Package ‘clusterProfiler’

December 21, 2016

Type Package
Title statistical analysis and visualization of functional profiles for genes and gene clusters
Version 3.2.8
Maintainer Guangchuang Yu <guangchuangyu@gmail.com>
Description This package implements methods to analyze and visualize functional profiles (GO and KEGG) of gene and gene clusters.
Depends R (>= 3.3.1), DOSE (>= 3.0.1)
Imports AnnotationDbi, ggplot2, GO.db, GOSemSim (>= 2.0.0), IRanges, magrittr, methods, plyr, qvalue, stats, stats4, tidyR, utils
Suggests AnnotationHub, BiocStyle, GSEABase, KEGG.db, knitr, org.Hs.evg.db, pathview, ReactomePA, testthat, topGO
VignetteBuilder knitr
ByteCompile true
License Artistic-2.0
URL https://guangchuangyu.github.io/clusterProfiler
BugReports https://github.com/GuangchuangYu/clusterProfiler/issues
biocViews Annotation, Clustering, GeneSetEnrichment, GO, KEGG, MultipleComparison, Pathways, Reactome, Visualization
RoxygenNote 5.0.1
NeedsCompilation no
Author Guangchuang Yu [aut, cre], Li-Gen Wang [ctb], Giovanni Dall’Olio [ctb] (formula interface of compareCluster)

R topics documented:

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clusterProfiler-package

statistical analysis and visualization of functional profiles for genes and gene clusters. The package implements methods to analyze and visualize functional profiles of gene and gene clusters.

Description

This package is designed to compare gene clusters functional profiles.

Details

Package: clusterProfiler
Type: Package
Version: 1.9.
Date: 06-13-2013
biocViews: GO, Clustering, Visualization
Depends: AnnotationDbi, GO.db, org.Hs.eg.db, ggplot2, plyr, methods
Description

Biological Id TRanslator

Usage

bitr(geneID, fromType, toType, OrgDb, drop = TRUE)

Arguments

geneID: input gene id
fromType: input id type
toType: output id type
OrgDb: annotation db
drop: drop NA or not

Value

data.frame

Author(s)

Guangchuang Yu
browseKEGG

bitr_kegg

Description
convert biological ID using KEGG API

Usage
bitr_kegg(geneID, fromType, toType, organism, drop = TRUE)

Arguments
geneID input gene id
fromType input id type
toType output id type
organism supported organism, can be search using search_kegg_organism function
drop drop NA or not

Value
data.frame

Author(s)
Guangchuang Yu

browseKEGG

Description
open KEGG pathway with web browser

Usage
browseKEGG(x, pathID)

Arguments
x an instance of enrichResult or gseaResult
pathID pathway ID

Value
url

Author(s)
Guangchuang Yu
buildGOmap

Description
building GO mapping files

Usage
buildGOmap(gomap)

Arguments
gomap data.frame with two columns of GO and gene ID

Details
provided by a data.frame of GO (column 1) and gene (column 2) direct annotation this function will building gene to GO and GO to gene mapping, with directly and indirectly (ancestor GO term) annotation.

Value
data.frame, GO annotation with indirect annotation

Author(s)
Yu Guangchuang

compareCluster

Compare gene clusters functional profile

Description
Given a list of gene set, this function will compute profiles of each gene cluster.

Usage
compareCluster(geneClusters, fun = "enrichGO", data = "", ...)

Arguments
geneClusters a list of entrez gene id. Alternatively, a formula of type Entrez~group
fun One of "groupGO", "enrichGO", "enrichKEGG", "enrichDO" or "enrichPathway".
data if geneClusters is a formula, the data from which the clusters must be extracted.
... Other arguments.
Value

A `clusterProfResult` instance.

