Package ‘PharmacoGx’

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Type Package

Title Analysis of Large-Scale Pharmacogenomic Data

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Description Contains a set of functions to perform large-scale analysis of pharmacogenomic data. These include the PharmacoSet object for storing the results of pharmacogenomic experiments, as well as a number of functions for computing common summaries of drug-dose response and correlating them with the molecular features in a cancer cell-line.

License GPL (>= 3)

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R topics documented:

'computeAUC.R' 'computeAUC_old.R' 'computeAmax.R'
'computeDSS.R' 'computeDrugSensitivity.R' 'computeGR.R'
'computeIC50.R' 'computeICn.R' 'computeSlope.R'
'computeSynergy.R' 'connectivityScore.R' 'cosinePerm.R'
'datasets.R' 'downloadPSet.R' 'downloadSignatures.R'
'drugDoseResponseCurve.R' 'drugPerturbationSig.R'
'filterNoisyCurves.R' 'geneDrugPerturbation.R'
'geneDrugSensitivityPCorr.R' 'getRawSensitivityMatrix.R'
'globals.R' 'intersectPSets.R' 'logLogisticRegression.R'
'matthewCor.R' 'mergePSets.R' 'methods-.R'
'methods-drugSensitivitySig.R' 'methods-intersect.R'
'methods-subsetTo.R' 'methods-summarizeMolecularProfiles.R'
'methods-summarizeSensitivityProfiles.R' 'plotPSetSig.R'
'rankGeneDrugPerturbation.R' 'rankGeneDrugSensitivity.R'
'rankGeneDrugPerturbation.R' 'sanityCheck.R' 'updateObject-methods.R' 'zzz.R'

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Vector-based version of computeZIPdelta

Description
Following the calculation of ZIP delta score as in Appendix A3. See reference for details.

Usage
.computeZIPdelta(
  treatment1id, # character a vector of identifiers for treatment 1
  treatment2id, # character a vector of identifiers for treatment 2
  treatment1dose, # numeric a vector of concentrations for treatment 1
  treatment2dose, # numeric a vector of concentrations for treatment 2
  sampleid, # character Cell-line ID of a drug combination screening experiment.
  HS_1, # numeric Hill coefficient of treatment 1
  HS_2, # numeric Hill coefficient of treatment 2
  EC50_1, # numeric relative EC50 of treatment 1.
  EC50_2, # numeric relative EC50 of treatment 2.
  E_inf_1, # numeric viability produced by the maximum attainable effect of treatment 1.
  E_inf_2, # numeric viability produced by the maximum attainable effect of treatment 2.
  combo_viability, # numeric observed viability of the two treatments combined.
  ZIP = NULL, #
  residual = "logcosh", #
  nthread = 1L, #
  show_Rsqr = FALSE #
)

Arguments
- treatment1id: character a vector of identifiers for treatment 1
- treatment2id: character a vector of identifiers for treatment 2
- treatment1dose: numeric a vector of concentrations for treatment 1
- treatment2dose: numeric a vector of concentrations for treatment 2
- sampleid: character Cell-line ID of a drug combination screening experiment.
- HS_1: numeric Hill coefficient of treatment 1
- HS_2: numeric Hill coefficient of treatment 2
- EC50_1: numeric relative EC50 of treatment 1.
- EC50_2: numeric relative EC50 of treatment 2.
- E_inf_1: numeric viability produced by the maximum attainable effect of treatment 1.
- E_inf_2: numeric viability produced by the maximum attainable effect of treatment 2.
- combo_viability: numeric observed viability of the two treatments combined.
ZIP numeric pre-computed ZIP reference values. If not provided, it will be computed during delta score calculation.

residual character Method used to minimise residual in fitting curves. 3 methods available: c("logcosh", "normal", "Cauchy"). The default method is logcosh. It minimises the logarithmic hyperbolic cosine loss of the residuals and provides the fastest estimation among the three methods, with fitting quality in between normal and Cauchy; recommended when fitting large-scale datasets. The other two methods minimise residuals by considering the truncated probability distribution (as in their names) for the residual. Cauchy provides the best fitting quality but also takes the longest to run.

nthread integer Number of cores used to perform computation. Default 1.

show_Rsqr logical Whether to show the 2-way curve fitting quality in the result. Default FALSE.

Value
numeric delta scores of every dose combinations for any given treatment combinations.

References

Examples
## Not run:
## ZIP is optional. Will be recomputed if not provided.
combo_profiles <- CoreGx::buildComboProfiles(tre, c("HS", "EC50", "E_inf", "ZIP", "combo_viability"))
combo_profiles[, .computeZIPdelta(
    treatment1id = treatment1id,
    treatment2id = treatment2id,
    treatment1dose = treatment1dose,
    treatment2dose = treatment2dose,
    sampleid = sampleid,
    HS_1 = HS_1, HS_2 = HS_2,
    EC50_1 = EC50_1, EC50_2 = EC50_2,
    E_inf_1 = E_inf_1, E_inf_2 = E_inf_2,
    combo_viability = combo_viability,
    ZIP = ZIP,
    nthread = 4,
    show_Rsqr = TRUE
) ] -> delta_scores

## End(Not run)
.summarizeSensProfiles

*Summarize the sensitivity profiles when the sensitivity slot is a LongTable*

**Description**

Summarize the sensitivity profiles when the sensitivity slot is a LongTable

**Usage**

```r
.summarizeSensProfiles(
  object,
  sensitivity.measure = "auc_recomputed",
  cell.lines,
  drugs,
  summary.stat,
  fill.missing = TRUE
)
```

**Value**

*matrix* A matrix with cell lines going down the rows, drugs across the columns, with the selected sensitivity statistic for each pair.

---

amcc

*Adaptive Matthews Correlation Coefficient*

**Description**

This function calculates an Adaptive Matthews Correlation Coefficient (AMCC) for two vectors of values of the same length. It assumes the entries in the two vectors are paired. The Adaptive Matthews Correlation Coefficient for two vectors of values is defined as the Maximum Matthews Coefficient over all possible binary splits of the ranks of the two vectors. In this way, it calculates the best possible agreement of a binary classifier on the two vectors of data. If the AMCC is low, then it is impossible to find any binary classification of the two vectors with a high degree of concordance.

**Usage**

```r
amcc(x, y, step.prct = 0, min.cat = 3, nperm = 1000, nthread = 1)
```
Arguments

x, y Two paired vectors of values. Could be replicates of observations for the same experiments for example.

step.prct Instead of testing all possible splits of the data, it is possible to test steps of a percentage size of the total number of ranks in x/y. If this variable is 0, function defaults to testing all possible splits.

min.cat The minimum number of members per category. Classifications with less members fitting into both categories will not be considered.

nperm The number of permutation to use for estimating significance. If 0, then no p-value is calculated.

nthread Number of threads to parallelize over. Both the AMCC calculation and the permutation testing is done in parallel.

Value

Returns a list with two elements. $amcc$ contains the highest ’mcc’ value over all the splits, the p value, as well as the rank at which the split was done.

Examples

amcc(0.6^(1:5), 0.5^(1:5))

availablePSets

Return a table of PharmacoSets available for download

Description

The function fetches a table of all PharmacoSets available for download. The table includes the dataset names, version information for the data in the PSet, the date of last update, the name of the PSet, and references for the data contained within, a DOI for the data, and a direct download link. Download can also be done using the downloadPSet function.

Usage

availablePSets(canonical = TRUE)

Arguments

canonical logical(1) Should available PSets show only official PSets, or should user generated PSets be included?

Details

Much more information on the processing of the data and data provenance can be found at: www.orcestra.ca
callingWaterfall

Value

A data.frame with details about the available PharmacoSet objects

Examples

```r
if (interactive()){
    availablePSets()
}
```

callingWaterfall  Drug sensitivity calling using waterfall plots

Description

1. Sensitivity calls were made using one of IC50, ActArea or Amax

Usage

```r
callingWaterfall(
    x,
    type = c("IC50", "AUC", "AMAX"),
    intermediate.fold = c(4, 1.2, 1.2),
    cor.min.linear = 0.95,
    name = "Drug",
    plot = FALSE
)
```

Arguments

- **x**: What type of object does this take in?
- **type**: ic50: IC50 values in micro molar (positive values) actarea: Activity Area, that is area under the drug activity curve (positive values) amax: Activity at max concentration (positive values)
- **intermediate.fold**: vector of fold changes used to define the intermediate sensitivities for ic50, actarea and amax respectively
- **cor.min.linear**: numeric The minimum linear correlation to require?
- **name**: character The name of the output to use in plot
- **plot**: boolean Whether to plot the results
Details

1. Sort log IC50s (or ActArea or Amax) of the samples to generate a “waterfall distribution”
2. Identify cutoff:
   3.1 If the waterfall distribution is non-linear (pearson cc to the linear fit <=0.95), estimate the major inflection point of the log IC50 curve as the point on the curve with the maximal distance to a line drawn between the start and end points of the distribution.
   3.2 If the waterfall distribution appears linear (pearson cc to the linear fit > 0.95), then use the median IC50 instead.

   1. Samples within a 4-fold IC50 (or within a 1.2-fold ActArea or 20% Amax difference) difference centered around this inflection point are classified as being “intermediate”, samples with lower IC50s (or ActArea/Amax values) than this range are defined as sensitive, and those with IC50s (or ActArea/Amax) higher than this range are called “insensitive”.
   2. Require at least x sensitive and x insensitive samples after applying these criteria (x=5 in our case).

Value

factor Containing the drug sensitivity status of each sample.

Examples

# Dummy example
1 + 1

Description

A small example version of the CCLE PharmacoSet, used in the documentation examples. All credit for the data goes to the CCLE group at the Broad Institute. This is not a full version of the dataset, most of of the dataset was removed to make runnable example code. For the full dataset, please download using the downloadPSet function.

Usage

data(CCLEsmall)

Format

PharmacoSet object

References

checkPsetStructure  

A function to verify the structure of a PharmacoSet

Description

This function checks the structure of a PharmacoSet, ensuring that the correct annotations are in place and all the required slots are filled so that matching of cells and drugs can be properly done across different types of data and with other studies.

Usage

checkPsetStructure(object, plotDist = FALSE, result.dir = ".")

Arguments

object  
A PharmacoSet to be verified

plotDist  
Should the function also plot the distribution of molecular data?

result.dir  
The path to the directory for saving the plots as a string

Value

Prints out messages whenever describing the errors found in the structure of the object object passed in.

Examples

data(CCLEsmall)
checkPsetStructure(CCLEsmall)

CMAPsmall  

Connectivity Map Example PharmacoSet

Description

A small example version of the Connectivity Map PharmacoSet, used in the documentation examples. All credit for the data goes to the Connectivity Map group at the Broad Institute. This is not a full version of the dataset, most of the dataset was removed to make runnable example code. For the full dataset, please download using the downloadPSet function.

Usage

data(CMAPsmall)
computeABC

Format

PharmacoSet object

References


__computeABC__

Fits dose-response curves to data given by the user and returns the ABC of the fitted curves.

Description

Fits dose-response curves to data given by the user and returns the ABC of the fitted curves.

Usage

```r
computeABC(
  conc1,
  conc2,
  viability1,
  viability2,
  Hill_fit1,
  Hill_fit2,
  conc_as_log = FALSE,
  viability_as_pct = TRUE,
  trunc = TRUE,
  verbose = TRUE
)
```

Arguments

- **conc1** numeric is a vector of drug concentrations.
- **conc2** numeric is a vector of drug concentrations.
- **viability1** numeric is a vector whose entries are the viability values observed in the presence of the drug concentrations whose logarithms are in the corresponding entries of conc1, expressed as percentages of viability in the absence of any drug.
- **viability2** numeric is a vector whose entries are the viability values observed in the presence of the drug concentrations whose logarithms are in the corresponding entries of conc2, expressed as percentages of viability in the absence of any drug.
- **Hill_fit1** list or vector In the order: c("Hill Slope", "E_inf", "EC50"), the parameters of a Hill Slope as returned by logLogisticRegression. If conc_as_log is set then the function assumes logEC50 is passed in, and if viability_as_pct flag is set, it assumes E_inf is passed in as a percent. Otherwise, E_inf is assumed to be a decimal, and EC50 as a concentration.
Hill_fit2  lis or vector  In the order: c("Hill Slope", "E_inf", "EC50"), the parameters of a Hill Slope as returned by logLogisticRegression. If conc_as_log is set then the function assumes logEC50 is passed in, and if viability_as_pct flag is set, it assumes E_inf is passed in as a percent. Otherwise, E_inf is assumed to be a decimal, and EC50 as a concentration.

conc_as_log  logical, if true, assumes that log10-concentration data has been given rather than concentration data.

viability_as_pct  logical, if false, assumes that viability is given as a decimal rather than a percentage, and returns ABC as a decimal. Otherwise, viability is interpreted as percent, and AUC is returned 0-100.

trunc  logical, if true, causes viability data to be truncated to lie between 0 and 1 before curve-fitting is performed.

verbose  logical, if true, causes warnings thrown by the function to be printed.

