

# Package ‘DrugVsDiseasedata’

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**Type** Package

**Title** Drug versus Disease Data

**Version** 1.40.0

**Date** 2013-03-15

**Author** C. Pacini

**Maintainer** J. Saez-Rodriguez <saezrodriguez@ebi.ac.uk>

**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)

**git\_url** <https://git.bioconductor.org/packages/DrugVsDiseasedata>

**git\_branch** RELEASE\_3\_19

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DrugVsDiseasedata-package

*DrugVsDisease Data Package*

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## Description

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

## Details

Package:	DrugVsDiseasedata
Type:	Package
Version:	1.0
Date:	2012-05-16
License:	GPL-2
LazyLoad:	yes

Data loaded automatically in the DrugVsDisease package.

## Author(s)

C. Pacini

Maintainer: Julio Saez-Rodriguezsaezrodriguez@ebi.ac.uk

## References

Disease Profiles: <http://www.ncbi.nlm.nih.gov/geo/>

## Examples

```
#load the disease Ranked lists:  
data(diseaseRL)
```

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annotationlist	<i>Annotation List Matrix</i>
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**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**

[1]Irizarry et al. (2003) Summaries of Affymetrix GeneChip probe level data. *Nucleic Acids Research*, 31(4); e15.

[2]Durinck et al. (2009). Mapping identifiers for the integration of genomic datasets with the R/Bioconductor package biomaRt. *Nature Protocols* 4, 1184-1191.

**Examples**

```
data(annotationlist)
```

---

cytodisease	<i>Cytodisease data frame</i>
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**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**

<http://www.ncbi.nlm.nih.gov/geo/>

**References**

Barrett T et al. (2011) NCBI GEO: archive for functional genomics data sets-10 years on. Nucl. Acids Res, 39, D1005-D1010.

Iorio et al. (2010) Discovery of drug mode of action and drug repositioning from transcriptional responses. PNAS, 107(33), 14621- 14626.

**Examples**

```
data(cytodisease)
```

---

diseaseClusters	<i>Disease Clusters Matrix</i>
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**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)
```

**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**

<http://www.ncbi.nlm.nih.gov/geo/>

**References**

<http://www.ncbi.nlm.nih.gov/geo/>

**Examples**

```
data(diseaseClusters)
```

---

diseaselabels	<i>Disease experiment names map to MeSH queries</i>
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**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**

```
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**

<http://www.ncbi.nlm.nih.gov/mesh/>

**References**

[1] Barrett T, Troup DB, Wilhite SE, Ledoux P, Evangelista C, Kim IF, Tomashevsky M, Marshall KA, Phillippy KH, Sherman PM, Muetter RN, Holko M, Ayanbule O, Yefanov A, Soboleva A. NCBI GEO: archive for functional genomics data sets 10 years on. *Nucleic Acids Res.* 2011 Jan;39(Database issue):D1005-10

**Examples**

```
data(diseaselabels)
```

---

`diseaseRL`*Disease Ranked List Matrix*

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**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**

<http://www.ncbi.nlm.nih.gov/geo/>

**References**

<http://www.ncbi.nlm.nih.gov/geo/>

**Examples**

```
data(diseaseRL)
```

---

`genelist`*Gene List Vector*

---

**Description**

List of HUGO genes included in the reference data sets.

**Usage**

```
data(genelist)
```

**Details**

A character vector listing those genes in the reference data sets. Obtained using BioMart annotations of the Affymetrix HGU-133A, HGU-133A2 and HGU-133Plus2 platforms.

**References**

Durinck et al. (2009). Mapping identifiers for the integration of genomic datasets with the R/Bioconductor package biomaRt. Nature Protocols 4, 1184-1191.

**Examples**

```
data(genelist)
```

---

GEOfactorvalues	<i>GEO Factor Values vector</i>
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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**

<http://www.ncbi.nlm.nih.gov/geo/>

**Examples**

```
data(GEOfactorvalues)
```

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