

# Package ‘DOSE’

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**Type** Package

**Title** Disease Ontology Semantic and Enrichment analysis

**Version** 4.1.0

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**Description** This package implements five methods proposed by Resnik, Schlicker, Jiang, Lin and Wang respectively for measuring semantic similarities among DO terms and gene products. Enrichment analyses including hypergeometric model and gene set enrichment analysis are also implemented for discovering disease associations of high-throughput biological data.

**Depends** R (>= 3.5.0)

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## Contents

DOSE-package . . . . .	3
clusterSim . . . . .	3
compareClusterResult-class . . . . .	4
computeIC . . . . .	5
DataSet . . . . .	6
doseSim . . . . .	6
enrichDGN . . . . .	7
enrichDGNv . . . . .	8
enrichDO . . . . .	9
enricher_internal . . . . .	10
enrichNCG . . . . .	11
enrichResult-class . . . . .	12
EXTID2NAME . . . . .	13
gene2DO . . . . .	13
geneID . . . . .	14
geneInCategory . . . . .	14
geneSim . . . . .	15
gseaResult-class . . . . .	16
GSEA_internal . . . . .	17
gseDGN . . . . .	18
gseDO . . . . .	19
gseNCG . . . . .	20
gsfilter . . . . .	21
mclusterSim . . . . .	21
parse_ratio . . . . .	22
reexports . . . . .	23
setReadable . . . . .	23
show . . . . .	24
simplot . . . . .	24
summary . . . . .	25
theme_dose . . . . .	26

**Index**

**27**

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DOSE-package

*DOSE: Disease Ontology Semantic and Enrichment analysis*

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### Description

This package implements five methods proposed by Resnik, Schlicker, Jiang, Lin and Wang respectively for measuring semantic similarities among DO terms and gene products. Enrichment analyses including hypergeometric model and gene set enrichment analysis are also implemented for discovering disease associations of high-throughput biological data.

### Author(s)

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### See Also

Useful links:

- <https://yulab-smu.top/biomedical-knowledge-mining-book/>
- Report bugs at <https://github.com/GuangchuangYu/DOSE/issues>

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clusterSim

*clusterSim*

---

### Description

semantic similarity between two gene clusters

### Usage

```
clusterSim(  
  cluster1,  
  cluster2,  
  ont = "HDO",  
  organism = "hsa",  
  measure = "Wang",  
  combine = "BMA"  
)
```

**Arguments**

cluster1	a vector of gene IDs
cluster2	another vector of gene IDs
ont	one of "HDO", "HPO" and "MPO"
organism	one of "hsa" and "mmu"
measure	One of "Resnik", "Lin", "Rel", "Jiang" and "Wang" methods.
combine	One of "max", "avg", "rcmax", "BMA" methods, for combining

**Details**

given two gene clusters, this function calculates semantic similarity between them.

**Value**

similarity

**Author(s)**

Yu Guangchuang

**Examples**

```
## Not run:
cluster1 <- c("835", "5261", "241", "994")
cluster2 <- c("307", "308", "317", "321", "506", "540", "378", "388", "396")
clusterSim(cluster1, cluster2)

## 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  
gene2Symbol gene ID to Symbol  
keytype Gene ID type  
readable logical flag of gene ID in symbol or not.  
.call function call  
termsim Similarity between term  
method method of calculating the similarity between nodes  
dr dimension reduction result

**Author(s)**

Guangchuang Yu <https://yulab-smu.top>

**See Also**

[enrichResult](#)

---

computeIC                      *compute information content*

---

**Description**

compute information content

**Usage**

```
computeIC(ont = "HDO")
```

**Arguments**

ont                      one of "DO", "HPO" and "MPO"

**Author(s)**

Guangchuang Yu <https://yulab-smu.top>

---

 DataSet
 

---

*Datasets*


---

**Description**

Information content and DO term to entrez gene IDs mapping

---

 doseSim
 

---

*doseSim*


---

**Description**

measuring similarities between two DO term vectors.

**Usage**