Value
The numeric area of the absolute difference between the two hill slopes

Author(s)
Mark Freeman

Examples

dose1 <- c(0.0025, 0.008, 0.025, 0.08, 0.25, 0.8, 2.53, 8)
viability1 <- c(108.67, 111, 102.16, 100.27, 90, 87, 74, 57)
dose2 <- c(0.0025, 0.008, 0.025, 0.08, 0.25, 0.8, 2.53, 8)
viability2 <- c(100.94, 112.5, 86, 104.16, 75, 68, 48, 29)
computeABC(dose1, dose2, viability1, viability2)

computeAmax  Fits dose-response curves to data given by the user and returns the Amax of the fitted curve. Amax: 100 - viability at maximum concentration (in fitted curve)

Description
Fits dose-response curves to data given by the user and returns the Amax of the fitted curve. Amax: 100 - viability at maximum concentration (in fitted curve)

Usage
computeAmax(concentration, viability, trunc = TRUE, verbose = FALSE)
computeAUC

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>concentration</td>
<td>numeric is a vector of drug concentrations.</td>
</tr>
<tr>
<td>viability</td>
<td>numeric is a vector whose entries are the viability values observed in the presence of the drug concentrations whose logarithms are in the corresponding entries of the log_conc, expressed as percentages of viability in the absence of any drug.</td>
</tr>
<tr>
<td>trunc</td>
<td>logical, if true, causes viability data to be truncated to lie between 0 and 1 before curve-fitting is performed.</td>
</tr>
<tr>
<td>verbose</td>
<td>logical should warnings be printed</td>
</tr>
</tbody>
</table>

Value

The numerical Amax

Examples

dose <- c(0.0025, 0.008, 0.025, 0.08, 0.25, 0.8, 2.53, 8)
viability <- c(108.67, 111, 102.16, 100.27, 90, 87, 74, 57)
computeAmax(dose, viability)

computeAUC

Computes the AUC for a Drug Dose Viability Curve

Description

Returns the AUC (Area Under the drug response Curve) given concentration and viability as input, normalized by the concentration range of the experiment. The area returned is the response (1-Viability) area, i.e. area under the curve when the response curve is plotted on a log10 concentration scale, with high AUC implying high sensitivity to the drug. The function can calculate both the area under a fitted Hill Curve to the data, and a trapz numeric integral of the actual data provided. Alternatively, the parameters of a Hill Slope returned by logLogisticRegression can be passed in if they already known.

Usage

computeAUC(
    concentration,
    viability,
    Hill_fit,
    conc_as_log = FALSE,
    viability_as_pct = TRUE,
    trunc = TRUE,
    area.type = c("Fitted", "Actual"),
    verbose = TRUE
)
Arguments

concentration numeric is a vector of drug concentrations.

viability numeric is a vector whose entries are the viability values observed in the presence of the drug concentrations whose logarithms are in the corresponding entries of conc, where viability 0 indicates that all cells died, and viability 1 indicates that the drug had no effect on the cells.

Hill_fit list or vector In the order: c("Hill Slope", "E_inf", "EC50"), the parameters of a Hill Slope as returned by logLogisticRegression. If conc_as_log is set then the function assumes logEC50 is passed in, and if viability_as_pct flag is set, it assumes E_inf is passed in as a percent. Otherwise, E_inf is assumed to be a decimal, and EC50 as a concentration.

conc_as_log logical, if true, assumes that log10-concentration data has been given rather than concentration data.

viability_as_pct logical, if false, assumes that viability is given as a decimal rather than a percentage, and returns AUC as a decimal. Otherwise, viability is interpreted as percent, and AUC is returned 0-100.

trunc logical, if true, causes viability data to be truncated to lie between 0 and 1 before curve-fitting is performed.

area.type Should the area be computed using the actual data ("Actual"), or a fitted curve ("Fitted")

verbose logical, if true, causes warnings thrown by the function to be printed.

Value

Numeric AUC value

Examples

dose <- c(0.0025,0.008,0.025,0.08,0.25,0.8,2.53,8)
viability <- c(108.67,111,102.16,100.27,90,87,74,57)
computeAUC(dose, viability)

computeBliss

Compute Bliss Null References

Description

Given two numeric containing viability of two monotherapy respectively, Compute Bliss null reference values for the expected response of the two treatments combined.

Usage

computeBliss(viability_1, viability_2)
computeHSA

Arguments

<table>
<thead>
<tr>
<th></th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>viability_1</td>
<td>numeric monotherapeutic response of treatment 1.</td>
</tr>
<tr>
<td>viability_2</td>
<td>numeric monotherapeutic response of treatment 2.</td>
</tr>
</tbody>
</table>

Value

numeric expected response of the two treatments combined using the highest response of the two (lower viability).

Examples

```r
(hsa <- computeHSA(0.75, 0.65))
```
computeIC50

**Description**

Returns the ICn for any given nth percentile when given concentration and viability as input, normalized by the concentration range of the experiment. A Hill Slope is first fit to the data, and the ICn is inferred from the fitted curve. Alternatively, the parameters of a Hill Slope returned by logLogisticRegression can be passed in if they already known.

**Usage**

```r
computeIC50(
  concentration,
  viability,
  Hill_fit,
  conc_as_log = FALSE,
  viability_as_pct = TRUE,
  verbose = TRUE,
  trunc = TRUE
)
```

```r
computeICn(
  concentration,
  viability,
  Hill_fit,
  n,
  conc_as_log = FALSE,
  viability_as_pct = TRUE,
  verbose = TRUE,
  trunc = TRUE
)
```

**Arguments**

- `concentration` numeric is a vector of drug concentrations.
- `viability` numeric is a vector whose entries are the viability values observed in the presence of the drug concentrations whose logarithms are in the corresponding entries of `conc`, where viability 0 indicates that all cells died, and viability 1 indicates that the drug had no effect on the cells.
- `Hill_fit` list or vector In the order: c("Hill Slope", "E_inf", "EC50"), the parameters of a Hill Slope as returned by logLogisticRegression. If conc_as_log is set then the function assumes logEC50 is passed in, and if viability_as_pct flag is set, it assumes E_inf is passed in as a percent. Otherwise, E_inf is assumed to be a decimal, and EC50 as a concentration.
computeLoewe

conc_as_log logical, if true, assumes that log10-concentration data has been given rather than concentration data, and that log10(ICn) should be returned instead of ICn.

viability_as_pct logical, if true, assumes that viability is given as a decimal rather than a percentage, and that E_inf passed in as decimal.

verbose logical, if true, causes warnings thrown by the function to be printed.

trunc logical, if true, causes viability data to be truncated to lie between 0 and 1 before curve-fitting is performed.

n numeric The percentile concentration to compute. If viability_as_pct set, assumed to be percentage, otherwise assumed to be a decimal value.

Value

numeric(1) The ICn of the Hill curve over the specified dose range.

a numeric value for the concentration of the nth percentile viability reduction

Functions

• computeIC50(): Returns the IC50 of a Drug Dose response curve

Examples

dose <- c(0.0025,0.008,0.025,0.08,0.25,0.8,2.5,8)
viability <- c(108.67,111,102.16,100.27,90,87,74,57)
computeIC50(dose, viability)
computeICn(dose, viability, n=10)

computeLoewe Computes Loewe Null References

Description

Predict the response of a treatment combination under the Loewe additive null assumption.

Usage

computeLoewe(
  treatment1dose,
  HS_1,
  E_inf_1,
  EC50_1,
  treatment2dose,
  HS_2,
  E_inf_2,
  EC50_2,
  tol = 0.1,
lower_bound = 0,
upper_bound = 1,
verbose = FALSE
)

Arguments

treatment1dose numeric a vector of concentrations for treatment 1
HS_1 numeric Hill coefficient of treatment 1
E_inf_1 numeric viability produced by the maximum attainable effect of treatment 1.
EC50_1 numeric relative EC50 of treatment 1.
treatment2dose numeric a vector of concentrations for treatment 2
HS_2 numeric Hill coefficient of treatment 2
E_inf_2 numeric viability produced by the maximum attainable effect of treatment 2.
EC50_2 numeric relative EC50 of treatment 2.
tol numeric Error tolerance for deviations from Loewe assumption. Loewe predictions with error higher than tol will be returned as NA. Default 0.1.
lower_bound numeric Lowest possible value for Loewe expected viability. Default 0.
upper_bound numeric Highest possible value for Loewe expected viability. Default 1.
verbose logical whether to display warning messages. Default FALSE.

Value
numeric expected viability under Loewe additive null assumption.

Examples

## Not run:
# run:
 tre |>
 endoaggregate(
   assay = "combo_viability",
   Loewe = computeLoewe(
     treatment1dose = treatment1dose,
     treatment2dose = treatment2dose,
     HS_1 = HS_1,
     HS_2 = HS_2,
     E_inf_1 = E_inf_1,
     E_inf_2 = E_inf_2,
     EC50_1 = EC50_1,
     EC50_2 = EC50_2
   ),
   by = assayKeys(tre, "combo_viability")
 ) -> tre

## End(Not run)
computeSlope

Return Slope (normalized slope of the drug response curve) for an experiment of a pSet by taking its concentration and viability as input.

Description

Return Slope (normalized slope of the drug response curve) for an experiment of a pSet by taking its concentration and viability as input.

Usage

computeSlope(concentration, viability, trunc = TRUE, verbose = TRUE)

Arguments

concentration numeric A concentration range that the AUC should be computed for that range. Concentration range by default considered as not logarithmic scaled. Converted to numeric by function if necessary.

viability numeric Viabilities corresponding to the concentration range passed as first parameter. The range of viability values by definition should be between 0 and 100. But the viabilities greater than 100 and lower than 0 are also accepted.

trunc logical(1) A flag that identify if the viability values should be truncated to be in the range of (0,100)

verbose logical(1) If 'TRUE' the function will retrun warnings and other informative messages.

Value

Returns the normalized linear slope of the drug response curve

Examples

dose <- c(0.0025,0.008,0.025,0.08,0.25,0.8,2.53,8)
viability <- c(108.67,111,102.16,100.27,90,87,74,57)
computeSlope(dose, viability)
computeZIP

Computes ZIP Null References

Description

Predict the additive response of a treatment combination under the ZIP null assumption.

Usage

computeZIP(
  treatment1dose,
  HS_1,
  EC50_1,
  E_inf_1,
  treatment2dose,
  HS_2,
  EC50_2,
  E_inf_2
)

Arguments

treatment1dose numeric a vector of concentrations for treatment 1
HS_1 numeric Hill coefficient of treatment 1
EC50_1 numeric relative EC50 of treatment 1.
E_inf_1 numeric viability produced by the maximum attainable effect of treatment 1. Default 0 by the original paper.
treatment2dose numeric a vector of concentrations for treatment 2
HS_2 numeric Hill coefficient of treatment 2
EC50_2 numeric relative EC50 of treatment 2.
E_inf_2 numeric viability produced by maximum effect of treatment 2. Default 0 by the original paper.

Value

numeric expected viability under ZIP null assumption.

