Package ‘clusterProfiler’

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Type Package

Title statistical analysis and visualization of functional profiles for genes and gene clusters

Version 3.2.14

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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.eg.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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### 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

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Author(s)
Guangchuang Yu <guangchuangyu@gmail.com>
Maintainer: Guangchuang Yu <guangchuangyu@gmail.com>

See Also
compareClusterResult, groupGOResult enrichResult

Description
Biological Id TRanslator

Usage

```r
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
**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

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

Class `compareClusterResult` 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.

Description

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**

**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**

**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 qvalueCutoff
species species
david.user david user

Value

A enrichResult instance

Author(s)

Guangchuang Yu
enrichGO

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

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

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

See Also

enrichResult-class, compareCluster

Examples

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

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

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

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

**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](http://ygc.name)

**See Also**

enrichResult-class, compareCluster

**Examples**

```r
data(geneList)
d <- names(geneList)[1:100]
y <- enrichMKEGG(d, pvalueCutoff=0.01)
head(summary(y))
#plot(y)
```

---

**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**

```r
enrichMKEGG(gene, organism = "hsa", keyType = "kegg", pvalueCutoff = 0.05,
pAdjustMethod = "BH", universe, minGSSize = 10, maxGSSize = 500,
qvalueCutoff = 0.2)
```
fortify.compareClusterResult

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

closestClusterResult 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  

**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)

---

**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

Description
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)

---

**groupGOResult-class**

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
Description

a universal gene set enrichment analysis tools

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

```r
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
gseMKEGG

Description

Gene Set Enrichment Analysis of KEGG Module

Usage

```r
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

**Description**
list ID types supported by annoDb

**Usage**
```
idType(OrgDb = "org.Hs.eg.db")
```

**Arguments**
- **OrgDb** annotation db

**Value**
character vector

**Author(s)**
Guangchuang Yu

---

### merge_result

**Description**
merge a list of enrichResult objects to compareClusterResult

**Usage**
```
merge_result(enrichResultList)
```

**Arguments**
- **enrichResultList** a list of enrichResult objects

**Value**
a compareClusterResult instance

**Author(s)**
Guangchuang Yu
Description

plot method generics

Usage

## 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)
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**  

**simplify method**

**Description**

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

**Usage**

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

```r
## 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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