

# Package ‘domainsignatures’

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**Type** Package

**Title** Geneset enrichment based on InterPro domain signatures

**Version** 1.18.0

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**Description** Find significantly enriched gene classifications in a list of functionally undescrbed genes based on their InterPro domain structure.

**Depends** R (>= 2.4.0), KEGG.db, prada, biomaRt, methods

**Imports** AnnotationDbi

**License** Artistic-2.0

**Collate** AllClasses.R methods-ipDataSource.R zzz.R getKEGGdata.R  
sage.test.R compSimilarities.R sim2Pathway.R  
getKEGGdescription.R resampleGeneLists.R dataSource.R gseDomain.R

**LazyLoad** yes

**biocViews** Annotation, Pathways, GeneSetEnrichment

## R topics documented:

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domainsignatures-package

*Geneset enrichment based on InterPro domain signatures.*

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**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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dataSource*Constructor for annotation object*

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**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**

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

---

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**

```
if(interactive())  
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")
```

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`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
```

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ipDataSource-class	<i>A class to store mapping information between genes, pathways and interPro domains</i>
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### 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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