Package ‘DOSE’

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Type Package

Title Disease Ontology Semantic and Enrichment analysis

Version 3.28.2

Maintainer Guangchuang Yu <guangchuangyu@gmail.com>

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)

Imports AnnotationDbi, HDO.db, BiocParallel, fgsea, ggplot2, GOSemSim (>= 2.27.1), methods, qvalue, reshape2, stats, utils, yulab.utils

Suggests prettydoc, clusterProfiler, gson (>= 0.0.5), knitr, rmarkdown, org.Hs.eg.db, MPO.db, HPO.db, testthat

VignetteBuilder knitr

ByteCompile true

License Artistic-2.0

Encoding UTF-8


BugReports https://github.com/GuangchuangYu/DOSE/issues

biocViews Annotation, Visualization, MultipleComparison, GeneSetEnrichment, Pathways, Software

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**Author**  Guangchuang Yu [aut, cre],
            Li-Gen Wang [ctb],
            Vladislav Petyuk [ctb],
            Giovanni Dall’Olio [ctb],
            Erqiang Hu [ctb]

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Disease Ontology Semantic and Enrichment analysis

Implemented five methods proposed by Resnik, Schlicker, Jiang, Lin and Wang respectively for measuring DO semantic similarities, and hypergeometric test for enrichment analysis.

Description

This package is designed to estimate DO-based semantic similarity measurement and enrichment analysis.

Details

Package: DOSE
Type: Package
Version: 2.3.5
Date: 2-27-2012
biocViews: Bioinformatics, Annotation
Depends:
Imports: methods, AnnotationDbi, HDO.dbb
Suggests: clusterProfiler, GOSemSim
License: Artistic-2.0

Author(s)

Guangchuang Yu, Li-Gen Wang

Maintainer: Guangchuang Yu <guangchuangyu@gmail.com>

See Also

enrichResult
Description

semantic similarity between two gene clusters

Usage

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

Arguments

cluster1 a vector of gene IDs
cluster2 another vector of gene IDs
ont one of "DO" and "MPO"
organism organism
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

cluster1 <- c("835", "5261", "241", "994")
clusterSim(cluster1, cluster2)
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](https://yulab-smu.top)

See Also

- `enrichResult`

computeIC

Description

compute information content

Usage

computeIC(ont = "DO")
Arguments

ont  one of "DO" and "MPO"

Author(s)

Guangchuang Yu [https://yulab-smu.top]

Description

Information content and DO term to entrez gene IDs mapping

doseSim  doSim

Description

measuring similarities between two DO term vectors.

Usage

doseSim(DOID1, DOID2, measure = "Wang", ont = "DO")

Arguments

DOID1  DO term, MPO term or HPO term vector
DOID2  DO term, MPO term or HPO term vector
measure  one of "Wang", "Resnik", "Rel", "Jiang", "Lin", and "TCSS".
ont  one of "DO" and "MPO"

Details

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

Value

score matrix
**doSim**

**Description**

measuring similarities between two MPO term vectors.

**Usage**

```r
doSim(DOID1, DOID2, measure = "Wang")
```

**Arguments**

- **DOID1**: DO term vector
- **DOID2**: DO term vector
- **measure**: one of "Wang", "Resnik", "Rel", "Jiang", "Lin", and "TCSS".

**Details**

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

**Value**

score matrix

**Author(s)**

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

---

**enrichDGN**


**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


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

snp      a vector of SNP
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

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

Description

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

Usage

enrichDO(
  gene,
  ont = "DO",
  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 DO and DOLite.
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 http://guangchuangyu.github.io

See Also

enrichResult-class
Examples

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

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
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.
**Description**

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

**Usage**

```r
enrichHPO(
  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)**

Erqiang Hu
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

enrichMPO

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

Description

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

Usage

enrichMPO(
  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)

Erqiang Hu
References


---

```
<table>
<thead>
<tr>
<th>enrichNCG</th>
<th>enrichNCG</th>
</tr>
</thead>
</table>
```

Description

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

Usage

