domainsignatures
April 19, 2009

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 entrezgene 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)
getKEGGdata

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: LGPL?

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, pathways)

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.

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 KEGG pathways it will fetch the necessary information and create an object of class ipDataSource which can later be used as input to gseDomain
getKEGGdescription

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

dataSource Object of class ipDataSource containing pathway and InterPro domain mappings
geneset Character vector of entrezgene identifiers
n Number of subsampling iterations
verbose Toggle progress report
samples 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

similarity Named vector of similarity measures for each pathway
pvalue The p-values of similarity to each pathway. A named vector.
dist A named list containing similarity measures for all the resamples

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

```r
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

Methods

- **show** display summary.

Author(s)

Florian Hahne

See Also

dataSource or getKEGGdata
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