Package ‘DvDdata’

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Type Package

Title Drug versus Disease Data

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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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**DvDdata-package**  
*DvD Data Package*

**Description**


**Details**

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<tr>
<td>Type:</td>
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<tr>
<td>Version:</td>
<td>1.0</td>
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<tr>
<td>Date:</td>
<td>2012-05-16</td>
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<td>License:</td>
<td>GPL-2</td>
</tr>
<tr>
<td>LazyLoad:</td>
<td>yes</td>
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</tbody>
</table>

Data loaded automatically in the DvD package.

**Author(s)**

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**References**


**Examples**

```r
#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**

```r
data(annotationlist)
```

**Format**

Matrix 3 rows, 2 columns.
cytodisease

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

References

Examples
data(annotationlist)

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

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
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
data(cytodrug)

diseaseClusters

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
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)
```

---

<table>
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<tr>
<th>diseaselabels</th>
<th>Disease experiment names map to MeSH queries</th>
</tr>
</thead>
</table>

**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.

**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**

`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)`


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**

`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.
**druglabels**

**Source**

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

**References**


**Examples**

```r
data(drugClusters)
```

<table>
<thead>
<tr>
<th>druglabels</th>
<th>Drug name maps to Drug Bank</th>
</tr>
</thead>
</table>

**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**

```r
data(druglabels)
```

**Source**

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

**References**


**Examples**

```r
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**

GEOfactorvalues

References

Examples
data(genelist)

---

GEOfactorvalues GEO Factor Values vector

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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