Author(s)

Guangchuang Yu [https://guangchuangyu.github.io](https://guangchuangyu.github.io)

See Also

`compareClusterResult-class`, `groupGO enrichGO`

Examples

```r
## Not run:
data(gcSample)
xx <- compareCluster(gcSample, fun="enrichKEGG",
                     organism="hsa", pvalueCutoff=0.05)
as.data.frame(xx)
# plot(xx, type="dot", caption="KEGG Enrichment Comparison")
## formula interface
mydf <- data.frame(Entrez=c(1, 100, 1000, 100101467,
                            100127206, 100128071),
                   group = c("A", "A", "A", "B", "B"),
                   othergroup = c("good", "good", "bad", "bad", "good", "bad"))
xx.formula <- compareCluster(Entrez~group, data=mydf,
                             fun='groupGO', OrgDb='org.Hs.eg.db')
as.data.frame(xx.formula)
## formula interface with more than one grouping variable
xx.formula.twogroups <- compareCluster(Entrez~group+othergroup, data=mydf,
                                        fun='groupGO', OrgDb='org.Hs.eg.db')
as.data.frame(xx.formula.twogroups)
## End(Not run)
```

---

**compareClusterResult-class**

This class represents the comparison result of gene clusters by GO categories at specific level or GO enrichment analysis.

Description

Class "compareClusterResult" This class represents the comparison result of gene clusters by GO categories at specific level or GO enrichment analysis.

Slots

- `compareClusterResult` cluster comparing result
- `geneClusters` a list of genes
- `fun` one of `groupGO`, `enrichGO` and `enrichKEGG`
- `.call` function call
Author(s)

Guangchuang Yu https://guangchuangyu.github.io

See Also

groupGOResult enrichResult compareCluster

dataset

Datasets gcSample contains a sample of gene clusters.
Datasets kegg_species contains kegg species information

dotplot, compareClusterResult-method

dotplot

Description

dot plot method

Usage

## S4 method for signature 'compareClusterResult'
dotplot(object, x = ~Cluster,
colorBy = "p.adjust", showCategory = 5, by = "geneRatio",
category = NULL, includeAll = TRUE, font.size = 12, title = "")

Arguments

object compareClusterResult object
x x variable
colorBy one of pvalue or p.adjust
showCategory category numbers
by one of geneRatio, Percentage or count
category ONTOLOGY or NULL
includeAll logical
font.size font size
title figure title
download KEgg

download KEgg

Description

download the latest version of KEGG pathway/module

Usage

```r
download KEgg(species, keggType = "KEGG", keyType = "kegg")
```

Arguments

- `species`: species
- `keggType`: one of 'KEGG' or 'MKEGG'
- `keyType`: supported keyType, see bitr_kegg

Value

list

Author(s)

Guangchuang Yu

---

dropGO

dropGO

Description

drop GO term of specific level or specific terms (mostly too general).

Usage

```r
dropGO(x, level = NULL, term = NULL)
```

Arguments

- `x`: an instance of 'enrichResult' or 'compareClusterResult'
- `level`: GO level
- `term`: GO term

Value

modified version of `x`

Author(s)

Guangchuang Yu
Description

enrichment analysis by DAVID

Usage

enrichDAVID(gene, idType = "ENTREZ_GENE_ID", listType = "Gene", 
minGSSize = 10, maxGSSize = 500, annotation = "GOTERM_BP_FAT", 
pvalueCutoff = 0.05, pAdjustMethod = "BH", qvalueCutoff = 0.2, 
species = NA, david.user)

Arguments

gene input gene
idType id type
listType list Type
minGSSize minimal size of genes annotated for testing
maxGSSize maximal size of genes annotated for testing
annotation david annotation
pvalueCutoff pvalueCutoff
pAdjustMethod one of "BH" and "bonferroni"
qvalueCutoff qvalutCutoff
species species
david.user david user

Value

A enrichResult instance

Author(s)

Guangchuang Yu
enricher

Description
A universal enrichment analyzer

Usage
enricher(gene, pvalueCutoff = 0.05, pAdjustMethod = "BH", universe,
minGSSize = 10, maxGSSize = 500, qvalueCutoff = 0.2, TERM2GENE,
TERM2NAME = NA)

Arguments
gene a vector of gene id
pvalueCutoff pvalue cutoff
pAdjustMethod one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
universe background genes
minGSSize minimal size of genes annotated for testing
maxGSSize maximal size of genes annotated for testing
qvalueCutoff qvalue cutoff
TERM2GENE user input annotation of TERM TO GENE mapping, a data.frame of 2 column
with term and gene
TERM2NAME user input of TERM TO NAME mapping, a data.frame of 2 column with term
and name

Value
A enrichResult instance

Author(s)
Guangchuang Yu

enrichGO

Description
GO Enrichment Analysis of a gene set. Given a vector of genes, this function will return the enrichment GO categories after FDR control.

