# Package 'ccdata'

April 13, 2017	
Title Data for Combination Connectivity Mapping (ccmap) Package	
Version 1.0.0	
Author Alex Pickering	
Maintainer Alex Pickering <alexvpickering@gmail.com></alexvpickering@gmail.com>	
<b>Description</b> This package contains microarray gene expression data generated from the Connectivity Map build 02. The data are used by the ccmap package to find drugs and drug combinations to mimic or reverse a gene expression signature.	
<b>Depends</b> R (>= 3.3)	
License MIT + file LICENSE	
LazyData false	
biocViews ExperimentData, MicroarrayData, ExpressionData	
RoxygenNote 5.0.1	
NeedsCompilation no	
R topics documented:	
cmap_es	
	_
cmap_es Effect size values for Connectivity Map build 02 drugs.	
Description	
Unbiased effect sizes values for all 1309 drugs in the Connectivity Map build 02.	
Usage	
data(cmap_es)	
1	

2 genes

#### **Format**

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

#### Value

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

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.

#### Value

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

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.

net1 3

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

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**

```
*Topic datasets
cmap_es, 1
cmap_var, 2
genes, 2
net1, 3
net2, 3
xgb_mod, 4

cmap_es, 1
cmap_var, 2
genes, 2
net1, 3
net2, 3
xgb_mod, 4
```