```
doseSim(DO1, DO2, measure = "Wang", ont = "HDO")
```

```
doSim(DO1, DO2, measure = "Wang", ont = "HDO")
```

**Arguments**

DO1	DO term, MPO term or HPO term vector
DO2	DO term, MPO term or HPO term vector
measure	one of "Wang", "Resnik", "Rel", "Jiang", "Lin", and "TCSS".
ont	one of "HDO", "HPO" and "MPO"

**Details**

provide two term vectors, this function will calculate their similarities.

**Value**

score matrix

**Author(s)**

Guangchuang Yu <https://yulab-smu.top>

---

enrichDGN	<i>Enrichment analysis based on the DisGeNET</i> ( <a href="http://www.disgenet.org/">http://www.disgenet.org/</a> )
-----------	--

---

### Description

given a vector of genes, this function will return the enrichment NCG categories with FDR control

### Usage

```
enrichDGN(  
  gene,  
  pvalueCutoff = 0.05,  
  pAdjustMethod = "BH",  
  universe,  
  minGSSize = 10,  
  maxGSSize = 500,  
  qvalueCutoff = 0.2,  
  readable = FALSE  
)
```

### Arguments

gene	a vector of entrez 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 by NCG category for testing
maxGSSize	maximal size of each geneSet for analyzing
qvalueCutoff	qvalue cutoff
readable	whether mapping gene ID to gene Name

### Value

A `enrichResult` instance

### Author(s)

Guangchuang Yu

### References

Janet et al. (2015) DisGeNET: a discovery platform for the dynamical exploration of human diseases and their genes. *Database* bav028 <http://database.oxfordjournals.org/content/2015/bav028.long>

---

`enrichDGNv`*enrichDGN*

---

## Description

Enrichment analysis based on the DisGeNET (<http://www.disgenet.org/>)

## Usage

```
enrichDGNv(  
  snp,  
  pvalueCutoff = 0.05,  
  pAdjustMethod = "BH",  
  universe,  
  minGSSize = 10,  
  maxGSSize = 500,  
  qvalueCutoff = 0.2,  
  readable = FALSE  
)
```

## Arguments

<code>snp</code>	a vector of SNP
<code>pvalueCutoff</code>	pvalue cutoff
<code>pAdjustMethod</code>	one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
<code>universe</code>	background genes
<code>minGSSize</code>	minimal size of genes annotated by NCG category for testing
<code>maxGSSize</code>	maximal size of each geneSet for analyzing
<code>qvalueCutoff</code>	qvalue cutoff
<code>readable</code>	whether mapping gene ID to gene Name

## Details

given a vector of genes, this function will return the enrichment NCG categories with FDR control

## Value

A `enrichResult` instance

## Author(s)

Guangchuang Yu



## References

Janet et al. (2015) DisGeNET: a discovery platform for the dynamical exploration of human diseases and their genes. *Database* bav028 <http://database.oxfordjournals.org/content/2015/bav028.long>

---

 enrichDO

*DO Enrichment Analysis*


---

## Description

Given a vector of genes, this function will return the enrichment DO categories with FDR control.

## Usage

```
enrichDO(
  gene,
  ont = "HDO",
  organism = "hsa",
  pvalueCutoff = 0.05,
  pAdjustMethod = "BH",
  universe,
  minGSSize = 10,
  maxGSSize = 500,
  qvalueCutoff = 0.2,
  readable = FALSE
)
```

## Arguments

gene	a vector of entrez gene id
ont	one of "HDO", "HPO" or "MPO".
organism	one of "hsa" and "mmu"
pvalueCutoff	pvalue cutoff
pAdjustMethod	one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
universe	background genes
minGSSize	minimal size of genes annotated by NCG category for testing
maxGSSize	maximal size of each geneSet for analyzing
qvalueCutoff	qvalue cutoff
readable	whether mapping gene ID to gene Name

## Value

A enrichResult instance.

**Author(s)**

Guangchuang Yu <https://yulab-smu.top>

**See Also**

[enrichResult-class](#)

**Examples**

```
data(geneList)
gene = names(geneList)[geneList > 1]
yy = enrichD0(gene, pvalueCutoff=0.05)
summary(yy)
```

---

enricher\_internal      *enrich.internal*

---

**Description**

internal method for enrichment analysis

**Usage**