Usage
enrichGO(gene, OrgDb, keytype = "ENTREZID", ont = "MF",
pvalueCutoff = 0.05, pAdjustMethod = "BH", universe, qvalueCutoff = 0.2,
minGSSize = 10, maxGSSize = 500, readable = FALSE)
**enrichKEGG**

**Arguments**

- `gene`: a vector of entrez gene id.
- `OrgDb`: `OrgDb`
- `keytype`: keytype of input gene
- `ont`: One of "MF", "BP", and "CC" subontologies.
- `pvalueCutoff`: Cutoff value of pvalue.
- `pAdjustMethod`: one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
- `universe`: background genes
- `qvalueCutoff`: qvalue cutoff
- `minGSSize`: minimal size of genes annotated by Ontology term for testing.
- `maxGSSize`: maximal size of genes annotated for testing
- `readable`: whether mapping gene ID to gene Name

**Value**

An `enrichResult` instance.

**Author(s)**

Guangchuang Yu [http://ygc.name](http://ygc.name)

**See Also**

`enrichResult-class`, `compareCluster`

**Examples**

```r
## Not run:
data(geneList)
de <- names(geneList)[1:100]
yy <- enrichKEGG(de, 'org.Hs.eg.db', ont="BP", pvalueCutoff=0.01)
head(yy)
## End(Not run)
```

**Description**

KEGG Enrichment Analysis of a gene set. Given a vector of genes, this function will return the enrichment KEGG categories with FDR control.

**Usage**

```r
enrichKEGG(gene, organism = "hsa", keyType = "kegg", pvalueCutoff = 0.05, 
pAdjustMethod = "BH", universe, minGSSize = 10, maxGSSize = 500, 
quvalueCutoff = 0.2, use_internal_data = FALSE)
```
Arguments

gene a vector of entrez gene id.
organism supported organism listed in 'http://www.genome.jp/kegg/catalog/org_list.html'
keyType one of "kegg", 'ncbi-geneid', 'ncib-proteinid' and 'uniprot'
pvalueCutoff Cutoff value of pvalue.
pAdjustMethod one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
universe background genes
minGSSize minimal size of genes annotated by Ontology term for testing.
maxGSSize maximal size of genes annotated for testing
qvalueCutoff qvalue cutoff
use_internal_data logical, use KEGG.db or latest online KEGG data

Value
A enrichResult instance.

Author(s)
Guangchuang Yu http://ygc.name

See Also
enrichResult-class, compareCluster

Examples

data(gcSample)
yy = enrichKEGG(gcSample[[5]], pvalueCutoff=0.01)
head(summary(yy))
#plot(yy)

---

enrichMKEGG

**KEGG Module Enrichment Analysis of a gene set. Given a vector of genes, this function will return the enrichment KEGG Module categories with FDR control.**

Description

KEGG Module Enrichment Analysis of a gene set. Given a vector of genes, this function will return the enrichment KEGG Module categories with FDR control.

Usage

enrichMKEGG(gene, organism = "hsa", keyType = "kegg", pvalueCutoff = 0.05, pAdjustMethod = "BH", universe, minGSSize = 10, maxGSSize = 500, qvalueCutoff = 0.2)
Arguments

gene  a vector of entrez gene id.
organism supported organism listed in 'http://www.genome.jp/kegg/catalog/org_list.html'
keyType  one of "kegg", 'ncbi-geneid', 'ncib-proteinid' and 'uniprot'
pvalueCutoff  Cutoff value of pvalue.
pAdjustMethod one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
universe  background genes
minGSSize  minimal size of genes annotated by Ontology term for testing.
maxGSSize  maximal size of genes annotated for testing
qvalueCutoff  qvalue cutoff

Value

A enrichResult instance.

