

domainsignatures

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dataSource

Constructor for annotation object

Description

This function creates the necessary annotation object of class `ipDataSource` containing the pathway and InterPro ID mappings.

Usage

```
dataSource(mapping, type = "generic")
```

Arguments

mapping	A named list providing a mapping between enterzgene identifiers and arbitrary groupings of genes or pathways.
type	The type of pathway. A character skalar.

Details

For genes without pathway membership, NA list items need to be included in `mapping`. The names of the list comprise the gene universe to test against. The function will access the `ensembl biomaRt` database in order to retrieve the necessary InterPro domain information.

Value

Object of class `ipDataSource`

Author(s)

Florian Hahne

See Also

[gseDomain](#), [getKEGGdata](#)

Examples

```
grouping <- list("653361"=c("pw1", "pw2"), "729230"="pw1",  
               "415117"="pw3")  
dataSource(grouping)
```

domainsignatures-package

Geneset enrichment based on InterPro domain signatures.

Description

Compute similarities to pathways for a set of entrezgene identifiers based on the InterPro domain signature

Details

Package: domainsignatures
 Type: Package
 Version: 1.0
 Date: 2007-07-02
 License: LPGL?

see help for [gseDomain](#) for details

Author(s)

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getKEGGdata

Fetch KEGG annotations and InterPro domains

Description

Get all available KEGG annotations and InterPro domains for a set of entrezgene identifiers from the KEGG annotation package and from the `ensembl biomaRt`.

Usage

```
getKEGGdata(universe=NULL, pathways=NULL, ensemblMart="hsapiens_gene_ensembl")
```

Arguments

universe	Character vector of entrezgene identifiers. This is the global universe of genes to test against.
pathways	Optional character vector of KEGG pathway identifiers. This can be used in order to test for over-representation of only a subset of all the available KEGG pathways.
ensemblMart	Character giving the type of <i>Biomart</i> to use. Defaults to <i>Human Ensembl</i> .

Details

This function is a wrapper around the `KEGG` annotation package and a customized query of the `ensembl biomaRt` database. For the gene identifiers in `universe` and all or a selection of `KEGG` pathways it will fetch the necessary information and create an object of class `ipDataSource` which can later be used as input to `gseDomain`

Value

An object of class `ipDataSource`.

Author(s)

Florian Hahne

See Also

[gseDomain](#)

Examples

```
getKEGGdata()
```

`getKEGGdescription` *KEGG description from ID*

Description

Get description of `KEGG` pathways from a list of `KEGG` identifiers.

Usage

```
getKEGGdescription(ids)
```

Arguments

`ids` Character vector of `KEGG` identifiers

Value

Character vector of `KEGG` descriptions

Author(s)

Florian Hahne

Examples

```
getKEGGdescription("hsa03050")
```

`gseDomain`*Geneset enrichment based on InterPro domain signatures*

Description

Compute the similarity to pathways specified through `dataSource` for a set of entrezgene identifiers.

Usage

```
gseDomain(dataSource, geneset, n=10000, verbose=TRUE, samples=FALSE)
```

Arguments

<code>dataSource</code>	Object of class <code>ipDataSource</code> containing pathway and InterPro domain mappings
<code>geneset</code>	Character vector of entrezgene identifiers
<code>n</code>	Number of subsampling iterations
<code>verbose</code>	Toggle progress report
<code>samples</code>	Logical indicating whether to return the similarity measures for all the resamples.

Details

Use this function to compute p-values for similarity of the domain signature of a gene set to all signatures of the pathways defined in `dataSource`. You should have created `dataSource` using either function `dataSource` or `getKEGGdata`.

Value

A list with items

<code>similarity</code>	Named vector of similarity measures for each pathway
<code>pvalue</code>	The p-values of similarity to each pathway. A named vector.

and optional item (if `samples=TRUE`)

<code>dist</code>	A named list containing similarity measures for all the resamples
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Author(s)

Florian Hahne

See Also

[gseDomain](#)

Examples

```
## see Vignette of this package for examples how to use this function
```

ipDataSource-class *A class to store mapping information between genes, pathways and interPro domains*

Description

This class represents the data necessary to run [gseDomain](#)

Details

You should always create these objects using either one of the functions [dataSource](#) or [getKEGGdata](#).

Creating Objects

Objects can be created using

```
new('ipDataSource',  
genes = ...., # Object of class character  
pathways = .... # Object of class character  
domains = .... # Object of class character  
gene2Domains = .... # Object of class environment  
path2Domains = .... # Object of class environment  
type = ...., # Object of class character  
)
```

or the functions [dataSource](#) or [getKEGGdata](#).

Slots

genes: Vector of unique entrezgene identifiers

pathways: Vector of unique pathway identifiers

domains: Vector of unique InterPro identifiers

gene2Domains: Hash table mapping entrezgene IDs to Interpro IDs

path2Domains: Hash table mapping pathway IDs to InterPro IDs

type: Type of pathway. A character skalar

dims: Numeric vector of dimensions

Methods

show display summary.

Author(s)

Florian Hahne

See Also

[dataSource](#) or [getKEGGdata](#)

Index

*Topic **IO**

- dataSource, 1
- getKEGGdata, 2
- getKEGGdescription, 3

*Topic **classes**

- ipDataSource-class, 5

*Topic **manip**

- gseDomain, 4

*Topic **package**

- domainsignatures-package, 2

dataSource, 1, 4, 5

domainsignatures
(domainsignatures-package),
2

domainsignatures-package, 2

getKEGGdata, 1, 2, 4, 5

getKEGGdescription, 3

gseDomain, 1-3, 4, 4, 5

ipDataSource

(ipDataSource-class), 5

ipDataSource-class, 5

show, ipDataSource-method

(ipDataSource-class), 5