Examples

(zip <- computeZIP(
  treatment1dose = c(0.1, 0.01, 0.001),
  treatment2dose = c(1, 0.1, 0.01),
  HS_1 = rep(1, 3), HS_2 = rep(1.2, 3),
  EC50_1 = rep(0.01, 3), EC50_2 = rep(0.1, 3),
  E_inf_1 = rep(0, 3), E_inf_2 = rep(0.1, 3)
))
computeZIPdelta

Generic to compute ZIP delta scores from an S4 object

Description

Generic to compute ZIP delta scores from an S4 object

Usage

computeZIPdelta(object, ...)

Arguments

object S4 An object to compute delta scores from.
... Allow new arguments to this generic.

Value

Depends on the implemented method.

Examples

print("Generics shouldn't need examples?")

computeZIPdelta, TreatmentResponseExperiment-method

Compute ZIP delta score

Description

Following the calculation of ZIP delta score as in Appendix A3. See reference for details.

Compute ZIP delta score as described in the original paper.

Usage

## S4 method for signature 'TreatmentResponseExperiment'
computeZIPdelta(object, residual = "logcosh", nthread = 1L, show_Rsqr = FALSE)
connectivityScore

Arguments

- **object**: `TreatmentResponseExperiment` The `TreatmentResponseExperiment` from which to extract assays `mono_profile` and `combo_viability` to compute ZIP delta scores.

- **residual**: character Method used to minimise residual in fitting curves. 3 methods available: c("logcosh", "normal", "Cauchy"). The default method is `logcosh`. It minimises the logarithmic hyperbolic cosine loss of the residuals and provides the fastest estimation among the three methods, with fitting quality in between `normal` and `Cauchy`; recommended when fitting large-scale datasets. The other two methods minimise residuals by considering the truncated probability distribution (as in their names) for the residual. `Cauchy` provides the best fitting quality but also takes the longest to run.

- **nthread**: integer Number of cores used to perform computation. Default 1.

- **show_Rsqr**: logical Whether to show the 2-way curve fitting quality in the result. Default FALSE.

Value

- `TreatmentResponseExperiment` with assay `combo_scores` containing `delta_scores`

References


Examples

```r
## Not run:
tre <- computeZIPdelta(tre, residual = "Cauchy", nthread = 2L)
## End(Not run)
```

connectivityScore

*Function computing connectivity scores between two signatures*

Description

A function for finding the connectivity between two signatures, using either the GSEA method based on the KS statistic, or the gwc method based on a weighted spearman statistic. The GSEA analysis is implemented in the piano package.
connectivityScore

Usage

connectivityScore(
  x,
  y,
  method = c("gsea", "fgsea", "gwc"),
  nperm = 10000,
  nthread = 1,
  gwc.method = c("spearman", "pearson"),
  ...
)

Arguments

  x  A matrix with the first gene signature. In the case of GSEA the vector of values per gene for GSEA in which we are looking for an enrichment. In the case of gwc, this should be a matrix, with the per gene responses in the first column, and the significance values in the second.
  y  A matrix with the second signature. In the case of GSEA, this is the vector of up and down regulated genes we are looking for in our signature, with the direction being determined from the sign. In the case of gwc, this should be a matrix of identical size to x, once again with the per gene responses in the first column, and their significance in the second.
  method character string identifying which method to use, out of 'fgsea' and 'gwc'
  nperm numeric, how many permutations should be done to determine significance through permutation testing? The minimum is 100, default is 1e4.
  nthread numeric, how many cores to run parallel processing on.
  gwc.method character, should gwc use a weighted spearman or pearson statistic?
  ...

Additional arguments passed down to gsea and gwc functions

Value

  numeric a numeric vector with the score and the p-value associated with it

References


Examples

  xValue <- c(1,5,23,4,8,9,2,19,11,12,13)
  xSig <- c(0.01, 0.01, .97, 0.01,0.01,0.28,0.7,0.01,0.01,0.01,0.01)
  yValue <- c(1,5,10,4,8,22,19,11,12,13)
  ySig <- c(0.01, 0.01, .97,0.01, 0.01,0.78,0.9,0.01,0.01,0.01,0.01)
\[ xx \leftarrow \text{cbind}(xValue, xSig) \]
\[ yy \leftarrow \text{cbind}(yValue, ySig) \]
\[ \text{rownames}(xx) \leftarrow \text{rownames}(yy) \leftarrow \text{c}(1', '2', '3', '4', '5', '6', '7', '8', '9', '10', '11') \]
\[ \text{data.cor} \leftarrow \text{connectivityScore}(xx, yy, \text{method} = 'gwc', \text{gwc.method} = 'spearman', nperm = 300) \]
**Examples**

```r
x <- factor(c(1,2,1,2,1))
y <- factor(c(2,2,1,1,1))
cosinePerm(x, y)
```

---

**dim,PharmacoSet-method**

*Get the dimensions of a PharmacoSet*

---

**Description**

Get the dimensions of a PharmacoSet

**Usage**

```r
## S4 method for signature 'PharmacoSet'
dim(x)
```

**Arguments**

- `x` : PharmacoSet

**Value**

A named vector with the number of Cells and Drugs in the PharmacoSet

---

**downloadPertSig**

*Download Drug Perturbation Signatures*

---

**Description**

This function allows you to download an array of drug perturbation signatures, as would be computed by the `drugPerturbationSig` function, for the available perturbation PharmacoSets. This function allows the user to skip these very lengthy calculation steps for the datasets available, and start their analysis from the already computed signatures

**Usage**

```r
downloadPertSig(
  name,
  saveDir = file.path(".", "PSets", "Sigs"),
  fileName,
  verbose = TRUE,
  ..., myfn
)
```
Arguments

name A character(1) string, the name of the PharmacoSet for which to download signatures. The name should match the names returned in the PSet Name column of availablePSets(canonical=FALSE).

saveDir A character(1) string with the folder path where the PharmacoSet should be saved. Defaults to "./PSet/Sigs/". Will create directory if it does not exist.

fileName character(1) What to name the downloaded file. Defaults to 'name_signature.RData' when excluded.

verbose logical(1) Should downloader show detailed messages?

... pairlist Force subsequent arguments to be named.

myfn character(1) A deprecated version of fileName. Still works for now, but will be deprecated in future releases.

Value

An array type object containing the signatures

Examples

```r
## Not run:
if (interactive()) downloadPertSig("CMAP_2016")

## End(Not run)
```

---

**downloadPSet**

*Download a PharmacoSet object*

Description

This function allows you to download a PharmacoSet object for use with this package. The PharmacoSets have been extensively curated and organised within a PharacoSet class, enabling use with all the analysis tools provided in PharmacoGx. Use availablePSets to discover which PSets are available.

Usage

```r
downloadPSet(
  name,
  saveDir = tempdir(),
  pSetFileName = NULL,
  verbose = TRUE,
  timeout = 600
)
```
drugDoseResponseCurve

Arguments

name Character string, the name of the PharmacoSet to download. Note that this is not the dataset name, but the PSet name - dataset names are not guaranteed to be unique.

saveDir Character string with the folder path where the PharmacoSet should be saved. Defaults to tempdir(). Will create directory if it does not exist.

pSetFileName character string, the file name to save the dataset under

verbose bool Should status messages be printed during download. Defaults to TRUE.

timeout numeric Parameter that lets you extend R’s default timeout for downloading large files. Defaults for this function to 600.

Value

A PSet object with the dataset

Warning

BREAKING CHANGES - this function now defaults to tempdir() as the download path! You must specify a saveDir or manually save the PSet if you want your download to persist past your current R session.

Examples

## Not run:
if (interactive()) downloadPSet("CTRPv2_2015")

## End(Not run)

drugDoseResponseCurve Plot drug response curve of a given drug and a given cell for a list of pSets (objects of the PharmacoSet class).

Description

Given a list of PharmacoSets, the function will plot the drug_response curve, for a given drug/cell pair. The y axis of the plot is the viability percentage and x axis is the log transformed concentrations. If more than one pSet is provided, a light gray area would show the common concentration range between pSets. User can ask for type of sensitivity measurement to be shown in the plot legend. The user can also provide a list of their own concentrations and viability values, as in the examples below, and it will be treated as experiments equivalent to values coming from a pset. The names of the concentration list determine the legend labels.
Usage

drugDoseResponseCurve(
  drug,
  cellline,
  pSets = list(),
  concentrations = list(),
  viabilities = list(),
  conc_as_log = FALSE,
  viability_as_pct = TRUE,
  trunc = TRUE,
  legends.label = c("ic50_published", "gi50_published", "auc_published",
                   "auc_recomputed", "ic50_recomputed"),
  ylim = c(0, 100),
  xlim,
  mycol,
  title,
  plot.type = c("Fitted", "Actual", "Both"),
  summarize.replicates = TRUE,
  lwd = 0.5,
  cex = 0.7,
  cex.main = 0.9,
  legend.loc = "topright",
  verbose = TRUE
)

Arguments

drug character(1) A drug name for which the drug response curve should be plotted. If the plot is desirable for more than one pharmaco set, A unique drug id should be provided.

cellline character(1) A cell line name for which the drug response curve should be plotted. If the plot is desirable for more than one pharmaco set, A unique cell id should be provided.

pSets list A list of PharmacoSet objects, for which the function should plot the curves.

concentrations, viabilities list A list of concentrations and viabilities to plot, the function assumes that concentrations[[i]] is plotted against viabilities[[i]]. The names of the concentration list are used to create the legend labels

conc_as_log logical, if true, assumes that log10-concentration data has been given rather than concentration data, and that log10(ICn) should be returned instead of ICn. Applies only to the concentrations parameter.

viability_as_pct logical, if false, assumes that viability is given as a decimal rather than a percentage, and that E_inf passed in as decimal. Applies only to the viabilities parameter.

trunc logical(1) Should the viability values be truncated to lie in [0-100] before doing the fitting
drugDoseResponseCurve

legends.label numeric A vector of sensitivity measurement types which could be any combination of ic50_published, auc_published, auc_recomputed and auc_recomputed_star. A legend will be displayed on the top right of the plot which each line of the legend is the values of requested sensitivity measurements for one of the requested pSets. If this parameter is missed no legend would be provided for the plot.

ylim numeric A vector of two numerical values to be used as ylim of the plot. If this parameter would be missed c(0,100) would be used as the ylim of the plot.
xlim numeric A vector of two numerical values to be used as xlim of the plot. If this parameter would be missed the minimum and maximum concentrations between all the pSets would be used as plot xlim.

mycol numeric A vector with the same length of the pSets parameter which will determine the color of the curve for the drug sets. If this parameter is missed default colors from Rcolorbrewer package will be used as curves color.
title character The title of the graph. If no title is provided, then it defaults to 'Drug': 'Cell Line'.

plot.type character Plot type which can be the actual one ("Actual") or the one fitted by log logistic regression ("Fitted") or both of them ("Both"). If this parameter is missed by default actual curve is plotted.

summarize.replicates character If this parameter is set to true replicates are summarized and replicates are plotted individually otherwise

lwd numeric The line width to plot with

cex numeric The cex parameter passed to plot

cex.main numeric The cex.main parameter passed to plot, controls the size of the titles

legend.loc And argument passable to xy.coords for the position to place the legend.

verbose logical(1) Should warning messages about the data passed in be printed?

Value

Plots to the active graphics device and returns an invisible NULL.

Examples

if (interactive()) {
  # Manually enter the plot parameters
drugDoseResponseCurve(concentrations=list("Experiment 1"=c(.008, .04, .2, 1)), viabilities=list(c(100,50,30,1)), plot.type="Both")

  # Generate a plot from one or more PSets
data(GDSCsmall)
drugDoseResponseCurve(drug="Doxorubicin", cellline="22RV", pSets=GDSCsmall)
}
drugPerturbationSig

Creates a signature representing gene expression (or other molecular profile) change induced by administering a drug, for use in drug effect analysis.

Description

Given a Pharmacoset of the perturbation experiment type, and a list of drugs, the function will compute a signature for the effect of drug concentration on the molecular profile of a cell. The algorithm uses a regression model which corrects for experimental batch effects, cell specific differences, and duration of experiment to isolate the effect of the concentration of the drug applied. The function returns the estimated coefficient for concentration, the t-stat, the p-value and the false discovery rate associated with that coefficient, in a 3 dimensional array, with genes in the first direction, drugs in the second, and the selected return values in the third.

