

goTools

November 11, 2009

R topics documented:

| | |
|--------------------|---|
| goTools | 1 |
| Internal functions | 2 |
| goTools | 2 |
| probeID | 3 |

| | |
|--------------|----------|
| Index | 4 |
|--------------|----------|

| | |
|---------|---------------------------------|
| goTools | <i>Reference GO nodes list.</i> |
|---------|---------------------------------|

Description

The function `EndNodeList` builds the default end node list used in `ontoCompare`. `CustomEndNodeList` helps you build a list of children nodes starting from a GO id of interest.

Usage

```
EndNodeList()  
CustomEndNodeList(id, rank=1)
```

Arguments

| | |
|-------------------|--|
| <code>id</code> | Valid GO id: "GO:XXXXXXX". |
| <code>rank</code> | Number of levels of children of the GO DAG under <code>id</code> you want to add to your nodes list. |

Value

`EndNodeList` returns a vector of all GO ids 1 level below `MF("GO:0003674")`, `BP("GO:0008150")` and `CC("GO:0005575")`. MF, BP and CC nodes are included. `CustomEndNodeList` returns a vector of all GO ids children of `id`, `rank` levels below it.

Author(s)

Yee Hwa (Jean) Yang, Agnes Paquet

See Also

[ontoCompare](#)

Examples

```
## Examples use the probeID dataset. For description type ? probeID.
## library(GO.db)
## EndNodeList()
## MFendnode <- CustomEndNodeList("GO:0003674", rank=2)

## Example (not run)
## data(probeID)
## ontoCompare(affylist, probeType="hgu133a", endnode=MFendnode, goType="MF")
```

Internal functions *Internal goTools functions*

Description

Internal goTools functions

Details

These are not to be called by the user.

goTools *Wrapper functions*

Description

This functions will allow you to describe and compare sets of oligo ids using Gene Ontology database

Usage

```
ontoCompare(genelist, probeType=c("GO", "hgu133a"),
goType="All", endnode, method=c("TGenes", "TIDS", "none"), plot=FALSE,
...)

ontoPlot(objM, beside=TRUE, las=2, legend.text=TRUE, ...)
```

Arguments

| | |
|-----------|--|
| genelist | list of list of valid probe ids. |
| method | method used to evaluate the percentage of oligos for each end-node. 'TGenes' = for each end node, return the number of direct children found / total number of probe ids. (default). This includes oligos which do not have GO annotations. 'TIDS' = for each end node, return the number of direct children found / total number of GO ids describing the list. 'none' = for each end node, return the number of direct children found. |
| probeType | type of input given to the function. Valid probe types include GO ids and any probes ids for which a BioC annotation package providing a mapping to GO is available. ontoCompare is expecting valid probe ids. |
| goType | help sort the data by type. If 'All' (default), all oligos are taken into account. 'BP' restricts information to Biological Process, 'CC' to Cellular Component, and 'MF' to Molecular Function. |
| plot | logical: if 'TRUE', results are output as a graph. |
| endnode | list of GO ids corresponding to end-nodes of interest. |
| objM | results from ontoCompare. |
| ... | extra layout parameters to be passed to ontoPlot. |

Value

Returns the percentage of probes children of nodes contained in endnode. If 'plot' = TRUE, results are plotted as a pie chart or a bargraph.

Author(s)

Yee Hwa (Jean) Yang, Agnes Paquet

Examples

```
# Examples use the probeID dataset. For description type ?probeID.
# Not run

#library(GO.db)
#data(probeID)
#ontoCompare(affylist, probeType="hgu133a", plot=TRUE)
#res <- ontoCompare(operonlist["L1"], probeType="operon", method="TIDS")
#ontoPlot(res, cex=0.7)
```

| | |
|---------|---|
| probeID | <i>List of probe ids from Affymetrix hgu133a chip and Operon Version 2 Human oligos</i> |
|---------|---|

Description

The probeID dataset consists of two lists of randomly chosen probe Ids. affylist contains 3 sets of ids from Affymetrix hgu133a. operonlist contains 2 sets of ids from Operon Version 2.

Usage

```
data(probeID)
```

Index

- *Topic **datasets**
 - probeID, 3
- *Topic **file**
 - goTools, 1, 2
- *Topic **hplot**
 - goTools, 2
- *Topic **manip**
 - goTools, 1
- *Topic **methods**
 - Internal functions, 2

affylist (*probeID*), 3

CustomEndNodeList (*goTools*), 1

EndNodeList (*goTools*), 1

getGOID (*Internal functions*), 2

getOntology (*Internal functions*),
2

goChildren (*Internal functions*), 2

goParents (*Internal functions*), 2

goTools, 1, 2

Internal functions, 2

isEndNode (*Internal functions*), 2

ontoCompare, 1

ontoCompare (*goTools*), 2

ontoCompare.main (*Internal functions*), 2

ontoPlot (*goTools*), 2

operonlist (*probeID*), 3

parentsVectWrapper (*Internal functions*), 2

probeID, 3