Package 'goTools'

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Title Functions for Gene Ontology database

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biocViews Microarray,GO,Visualization

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Description Wraper functions for description/comparison of oligo ID list using Gene Ontology database

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EndNodeList *Reference GO nodes list.*

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

id	Valid GO id: "GO:XXXXXXX".
rank	Number of levels of children of the GO DAG under id 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)

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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")
```

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, names.arg=NULL,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.
beside	Logical. If 'TRUE', the bars of the barplot are portrayed as juxtaposed bars. See ?barplot for more details.
las	numeric: if las=2, the axis labels are displayed perpendicular to the axis. See ?par for more details.
legend.text	vector of text used to construct a legend for the plot. See ?barplot for more details.
objM	results from ontoCompare.
names.arg	Labels to use in ontoPlot.
...	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)
```

Internal functions *Internal goTools functions*

Description

Internal goTools functions

Details

These are not to be called by the user.

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probeID *List of probe ids from Affymetrix hgu133a chip and Operon Version 2 Human oligos*

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)
```

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