Usage

```r
drugPerturbationSig(
  pSet,
  mDataType,
  drugs,
  cells,
  features,
  nthread = 1,
  returnValues = c("estimate", "tstat", "pvalue", "fdr"),
  verbose = FALSE
)
```

Arguments

- `pSet`: PharmacoSet a PharmacoSet of the perturbation experiment type
- `mDataType`: character which one of the molecular data types to use in the analysis, out of dna, rna, rnaseq, snp, cnv
- `drugs`: character a vector of drug names for which to compute the signatures. Should match the names used in the PharmacoSet.
- `cells`: character a vector of cell names to use in computing the signatures. Should match the names used in the PharmacoSet.
- `features`: character a vector of features for which to compute the signatures. Should match the names used in correspondant molecular data in PharmacoSet.
- `nthread`: numeric if multiple cores are available, how many cores should the computation be parallelized over?
- `returnValues`: character Which of estimate, t-stat, p-value and fdr should the function return for each gene drug pair?
- `verbose`: logical(1) Should diagnostic messages be printed? (default false)
Value

list a 3D array with genes in the first dimension, drugs in the second, and return values in the third.

Examples

data(CMAPsmall)
drug.perturbation <- drugPerturbationSig(CMAPsmall, mDataType="rna", nthread=1)
print(drug.perturbation)

---

drugSensitivitySig,PharmacoSet-method

Creates a signature representing the association between gene expression (or other molecular profile) and drug dose response, for use in drug sensitivity analysis.

Description

Given a Pharmacoset of the sensitivity experiment type, and a list of drugs, the function will compute a signature for the effect gene expression on the molecular profile of a cell. The function returns the estimated coefficient, the t-stat, the p-value and the false discovery rate associated with that coefficient, in a 3 dimensional array, with genes in the first direction, drugs in the second, and the selected return values in the third.

Usage

## S4 method for signature 'PharmacoSet'
drugSensitivitySig(
  object,
  mDataType,
  drugs,
  features,
  cells,
  tissues,
  sensitivity.measure = "auc_recomputed",
  molecular.summary.stat = c("mean", "median", "first", "last", "or", "and"),
  sensitivity.summary.stat = c("mean", "median", "first", "last"),
  returnValues = c("estimate", "pvalue", "fdr"),
  sensitivity.cutoff,
  standardize = c("SD", "rescale", "none"),
  molecular.cutoff = NA,
  molecular.cutoff.direction = c("less", "greater"),
  nthread = 1,
  parallel.on = c("drug", "gene"),
  modeling.method = c("anova", "pearson"),
  inference.method = c("analytic", "resampling"),
)
verbose = TRUE,
...)

Arguments

object                   PharmacoSet a PharmacoSet of the perturbation experiment type
mDataType                character which one of the molecular data types to use in the analysis, out of
                          dna, rna, rnaseq, snp, cnv
drugs                    character a vector of drug names for which to compute the signatures. Should
                          match the names used in the PharmacoSet.
features                 character a vector of features for which to compute the signatures. Should
                          match the names used in correspondant molecular data in PharmacoSet.
cells                    character allows choosing exactly which cell lines to include for the signature
                          fitting. Should be a subset of sampleNames(pSet)
tissues                  character a vector of which tissue types to include in the signature fitting. Should be a
                          subset of sampleInfo(pSet)$tissueid
sensitivity.measure      character which measure of the drug dose sensitivity should the function use
                          for its computations? Use the sensitivityMeasures function to find out what
                          measures are available for each PSet.
molecular.summary.stat    character What summary statistic should be used to summarize duplicates for
                          cell line molecular profile measurements?
sensitivity.summary.stat character What summary statistic should be used to summarize duplicates for
                          cell line sensitivity measurements?
returnValues             character Which of estimate, t-stat, p-value and fdr should the function return
                          for each gene drug pair?
sensitivity.cutoff       numeric Allows the user to binarize the sensitivity data using this threshold.
standardize              character One of "SD", "rescale", or "none", for the form of standardization
                          of the data to use. If "SD", the the data is scaled so that SD = 1. If rescale, then
                          the data is scaled so that the 95% interquantile range lies in [0,1]. If none
                          no rescaling is done.
molecular.cutoff         numeric Allows the user to binarize the sensitivity data using this threshold.
molecular.cutoff.direction character One of "less" or "greater", allows to set direction of binarization.
nthread                  numeric if multiple cores are available, how many cores should the computation
                          be parallelized over?
parallel.on              One of "gene" or "drug", chooses which level to parallelize computation (by
gene, or by drug).
effectToDose

modeling.method
One of "anova" or "pearson". If "anova", nested linear models (including and excluding the molecular feature) adjusted for are fit after the data is standardized, and ANOVA is used to estimate significance. If "pearson", partial correlation adjusted for tissue of origin are fit to the data, and a Pearson t-test (or permutation) test are used. Note that the difference is in whether standardization is done across the whole dataset (anova) or within each tissue (pearson), as well as the test applied.

inference.method
Should "analytic" or "resampling" (permutation testing + bootstrap) inference be used to estimate significance. For permutation testing, QUICK-STOP is used to adaptively stop permutations. Resampling is currently only implemented for "pearson" modelling method.

verbose logical 'TRUE' if the warnings and other informative message should be displayed

... additional arguments not currently fully supported by the function

Value
array a 3D array with genes in the first dimension, drugs in the second, and return values in the third.

Examples

data(GDSCsmall)
drug.sensitivity <- drugSensitivitySig(GDSCsmall,
    mDataType = "rna",
    nthread = 1, features = fNames(GDSCsmall, "rna")[1]
)
print(drug.sensitivity)

effectToDose
Inverse function of Hill equation

Description
For the dose-response Hill equation of a drug defined by \( E(x) = E_{\text{inf}} + \frac{1-E_{\text{inf}}}{1+(x/\text{EC}_{50})^{1/HS}} \), that computes the response in viability from a dose in micromole for a drug, this function is the inverse function of the Hill curve that computes the dose required to produce a given response: \( f^{-1}(E) = \text{EC}_{50}(\frac{1-E}{E-E_{\text{inf}}})^{\frac{1}{HS}} \)

Usage
effectToDose(viability, EC50, HS, E_inf, is_pct = FALSE)
**estimateProjParams**

Estimate the projected Hill coefficient, efficacy, and potency

**Description**

Estimate the projected shape parameter HS, efficacy E_inf and potency EC50 in the new dose-response curve of a drug after adding another drug to it by fitting a 2-parameter dose-response curve.

**Usage**

```r
estimateProjParams(
  dose_to,
  combo_viability,
  dose_add,
  EC50_add,
  HS_add,
  E_inf_add = 0,
  residual = c("logcosh", "normal", "Cauchy"),
  show_Rsqr = TRUE,
  conc_as_log = FALSE,
  optim_only = FALSE,
  loss_args = list()
)
```

**Arguments**

- **viability** numeric is a vector whose entries are the viability values in the range \([0, 1]\) if is_pct is FALSE or \([0, 100]\) if it is TRUE.
- **EC50** numeric is a vector of relative EC50 for drug-response equation.
- **HS** numeric Hill coefficient of the drug-response equation that represents the sigmoidity of the curve.
- **E_inf** numeric the maximum attainable effect of a drug when it is administered with a infinitely high concentration.
- **is_pct** logical whether both the input viability and E_inf are given in percentage \((0, 100]\) rather than decimal \((0, 1]\). Default FALSE.

**Value**

numeric concentrations in micromoles required to produce viability in the corresponding entries.

**Examples**

```r
dose <- effectToDose(viability = 80,
                      EC50 = 42,
                      HS = 1,
                      E_inf = 10,
                      is_pct = TRUE)
```

Arguments

dose_to numeric a vector of concentrations of the drug being added to
combo_viability numeric observed viability of two treatments; target for fitting curve.
dose_add numeric a vector of concentrations of the drug added.
EC50_add numeric relative EC50 of the drug added.
HS_add numeric Hill coefficient of the drug added.
E_inf_add numeric Efficacy of the drug added.
residual character Method used to minimise residual in fitting curves. 3 methods available: logcosh, normal, Cauchy. The default method is logcosh. It minimises the logarithmic hyperbolic cosine loss of the residuals and provides the fastest estimation among the three methods, with fitting quality in between normal and Cauchy; recommended when fitting large-scale datasets. The other two methods minimise residuals by considering the truncated probability distribution (as in their names) for the residual. Cauchy provides the best fitting quality but also takes the longest to run.
show_Rsqr logical whether to show goodness-of-fit value in the result.
conc_as_log logical indicates whether input concentrations are in log10 scale.
optim_only logical(1) Should the fall back methods when optim fails
loss_args list Additional argument to the loss function. These get passed to losses via do.call analogously to using ....

Value

list * HS_proj: Projected Hill coefficient after adding a drug * E_inf_proj: Projected efficacy after adding a drug * EC50_proj: Projected potency after adding a drug * E_ninf_proj: Projected baseline viability by the added drug * Rsqr: if show_Rsqr is TRUE, it will include the R squared value indicating the quality of the fit in the result.

References

Description

Viability measurements in dose-response curves must remain stable or decrease monotonically reflecting response to the drug being tested. filterNoisyCurves flags dose-response curves that strongly violate these assumptions.

Usage

```r
filterNoisyCurves(
  pSet,
  epsilon = 25,
  positive.cutoff.percent = 0.8,
  mean.viability = 200,
  nthread = 1
)
```

Arguments

- **pSet**: `PharmacoSet` a PharmacoSet object
- **epsilon**: numeric a value indicates assumed threshold for the distance between to consecutive viability values on the drug-response curve in the analysis, out of dna, rna, rnaseq, snp, cnv
- **positive.cutoff.percent**: numeric This value indicates that function may violate epsilon rule for how many points on drug-response curve
- **mean.viability**: numeric average expected viability value
- **nthread**: numeric if multiple cores are available, how many cores should the computation be parallelized over?

Value

a list with two elements 'noisy' containing the rownames of the noisy curves, and 'ok' containing the rownames of the non-noisy curves

Examples

```r
data(GDSCsmall)
filterNoisyCurves(GDSCsmall)
```

---

fitTwowayZIP

Two-way fitting for projected dose-response curve.

Description

Fit projected dose-response curves with \( E_{\text{min}} \) as the viability of the treatment being added to the other treatment at a fixed dose.
Usage

```r
fitTwowayZIP(
  combo_profiles,
  residual = "logcosh",
  show_Rsqr = TRUE,
  nthread = 1L,
  optim_only = TRUE,
  loss_args = list()
)
```

Arguments

- **combo_profiles** - `data.table` contains three parameters of dose-response curves for each single agent in a drug combination, and the observed viability of two treatments combined.
- **residual** - character. Method used to minimise residual in fitting curves. 3 methods available: c("logcosh", "normal", "Cauchy"). The default method is logcosh. It minimises the logarithmic hyperbolic cosine loss of the residuals and provides the fastest estimation among the three methods, with fitting quality in between normal and Cauchy; recommended when fitting large-scale datasets. The other two methods minimise residuals by considering the truncated probability distribution (as in their names) for the residual. Cauchy provides the best fitting quality but also takes the longest to run.
- **show_Rsqr** - logical. Whether to show goodness-of-fit value in the result.
- **nthread** - integer. Number of cores used to perform computation. Default 1.
- **optim_only** - logical(1). Should the fallback methods when optim fails
- **loss_args** - list. Additional argument to the `loss` function. These get passed to `losss` via `do.call` analogously to using `...`.

Value

- `data.table` contains parameters of projected dose-response curves for adding one treatment to the other.

References


Examples

```r
## Not run:
combo_profiles <- CoreGx::buildComboProfiles(tre, c("HS", "EC50", "E_inf", "viability"))
combo_twowayFit <- fitTwowayZIP(combo_profiles)
```

## End(Not run)
GDSCsmall  Genomics of Drug Sensitivity in Cancer Example PharmacoSet

Description

A small example version of the Genomics of Drug Sensitivity in Cancer Project PharmacoSet, used in the documentation examples. All credit for the data goes to the Genomics of Drug Sensitivity in Cancer Project group at the Sanger. This is not a full version of the dataset, most of the dataset was removed to make runnable example code. For the full dataset, please download using the downloadPSet function.

