Package 'cMap2data'

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Type Package

Title Connectivity Map (version 2) Data

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Description Data package which provides default drug profiles for the DrugVsDisease package as well as associated gene lists and data clusters used by the DrugVsDisease package.

License GPL-3

biocViews Homo_sapiens_Data, MicroarrayData, GEO

LazyLoad yes

LazyData yes

Depends R (>= 2.10)

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cMap2data-package *cMap2 Data Package*

Description

Data package to provide default ranked profiles, clusters and Cytoscape http://www.cytoscape.org/ file format for the DrugVsDisease package. The data is from drug screenings in the connectivity map (version 2) which is a project based at the Broad Institute of MIT and Harvard in Cambridge, Massachusetts (USA).

Details

Package:	cMap2data
Type:	Package
Version:	0.99.0
Date:	2012-09-20
License:	GPL-3
LazyLoad:	yes

Data loaded automatically in the DrugVsDisease package.

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References

Drug Profiles: http://www.broadinstitute.org/cmap/ Disease Profiles: http://www.ncbi.nlm.nih.gov/geo/

Examples

```
#load the gene Ranked lists:
data(drugRL)
```

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

```
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

Lamb J et al. (2006) The Connectivity Map: Using Gene- Expression Signatures to Connect Small Molecules, Genes, and Disease. Science, 313(5795), 1929-1935.

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

Examples

```
data(cytodrug)
```

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. The drug profiles are derived from the Connectivity Map version 2 which is a project based at the Broad Institute of MIT and Harvard Cambridge, Massachusetts (USA)

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.

Source

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

References

Lamb J et al. (2006) The Connectivity Map: Using Gene- Expression Signatures to Connect Small Molecules, Genes, and Disease. Science, 313(5795), 1929-1935.

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

Examples

```
data(drugClusters)
```

druglabels *Drug name maps to Drug Bank*

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

[1] DrugBank 3.0: a comprehensive resource for 'omics' research on drugs. Knox C, Law V, Jewison T, Liu P, Ly S, Frolkis A, Pon A, Banco K, Mak C, Neveu V, Djoumbou Y, Eisner R, Guo AC, Wishart DS. Nucleic Acids Res. 2011 Jan;39(Database issue):D1035-41.

[2] The Connectivity Map: Using Gene-Expression Signatures to Connect Small Molecules, Genes, and Disease. Lamb J et al. Science 29 September 2006: 313 (5795), 1929-1935. [DOI:10.1126/science.1132939]

Examples

```
data(druglabels)
```

drugRL *Drug Ranked List Matrix*

Description

Ranked Lists by expression of genes for reference set of drug profiles. These drug profiles are derived from the Connectivity map (version 2) project which is based at the Broad Institute of MIT and Harvard in Cambridge, Massachusetts (USA)

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

Lamb J et al. (2006) The Connectivity Map: Using Gene- Expression Signatures to Connect Small Molecules, Genes, and Disease. Science, 313(5795), 1929-1935.

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

Examples

```
data(drugRL)
```

---

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)
```

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