goTools
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- 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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>id</td>
<td>Valid GO id: &quot;GO:XXXXXXX&quot;.</td>
</tr>
<tr>
<td>rank</td>
<td>Number of levels of children of the GO DAG under id you want to add to your nodes list.</td>
</tr>
</tbody>
</table>

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.

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, ...)
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.
- **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)**

Yee Hwa (Jean) Yang, Agnes Paquet

**Examples**

```r
# 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)
```

**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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