

# goTools

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goTools

*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 <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")
```

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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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goTools *Wrapper functions*

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**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, 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**

```
# 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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|         |   |
|---------|---|
| probeID | <i>List of probe ids from Affymetrix hgu133a chip and Operon Version 2 Human oligos</i> |
|---------|---|

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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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