

# Package ‘goTools’

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**Title** Functions for Gene Ontology database

**Depends** GO.db

**Imports** AnnotationDbi, GO.db, graphics, grDevices

**Suggests** hgu133a.db

**biocViews** Microarray,GO,Visualization

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

**License** GPL-2

**LazyLoad** yes

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## R topics documented:

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EndNodeList

*Reference GO nodes list.*

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### 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

|                   |   |
|-------------------|---|
| <code>id</code>   | Valid GO id: "GO:XXXXXXXX".   |
| <code>rank</code> | 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)
```

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Internal functions      *Internal goTools functions*

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**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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