goTools
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goTools
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:xxxxxxxx".

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)

Yee Hwa (Jean) Yang, Agnes Paquet

See Also

ontoCompare
Examples

```r
## 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.

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goTools Wrapper functions

Description

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

Usage

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

```r
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.
probeID

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)
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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  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.

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