Description

convert compareClusterResult to a data.frame that ready for plot

Usage

## S3 method for class 'compareClusterResult'
fortify(model, data, showCategory = 5,
        by = "geneRatio", category = NULL, includeAll = TRUE)

Arguments

model  compareClusterResult object
data  not use here
showCategory  category numbers
by  one of geneRatio, Percentage or count
category  ONTOLOGY or NULL
includeAll  logical

Value

data.frame

Author(s)

Guangchuang Yu
**getGOLevel**  
*get GOIDs at a specific level*

**Description**  
query GOIDs at a specific level.

**Usage**  
getGOLevel(ont, level)

**Arguments**  
- **ont**: Ontology
- **level**: GO level

**Value**  
a vector of GOIDs

**Author(s)**  
Guangchuang Yu [http://guangchuangyu.github.io](http://guangchuangyu.github.io)

---

**Gff2GeneTable**  
*Gff2GeneTable*

**Description**  
read GFF file and build gene information table

**Usage**  
Gff2GeneTable(gffFile, compress = TRUE)

**Arguments**  
- **gffFile**: GFF file
- **compress**: compress file or not

**Details**  
given a GFF file, this function extracts information from it and save it in working directory

**Value**  
file save.

**Author(s)**  
Yu Guangchuang
go2ont

Description
convert goid to ontology (BP, CC, MF)

Usage
go2ont(goid)

Arguments
  goid  a vector of GO IDs

Value
data.frame

Author(s)
Guangchuang Yu

---

go2term

Description
convert goid to descriptive term

Usage
go2term(goid)

Arguments
  goid  a vector of GO IDs

Value
data.frame

Author(s)
Guangchuang Yu
gofilter

Description
filter GO enriched result at specific level

Usage
gofilter(x, level = 4)

Arguments
x          output from enrichGO or compareCluster
level      GO level

Value
updated object

Author(s)
Guangchuang Yu

---

groupGO

Functional Profile of a gene set at specific GO level. Given a vector of genes, this function will return the GO profile at a specific level.

Usage
groupGO(gene, OrgDb, keytype = "ENTREZID", ont = "CC", level = 2,
readable = FALSE)

Arguments
gene         a vector of entrez gene id.
OrgDb        OrgDb
keytype      keytype of input gene
ont          One of "MF", "BP", and "CC" subontologies.
level        Specific GO Level.
readable     if readable is TRUE, the gene IDs will mapping to gene symbols.
Value

A groupGOResult instance.

Author(s)

Guangchuang Yu http://ygc.name

See Also

groupGOResult-class, compareCluster

Examples

data(gcSample)
yy <- groupGO(gcSample[[1]], 'org.Hs.eg.db', ont="BP", level=2)
head(summary(yy))
#plot(yy)

---

Class "groupGOResult" This class represents the result of functional Profiles of a set of gene at specific GO level.

Description

Class "groupGOResult" This class represents the result of functional Profiles of a set of gene at specific GO level.

Slots

result  GO classification result
ontology  Ontology
level  GO level
organism  one of "human", "mouse" and "yeast"
gene  Gene IDs
readable  logical flag of gene ID in symbol or not.

Author(s)

Guangchuang Yu http://ygc.name

See Also

compareClusterResult compareCluster groupGO
GSEA

Description

a universal gene set enrichment analysis tool

Usage

GSEA(geneList, exponent = 1, nPerm = 1000, minGSSize = 10,
maxGSSize = 500, pvalueCutoff = 0.05, pAdjustMethod = "BH", TERM2GENE,
TERM2NAME = NA, verbose = TRUE, seed = FALSE, by = "fgsea")

Arguments

geneList | order ranked geneList
exponent | weight of each step
nPerm | number of permutations
minGSSize | minimal size of each geneSet for analyzing
maxGSSize | maximal size of genes annotated for testing
pvalueCutoff | pvalue cutoff
pAdjustMethod | p value adjustment method
TERM2GENE | user input annotation of TERM TO GENE mapping, a data.frame of 2 column with term and gene
TERM2NAME | user input of TERM TO NAME mapping, a data.frame of 2 column with term and name
verbose | logical
seed | logical
by | one of ‘fgsea’ or ‘DOSE’

Value

gseaResult object

Author(s)

Guangchuang Yu
Description

Gene Set Enrichment Analysis of Gene Ontology

Usage

gseGO(geneList, ont = "BP", OrgDb, keytype = "ENTREZID", exponent = 1, 
nPerm = 1000, minGSSize = 10, maxGSSize = 500, pvalueCutoff = 0.05, 
pAdjustMethod = "BH", verbose = TRUE, seed = FALSE, by = "fgsea")