Usage

data(GDSCsmall)

Format

PharmacoSet object

References


geneDrugSensitivity  Calculate The Gene Drug Sensitivity

Description

TODO:: Write a description!

Usage

geneDrugSensitivity(
x, type, batch, drugpheno, interaction.type gene = FALSE, model = FALSE, standardize = c("SD", "rescale", "none"), verbose = FALSE)
Arguments

- **x**  
  A numeric vector of gene expression values

- **type**  
  A vector of factors specifying the cell lines or type types

- **batch**  
  A vector of factors specifying the batch

- **drugpheno**  
  A numeric vector of drug sensitivity values (e.g., IC50 or AUC)

- **interaction.typegene**  
  boolean Should interaction between gene expression and cell/type type be computed? Default set to FALSE

- **model**  
  boolean Should the full linear model be returned? Default set to FALSE

- **standardize**  
  character One of 'SD', 'rescale' or 'none'

- **verbose**  
  boolean Should the function display messages?

Value

A vector reporting the effect size (estimate of the coefficient of drug concentration), standard error (se), sample size (n), t statistic, and F statistics and its corresponding p-value.

Examples

```
print("TODO::")
```

---

**geneDrugSensitivityPBCorr**

*Calculate The Gene Drug Sensitivity*

Description

This version of the function uses a partial correlation instead of standardized linear models, for discrete predictive features Requires at least 3 observations per group.

Usage

```
geneDrugSensitivityPBCorr(
  x,  
  type,  
  batch,  
  drugpheno,  
  test = c("resampling", "analytic"),  
  req_alpha = 0.05,  
  nBoot = 1000,  
  conf.level = 0.95,  
  max_perm =getOption("PharmacoGx_Max_Perm", ceiling(1/req_alpha * 100)),  
  verbose = FALSE
)
```
Arguments

- **x**: A numeric vector of gene expression values.
- **type**: A vector of factors specifying the cell lines or type types.
- **batch**: A vector of factors specifying the batch.
- **drugpheno**: A numeric vector of drug sensitivity values (e.g., IC50 or AUC).
- **test**: A character string indicating whether resampling or analytic based tests should be used.
- **req_alpha**: numeric, number of permutations for p value calculation.
- **nBoot**: numeric, number of bootstrap resamplings for confidence interval estimation.
- **conf.level**: numeric, between 0 and 1. Size of the confidence interval required.
- **max_perm**: numeric the maximum number of permutations that QUICKSTOP can do before giving up and returning NA. Can be set globally by setting the option "PharmacoGx_Max_Perm", or left at the default of ceiling(1/req_alpha*100).
- **verbose**: boolean Should the function display messages?

Value

A vector reporting the effect size (estimate of the coefficient of drug concentration), standard error (se), sample size (n), t statistic, and F statistics and its corresponding p-value.

Examples

```
print("TODO::")
```

---

**geneDrugSensitivityPCorr**

*Calculate The Gene Drug Sensitivity*

Description

This version of the function uses a partial correlation instead of standardized linear models.

Usage

```
geneDrugSensitivityPCorr(
  x,
  type,
  batch,
  drugpheno,
  test = c("resampling", "analytic"),
  req_alpha = 0.05,
  nBoot = 1000,
  conf.level = 0.95,
  max_perm = getOption("PharmacoGx_Max_Perm", ceiling(1/req_alpha * 100)),
  verbose = FALSE
)
```
Arguments

x  A numeric vector of gene expression values

type  A vector of factors specifying the cell lines or type types

batch  A vector of factors specifying the batch

drugpheno  A numeric vector of drug sensitivity values (e.g., IC50 or AUC)

test  A character string indicating whether resampling or analytic based tests should be used

req_alpha  numeric, number of permutations for p value calculation

nBoot  numeric, number of bootstrap resamplings for confidence interval estimation

conf.level  numeric, between 0 and 1. Size of the confidence interval required

max_perm  numeric the maximum number of permutations that QUICKSTOP can do before giving up and returning NA. Can be set globally by setting the option "Pharmacogx_Max_Perm", or left at the default of ceiling(1(req_alpha*100).

verbose  boolean Should the function display messages?

Value

A vector reporting the effect size (estimate of the coefficient of drug concentration), standard error (se), sample size (n), t statistic, and F statistics and its corresponding p-value.

Examples

print("TODO::")

---

gwc GWC Score

Description

Calculate the gwc score between two vectors, using either a weighted spearman or pearson correlation

Usage

gwc(
  x1,  
p1,  
x2,  
p2,  
  method.cor = c("pearson", "spearman"),
  nperm = 10000,
  truncate.p = 1e-16,

  ...  
)
Arguments

x1  numeric vector of effect sizes (e.g., fold change or t statistics) for the first experiment
p1  numeric vector of p-values for each corresponding effect size for the first experiment
x2  numeric effect size (e.g., fold change or t statistics) for the second experiment
p2  numeric vector of p-values for each corresponding effect size for the second experiment
method.cor character string identifying if a pearson or spearman correlation should be used
nperm numeric how many permutations should be done to determine
truncate.p numeric Truncation value for extremely low p-values
...
Other passed down to internal functions

Value

numeric a vector of two values, the correlation and associated p-value.

Examples

data(CCLEsmall)
x <- molecularProfiles(CCLEsmall,"rna")[,1]
y <- molecularProfiles(CCLEsmall,"rna")[,2]
x_p <- rep(0.05, times=length(x))
y_p <- rep(0.05, times=length(y))
names(x_p) <- names(x)
names(y_p) <- names(y)
gwc(x,x_p,y,y_p, nperm=100)

<table>
<thead>
<tr>
<th>HDAC_genes</th>
<th>HDAC Gene Signature</th>
</tr>
</thead>
</table>

Description

A gene signature for HDAC inhibitors, as detailed by Glaser et al. The signature is mapped from the probe to gene level using probeGeneMapping

Usage

data(HDAC_genes)

Format

a 13x2 data.frame with gene identifiers in the first column and direction change in the second
References


---

**hillsCurve**

**4-Parameter Hill Equation for Stimuli-Response Curves**

**Description**

Sigmoidal function which fits well to many stimuli-response associations observed in biology and pharmacology. In the context of PharmacoGx we are using it to model treatment-response associations in cancer cell lines.

**Usage**

```r
hillsCurve(dose, HS, EC50, E_inf, E_ninf)
```

**Arguments**

- **dose** numeric() A vector of log10(dose) values (or equivalent for the stimuli being modelled).
- **HS** numeric(1) Hill coefficient (n) which defines the slope of the dose-response curve at the mid-point. This parameter describes the degree of sigmoidicity of the Hill curve. HS = 1 corresponds to the rectangular hyperbola in dose-response space.
- **EC50** numeric(1) The dose required to produce 50% of the theoretically maximal response in the system, E_inf. Should be in the same units as dose!
- **E_inf** numeric(1) Theoretical maximal response (minimal viability) in the system as a proportion in the range \([0, 1]\). Note that since we are predicting viability (percent of cells alive after treatment) instead of response, this value should be low (i.e., more cell killing).
- **E_ninf** numeric(1) Theoretical minimum response (basal response). Defaults to 1, which should be the case for most viability experiments since we expect no cell killing to occur prior to applying a treatment.

**Value**

numeric() Vector of predicted viabilities for the Hill curve defined by EC50, E_inf, E_ninf and HS for each supplied value of dose.

**Author(s)**

Feifei Li Petr Smirnov Christopher Eeles
References


Examples

```r
(viability <- hillCurve(
  dose=c(0.1, 0.01, 0.001),
  HS=1.1,
  EC50=0.01,
  E_ninf=1,
  E_inf=0
))
```

---

**intersectPSet**

Intersects objects of the PharmacoSet class, subsetting them to the common drugs and/or cell lines as selected by the user.

**Description**

Given a list of PharmacoSets, the function will find the common drugs, and/or cell lines, and return PharmacoSets that contain data only pertaining to the common drugs, and/or cell lines. The mapping between dataset drug and cell names is done using annotations found in the PharmacoSet object’s internal curation slot.

**Usage**

```r
intersectPSet(
  pSets,
  intersectOn = c("drugs", "cell.lines", "concentrations"),
  cells,
  drugs,
  strictIntersect = FALSE,
  verbose = TRUE,
  nthread = 1
)
```

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>pSets</td>
<td>list a list of PharmacoSet objects, of which the function should find the intersection</td>
</tr>
<tr>
<td>intersectOn</td>
<td>character which identifiers to intersect on, drugs, cell lines, or concentrations</td>
</tr>
</tbody>
</table>
loeweCI

a character vector of common cell lines between pSets. In case user is interested on getting intersection on certain cell lines, they can provide their list of cell lines.

drugs

a character vector of common drugs between pSets. In case user is interested on getting intersection on certain drugs, they can provide their list of drugs.

strictIntersect

boolean Should the intersection keep only the drugs and cell lines that have been tested on together?

verbose

boolean Should the function announce its key steps?

nthread

numeric The number of cores to use to run intersection on concentrations

Value

A list of pSets, containing only the intersection

Examples

data(GDSCsmall)
data(CCLEsmall)
common <- intersectPSet(list('GDSC'=GDSCsmall,'CCLE'=CCLEsmall),
                         intersectOn = c("drugs", "cell.lines"))
common$CGP
common$CCLE

---

loeweCI  

**Loewe Additive Combination Index (CI)**

Description

Computes the Loewe additive combination index (CI) from its definition $CI = \frac{x_1}{f_1(E)} + \frac{x_2}{f_2(E)}$.

Usage

loeweCI(
  viability,
  treatment1dose,
  HS_1,
  E_inf_1,
  EC50_1,
  treatment2dose,
  HS_2,
  E_inf_2,
  EC50_2,
  is_pct = FALSE
)
Arguments

- **viability** numeric is a vector whose entries are the viability values in the range [0, 1].
- **treatment1dose** numeric a vector of concentrations for treatment 1
- **HS_1** numeric Hill coefficient of treatment 1
- **E_inf_1** numeric the maximum attainable effect of treatment 1.
- **EC50_1** numeric relative EC50 of treatment 1.
- **treatment2dose** numeric a vector of concentrations for treatment 2
- **HS_2** numeric Hill coefficient of treatment 2
- **E_inf_2** numeric the maximum attainable effect of treatment 2.
- **EC50_2** numeric relative EC50 of treatment 2.
- **is_pct** logical whether both the input viability and E_inf are given in percentage ([0, 100]) rather than decimal ([0, 1]). Default FALSE.

Value

CI under Loewe additive definition

Examples

```r
## Not run:
tre |> 
endoaggregate(
  assay="combo_viability",
  Loewe = PharmacoGx::computeLoewe(
    treatment1dose = treatment1dose,
    treatment2dose = treatment2dose,
    HS_1 = HS_1,
    HS_2 = HS_2,
    E_inf_1 = E_inf_1,
    E_inf_2 = E_inf_2,
    EC50_1 = EC50_1,
    EC50_2 = EC50_2
  ),
  by = assayKeys(tre, "combo_viability")
) -> tre

## End(Not run)
```

logLogisticRegression  Fits curves of the form \( E = E_{\text{inf}} + (1 - E_{\text{inf}})/(1 + (c/EC50)^HS) \) to dose-response data points \((c, E)\) given by the user and returns a vector containing estimates for \(HS, E_{\text{inf}}, \text{and } EC50\).
Description

By default, logLogisticRegression uses an L-BFGS algorithm to generate the fit. However, if this fails to converge to solution, logLogisticRegression samples lattice points throughout the parameter space. It then uses the lattice point with minimal least-squares residual as an initial guess for the optimal parameters, passes this guess to drm, and re-attempts the optimization. If this still fails, logLogisticRegression uses the PatternSearch algorithm to fit a log-logistic curve to the data.

