

# Package ‘ccdata’

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**Title** Data for Combination Connectivity Mapping (ccmap) Package

**Version** 1.32.0

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**Description** This package contains microarray gene expression data generated from the Connectivity Map build 02 and LINCS 11000. 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

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cmap\_es

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

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### **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.

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cmap\_var

*Variance values for Connectivity Map build 02 drugs.*

---

### **Description**

Variations 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.

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|       |  |
|-------|--|
| genes | <i>HGNC symbols used for NNet predictions.</i> |
|-------|--|

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**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.

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|          |   |
|----------|---|
| 11000_es | <i>Effect size values for LINCS 11000 signatures.</i> |
|----------|---|

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**Description**

Moderated unbiased effect sizes values for all 230829 LINCS 11000 signatures.

**Usage**

```
data(11000_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.

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net1

*Neural network model 1 for treatment combinations.*

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**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.

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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.

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`xgb_mod`*XGBoost model for treatment combinations.*

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**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`

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