```
enricher_internal(
  gene,
  pvalueCutoff,
  pAdjustMethod = "BH",
  universe = NULL,
  minGSSize = 10,
  maxGSSize = 500,
  qvalueCutoff = 0.2,
  USER_DATA
)
```

**Arguments**

gene	a vector of entrez gene id.
pvalueCutoff	Cutoff value of pvalue.
pAdjustMethod	one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
universe	background genes, default is the intersection of the 'universe' with genes that have annotations. Users can set 'options(enrichment_force_universe = TRUE)' to force the 'universe' untouched.
minGSSize	minimal size of genes annotated by Ontology term for testing.
maxGSSize	maximal size of each geneSet for analyzing
qvalueCutoff	cutoff of qvalue
USER_DATA	ontology information

**Details**

using the hypergeometric model

**Value**

A `enrichResult` instance.

**Author(s)**

Guangchuang Yu <https://yulab-smu.top>

---

enrichNCG

*enrichNCG*


---

**Description**

Enrichment analysis based on the Network of Cancer Genes database (<http://ncg.kcl.ac.uk/>)

**Usage**

```
enrichNCG(
  gene,
  pvalueCutoff = 0.05,
  pAdjustMethod = "BH",
  universe,
  minGSSize = 10,
  maxGSSize = 500,
  qvalueCutoff = 0.2,
  readable = FALSE
)
```

**Arguments**

<code>gene</code>	a vector of entrez gene id
<code>pvalueCutoff</code>	pvalue cutoff
<code>pAdjustMethod</code>	one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
<code>universe</code>	background genes
<code>minGSSize</code>	minimal size of genes annotated by NCG category for testing
<code>maxGSSize</code>	maximal size of each <code>geneSet</code> for analyzing
<code>qvalueCutoff</code>	qvalue cutoff
<code>readable</code>	whether mapping gene ID to gene Name

**Details**

given a vector of genes, this function will return the enrichment NCG categories with FDR control

**Value**

A enrichResult instance

**Author(s)**

Guangchuang Yu

---

enrichResult-class	<i>Class "enrichResult" This class represents the result of enrichment analysis.</i>
--------------------	--

---

**Description**

Class "enrichResult" This class represents the result of enrichment analysis.

**Slots**

result enrichment analysis  
 pvalueCutoff pvalueCutoff  
 pAdjustMethod pvalue adjust method  
 qvalueCutoff qvalueCutoff  
 organism only "human" supported  
 ontology biological ontology  
 gene Gene IDs  
 keytype Gene ID type  
 universe background gene  
 gene2Symbol mapping gene to Symbol  
 geneSets gene sets  
 readable logical flag of gene ID in symbol or not.  
 termsim Similarity between term  
 method method of calculating the similarity between nodes  
 dr dimension reduction result

**Author(s)**

Guangchuang Yu <https://yulab-smu.top>

**See Also**

[enrichDO](#)

---

EXTID2NAME	<i>EXTID2NAME</i>
------------	-------------------

---

**Description**

mapping gene ID to gene Symbol

**Usage**

```
EXTID2NAME(OrgDb, geneID, keytype)
```

**Arguments**

OrgDb	OrgDb
geneID	entrez gene ID
keytype	keytype

**Value**

gene symbol

**Author(s)**

Guangchuang Yu <https://yulab-smu.top>

---

gene2DO	<i>convert Gene ID to DO Terms</i>
---------	------------------------------------

---

**Description**

provide gene ID, this function will convert to the corresponding DO Terms

**Usage**

```
gene2DO(gene, organism = "hsa", ont = "HDO")
```

**Arguments**

gene	entrez gene ID
organism	organism
ont	ont

**Value**

DO Terms

**Author(s)**

Guangchuang Yu <https://yulab-smu.top>

---

geneID                      *geneID generic*

---

**Description**

geneID generic

**Usage**

geneID(x)

**Arguments**

x                      enrichResult object

**Value**

'geneID' return the 'geneID' column of the enriched result which can be converted to data.frame via 'as.data.frame'

**Examples**

