Package ‘goTools’

March 28, 2017

Version 1.48.0  
Date 2009-10-23  
Title Functions for Gene Ontology database  
Depends GO.db  
Imports AnnotationDbi, GO.db, graphics, grDevices  
Suggests hgu133a.db  
biocViews Microarray, GO, Visualization  
Author Yee Hwa (Jean) Yang <jean@biostat.ucsf.edu>, Agnes Paquet <paquetagnes@yahoo.com>  
Maintainer Agnes Paquet <paquetagnes@yahoo.com>  
Description Wrapper functions for description/comparison of oligo ID list using Gene Ontology database  
License GPL-2  
LazyLoad yes  
NeedsCompilation no

R topics documented:

EndNodeList ......................................................... 1  
goTools .......................................................... 2  
Internal functions ................................................. 4  
probeID ............................................................ 4

Index  5

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)

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")

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)
<table>
<thead>
<tr>
<th>Internal functions</th>
<th>Internal goTools functions</th>
</tr>
</thead>
</table>

**Description**

Internal goTools functions

**Details**

These are not to be called by the user.

<table>
<thead>
<tr>
<th>probeID</th>
<th>List of probe ids from Affymetrix hgu133a chip and Operon Version 2 Human oligos</th>
</tr>
</thead>
</table>

**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, 4
*Topic file
  EndNodeList, 1
gotoTools, 2
*Topic hplot
gotoTools, 2
*Topic manip
  EndNodeList, 1
*Topic methods
  Internal functions, 4

affylist (probeID), 4

CustomEndNodeList (EndNodeList), 1

EndNodeList, 1

gtGOID (Internal functions), 4
gtOntology (Internal functions), 4
goChildren (Internal functions), 4
goParents (Internal functions), 4
goTools, 2

Internal functions, 4

isEndNode (Internal functions), 4

ontoCompare, 1, 2
ontoCompare (gotoTools), 2
ontoCompare.main (Internal functions), 4
ontoPlot (gotoTools), 2
operonlist (probeID), 4

parentsVectorWrapper (Internal functions), 4

probeID, 4