

DOSE

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DO2EG

Map DO term to entrez gene IDs

Description

This data contain a list of DO terms annotated with entrez gene IDs.

DOParams-class

Class "DOParams"

Description

A `DOParams` contains parameters for calculating DO semantic similarity among DO term or Gene list.

Slots

IDs: containing a list of DO terms or Gene IDs.

type: specify the type of IDs, one of "DOID", "GeneID".

ontology: must set to "DO".

organism: currently, only "human" supported.

method: Method for calculating DO semantic similarity, one of "Resnik", "Jiang", "Lin", "Rel", "Wang".

combine: Method for combining DO semantic similarity scores, one of "avg", "max", "rmax", "rmax.avg"

dropCodes: dropCodes for mapping Gene to DO Terms.

Methods

sim signature(object = "DOParams"): calculates semantic similarities of DOParams.

Author(s)

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See Also[sim](#)**Examples**

```
data(DO2EG)
set.seed(123)
id <- list(a=sample(names(DO2EG), 5), b= sample(names(DO2EG), 6))
## Setting Parameters...
params <- new("DOParams", IDs=id, type="DOID", method="Wang", combine="rcmax.avg")
## Calculating Semantic Similarities...
sim(params)
```

DOSE-package

Disease Ontology Semantic and Enrichment analysis

Description

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

Details

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

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See Also

[DOParams](#), [enrichDOResult](#)

EG2DO

Map entrez gene ID to DO terms

Description

This data contain a list of entrez gene IDs annotated with DO terms.

IC	<i>Information content of DO terms</i>
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Description

These datasets are the information contents of DO terms.

enrichDO	<i>DO Enrichment Analysis of a gene set.</i>
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Description

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

Usage

```
enrichDO(gene, organism="human", pvalueCutoff = 0.05)
```

Arguments

gene a vector of entrez gene id.
 organism Currently, only "human" and "mouse" supported.
 pvalueCutoff Cutoff value of pvalue.

Value

A `enrichDOResult` instance.

See Also

[enrichDOResult-class](#),

Examples

```
set.seed(123)
data(EG2DO)
gene = sample(names(EG2DO), 30)
yy = enrichDO(gene, pvalueCutoff=0.05)
summary(yy)
```

enrichDOResult-class

Class "enrichDOResult"

Description

This class represents the result of DO enrichment analysis.

Objects from the Class

Objects can be created by calls of the form `new("enrichDOResult", ...)`.

Slots

enrichDOResult: containing a dataframe of DO enrichment analysis result.

pvalueCutoff: Cutoff value of pvalue.

Organism: Organism.

Gene: input gene vector.

Methods

show signature(object="enrichDOResult")

summary signature(object="enrichDOResult")

Author(s)

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See Also

[enrichDO](#)

Examples

```
set.seed(123)
data(EG2DO)
gene = sample(names(EG2DO), 30)
yy = enrichDO(gene, pvalueCutoff=0.05)
## yy is an enrichDOResult instance, which stored the enrichment analysis result.
YY
summary(yy)
```

Description

Given a `DOParams` instance containing a list of DO terms or Entrez Gene IDs, the ID type, the method for calculating similarity, and the combine method for combining similarity scores, this method will compute semantic similarity among DO terms or genes.

Arguments

`params` A `DOParams` instance

See Also

[DOParams-class](#)

Examples

```
data(DO2EG)
set.seed(123)
id <- list(a=sample(names(DO2EG), 5), b= sample(names(DO2EG), 6))
## Setting Parameters...
params <- new("DOParams", IDs=id, type="DOID", method="Wang", combine="rcmax.avg")
## Calculating Semantic Similarities...
sim(params)
```

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