Usage

logLogisticRegression(
  conc,
  viability,
  density = c(2, 10, 5),
  step = 0.5/density,
  precision = 1e-04,
  lower_bounds = c(0, 0, -6),
  upper_bounds = c(4, 1, 6),
  scale = 0.07,
  family = c("normal", "Cauchy"),
  median_n = 1,
  conc_as_log = FALSE,
  viability_as_pct = TRUE,
  trunc = TRUE,
  verbose = TRUE
)

Arguments

conc numeric is a vector of drug concentrations.
viability numeric is a vector whose entries are the viability values observed in the presence of the drug concentrations whose logarithms are in the corresponding entries of the log_conc, where viability 0 indicates that all cells died, and viability 1 indicates that the drug had no effect on the cells.
density numeric is a vector of length 3 whose components are the numbers of lattice points per unit length along the HS, E_inf, and base-10 logarithm of the EC50-dimensions of the parameter space, respectively.
step numeric is a vector of length 3 whose entries are the initial step sizes in the HS, E_inf, and base-10 logarithm of the EC50 dimensions, respectively, for the PatternSearch algorithm.
precision is a positive real number such that when the ratio of current step size to initial step size falls below it, the PatternSearch algorithm terminates. A smaller value will cause LogisticPatternSearch to take longer to complete optimization, but will produce a more accurate estimate for the fitted parameters.
lower_bounds numeric is a vector of length 3 whose entries are the lower bounds on the HS, E_inf, and base-10 logarithm of the EC50 parameters, respectively.
upper_bounds numeric is a vector of length 3 whose entries are the upper bounds on the HS, E_inf, and base-10 logarithm of the EC50 parameters, respectively.
scale is a positive real number specifying the shape parameter of the Cauchy distribution.

family character, if "cauchy", uses MLE under an assumption of Cauchy-distributed errors instead of sum-of-squared-residuals as the objective function for assessing goodness-of-fit of dose-response curves to the data. Otherwise, if "normal", uses MLE with a gaussian assumption of errors.

median_n If the viability points being fit were medians of measurements, they are expected to follow a median of family distribution, which is in general quite different from the case of one measurement. Median_n is the number of measurements the median was taken of. If the measurements are means of values, then both the Normal and the Cauchy distributions are stable, so means of Cauchy or Normal distributed variables are still Cauchy and normal respectively.

conc_as_log logical, if true, assumes that log10-concentration data has been given rather than concentration data, and that log10(EC50) should be returned instead of EC50.

viability_as_pct logical, if false, assumes that viability is given as a decimal rather than a percentage, and that E_inf should be returned as a decimal rather than a percentage.

trunc logical, if true, causes viability data to be truncated to lie between 0 and 1 before curve-fitting is performed.

verbose logical, if true, causes warnings thrown by the function to be printed.

Value
A list containing estimates for HS, E_inf, and EC50. It is annotated with the attribute Rsquared, which is the R^2 of the fit. Note that this is calculated using the values actually used for the fit, after truncation and any transform applied. With truncation, this will be different from the R^2 compared to the variance of the raw data. This also means that if all points were truncated down or up, there is no variance in the data, and the R^2 may be NaN.

Examples

dose <- c(0.0025,0.008,0.025,0.08,0.25,0.8,2.53,8)
viability <- c(108.67,111,102.16,100.27,90,87,74,57)
computeAUC(dose, viability)

mcc Compute a Mathews Correlation Coefficient

Description
The function computes a Matthews correlation coefficient for two factors provided to the function. It assumes each factor is a factor of class labels, and the entries are paired in order of the vectors.
Usage

\[ \text{mcc}(x, y, \text{nperm} = 1000, \text{nthread} = 1) \]

Arguments

- **x**, **y**: factor of the same length with the same number of levels
- **nperm**: numeric number of permutations for significance estimation. If 0, no permutation testing is done
- **nthread**: numeric can parallelize permutation testing using BiocParallels `bplapply`

Details

Please note: we recommend you call `set.seed()` before using this function to ensure the reproducibility of your results. Write down the seed number or save it in a script if you intend to use the results in a publication.

Value

A list with the MCC as the `estimate`, and p value as `p.value`

Examples

```r
x <- factor(c(1,2,1,2,3,1))
y <- factor(c(2,1,1,1,2,2))
mcc(x, y)
```

---

**Description**

This function will test whether the observed partial correlation is significant at a level of `req_alpha`, doing up to MaxIter permutations. Currently, it supports only grouping by discrete categories when calculating a partial correlation. Currently, only does two sided tests.

Usage

```r
\text{partialCorQUICKSTOP}(\text{pin}_x, \text{pin}_y, \text{pobsCor}, \text{pGroupFactor}, \text{pGroupSize}, \text{pnumGroup}, \text{pMaxIter}, \text{pn}, \text{preq_alpha})
```
Arguments

pin_x       one of the two vectors to correlate.
pin_y       the other vector to calculate
pobsCor     the observed (partial) correlation between these variables
pGroupFactor an integer vector labeling group membership, to correct for in the partial corre-
              lation. NEEDS TO BE ZERO BASED!
pGroupSize  an integer vector of size length(unique(pGroupFactor)), counting the number of
              members of each group (basically table(pGroupFactor)) as integer vector
pnumGroup   how many groups are there (len(pGroupSize))
pMaxIter    maximum number of iterations to do, as a REAL NUMBER
pn          length of x and y, as a REAL NUMBER
preq_alpha  the required alpha for significance
ptolerance_par the tolerance region for quickstop. Suggested to be 1/100th of req_alpha'
plog_decision_boundary log (base e) of 1/probability of incorrectly calling significance, as per quickstop
              paper (used to determine the log-odds)
pseed       A numeric vector of length 2, used to seed the internal xoroshiro128+ 1.0 ran-
              dom number generator. Note that currently, these values get modified per call,
              so pass in a copy if you wish to keep a seed for running same simulation twice

Value

a double vector of length 4, entry 1 is either 0, 1 (for TRUE/FALSE) or NA_REAL_ for signifi-
ance determination NA_REAL_ is returned when the MaxIter were reached before a decision is
made. Usually, this occurs when the real p value is close to, or falls within the tolerance region
of (req_alpha, req_alpha+tolerance_par). Entry 2 is the current p value estimate. entry 3 is the
total number of iterations performed. Entry 4 is the number of time a permuted value was larger in
absolute value than the observed cor.

PharmacoSet constructor

Description

A constructor that simplifies the process of creating PharmacoSets, as well as creates empty objects
for data not provided to the constructor. Only objects returned by this constructor are expected to
work with the PharmacoSet methods. For a much more detailed instruction on creating Pharma-
coSets, please see the "CreatingPharmacoSet" vignette.
PharmacoSet

Usage

PharmacoSet(
  name,
  molecularProfiles = list(),
  sample = data.frame(),
  treatment = data.frame(),
  sensitivityInfo = data.frame(),
  sensitivityRaw = array(dim = c(0, 0, 0)),
  sensitivityProfiles = matrix(),
  sensitivityN = matrix(nrow = 0, ncol = 0),
  perturbationN = array(NA, dim = c(0, 0, 0)),
  curationTreatment = data.frame(),
  curationSample = data.frame(),
  curationTissue = data.frame(),
  datasetType = c("sensitivity", "perturbation", "both"),
  verify = TRUE,
  ...)

Arguments

name A character string detailing the name of the dataset
molecularProfiles A list of SummarizedExperiment objects containing molecular profiles for each molecular data type.
sample A data.frame containing the annotations for all the sample profiled in the data set, across all data types. Must contain the mandatory sampleid column which uniquely identifies each sample in the object.
treatment A data.frame containing annotations for all treatments profiled in the dataset. Must contain the mandatory treatmentid column which uniquely identifies each treatment in the object.
sensitivityInfo A data.frame containing the information for the sensitivity experiments. Must contain a 'sampleid' column with unique identifiers to each sample, matching the sample object and a 'treatmentid' columns with unique identifiers for each treatment, matching the treatment object.
sensitivityRaw A 3 Dimensional array containing the raw drug dose response data for the sensitivity experiments
sensitivityProfiles data.frame containing drug sensitivity profile statistics such as IC50 and AUC
sensitivityN, perturbationN A data.frame summarizing the available sensitivity/perturbation data
curationSample, curationTissue, curationTreatment A data.frame mapping the names for samples, tissues and treatments used in the data set to universal identifiers used between different CoreSet objects
datasetType A character(1) string of 'sensitivity', 'preturbation', or 'both' detailing what type of data can be found in the CoreSet, for proper processing of the data

verify logical(1) Should the function verify the CoreSet and print out any errors it finds after construction?

Value

An object of class PharmacoSet

Examples

## For help creating a PharmacoSet object, please see the following vignette:
browseVignettes("PharmacoGx")

PharmacoSet-accessors Accessing and modifying information in a PharmacoSet

Description

Documentation for the various setters and getters which allow manipulation of data in the slots of a PharmacoSet object.

Usage

drugInfo(...)  
drugInfo(...) <- value  
drugNames(...)  
drugNames(...) <- value

## S4 method for signature 'PharmacoSet'
annotation(object)

## S4 replacement method for signature 'PharmacoSet,list'
annotation(object) <- value

## S4 method for signature 'PharmacoSet'
dateCreated(object)

## S4 replacement method for signature 'PharmacoSet,character'
dateCreated(object) <- value

## S4 method for signature 'PharmacoSet'
name(object)
## S4 replacement method for signature 'PharmacoSet'
name(object) <- value

## S4 method for signature 'PharmacoSet'
sampleInfo(object)
## S4 replacement method for signature 'PharmacoSet,data.frame'
sampleInfo(object) <- value

## S4 method for signature 'PharmacoSet'
sampleNames(object)
## S4 replacement method for signature 'PharmacoSet,character'
sampleNames(object) <- value

## S4 method for signature 'PharmacoSet'
curation(object)
## S4 replacement method for signature 'PharmacoSet,list'
curation(object) <- value

## S4 method for signature 'PharmacoSet'
datasetType(object)
## S4 replacement method for signature 'PharmacoSet,character'
datasetType(object) <- value

## S4 method for signature 'PharmacoSet'
molecularProfiles(object, mDataType, assay)
## S4 replacement method for signature 'PharmacoSet,character,matrix'
molecularProfiles(object, mDataType, assay) <- value

## S4 method for signature 'PharmacoSet'
featureInfo(object, mDataType)
## S4 replacement method for signature 'PharmacoSet,character,data.frame'
featureInfo(object, mDataType) <- value

## S4 method for signature 'PharmacoSet,character'
phenoInfo(object, mDataType)
## S4 replacement method for signature 'PharmacoSet,character,data.frame'
phenoInfo(object, mDataType) <- value

## S4 method for signature 'PharmacoSet,character'
fNames(object, mDataType)

## S4 replacement method for signature 'PharmacoSet,character,character'
fNames(object, mDataType) <- value

## S4 method for signature 'PharmacoSet'
mDataNames(object)

## S4 replacement method for signature 'PharmacoSet'
mDataNames(object) <- value

## S4 method for signature 'PharmacoSet'
molecularProfilesSlot(object)

## S4 replacement method for signature 'PharmacoSet,list_OR_MAE'
molecularProfilesSlot(object) <- value

## S4 method for signature 'PharmacoSet'
sensitivityInfo(object, dimension, ...)

## S4 replacement method for signature 'PharmacoSet,data.frame'
sensitivityInfo(object, dimension, ...) <- value

## S4 method for signature 'PharmacoSet'
sensitivityMeasures(object)

## S4 replacement method for signature 'PharmacoSet,character'
sensitivityMeasures(object) <- value

## S4 method for signature 'PharmacoSet'
sensitivityProfiles(object)

## S4 replacement method for signature 'PharmacoSet,data.frame'
sensitivityProfiles(object) <- value

## S4 method for signature 'PharmacoSet'
sensitivityRaw(object)

## S4 replacement method for signature 'PharmacoSet,array'
sensitivityRaw(object) <- value

## S4 method for signature 'PharmacoSet'
treatmentResponse(object)

## S4 replacement method for signature 'PharmacoSet,list_OR_LongTable'
treatmentResponse(object) <- value

## S4 method for signature 'PharmacoSet'
sensNumber(object)
## S4 replacement method for signature 'PharmacoSet,matrix'
sensNumber(object) <- value

## S4 method for signature 'PharmacoSet'
pertNumber(object)
## S4 replacement method for signature 'PharmacoSet,array'
pertNumber(object) <- value

Arguments

... See details.
value See details.
o bject A PharmacoSet object.
mDataType character(1) The name of a molecular datatype to access from the molecularProfiles of a PharmacoSet object.
assay character(1) A valid assay name in the SummarizedExperiment of @molecularProfiles of a PharmacoSet object for data type mDataType.
dimension See details.

