Package ‘ConnectivityMap’

October 1, 2024

Type Package

Title Functional connections between drugs, genes and diseases as revealed by common gene-expression changes

Version 1.41.0

Date 2013-03-15

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Depends R (>= 2.15.1)

Suggests RUnit, BiocGenerics

Description The Broad Institute's Connectivity Map (cmap02) is a ``large reference catalogue of gene-expression data from cultured human cells perturbed with many chemicals and genetic reagents", containing more than 7000 gene expression profiles and 1300 small molecules.

biocViews ExperimentData, CancerData, MicroarrayData

License GPL-3

git_url https://git.bioconductor.org/packages/ConnectivityMap

git_branch devel

git_last_commit 94489a2

git_last_commit_date 2024-04-30

Repository Bioconductor 3.20

Date/Publication 2024-10-01

Contents

`ConnectivityMap` *ConnectivityMap: Functional connections between drugs, genes and diseases as revealed by common gene-expression changes*

Description

The Broad Institute's Connectivity Map (cmap02) http://www.broadinstitute.org/cmap/

is a "large reference catalogue of gene-expression data from cultured human cells perturbed with many chemicals and genetic reagents", containing more than 7000 gene expression profiles and 1300 small molecules. Quoting further:

To pursue a systematic approach to the discovery of functional connections among diseases, genetic perturbation, and drug action, we have created the first installment of a reference collection of gene-expression profiles from cultured human cells treated with bioactive small molecules, together with pattern-matching software to mine these data. We demonstrate that this "Connectivity Map" resource can be used to find connections among small molecules sharing a mechanism of action, chemicals and physiological processes, and diseases and drugs. These results indicate the feasibility of the approach and suggest the value of a large-scale community Connectivity Map project.

This data package contains two data objects, obtained with permission from the Broad Institute, transformed very modestly, and presented as serialied *RData* objecgs:

- *rankMatrix*: 22283 rows (human Affymetrix probeIDs) x 6100 perturbation "instances"
- *instances*: 14 columns of metadata describing each of the 6100 instances.

The metadata matrix, *instances* has these columns:

- instance_id
- batch_id
- cmap_name
- INN1
- concentration (M) (appears as "conentration..M.")
- duration (h) (appears as "duration..h.")
- cell2
- array3
- perturbation_scan_id
- vehicle_scan_id4
- scanner
- vehicle
- vendor
- catalog_number
- catalog_name

References

Lamb, Justin, et al. "The Connectivity Map: using gene-expression signatures to connect small molecules, genes, and disease." Science Signalling 313.5795 (2006): 1929.

Lamb, Justin. "The Connectivity Map: a new tool for biomedical research." Nature Reviews Cancer 7.1 (2007): 54-60.

Examples

```
library(ConnectivityMap)
data(rankMatrix)
data(instances)
print(table(instances$cell2))
   # identify the pertubrations in the rankMatrix from the SKMEL5 skin
   # melanoma cell line
skmel.instance.names <- rownames(subset(instances, cell2=="SKMEL5"))
matrix.skmel <- rankMatrix[, skmel.instance.names]
```

Index