

Package ‘geneListPie’

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Type Package

Title Profiling a gene list into GOSlim or KEGG function pie

Version 1.0

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Description “geneListPie” package is for mapping a gene list to function categories defined in GOSlim or Kegg. The results can be plotted as a pie chart to provide a quick view of the genes distribution of the gene list among the function categories. The gene list must contain a list of gene symbols. The package contains a set of pre-processed gene sets obtained from Gene Ontology and MSigDB including human, mouse, rat and yeast. To provide a high level concise view, only GO slim and kegg are provided. The gene sets are regularly updated. User can also use customized gene sets. User can use the R Pie() or Pie3D() function for plotting the pie chart. Users can also choose to output the gene function mapping results and use external software such as Excel(R) for plotting.

Suggests plotrix

License GPL-3

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geneListPie-package *Profiling a gene list into GOSlim or KEGG function pie*

Description

geneListPie package is for mapping a gene list to function categories defined in GOSlim or Kegg. The results can be plotted as a pie chart to provide a quick view of the genes distribution of the gene list among the function categories. The gene list must contain a list of gene symbols. The package contains a set of pre-processed gene sets obtained from Gene Ontology and MSigDB including human, mouse, rat and yeast. To provide a high level concise view, only GO slim and kegg are provided. The gene sets are regularly updated. User can also use customized gene sets. User can use the R Pie() or Pie3D() function for plotting the pie chart. Users can also choose to output the gene function mapping results and use external software such as Excel(R) for plotting.

Details

Package:	geneListPie
Type:	Package
Version:	1.0
Date:	2009-10-06
License:	GPL-3
LazyLoad:	yes

load.genelist() to load a list of gene symbols from a text file.

load.genesets() to load customized gene sets from a file. Otherwise use pre-packaged gene sets

including gene sets from Human, Mouse, Rat, and Yeast for Biological Processes, Molecular Functions, and Cellular Components.

```
goslim.human.all
goslim.human.BP
goslim.human.CC
goslim.human.MF
goslim.mouse.all
goslim.mouse.BP
goslim.mouse.CC
goslim.mouse.MF
goslim.rat.all
goslim.rat.BP
goslim.rat.CC
goslim.rat.MF
goslim.yeast.all
goslim.yeast.BP
goslim.yeast.CC
goslim.yeast.MF
kegg2.5.generic
```

geneListProfile() will then generates the results for plotting function distribution or pie.
printGeneListProfile() can be used for generating mapping results in text format

Author(s)

Xutao Deng

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References

Gene Ontology <http://www.geneontology.org/> MSigDB <http://www.broadinstitute.org/gsea/msigdb/>

Examples

```
data(goslim.human.BP)
glist<-c("ABCB7", "ABCF1", "ABHD2", "ACAD9", "ACIN1", "AMOTL1", "ANLN", "ANXA4", "APBA2", "APBA3", "BAI3", "BCLAF1", "BEST1", "BHLHE40", "BHLHE41", "BHLHE42", "BHLHE43", "BHLHE44", "BHLHE45", "BHLHE46", "BHLHE47", "BHLHE48", "BHLHE49", "BHLHE50", "BHLHE51", "BHLHE52", "BHLHE53", "BHLHE54", "BHLHE55", "BHLHE56", "BHLHE57", "BHLHE58", "BHLHE59", "BHLHE60", "BHLHE61", "BHLHE62", "BHLHE63", "BHLHE64", "BHLHE65", "BHLHE66", "BHLHE67", "BHLHE68", "BHLHE69", "BHLHE70", "BHLHE71", "BHLHE72", "BHLHE73", "BHLHE74", "BHLHE75", "BHLHE76", "BHLHE77", "BHLHE78", "BHLHE79", "BHLHE80", "BHLHE81", "BHLHE82", "BHLHE83", "BHLHE84", "BHLHE85", "BHLHE86", "BHLHE87", "BHLHE88", "BHLHE89", "BHLHE90", "BHLHE91", "BHLHE92", "BHLHE93", "BHLHE94", "BHLHE95", "BHLHE96", "BHLHE97", "BHLHE98", "BHLHE99", "BHLHE100")
r<-geneListProfile(goslim.human.BP, glist, threshold=1)
labels<-sub("_", "__", r$labels) #remove the GO id labels for display, optional
labels<-sub(".*_", "", labels)
pie(r$sizes, labels=labels, main="GO Slim Biological Process Mapping")

##prepare a gene list in a single column or row
#glist<-load.genelist("genelist.txt", format="column")
##this is how to load a customize gene set in a file
#gs<-load.genesets("customized-genesets.txt")
#r<-geneListProfile(gs, glist, threshold=5)
```

```
#library(plotrix)
#pie3D(r$sizes,labels=r$labels, main="customized Mapping")
#printGeneListProfile(r)
```