```
data(geneList, package="DOSE")
de <- names(geneList)[1:100]
x <- enrichDO(de)
geneID(x)
```

---

geneInCategory            *geneInCategory generic*

---

**Description**

geneInCategory generic

**Usage**

geneInCategory(x)

**Arguments**

x                      enrichResult

**Value**

'geneInCategory' return a list of genes, by splitting the input gene vector to enriched functional categories

**Examples**

```
data(geneList, package="DOSE")
de <- names(geneList)[1:100]
x <- enrichDO(de)
geneInCategory(x)
```

---

 geneSim

*geneSim*


---

**Description**

measuring similarities between two gene vectors.

**Usage**

```
geneSim(
  geneID1,
  geneID2 = NULL,
  ont = "HDO",
  organism = "hsa",
  measure = "Wang",
  combine = "BMA"
)
```

**Arguments**

geneID1	entrez gene vector
geneID2	entrez gene vector
ont	one of "HDO" and "MPO"
organism	one of "hsa" and "mmu"
measure	one of "Wang", "Resnik", "Rel", "Jiang", and "Lin".
combine	One of "max", "avg", "rcmax", "BMA" methods, for combining semantic similarity scores of multiple DO terms associated with gene/protein.

**Details**

provide two entrez gene vectors, this function will calculate their similarity.

**Value**

score matrix

**Author(s)**

Guangchuang Yu <https://yulab-smu.top>

**Examples**

```
g <- c("835", "5261", "241", "994")
geneSim(g)
```

---

gseaResult-class

*Class "gseaResult" This class represents the result of GSEA analysis*

---

**Description**

Class "gseaResult" This class represents the result of GSEA analysis

**Slots**

result GSEA analysis

organism organism

setType setType

geneSets geneSets

geneList order rank geneList

keytype ID type of gene

permScores permutation scores

params parameters

gene2Symbol gene ID to Symbol

readable whether convert gene ID to symbol

dr dimension reduction result

**Author(s)**

Guangchuang Yu <https://yulab-smu.top>



---

GSEA\_internal                      *GSEA\_internal*

---

### Description

generic function for gene set enrichment analysis

### Usage

```
GSEA_internal(
  geneList,
  exponent,
  minGSSize,
  maxGSSize,
  eps,
  pvalueCutoff,
  pAdjustMethod,
  verbose,
  seed = FALSE,
  USER_DATA,
  by = "fgsea",
  ...
)
```

### Arguments

geneList	order ranked geneList
exponent	weight of each step
minGSSize	minimal size of each geneSet for analyzing
maxGSSize	maximal size of each geneSet for analyzing
eps	This parameter sets the boundary for calculating the p value.
pvalueCutoff	p value Cutoff
pAdjustMethod	p value adjustment method
verbose	print message or not
seed	set seed inside the function to make result reproducible. FALSE by default.
USER_DATA	annotation data
by	one of 'fgsea' or 'DOSE'
...	other parameter

### Value

gseaResult object

### Author(s)

Yu Guangchuang

---

gseDGN

*DisGeNET Gene Set Enrichment Analysis*

---

## Description

perform gsea analysis

## Usage

```
gseDGN(  
  geneList,  
  exponent = 1,  
  minGSSize = 10,  
  maxGSSize = 500,  
  pvalueCutoff = 0.05,  
  pAdjustMethod = "BH",  
  verbose = TRUE,  
  seed = FALSE,  
  by = "fgsea",  
  ...  
)
```

## Arguments

geneList	order ranked geneList
exponent	weight of each step
minGSSize	minimal size of each geneSet for analyzing
maxGSSize	maximal size of each geneSet for analyzing
pvalueCutoff	pvalue Cutoff
pAdjustMethod	p value adjustment method
verbose	print message or not
seed	logical
by	one of 'fgsea' or 'DOSE'
...	other parameter

## Value

gseaResult object

## Author(s)

Yu Guangchuang

gseDO

*DO Gene Set Enrichment Analysis***Description**

perform gsea analysis

**Usage**