Arguments

geneList  order ranked geneList
ont        one of "BP", "MF", "CC" or "GO"
OrgDb      OrgDb
keytype    keytype of gene
exponent   weight of each step
nPerm      permutation numbers
minGSSize  minimal size of each geneSet for analyzing
maxGSSize  maximal size of genes annotated for testing
pvalueCutoff  pvalue Cutoff
pAdjustMethod  pvalue adjustment method
verbose    print message or not
seed       logical
by         one of ‘fgsea’ or ‘DOSE’

Value

gseaResult object

Author(s)

Yu Guangchuang
Description

Gene Set Enrichment Analysis of KEGG

Usage

gseKEGG(geneList, organism = "hsa", keyType = "kegg", exponent = 1,
        nPerm = 1000, minGSSize = 10, maxGSSize = 500, pvalueCutoff = 0.05,
        pAdjustMethod = "BH", verbose = TRUE, use_internal_data = FALSE,
        seed = FALSE, by = "fgsea")

Arguments

geneList          order ranked geneList
organism          supported organism listed in 'http://www.genome.jp/kegg/catalog/org_list.html'
keyType           one of "kegg", 'ncbi-geneid', 'ncib-proteinid' and 'uniprot'
exponent          weight of each step
nPerm              permutation numbers
minGSSize          minimal size of each geneSet for analyzing
maxGSSize          maximal size of genes annotated for testing
pvalueCutoff       pvalue Cutoff
pAdjustMethod      pvalue adjustment method
verbose            print message or not
use_internal_data  logical, use KEGG.db or latest online KEGG data
seed               logical
by                 one of 'fgsea' or 'DOSE'

Value

gseaResult object

Author(s)

Yu Guangchuang
Description

Gene Set Enrichment Analysis of KEGG Module

Usage

gseMKEGG(geneList, organism = "hsa", keyType = "kegg", exponent = 1,
        nPerm = 1000, minGSSize = 10, maxGSSize = 500, pvalueCutoff = 0.05,
        pAdjustMethod = "BH", verbose = TRUE, seed = FALSE, by = "fgsea")

Arguments

geneList          order ranked geneList
organism          supported organism listed in ’http://www.genome.jp/kegg/catalog/org_list.html’
keyType           one of "kegg", 'ncbi-geneid', 'ncib-proteinid' and 'uniprot'
exponent          weight of each step
nPerm             permutation numbers
minGSSize         minimal size of each geneSet for analyzing
maxGSSize         maximal size of genes annotated for testing
pvalueCutoff      pvalue Cutoff
pAdjustMethod     pvalue adjustment method
verbose           print message or not
seed              logical
by                one of ’fgsea’ or ’DOSE’

Value

gseaResult object

Author(s)

Yu Guangchuang
**idType**

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<th>Description</th>
<th>list ID types supported by annoDb</th>
</tr>
</thead>
<tbody>
<tr>
<td>Usage</td>
<td><code>idType(OrgDb = &quot;org.Hs.eg.db&quot;)</code></td>
</tr>
<tr>
<td>Arguments</td>
<td>OrgDb: annotation db</td>
</tr>
<tr>
<td>Value</td>
<td>character vector</td>
</tr>
<tr>
<td>Author(s)</td>
<td>Guangchuang Yu</td>
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</tbody>
</table>

**merge_result**

<table>
<thead>
<tr>
<th>Description</th>
<th>merge a list of enrichResult objects to compareClusterResult</th>
</tr>
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<tr>
<td>Usage</td>
<td><code>merge_result(enrichResultList)</code></td>
</tr>
<tr>
<td>Arguments</td>
<td>enrichResultList: a list of enrichResult objects</td>
</tr>
<tr>
<td>Value</td>
<td>a compareClusterResult instance</td>
</tr>
<tr>
<td>Author(s)</td>
<td>Guangchuang Yu</td>
</tr>
</tbody>
</table>
### plot