Details

treatmentInfo: data.frame Metadata for all treatments in a PharmacoSet object. Arguments:

  object: PharmacoSet An object to retrieve treatment metadata from.

treatmentInfo<-: PharmacoSet object with updated treatment metadata. object. Arguments:

  object: PharmacoSet An object to set treatment metadata for.
  value: data.frame A new table of treatment metadata for object.

treatmentNames: character Names for all treatments in a PharmacoSet object. Arguments:

  object: PharmacoSet An object to retrieve treatment names from.

treatmentNames<-: PharmacoSet Object with updates treatment names. object. Arguments:

  object: PharmacoSet An object to set treatment names from.
  value: character A character vector of updated treatment names.

@annotation:
annotation: A list of PharmacoSet annotations with items: 'name', the name of the object; 'dateCreated', date the object was created; 'sessionInfo', the sessionInfo() when the object was created; 'call', the R constructor call; and 'version', the object version.

annotation<-: Setter method for the annotation slot. Arguments:

  value: a list of annotations to update the PharmacoSet with.
@dateCreated:

dateCreated: character(1) The date the PharmacoSet object was created, as returned by the date() function.

dateCreated<-: Update the 'dateCreated' item in the annotation slot of a PharmacoSet object.
Arguments:
  • value: A character(1) vector, as returned by the date() function.

name: character(1) The name of the PharmacoSet, retrieved from the @annotation slot.

name<-: Update the @annotation$name value in a PharmacoSet object.
Arguments:
  • value: character(1) The name of the PharmacoSet object.

cellInfo: data.frame Metadata for all sample in a PharmacoSet object.

sampleInfo<-: assign updated sample annotations to the PharmacoSet object. Arguments:
  • value: a data.frame object.

sampleNames: character Retrieve the rownames of the data.frame in the sample slot from a PharmacoSet object.

sampleNames<-: assign new rownames to the sampleInfo data.frame for a PharmacoSet object. Arguments:
  • value: character vector of rownames for the sampleInfo(object) data.frame.

@curation:

curation: A list of curated mappings between identifiers in the PharmacoSet object and the original data publication. Contains three data.frames, 'cell' with cell-line ids and 'tissue' with tissue ids and 'drug' with drug ids.

curation<-: Update the curation slot of a PharmacoSet object. Arguments:
  • value: A list of data.frames, one for each type of curated identifier. For a PharmacoSet object the slot should contain tissue, cell-line and drug id data.frames.

datasetType slot:

datasetType: character(1) The type treatment response in the sensitivity slot. Valid values are 'sensitivity', 'perturbation' or 'both'.

datasetType<-: Update the datasetType slot of a PharmacoSet object. Arguments:
  • value: A character(1) vector with one of 'sensitivity', 'perturbation' or 'both'

@molecularProfiles:

molecularProfiles: matrix() Retrieve an assay in a SummarizedExperiment from the molecularProfiles slot of a PharmacoSet object with the specified mDataType. Valid mDataType arguments can be found with mDataNames(object). Exclude mDataType and assay to access the entire slot. Arguments:
• assay: Optional character(1) vector specifying an assay in the SummarizedExperiment of the molecularProfiles slot of the PharmacoSet object for the specified mDataType. If excluded, defaults to modifying the first assay in the SummarizedExperiment for the given mDataType.

molecularProfiles<-: Update an assay in a SummarizedExperiment from the molecularProfiles slot of a PharmacoSet object with the specified mDataType. Valid mDataType arguments can be found with mDataNames(object). Omit mDataType and assay to update the slot.

• assay: Optional character(1) vector specifying an assay in the SummarizedExperiment of the molecularProfiles slot of the PharmacoSet object for the specified mDataType. If excluded, defaults to modifying the first assay in the SummarizedExperiment for the given mDataType.
• value: A matrix of values to assign to the assay slot of the SummarizedExperiment for the selected mDataType. The rownames and column names must match the associated SummarizedExperiment.

featureInfo: Retrieve a DataFrame of feature metadata for the specified mDataType from the molecularProfiles slot of a PharmacoSet object. More specifically, retrieve the @rowData slot from the SummarizedExperiment from the @molecularProfiles of a PharmacoSet object with the name mDataType.

featureInfo<-: Update the featureInfo(object, mDataType) DataFrame with new feature metadata. Arguments:

• value: A data.frame or DataFrame with updated feature metadata for the specified molecular profile in the molecularProfiles slot of a PharmacoSet object.

phenoInfo: Return the @colData slot from the SummarizedExperiment of mDataType, containing sample-level metadata, from a PharmacoSet object.

phenoInfo<-: Update the @colData slot of the SummarizedExperiment of mDataType in the @molecularProfiles slot of a PharmacoSet object. This updates the sample-level metadata in-place.

• value: A data.frame or DataFrame object where rows are samples and columns are sample metadata.

fNames: character() The features names from the rowData slot of a SummarizedExperiment of mDataType within a PharmacoSet object.

fNames: Updates the rownames of the feature metadata (i.e., rowData) for a SummarizedExperiment of mDataType within a PharmacoSet object.

• value: character() A character vector of new features names for the rowData of the SummarizedExperiment of mDataType in the @molecularProfiles slot of a PharmacoSet object. Must be the same length as nrow(featureInfo(object, mDataType)), the number of rows in the feature metadata.

mDataNames: character Retrieve the names of the molecular data types available in the molecularProfiles slot of a PharmacoSet object. These are the options which can be used in the mDataType parameter of various molecularProfiles slot accessors methods.

mDataNames: Update the molecular data type names of the molecularProfiles slot of a PharmacoSet object. Arguments:
• value: character vector of molecular datatype names, with length equal to length(molecularProfilesSlot(object)).

molecularProfilesSlot: Return the contents of the @molecularProfiles slot of a PharmacoSet object. This will either be a list or MultiAssayExperiment of SummarizedExperiments.

molecularProfilesSlot<-: Update the contents of the @molecularProfiles slot of a PharmacoSet object. Arguments:
• value: A list or MultiAssayExperiment of SummarizedExperiments. The list and assays should be named for the molecular datatype in each SummarizedExperiment.

@treatmentResponse:
Arguments::
• dimension: Optional character(1) One of 'treatment', 'sample' or 'assay' to retrieve rowData, colData or the 'assay_metadata' assay from the PharmacoSet@sensitivity LongTable object, respectively. Ignored with warning if @treatmentResponse is not a LongTable object.
• ...: Additional arguments to the rowData or colData. LongTable methods. Only used if the sensitivity slot contains a LongTable object instead of a list and the dimension argument is specified.

Methods::
sensitivityInfo: DataFrame or data.frame of sensitivity treatment combo by sample metadata for the PharmacoSet object. When the dimension parameter is used, it allows retrieval of the dimension specific metadata from the LongTable object in @treatmentResponse of a PharmacoSet object.

dimension<-: Update the @treatmentResponse slot metadata for a PharmacoSet object. When used without the dimension argument is behaves similar to the old PharmacoSet implementation, where the @treatmentResponse slot contained a list with a $info data.frame item. When the dimension argument is used, more complicated assignments can occur where 'sample' modifies the @sensitivity LongTable colData, 'treatment' the rowData and 'assay' the 'assay_metadata' assay. Arguments:
• value: A data.frame of treatment response experiment metadata, documenting experiment level metadata (mapping to treatments and samples). If the @treatmentResponse slot doesn't contain a LongTable and dimension is not specified, you can only modify existing columns as returned by sensitivityInfo(object).

sensitivityMeasures: Get the 'sensitivityMeasures' available in a PharmacoSet object. Each measure represents some summary of sample sensitivity to a given treatment, such as ic50, ec50, AUC, AAC, etc. The results are returned as a character vector with all available metrics for the PSet object.

sensitivityMeasures: Update the sensitivity measure in a PharmacoSet object. These values are the column names of the 'profiles' assay and represent various computed sensitivity metrics such as ic50, ec50, AUC, AAC, etc.
• value: A character vector of new sensitivity measure names, the then length of the character vector must match the number of columns of the 'profiles' assay, excluding metadata and key columns.
sensitivityProfiles:: Return the sensitivity profile summaries from the sensitivity slot. This data.frame contains various sensitivity summary metrics, such as ic50, amax, EC50, aac, HS, etc as columns, with rows as treatment by sample experiments.

sensitivityProfiles<-:: Update the sensitivity profile summaries the sensitivity slot. Arguments: - value: A data.frame the the same number of rows as as returned by sensitivityProfiles(object), but potentially modified columns, such as the computation of additional summary metrics.

sensitivityRaw:: Access the raw sensitivity measurements for a PharmacoSet object. A 3D array where rows are experiment_ids, columns are doses and the third dimension is metric, either 'Dose' for the doses used or 'Viability' for the sample viability at that dose.

sensitivityRaw<-:: Update the raw dose and viability data in a PharmacoSet.

  • value: A 3D array object where rows are experiment_ids, columns are replicates and pages are c('Dose', 'Viability'), with the corresponding dose or viability measurement for that experiment_id and replicate.

sensNumber:: Return a count of viability observations in a PharmacoSet object for each treatment-combo by sample combination.

sensNumber<-:: Update the 'n' item, which holds a matrix with a count of treatment by sample-line experiment counts, in the list in @treatmentResponse slot of a PharmacoSet object. Will error when @sensitivity contains a LongTable object, since the counts are computed on the fly. Arguments:

  • value: A matrix where rows are samples and columns are treatments, with a count of the number of experiments for each combination as the values.

pertNumber:: array Summary of available perturbation experiments from in a PharmacoSet object. Returns a 3D array with the number of perturbation experiments per treatment and sample, and data type.

pertNumber<-:: Update the @perturbation$n value in a PharmacoSet object, which stores a summary of the available perturbation experiments. Arguments:

  • value: A new 3D array with the number of perturbation experiments per treatment and sample, and data type

Value

Accessors: See details.

Setters: An updated PharmacoSet object, returned invisibly.

Examples

data(CCLEsmall)
treatmentInfo(CCLEsmall)

treatmentInfo(CCLEsmall) <- treatmentInfo(CCLEsmall)

treatmentNames(CCLEsmall)

treatmentNames(CCLEsmall) <- treatmentNames(CCLEsmall)
## @annotation
annotation(CCLEsmall)

annotation(CCLEsmall) <- annotation(CCLEsmall)

dateCreated(CCLEsmall)

## dateCreated
dateCreated(CCLEsmall) <- date()

name(CCLEsmall)

name(CCLEsmall) <- 'new_name'

sampleInfo(CCLEsmall) <- sampleInfo(CCLEsmall)

sampleNames(CCLEsmall)

sampleNames(CCLEsmall) <- sampleNames(CCLEsmall)

## curation
curation(CCLEsmall)

curation(CCLEsmall) <- curation(CCLEsmall)

datasetType(CCLEsmall)

datasetType(CCLEsmall) <- 'both'

# No assay specified
molecularProfiles(CCLEsmall, 'rna') <- molecularProfiles(CCLEsmall, 'rna')

# Specific assay
molecularProfiles(CCLEsmall, 'rna', 'exprs') <-
    molecularProfiles(CCLEsmall, 'rna', 'exprs')

# Replace the whole slot
molecularProfiles(CCLEsmall) <- molecularProfiles(CCLEsmall)

featureInfo(CCLEsmall, 'rna')

featureInfo(CCLEsmall, 'rna') <- featureInfo(CCLEsmall, 'rna')

phenoInfo(CCLEsmall, 'rna')

phenoInfo(CCLEsmall, 'rna') <- phenoInfo(CCLEsmall, 'rna')

fNames(CCLEsmall, 'rna')

fNames(CCLEsmall, 'rna') <- fNames(CCLEsmall, 'rna')
PharmacoSet-class

A Class to Contain PharmacoGenomic datasets together with their curations

Description

The PharmacoSet (pSet) class was developed to contain and organise large PharmacoGenomic datasets, and aid in their metanalysis. It was designed primarily to allow bioinformaticians and biologists to work with data at the level of genes, drugs and cell lines, providing a more naturally intuitive interface and simplifying analyses between several datasets. As such, it was designed to be flexible enough to hold datasets of two different natures while providing a common interface. The
class can accommodate datasets containing both drug dose response data, as well as datasets containing genetic profiles of cell lines pre and post treatment with compounds, known respectively as sensitivity and perturbation datasets.

