

# Package ‘ConnectivityMap’

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**Type** Package

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

**Version** 1.44.0

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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

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## Contents

ConnectivityMap . . . . .	2
<b>Index</b>	<b>4</b>

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

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## 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 serialised *RData* objects:

- *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 "concentration..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 perturbations 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

## \* **datasets**

ConnectivityMap, [2](#)

ConnectivityMap, [2](#)

instances (ConnectivityMap), [2](#)

rankMatrix (ConnectivityMap), [2](#)