Package 'DrugVsDiseasedata'

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Type Package

Title Drug versus Disease Data

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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)

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`DrugVsDiseasedata-package`
DrugVsDisease Data Package

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.

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References

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

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

[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 *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

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

References

Barrett T et al. (2011) NCBI GEO: archive for func- tional 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 *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

```
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` *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

```
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, Muertter 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*

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` *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

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

Examples

```
data(GEOfactorvalues)
```

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