Package ‘cMap2data’

February 1, 2017

Type Package
Title Connectivity Map (version 2) Data
Version 1.10.0
Date 2012-07-24
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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)
NeedsCompilation no

R topics documented:

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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).
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

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

---

**cytodrug**

*Cytodrug data frame*

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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
```r
data(cytodrug)
```

drugClustes 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

Examples
```r
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**

```r
data(druglabels)
```

**Source**


**References**


**Examples**

```r
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**

```r
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](http://www.broadinstitute.org/genome_bio/connectivitymap.html)
References


Examples

data(drugRL)

genelist

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Description

List of HUGO genes included in the reference data sets.

Usage

data(genelist)

Details


References


Examples

data(genelist)
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