#### Description

plot method generics

#### Usage

```r
## S4 method for signature 'compareClusterResult,ANY'
plot(x, type = "dot",
    colorBy = "p.adjust", showCategory = 5, by = "geneRatio",
    category = NULL, includeAll = TRUE, font.size = 12, title = "")
```

#### Arguments

- `x`: compareClusterResult object
- `type`: one of bar or dot
- `colorBy`: one of pvalue or p.adjust
- `showCategory`: category numbers
- `by`: one of geneRatio, Percentage or count
- `category`: ONTOLOGY or NULL
- `includeAll`: logical
- `font.size`: font size
- `title`: figure title
- `...`: Additional argument list

#### Value

plot

#### Author(s)

Guangchuang Yu [http://ygc.name](http://ygc.name)

---

### plotGOgraph

#### Description

plot GO graph

#### Usage

```r
plotGOgraph(x, firstSigNodes = 10, useInfo = "all", sigForAll = TRUE,
             useFullNames = TRUE, ...)
```
plotting.clusterProfile

Arguments

x output of enrichGO or gseGO
firstSigNodes number of significant nodes (rectangle nodes in the graph)
useInfo additional info
sigForAll if TRUE the score/p-value of all nodes in the DAG is shown, otherwise only score will be shown
useFullNames logical
... additional parameter of showSigOfNodes, please refer to topGO

Value

GO DAG graph

Author(s)

Guangchuang Yu

See Also

showSigOfNodes

Description

Internal plot function for plotting compareClusterResult

Usage

plotting.clusterProfile(clProf.reshape.df, x = ~Cluster, type = "dot",
colorBy = "p.adjust", by = "geneRatio", title = "", font.size = 12)

Arguments

clProf.reshape.df data frame of compareCluster result
x x variable
type one of dot and bar
colorBy one of pvalue or p.adjust
by one of percentage and count
title graph title
font.size graph font size

Value

ggplot object
**read.gmt**

**Author(s)**
Guangchuang Yu [http://ygc.name](http://ygc.name)

---

**Description**
parse gmt file to a data.frame

**Usage**

```r
read.gmt(gmtfile)
```

**Arguments**

- `gmtfile` gmt file

**Value**
data.frame

**Author(s)**
Guangchuang Yu

---

**search_kegg_organism**

**Description**
search kegg organism, listed in [http://www.genome.jp/kegg/catalog/org_list.html](http://www.genome.jp/kegg/catalog/org_list.html)

**Usage**

```r
search_kegg_organism(str, by = "scientific_name", ignore.case = FALSE)
```

**Arguments**

- `str` string
- `by` one of `kegg.code`, `scientific_name` and `common_name`
- `ignore.case` TRUE or FALSE

**Value**
data.frame

**Author(s)**
Guangchuang Yu
simplify

Description

simplify output from enrichGO by removing redundancy of enriched GO terms
simplify output from compareCluster by removing redundancy of enriched GO terms

Usage

## S4 method for signature 'enrichResult'
simplify(x, cutoff = 0.7, by = "p.adjust",
select_fun = min, measure = "Wang", semData = NULL)

## S4 method for signature 'compareClusterResult'
simplify(x, cutoff = 0.7, by = "p.adjust",
select_fun = min, measure = "Wang", semData = NULL)

Arguments

x output of enrichGO
cutoff similarity cutoff
by feature to select representative term, selected by 'select_fun' function
select_fun function to select feature passed by 'by' parameter
measure method to measure similarity
semData GOSemSimDATA object

Value

updated enrichResult object
updated compareClusterResult object

Author(s)

Guangchuang Yu
Guangchuang Yu

References

issue #28 https://github.com/GuangchuangYu/clusterProfiler/issues/28
viewKEGG function is for visualize KEGG pathways works with enrichResult object to visualize enriched KEGG pathway

Description

viewKEGG function is for visualize KEGG pathways works with enrichResult object to visualize enriched KEGG pathway

Usage

viewKEGG(obj, pathwayID, foldChange, color.low = "green", color.high = "red", kegg.native = TRUE, out.suffix = "clusterProfiler")

Arguments

  obj  enrichResult object  
  pathwayID  pathway ID or index  
  foldChange  fold change values  
  color.low  color of low foldChange genes  
  color.high  color of high foldChange genes  
  kegg.native  logical  
  out.suffix  suffix of output file

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