

domainsignatures

October 5, 2010

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 *Biomart* to use. Defaults to *Human Ensembl*.

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](#)

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