Package ‘ccdata’

November 18, 2025

Title Data for Combination Connectivity Mapping (ccmap) Package

Version 1.37.0

Author Alex Pickering

Maintainer Alex Pickering <`alexvpickering@gmail.com`>

Description This package contains microarray gene expression data generated from the Connectivity Map build 02 and LINCS l1000. The data are used by the ccmap package to find drugs and drug combinations to mimic or reverse a gene expression signature.

Depends R (>= 3.3)

License MIT + file LICENSE

LazyData false

biocViews ExperimentData, MicroarrayData, ExpressionData

RoxygenNote 6.0.1

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

git_branch devel

git_last_commit 0d2b81b

git_last_commit_date 2025-10-29

Repository Bioconductor 3.23

Date/Publication 2025-11-18

Contents

`cmap_es` *Effect size values for Connectivity Map build 02 drugs.*

Description

Moderated unbiased effect sizes values for all 1309 drugs in the Connectivity Map build 02.

Usage

```
data(cmap_es)
```

Format

An object of class `matrix` with 13832 rows and 1309 columns.

Details

Calculated as described by Marot et al (see reference) using `toptable` from limma and `effectsize` from metaMA.

Value

A matrix where columns correspond to drugs and rows to gene symbols.

References

Marot G, Foulley JL, Mayer CD, Jaffrézic F. Moderated effect size and P-value combinations for microarray meta-analyses. Bioinformatics. 2009 Oct 15;25(20):2692-9. doi: 10.1093/bioinformatics/btp444.

`cmap_var` *Variance values for Connectivity Map build 02 drugs.*

Description

Variances of unbiased effect sizes values for all 1309 drugs in the Connectivity Map build 02.

Usage

```
data(cmap_var)
```

Format

An object of class `matrix` with 13832 rows and 1309 columns.

Details

Calculated as described by Marot et al (see reference) using `toptable` from limma and `effectsize` from metaMA.

Value

A matrix where columns correspond to drugs and rows to gene symbols.

References

Marot G, Foulley JL, Mayer CD, Jaffrézic F. Moderated effect size and P-value combinations for microarray meta-analyses. Bioinformatics. 2009 Oct 15;25(20):2692-9. doi: 10.1093/bioinformatics/btp444.

`genes` *HGNC symbols used for NNet predictions.*

Description

Order is as required for input and produced by output of net1/net2 predictions.

Usage

```
data(genes)
```

Format

An object of class `character` of length 11525.

Value

A character vector of 11525 HGNC symbols.

`l1000_es` *Effect size values for LINCS l1000 signatures.*

Description

Moderated unbiased effect sizes values for all 230829 LINCS l1000 signatures.

Usage

```
data(l1000_es)
```

Format

An object of class `matrix` with 1001 rows and 230829 columns.

Details

Calculated as described by Marot et al (see reference) using `toptable` from limma and `effectsize` from metaMA.

Value

A matrix where columns correspond to perturbagens and rows to gene symbols.

References

Marot G, Foulley JL, Mayer CD, Jaffrézic F. Moderated effect size and P-value combinations for microarray meta-analyses. Bioinformatics. 2009 Oct 15;25(20):2692-9. doi: 10.1093/bioinformatics/btp444.

`net1` *Neural network model 1 for treatment combinations.*

Description

Contains weight matrices and bias vectors needed to make predictions.

Usage

```
#NA
```

Format

An object of class `list` of length 4.

Value

List with matrices W1/W2 and vectors b1/b2.

`net2` *Neural network model 2 for treatment combinations.*

Description

Contains weight matrices and bias vectors needed to make predictions.

Usage

```
#NA
```

Format

An object of class `list` of length 4.

Value

List with matrices W1/W2 and vectors b1/b2.

`xgb_mod` *XGBoost model for treatment combinations.*

Description

Model stacks predictions from net1 and net2 with effect size values from cmap_es and variance values from cmap_var.

Usage

```
#NA
```

Format

An object of class `xgb.Booster` of length 2.

Value

Object of class xgb.Booster

Index