0.729
338  0.847 0.643 0.610
```

DOSE implement `simplot` to visualize the semantic similarity matrix.

```
> simplot(x)
```

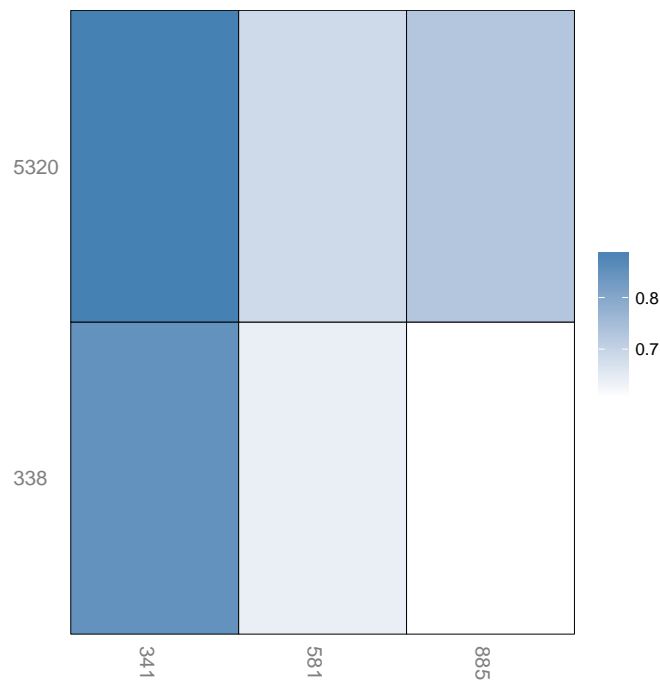


Figure 1: Heatmap plot for semantic similarity matrix

- Enrichment analysis of a list of genes can also be performed as shown in the following examples.

```
> data(AL1)
> x <- enrichDO(AL1, pvalueCutoff=0.05)
> head(summary(x))
```

	ID	Description	GeneRatio	BgRatio
DOLite:214	DOLite:214	Gigantism	1/62	1/4051
DOLite:310	DOLite:310	Lewy body disease	1/62	1/4051
DOLite:258	DOLite:258	Hyperglycemia	3/62	39/4051
DOLite:168	DOLite:168	Encephalopathies	3/62	51/4051

	pvalue	qvalue	geneID	Count
DOLite:214	0.01530486	0.5978242	2597	1
DOLite:310	0.01530486	0.5978242	10376	1
DOLite:258	0.02109968	0.5978242	10135/9588/2739	3
DOLite:168	0.04227576	0.7876214	2184/1967/2023	3

User can use the following command for mapping gene IDs to their corresponding gene symbol.

```
> setReadable(x) <- TRUE
> head(summary(x))
```

	ID	Description	GeneRatio	BgRatio
DOLite:214	DOLite:214	Gigantism	1/62	1/4051
DOLite:310	DOLite:310	Lewy body disease	1/62	1/4051
DOLite:258	DOLite:258	Hyperglycemia	3/62	39/4051
DOLite:168	DOLite:168	Encephalopathies	3/62	51/4051

	pvalue	qvalue	geneID	Count
DOLite:214	0.01530486	0.5978242	GAPDH	1
DOLite:310	0.01530486	0.5978242	TUBA1B	1
DOLite:258	0.02109968	0.5978242	NAMPT/PRDX6/GL01	3
DOLite:168	0.04227576	0.7876214	FAH/EIF2B1/ENO1	3

DOSE package implement bar plot and gene-category network plot for visualization.

In the category-network plot, if expression values is provided, the plot function will use them to label the gene nodes. Red indicates up-regulated and green indicates down-regulated.

```
> AL1expr
```

396	8349	7334	10539	7178	11332	5034	1891	1072	5094
-4.12	-2.14	-2.07	-3.03	2.40	2.34	2.39	2.07	2.22	2.56
8668	7384	6282	708	3735	4436	10135	5713	811	811
-2.34	-3.72	2.53	2.13	-2.06	-2.82	2.03	4.04	-3.06	2.01

```
> plot(x, type="bar")
```

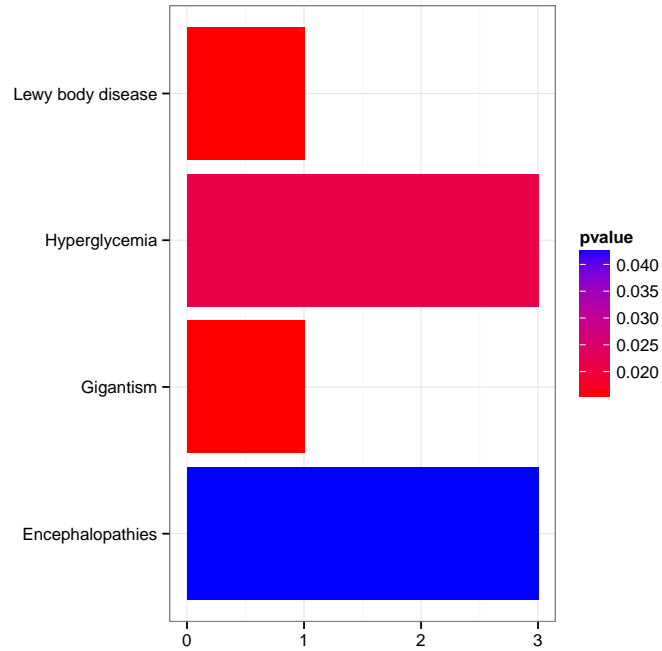


Figure 2: Bar Plot of Enrichment Result

