Package ‘DvDdata’

March 23, 2017

Type Package

Title Drug versus Disease Data

Version 1.10.0

Date 2012-07-24

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Description Data package which provides default drug and disease expression profiles for the DvD package.

License GPL-3

LazyLoad yes

LazyData yes

Depends R (>= 2.10)

biocViews GEO

NeedsCompilation no

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DvD Data Package

Description

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

Details

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<tr>
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<td>Version:</td>
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<td>2012-05-16</td>
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<td>LazyLoad:</td>
<td>yes</td>
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Data loaded automatically in the DvD package.

Author(s)

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References


Examples

#load the disease Ranked lists:
data(diseaseRL)

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(annotlist)

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**

---

**cytodrug**  
* Cytodrug data frame

**Description**

Data frame containing information for input into Cytoscape SIF file format. Contains the connections between the affinity propagation clustering of the drug profiles.

**Usage**

```r
data(cytodrug)
```

**Format**

A data frame with 1309 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**

http://www.broadinstitute.org/genome_bio/connectivitymap.html

**References**


**Examples**

```r
data(cytodrug)
```

---

**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)
```
**diseaselabels**

**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 DvD data reference set in the first column [1]. Second column contains the corresponding search term that can be used in the MeSH browser.

**Source**


**References**


**Examples**

```r
data(diseaselabels)
```
**diseaseRL**

*Disease Ranked List Matrix*

**Description**

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

**Usage**

```r
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**

```r
data(diseaseRL)
```

---

**drugClusters**

*Drug Clusters Matrix*

**Description**

Containing the names of the drug 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(drugClusters)
```

**Format**

A data frame with 1309 observations on 2 variables.

**Details**

A Data frame containing the names of the compounds in the DvDdata reference set in the first column. The second column contains the cluster they were assigned to using GSEA to calculate similarity between profiles used as input into affinity propagation clustering.
Source

http://www.broadinstitute.org/genome_bio/connectivitymap.html

References


Examples

data(drugClusters)

druglabels

<table>
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<th>Drug name maps to Drug Bank</th>
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<tr>
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Description

Data frame containing the names of the compounds in the DvDdata drug profiles, with corresponding names to search the DrugBank [1] database through its web browser.

Usage

data(druglabels)

Source

http://www.broadinstitute.org/cmap/

References


Examples

data(druglabels)
**Drug Ranked List Matrix**

**Description**

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

**Usage**

`data(drugRL)`

**Details**

A matrix containing the ranked lists of expression profiles for the 1309 drug compounds in the Connectivity Map (version 2) screening. Rows are the genes and the columns contain ranked lists for different drugs. The profiles are in rank decreasing order.

**Source**

http://www.broadinstitute.org/genome_bio/connectivitymap.html

**References**


**Examples**

`data(drugRL)`

**Gene List Vector**

**Description**

List of HUGO genes included in the reference data sets.

**Usage**

`data(genelist)`

**Details**

References

Examples
data(genelist)

---

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<th>GEOfactorvalues</th>
<th>GEO Factor Values vector</th>
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Description
List of possible factor values the GEO data sets can have.

Usage
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
data(GEOfactorvalues)
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