

# Package ‘goTools’

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**Title** Functions for Gene Ontology database

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**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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EndNodeList	<i>Reference GO nodes list.</i>
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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 <code>id</code> 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*

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**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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