```
811 811 10102 839 10935 3315 8533 3417 7001 7001
-3.06 2.01 2.13 2.62 -2.57 -2.04 3.52 2.48 -7.47 -2.45
7001 7001 5690 80273 25796 2184 9342 9380 28970 4678
-7.47 -2.45 2.51 -2.05 2.36 2.50 -2.17 -2.69 2.37 2.32
3050 2288 2597 10327 9588 6636 2739 7520 1967 10015
2.59 -2.06 2.53 3.04 2.25 3.34 -2.91 2.41 3.55 2.01
8574 30968 23193 689 5478 2023 3925 7203 5721 10694
2.51 2.24 2.33 2.38 2.77 3.06 2.17 2.23 -2.61 -3.23
10376 7296
-2.01 2.01
```

The plot was re-generate by using this log fold change expression values as follows:

5 Session Information

The version number of R and packages loaded for generating the vignette were:

```
> plot(x, categorySize="geneNum", output="fixed")
```

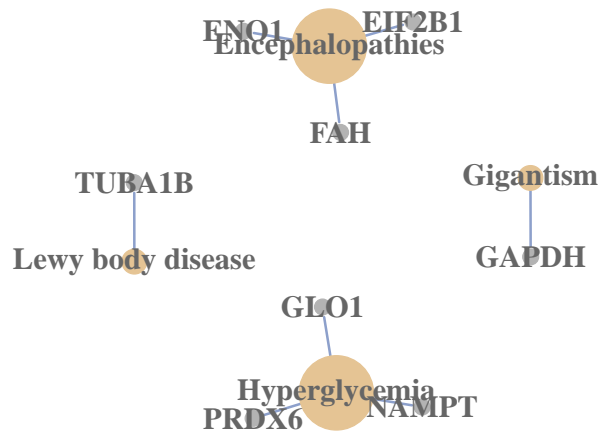


Figure 3: Category-Network Plot of Enrichment Result

```
R version 2.15.1 (2012-06-22)
Platform: x86_64-unknown-linux-gnu (64-bit)

locale:
 [1] LC_CTYPE=en_US.UTF-8      LC_NUMERIC=C
 [3] LC_TIME=en_US.UTF-8      LC_COLLATE=C
 [5] LC_MONETARY=en_US.UTF-8  LC_MESSAGES=en_US.UTF-8
 [7] LC_PAPER=C                LC_NAME=C
 [9] LC_ADDRESS=C              LC_TELEPHONE=C
[11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C

attached base packages:
[1] stats      graphics  grDevices  utils      datasets
[6] methods   base

other attached packages:
[1] org.Hs.eg.db_2.8.0  DO.db_2.5.0
```



```
> plot(x,showCategory=5, logFC=AL1expr, categorySize="geneNum",output="fixed")
```

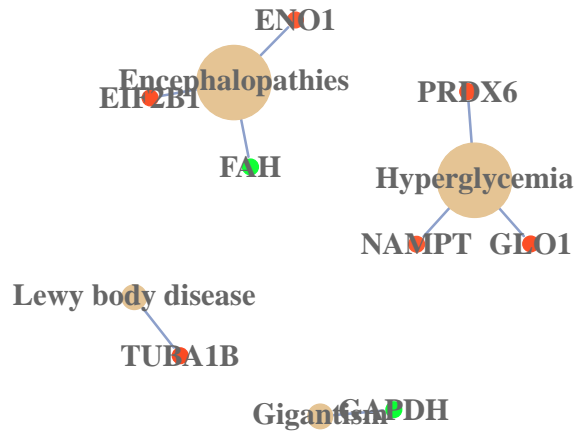


Figure 4: Category-Network Plot of Enrichment Result

```
[3] DOSE_1.4.0          AnnotationDbi_1.20.0
[5] Biobase_2.18.0      BiocGenerics_0.4.0
[7] RSQLite_0.11.2     DBI_0.2-5
[9] ggplot2_0.9.2.1
```

loaded via a namespace (and not attached):

```
[1] GO.db_2.8.0          GOSemSim_1.16.0
[3] IRanges_1.16.0      MASS_7.3-21
[5] RColorBrewer_1.0-5  colorspace_1.1-1
[7] dichromat_1.2-4     digest_0.5.2
[9] grid_2.15.1         gtable_0.1.1
[11] igraph_0.6-2        labeling_0.1
[13] memoise_0.1         munsell_0.4
[15] parallel_2.15.1     plyr_1.7.1
[17] proto_0.3-9.2       qvalue_1.32.0
[19] reshape2_1.2.1     scales_0.2.2
[21] stats4_2.15.1       stringr_0.6.1
```

References

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