Package ‘DrugVsDiseasedata’

February 1, 2017

Type Package
Title Drug versus Disease Data
Version 1.10.0
Date 2013-03-15
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Description Data package which provides default disease expression profiles, clusters and annotation information for use with the DrugVsDisease package.

biocViews Homo_sapiens_Data, MicroarrayData
License GPL-3
LazyLoad yes
LazyData yes
Depends R (>= 2.10)
NeedsCompilation no

R topics documented:

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DrugVsDiseasedata-package

Description

Data package to provide default ranked disease profiles, clusters and Cytoscape http://www.cytoscape.org/ file format for the DrugVsDisease package.

Details

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Data loaded automatically in the DrugVsDisease package.

Author(s)

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References


Examples

# load the disease Ranked lists:
data(diseaseRL)

annotationlist Annotation List Matrix

Description

Maps the annotation of Affymetrix platforms from the affy [1] package to the annotation names in BioMaRt [2]

Usage

data(annotationlist)

Format

Matrix 3 rows, 2 columns.
Details

Provided for three Affymetrix platforms HG-U133A, HG-U133A2 and HG-U133Plus2.

References


Examples

data(annocationlist)

---

## cytodisease

### Cytodisease data frame

#### Description

Data frame containing information for generating the Cytoscape SIF file. Contains the connections between the affinity propagation clustering of the disease profiles.

#### Usage

data(cytodisease)

#### Format

A data frame with 85 observations on 4 variables.

#### Details

Columns 1 and 2 contain the names of the nodes connected in the network. The third have the distances according to the GSEA scores and the fourth column is edge type the Running sum Peak Sign (RPS) for which 1 denotes positive correlation and (-1) a negative correlation.

#### Source


#### References


#### Examples

data(cytodisease)
### diseaseClusters

**Disease Clusters Matrix**

**Description**

Containing the names of the disease profiles and the numbers of the clusters for each node, as determined by affinity propagation clustering using GSEA scores for similarity matrix.

**Usage**

```r
data(diseaseClusters)
```

**Format**

A data frame with 85 observations on 2 variables.

**Details**

Contains the cluster assignments for each of the disease profiles. The clusters were obtained using similarity scores from GSEA as input to the affinity propagation clustering method.

**Source**


**References**


**Examples**

```r
data(diseaseClusters)
```

### diseaselabels

**Disease experiment names map to MeSH queries**

**Description**

Data frame containing the names of the experiments in the disease clusters, with the corresponding search terms to use in the MeSH browser through NCBI.

**Usage**

```r
data(diseaselabels)
```

**Details**

Character matrix containing the names of the disease profiles in the DvDdata reference set in the first column [1]. Second column contains the corresponding search term that can be used in the MeSH browser.
diseaseRL

Source


References


Examples

data(diseaseRL)

diseaseRL  Disease Ranked List Matrix

Description

Ranked Lists by expression of genes for reference set of disease profiles.

Usage

data(diseaseRL)

Details

Matrix containing ranks of genes (rows) for a set of disease profiles (columns). The ranks are in decreasing order of differential expression.

Source


References


Examples

data(diseaseRL)
genelist  

**Gene List Vector**

**Description**
List of HUGO genes included in the reference data sets.

**Usage**
```r
data(genelist)
```

**Details**

**References**

**Examples**
```r
data(genelist)
```

---

GEOfactorvalues  

**GEO Factor Values vector**

**Description**
List of possible factor values the GEO data sets can have.

**Usage**
```r
data(GEOfactorvalues)
```

**Details**
This character vector lists all the available experimental factors which are available in the GEO which can be used explanatory factors in a linear regression model.

**Source**

**Examples**
```r
data(GEOfactorvalues)
```
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