Package ‘goTools’

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Title Functions for Gene Ontology database

Depends GO.db

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Suggests hgu133a.db

biocViews Microarray,GO,Visualization

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

License GPL-2

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Contents

`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.

`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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