geneListProfile	<i>Profiling a gene list against gene sets</i>
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Description

number is the number of overlapping genes between the gene list and the gene set.

Usage

```
geneListProfile(gs, glist, threshold = 10)
```

Arguments

gs	gene sets, use prepackaged or user loaded
glist	gene list loaded by user
threshold	specify the minimum number of overlapping genes in a gene set to output. This is to avoid displaying gene sets with very few overlapping genes. For each gene set, if the number of overlapping genes is smaller than the threshold, the set of overlapping genes will be combined to a gene set labeled "Others"

Value

labels	the labels of the gene sets
sizes	the number of overlapping genes of gene sets against gene list
symbols	the gene symbols of overlapping genes

Author(s)

Xutao Deng

Examples

```
data(goslim.human.BP)
glist<-c("ABCB7","ABCF1","ABHD2","ACAD9","ACIN1","AMOTL1","ANLN","ANXA4","APBA2","APBA3","BAI3","BCLAF1","BEST
r<-geneListProfile(goslim.human.BP, glist, threshold=1)
labels<-sub("_", "__", r$labels) #remove the GO id labels for display, optional
labels<-sub(".*__", "", labels)
pie(r$sizes,labels=labels, main="GO Slim Biological Process Mapping")
```

`goslim.human.all` *goslim.human.all*

Description

The data set is pre-loaded using `load.genesets()` function from MSigDB text format

Usage

```
data(goslim.human.all)
```

Examples

```
data(goslim.human.all)
```

`goslim.human.BP` *goslim.human.BP*

Description

The data set is pre-loaded using `load.genesets()` function from MSigDB text format

Usage

```
data(goslim.human.BP)
```

Examples

```
data(goslim.human.BP)
```

`goslim.human.CC` *goslim.human.CC*

Description

The data set is pre-loaded using `load.genesets()` function from MSigDB text format

Usage

```
data(goslim.human.CC)
```

Examples

```
data(goslim.human.CC)
```

<code>goslim.human.MF</code>	<i>goslim.human.MF</i>
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Description

The data set is pre-loaded using `load.genesets()` function from MSigDB text format

Usage

```
data(goslim.human.MF)
```

Examples

```
data(goslim.human.MF)
```

<code>goslim.mouse.all</code>	<i>goslim.mouse.all</i>
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Description

The data set is pre-loaded using `load.genesets()` function from MSigDB text format

Usage

```
data(goslim.mouse.all)
```

Examples

```
data(goslim.mouse.all)
```

<code>goslim.mouse.BP</code>	<i>goslim.mouse.BP</i>
------------------------------	------------------------

Description

The data set is pre-loaded using `load.genesets()` function from MSigDB text format

Usage

```
data(goslim.mouse.BP)
```

Examples

```
data(goslim.mouse.BP)
```

`goslim.mouse.CC` *goslim.mouse.CC*

Description

The data set is pre-loaded using `load.genesets()` function from MSigDB text format

Usage

```
data(goslim.mouse.CC)
```

Examples

```
data(goslim.mouse.CC)
```

`goslim.mouse.MF` *goslim.mouse.MF*

Description

The data set is pre-loaded using `load.genesets()` function from MSigDB text format

Usage

```
data(goslim.mouse.MF)
```

Examples

```
data(goslim.mouse.MF)
```

`goslim.rat.all` *goslim.rat.all*

Description

The data set is pre-loaded using `load.genesets()` function from MSigDB text format