```

gseDO(
  geneList,
  ont = "HDO",
  organism = "hsa",
  exponent = 1,
  minGSSize = 10,
  maxGSSize = 500,
  pvalueCutoff = 0.05,
  pAdjustMethod = "BH",
  verbose = TRUE,
  seed = FALSE,
  by = "fgsea",
  ...
)

```

**Arguments**

geneList	order ranked geneList
ont	one of "HDO", "HPO" or "MPO"
organism	one of "hsa" and "mmu"
exponent	weight of each step
minGSSize	minimal size of each geneSet for analyzing
maxGSSize	maximal size of each geneSet for analyzing
pvalueCutoff	pvalue Cutoff
pAdjustMethod	p value adjustment method
verbose	print message or not
seed	logical
by	one of 'fgsea' or 'DOSE'
...	other parameter

**Value**

gseaResult object

**Author(s)**

Yu Guangchuang

---

`gseNCG`*NCG Gene Set Enrichment Analysis*

---

**Description**

perform gsea analysis

**Usage**

```
gseNCG(  
  geneList,  
  exponent = 1,  
  minGSSize = 10,  
  maxGSSize = 500,  
  pvalueCutoff = 0.05,  
  pAdjustMethod = "BH",  
  verbose = TRUE,  
  seed = FALSE,  
  by = "fgsea",  
  ...  
)
```

**Arguments**

<code>geneList</code>	order ranked geneList
<code>exponent</code>	weight of each step
<code>minGSSize</code>	minimal size of each geneSet for analyzing
<code>maxGSSize</code>	maximal size of each geneSet for analyzing
<code>pvalueCutoff</code>	pvalue Cutoff
<code>pAdjustMethod</code>	p value adjustment method
<code>verbose</code>	print message or not
<code>seed</code>	logical
<code>by</code>	one of 'fgsea' or 'DOSE'
<code>...</code>	other parameter

**Value**

`gseaResult` object

**Author(s)**

Yu Guangchuang

---

gsfilter	<i>gsfilter</i>
----------	-----------------

---

**Description**

filter enriched result by gene set size or gene count

**Usage**

```
gsfilter(x, by = "GSSize", min = NA, max = NA)
```

**Arguments**

x	instance of enrichResult or compareClusterResult
by	one of 'GSSize' or 'Count'
min	minimal size
max	maximal size

**Value**

update object

**Author(s)**

Guangchuang Yu

---

mclusterSim	<i>mclusterSim</i>
-------------	--------------------

---

**Description**

Pairwise semantic similarity for a list of gene clusters

**Usage**

```
mclusterSim(  
  clusters,  
  ont = "HDO",  
  organism = "hsa",  
  measure = "Wang",  
  combine = "BMA"  
)
```

**Arguments**

clusters	A list of gene clusters
ont	one of "HDO", "HPO" and "MPO"
organism	organism
measure	one of "Wang", "Resnik", "Rel", "Jiang", and "Lin".
combine	One of "max", "avg", "rcmax", "BMA" methods, for combining semantic similarity scores of multiple DO terms associated with gene/protein.

**Value**

similarity matrix

**Author(s)**

Guangchuang Yu

**Examples**

```
## Not run:
cluster1 <- c("835", "5261", "241")
cluster2 <- c("578", "582")
cluster3 <- c("307", "308", "317")
clusters <- list(a=cluster1, b=cluster2, c=cluster3)
mclusterSim(clusters, measure="Wang")

## End(Not run)
```

---

parse\_ratio

*parse\_ratio*

---

**Description**

parse character ratio to double value, such as 1/5 to 0.2

**Usage**

```
parse_ratio(ratio)
```

**Arguments**

ratio	character vector of ratio to parse
-------	------------------------------------

**Value**

A numeric vector (double) of parsed ratio

**Author(s)**

Guangchuang Yu

---

reexports	<i>Objects exported from other packages</i>
-----------	---

---

**Description**

These objects are imported from other packages. Follow the links below to see their documentation.

**ggplot2** [facet\\_grid](#)

---

setReadable	<i>setReadable</i>
-------------	--------------------

---

**Description**

mapping geneID to gene Symbol

**Usage**

```
setReadable(x, OrgDb, keyType = "auto")
```

**Arguments**

x	enrichResult Object
OrgDb	OrgDb
keyType	keyType of gene

**Value**

enrichResult Object

**Author(s)**

Yu Guangchuang

show *show method*

---

**Description**

show method for gseaResult instance  
show method for enrichResult instance

**Usage**