```r
enrichNCG(
  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

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

**Description**

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

**Slots**

- `result`: enrichment analysis
- `pvalueCutoff`: p-value cutoff
- `pAdjustMethod`: p-value adjust method
- `qvalueCutoff`: q-value cutoff
- `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](https://yulab-smu.top)

**See Also**

-enrichDO
EXTID2NAME

**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](https://yulab-smu.top)

gene2DO

**Description**

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

**Usage**

gene2DO(gene, organism = "hsa", ont = "DO")

**Arguments**

- gene: entrez gene ID
- organism: organism
- ont: ont

**Value**

DO Terms
geneID

Author(s)
Guangchuang Yu https://yulab-smu.top

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 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)

desc

geneSim
geneSim

description

measuring similarities between two gene vectors.

Usage

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

Arguments

geneID1 entrez gene vector
geneID2 entrez gene vector
ont one of "DO" 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.

Details

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

Value

score matrix
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 http://ygc.name

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**

```r
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
DO Gene Set Enrichment Analysis

Description
perform gsea analysis

Usage

\[
gseDO( 
  geneList, 
  organism = "hsa", 
  exponent = 1, 
  minGSSize = 10, 
  maxGSSize = 500, 
  pvalueCutoff = 0.05, 
  pAdjustMethod = "BH", 
  verbose = TRUE, 
  seed = FALSE, 
  by = "fgsea", 
  \ldots 
)
\]

Arguments

- **geneList**: order ranked geneList
- **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'
- **\ldots**: other parameter

Value
gseaResult object

Author(s)
Yu Guangchuang
gseHPO

MPO Gene Set Enrichment Analysis

Description

perform gsea analysis

Usage

gseHPO(
  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)

Erqiang Hu
Description

perform gsea analysis

Usage

gseMPO(
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)

Erqiang Hu
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

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
**gsfilter**

**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

---

**hpoSim**

**doSim**

**Description**
measuring similarities between two MPO term vectors.

**Usage**
hpoSim(DOID1, DOID2, measure = "Wang")

**Arguments**
- **DOID1**: HPO term vector
- **DOID2**: HPO term vector
- **measure**: one of "Wang", "Resnik", "Rel", "Jiang", "Lin", and "TCSS".
Details
provide two HPO term vectors, this function will calculate their similarities.

Value
score matrix

Description
Pairwise semantic similarity for a list of gene clusters

Usage
mclusterSim(
  clusters,
  ont = "DO",
  organism = "hsa",
  measure = "Wang",
  combine = "BMA"
)

Arguments
clusters A list of gene clusters
ont one of "DO" 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)
Yu Guangchuang

Examples
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")
mpoSIm  
doSim

**Description**
measuring similarities between two MPO term vectors.

**Usage**

```r
mpoSIm(DOID1, DOID2, measure = "Wang")
```

**Arguments**

- **DOID1**: MPO term vector
- **DOID2**: MPO term vector
- **measure**: one of "Wang", "Resnik", "Rel", "Jiang", "Lin", and "TCSS".

**Details**

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

**Value**

score matrix

---

`parse_ratio`

**Description**

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

**Usage**

```r
parse_ratio(ratio)
```

**Arguments**

- **ratio**: character vector of ratio to parse

**Value**

A numeric vector (double) of parsed ratio

**Author(s)**

Guangchuang Yu
rebuildAnnoData

Description
rebuilding entrez and DO mapping datasets

Usage
rebuildAnnoData(file)

Arguments

file
do_rif.human.txt

Author(s)
Guangchuang Yu https://yulab-smu.top

reexports

Objects exported from other packages

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

**ggplot2** facet_grid

setReadable

setReadable

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

Description

show method for gseaResult instance
show method for enrichResult instance

Usage

show(object)

Arguments

object A enrichResult instance.

Value

message

message

Author(s)

Guangchuang Yu https://yulab-smu.top
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 label size
font.size font size

Value
ggplot object

Author(s)
Yu Guangchuang
```r
# theme_dose

## Description

ggplot theme of DOSE

## Usage

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

## Arguments

- `font.size` : font size

---

```r
# summary

## Description

summary method for gseaResult instance

summary method for enrichResult instance

## Usage

```r
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](https://guangchuangyu.github.io)

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```
theme_dose

Value

ggplot theme

Examples

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