Usage

```
data(goslim.rat.all)
```

Examples

```
data(goslim.rat.all)
```

<code>goslim.rat.BP</code>	<i>goslim.rat.BP</i>
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Description

The data set is pre-loaded using `load.genesets()` function from MSigDB text format

Usage

```
data(goslim.rat.BP)
```

Examples

```
data(goslim.rat.BP)
```

<code>goslim.rat.CC</code>	<i>goslim.rat.CC</i>
----------------------------	----------------------

Description

The data set is pre-loaded using `load.genesets()` function from MSigDB text format

Usage

```
data(goslim.rat.CC)
```

Examples

```
data(goslim.rat.CC)
```

<code>goslim.rat.MF</code>	<i>goslim.rat.MF</i>
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Description

The data set is pre-loaded using `load.genesets()` function from MSigDB text format

Usage

```
data(goslim.rat.MF)
```

Examples

```
data(goslim.rat.MF)
```

`goslim.yeast.all` *goslim.yeast.all*

Description

The data set is pre-loaded using `load.genesets()` function from MSigDB text format

Usage

```
data(goslim.yeast.all)
```

Examples

```
data(goslim.yeast.all)
```

`goslim.yeast.BP` *goslim.yeast.BP*

Description

The data set is pre-loaded using `load.genesets()` function from MSigDB text format

Usage

```
data(goslim.yeast.BP)
```

Examples

```
data(goslim.yeast.BP)
```

`goslim.yeast.CC` *goslim.yeast.CC*

Description

The data set is pre-loaded using `load.genesets()` function from MSigDB text format

Usage

```
data(goslim.yeast.CC)
```

Examples

```
data(goslim.yeast.CC)
```

goslim.yeast.MF	<i>goslim.yeast.MF</i>
-----------------	------------------------

Description

The data set is pre-loaded using load.genesets() function from MSigDB text format

Usage

```
data(goslim.yeast.MF)
```

Examples

```
data(goslim.yeast.MF)
```

kegg2.5.generic	<i>kegg2.5.generic</i>
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Description

The data set is pre-loaded using load.genesets() function from MSigDB text format

Usage

```
data(kegg2.5.generic)
```

Examples

```
data(kegg2.5.generic)
```

load.genelist	<i>load a gene list into workspace</i>
---------------	--

Description

load a gene list consisting of a set of symbols; return a character vector

Usage

```
load.genelist(file = "genelist.txt", format = "column", sep = "\t")
```

Arguments

file	file name
format	"row" or "column"
sep	default separator is tab

Details

The list can be either in a row or a column. If in a row format, separator needs to be specified

Value

return a character vector consisting of the gene symbols in the list

Author(s)

Xutao Deng

load.genesets

Load customized gene sets into work space

Description

Load customized gene sets into work space. Pre-packaged genesets can also be used

goslim.human.all
goslim.human.BP
goslim.human.CC
goslim.human.MF
goslim.mouse.all
goslim.mouse.BP
goslim.mouse.CC
goslim.mouse.MF
goslim.rat.all
goslim.rat.BP
goslim.rat.CC
goslim.rat.MF
goslim.yeast.all
goslim.yeast.BP
goslim.yeast.CC
goslim.yeast.MF
kegg2.5.generic

Usage

```
load.genesets(file = "geneset.gmt.txt")
```

Arguments

file file name of customized gene sets in MSigDB format. <http://www.broadinstitute.org/gsea/msigdb/>

Value

A character vector of length the number of lines read. Each line is a gene set.

Author(s)

Xutao Deng

printGeneListProfile *Print the profiling results*

Description

Print the results from geneListProfile(). The printing format can be MSigDB or 2 column (Gene_Set, number) format, where Gene_Set is the name of a gene set and number is the number of overlapping genes between the gene list and the gene set. In the MSigDB format the output contains all the overlapping gene symbols. The output can be stdin or directed to a file.

Usage

```
printGeneListProfile(r, file = "", format = NULL)
```

Arguments

r profiling mapping results from geneListProfile
file filename, default to stdin
format "MSigDB" format or NULL

Author(s)

Xutao Deng

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