Package ‘goTools’

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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 function 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)
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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)

________________________________________________________

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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