```
show(object)
```

```
show(object)
```

**Arguments**

object            A enrichResult instance.

**Value**

message

message

**Author(s)**

Guangchuang Yu <https://yulab-smu.top>

---

simplot *simplot*

---

**Description**

plotting similarity matrix

**Usage**

```
simplot(  
  sim,  
  xlab = "",  
  ylab = "",  
  color.low = "white",  
  color.high = "red",  
  labs = TRUE,  
  digits = 2,  
  labs.size = 3,  
  font.size = 14  
)
```



**Arguments**

sim	similarity matrix
xlab	xlab
ylab	ylab
color.low	color of low value
color.high	color of high value
labs	logical, add text label or not
digits	round digit numbers
labs.size	lable size
font.size	font size

**Value**

ggplot object

**Author(s)**

Yu Guangchuang

---

summary	<i>summary method</i>
---------	-----------------------

---

**Description**

summary method for gseaResult instance  
summary method for enrichResult instance

**Usage**

```
summary(object, ...)
```

```
summary(object, ...)
```

**Arguments**

object	A enrichResult instance.
...	additional parameter

**Value**

A data frame  
A data frame

**Author(s)**

Guangchuang Yu <https://guangchuangyu.github.io>

Guangchuang Yu <http://guangchuangyu.github.io>

---

theme\_dose

*theme\_dose*

---

**Description**

ggplot theme of DOSE

**Usage**

```
theme_dose(font.size = 14)
```

**Arguments**

font.size      font size

**Value**

ggplot theme

**Examples**

```
library(ggplot2)
qplot(1:10) + theme_dose()
```

# Index

- \* **classes**
  - compareClusterResult-class, 4
  - enrichResult-class, 12
  - gseaResult-class, 16
- \* **datasets**
  - DataSet, 6
- \* **internal**
  - DOSE-package, 3
  - reexports, 23
- \* **manip**
  - enrichDO, 9
  - enricher\_internal, 10
  - gseDGN, 18
  - gseDO, 19
  - gseNCG, 20
- clusterSim, 3
- compareClusterResult-class, 4
- computeIC, 5
- DataSet, 6
- DGN\_EXTID2PATHID (DataSet), 6
- DGN\_PATHID2EXTID (DataSet), 6
- DGN\_PATHID2NAME (DataSet), 6
- DOSE (DOSE-package), 3
- DOSE-package, 3
- doseSim, 6
- doSim (doseSim), 6
- enrichDGN, 7
- enrichDGNv, 8
- enrichDO, 9, 12
- enricher\_internal, 10
- enrichNCG, 11
- enrichResult, 5
- enrichResult-class, 12
- EXTID2NAME, 13
- facet\_grid, 23
- facet\_grid (reexports), 23
- gene2DO, 13
- geneID, 14
- geneInCategory, 14
- geneList (DataSet), 6
- geneSim, 15
- GSEA\_internal, 17
- gseahResult-class (gseaResult-class), 16
- gseaResult-class, 16
- gseDGN, 18
- gseDO, 19
- gseNCG, 20
- gsfilter, 21
- mclusterSim, 21
- NCG\_EXTID2PATHID (DataSet), 6
- NCG\_PATHID2EXTID (DataSet), 6
- NCG\_PATHID2NAME (DataSet), 6
- parse\_ratio, 22
- plot, compareClusterResult-method  
(compareClusterResult-class), 4
- reexports, 23
- setReadable, 23
- show, 24
- show, compareClusterResult-method  
(compareClusterResult-class), 4
- show, enrichResult-method  
(enrichResult-class), 12
- show, gseaResult-method  
(gseaResult-class), 16
- simplot, 24
- summary, 25
- summary, compareClusterResult-method  
(compareClusterResult-class), 4
- summary, enrichResult-method  
(enrichResult-class), 12
- summary, gseaResult-method  
(gseaResult-class), 16

theme\_dose, [26](#)

VDGN\_EXTID2PATHID (DataSet), [6](#)

VDGN\_PATHID2EXTID (DataSet), [6](#)

VDGN\_PATHID2NAME (DataSet), [6](#)