**Arguments**

- `object`: A PharmacoSet object
- `mDataType`: A character with the type of molecular data to return/update
- `value`: A replacement value

**Value**

An object of the PharmacoSet class

**Slots**

- `annotation`: A list of annotation data about the PharmacoSet, including the `$name` and the session information for how the object was creating, detailing the exact versions of R and all the packages used
- `molecularProfiles`: A list containing SummarizedExperiment type object for holding data for RNA, DNA, SNP and CNV measurements, with associated fData and pData containing the row and column metadata
- `sample`: A data.frame containing the annotations for all the cell lines profiled in the data set, across all data types
- `treatment`: A data.frame containing the annotations for all the drugs profiled in the data set, across all data types
- `treatmentResponse`: A list containing all the data for the sensitivity experiments, including `$info`, a data.frame containing the experimental info, `$raw` a 3D array containing raw data, `$profiles`, a data.frame containing sensitivity profiles statistics, and `$n`, a data.frame detailing the number of experiments for each cell-drug pair
- `perturbation`: A list containing `$n`, a data.frame summarizing the available perturbation data,
- `curation`: A list containing mappings for `$treatment`, `$cell`, `$tissue` names used in the data set to universal identifiers used between different PharmacoSet objects
- `datasetType`: A character string of 'sensitivity', 'perturbation', or both detailing what type of data can be found in the PharmacoSet, for proper processing of the data

---

**PharmacoSet-utils**

Utility methods for a PharmacoSet object.

**Description**

Documentation for utility methods for a PharmacoSet object, such as set operations like subset and intersect. See @details for information on different types of methods and their implementations.
Usage

## S4 method for signature 'PharmacoSet'
subsetBySample(x, samples)

## S4 method for signature 'PharmacoSet'
subsetByTreatment(x, treatments)

## S4 method for signature 'PharmacoSet'
subsetByFeature(x, features, mDataTypes)

Arguments

- **x**
  - A PharmacoSet object.

- **samples**
  - character() vector of sample names. Must be valid rownames from sampleInfo(x).

- **treatments**
  - character() vector of treatment names. Must be valid rownames from treatmentInfo(x). This method does not work with CoreSet objects yet.

- **features**
  - character() vector of feature names. Must be valid feature names for a given mDataType

- **mDataTypes**
  - character() One or more molecular data types to to subset features by. Must be valid rownames for the selected SummarizedExperiment mDataTypes.

Details

**subset methods:**

**subsetBySample:** Subset a PharmacoSet object by sample identifier.

- value: a PharmacoSet object containing only samples.

**subset methods:**

**subsetByTreatment:** Subset a PharmacoSet object by treatment identifier.

- value: a PharmacoSet object containing only treatments.

**subset methods:**

**subsetByFeature:** Subset a PharmacoSet object by molecular feature identifier.

- value: a PharmacoSet object containing only features.

Value

See details.

Examples

data(CCLEsmall)

## subset methods

### subsetBySample

samples <- sampleInfo(CCLEsmall)$sampleid[seq_len(10)]
PharmacoSet2 <- subsetBySample(CCLEsmall, samples)

## subset methods

### subsetByTreatment
treatments <- drugInfo(CCLEsmall)$drugid[seq_len(10)]
CCLEsmall_sub <- subsetByTreatment(CCLEsmall, treatments)

## subset methods

### subsetByFeature
features <- fNames(CCLEsmall, 'rna')[seq_len(5)]
CCLEsmall_sub <- subsetByFeature(CCLEsmall, features, 'rna')

---

PharmacoSet2  

Make a CoreSet with the updated class structure

Description

New implementation of the CoreSet constructor to support MAE and TRE. This constructor will be swapped with the original CoreSet constructor as part of an overhaul of the CoreSet class structure.

Usage

PharmacoSet2(
  name = "emptySet",
  treatment = data.frame(),
  sample = data.frame(),
  molecularProfiles = MultiAssayExperiment(),
  treatmentResponse = TreatmentResponseExperiment(),
  perturbation = list(),
  curation = list(sample = data.frame(), treatment = data.frame(), tissue = data.frame()),
  datasetType = "sensitivity"
)

Arguments

- **name**: A character(1) vector with the PharmacoSet objects name.
- **treatment**: A data.frame with treatment level metadata. Treatments in a PharmacoSet represent pharmaceutical compounds.
- **sample**: A data.frame with sample level metadata for the union of samples in treatmentResponse and molecularProfiles. Samples in a PharmacoSet represent cancer cell-lines.
molecularProfiles
A MultiAssayExperiment containing one SummarizedExperiment object for each molecular data type.

treatmentResponse
A LongTable or LongTableDataMapper object containing all treatment response data associated with the PharmacoSet object.

perturbation
A deprecated slot in a PharmacoSet object included for backwards compatibility. This may be removed in future releases.

curation
This class requires an additional curation item, tissue, which maps from published to standardized tissue identifiers.

datasetType
A deprecated slot in a PharmacoSet object included for backwards compatibility. This may be removed in future releases.

Value
A CoreSet object storing standardized and curated treatment response and multiomic profile data associated with a given publication.

Examples

```r
data(CCLEsmall)
CCLEsmall
```
Arguments

- **Data**
  of data to build the signature from
- **PSetName**
  character vector containing name of PSet, defaults to ""
- **DateCreated**
  date date the signature was created, defaults to `date()`
- **SigType**
  character vector specifying whether the signature is sensitivity or perturbation, defaults to 'sensitivity'
- **SessionInfo**
  sessionInfo object as returned by `sessionInfo()` function, defaults to `sessionInfo()`
- **Call**
  character or call specifying the constructor call used to make the object, defaults to 'No Call Recorded'
- **Arguments**
  list a list of additional arguments to the constructor

Value

A PharmacoSig object build from the provided signature data

Examples

PharmacoSig()

---

**plot.PharmacoSig**

Plots a PharmacoSig object into a Volcano Plot

Description

Given a PharmacoSig, this will plot a volcano plot, with parameters to set cutoffs for a significant effect size, p value, to pick multiple testing correction strategy, and to change point colors. Built on top of ggplot, it will return the plot object which can be easily customized as any other ggplot.

Usage

```r
## S3 method for class 'PharmacoSig'
plot(
  x,
  adjust.method,
  drugs,
  features,
  effect_cutoff,
  signif_cutoff,
  color,
  ...
)
```
Arguments

- **x**: A `PharmacoSig` object, result of `drugSensitivitySig` or `drugPerturbationSig`.
- **adjust.method**: A character(1) or logical(1) either FALSE for no adjustment, or one of the methods implemented by `p.adjust`. Defaults to FALSE for no correction.
- **drugs**: A character vector of drug names for which to plot the estimated associations with gene expression.
- **features**: A character vector of features for which to plot the estimated associations with drug treatment.
- **effect_cutoff**: The cutoff to use for coloring significant effect sizes.
- **signif_cutoff**: The cutoff to use for coloring significance by p value or adjusted p values. Not on log scale.
- **color**: One color if no cutoffs set for plotting. A vector of colors otherwise used to color points in three categories above.
- **...**: Additional arguments, not currently used, but left here for consistency with `plot`.

Value

Returns a ggplot object, which by default will be evaluated and the plot displayed, or can be saved to a variable for further customization by adding ggplot elements to the returned graph.

Examples

```r
data(GDSCsmall)
drug.sensitivity <- drugSensitivitySig(GDSCsmall, mDataType="rna",
    nthread=1, features = fNames(GDSCsmall, "rna")[1])
plot(drug.sensitivity)
```

Description

Show a PharmacoSet

Usage

```r
## S4 method for signature 'PharmacoSet'

show(object)
```

Arguments

- **object**: A PharmacoSet
show.PharmacoSig-method

Show PharmacoGx Signatures

Description

Show PharmacoGx Signatures

Usage

## S4 method for signature 'PharmacoSig'
show(object)

Arguments

object PharmacoSig

Value

Prints the PharmacoGx Signatures object to the output stream, and returns invisible NULL.

Examples

data(GDSCsmall)
drug.sensitivity <- drugSensitivitySig(GDSCsmall, mDataType="rna", nthread=1, features = fNames(GDSCsmall, "rna")[1])
drug.sensitivity
showSigAnnot,PharmacoSig-method

Show the Annotations of a signature object

Description

This function prints out the information about the call used to compute the drug signatures, and the session info for the session in which the computation was done. Useful for determining the exact conditions used to generate signatures.

Usage

```r
## S4 method for signature 'PharmacoSig'
showSigAnnot(object)
```

Arguments

- `object` An object of the PharmacoSig Class, as returned by drugPerturbationSig or drugSensitivitySig

Value

Prints the PharmacoGx Signatures annotations to the output stream, and returns invisible NULL.

Examples

```r
data(GDSCsmall)
drug.sensitivity <- drugSensitivitySig(GDSCsmall, mDataType="rna",
nthread=1, features = fNames(GDSCsmall, "rna")[1])
showSigAnnot(drug.sensitivity)
```

subsetTo,PharmacoSet-method

A function to subset a PharmacoSet to data containing only specified drugs, cells and genes

Description

This is the preferred method of subsetting a PharmacoSet. This function allows abstraction of the data to the level of biologically relevant objects: drugs and cells. The function will automatically go through all of the combined data in the PharmacoSet and ensure only the requested drugs and cell lines are found in any of the slots. This allows quickly picking out all the experiments for a drug or cell of interest, as well removes the need to keep track of all the metadata conventions between different datasets.
Usage

```r
## S4 method for signature 'PharmacoSet'
subsetTo(
  object,
  cells = NULL,
  drugs = NULL,
  molecular.data.cells = NULL,
  keep.controls = TRUE,
  ...
)
```

Arguments

- `object`: A PharmacoSet to be subsetted
- `cells`: A list or vector of cell names as used in the dataset to which the object will be subsetted. If left blank, then all cells will be left in the dataset.
- `drugs`: A list or vector of drug names as used in the dataset to which the object will be subsetted. If left blank, then all drugs will be left in the dataset.
- `molecular.data.cells`: A list or vector of cell names to keep in the molecular data
- `keep.controls`: If the dataset has perturbation type experiments, should the controls be kept in the dataset? Defaults to true.
- `...`: Other arguments passed by other function within the package

Value

A PharmacoSet with only the selected drugs and cells

Examples

```r
data(CCLEsmall)
CCLEdrugs <- treatmentNames(CCLEsmall)
CCLEcells <- sampleNames(CCLEsmall)
pSet <- subsetTo(CCLEsmall, drugs = CCLEdrugs[1], cells = CCLEcells[1])
pSet
```

Description

Given a PharmacoSet with molecular data, this function will summarize the data into one profile per cell line, using the chosen summary.stat. Note that this does not really make sense with perturbation type data, and will combine experiments and controls when doing the summary if run on a perturbation dataset.
Usage

## S4 method for signature 'PharmacoSet'
summarizeMolecularProfiles(
  object,
  mDataType,
  cell.lines,
  features,
  summary.stat = c("mean", "median", "first", "last", "and", "or"),
  fill.missing = TRUE,
  summarize = TRUE,
  verbose = TRUE,
  binarize.threshold = NA,
  binarize.direction = c("less", "greater"),
  removeTreated = TRUE
)

Arguments

object PharmacoSet The PharmacoSet to summarize
mDataType character which one of the molecular data types to use in the analysis, out of all the molecular data types available for the pset for example: rna, rnaseq, snp
cell.lines character The cell lines to be summarized. If any cell.line has no data, missing values will be created
features character A vector of the feature names to include in the summary
summary.stat character which summary method to use if there are repeated cell.lines? Choices are "mean", "median", "first", or "last" In case molecular data type is mutation or fusion "and" and "or" choices are available
fill.missing boolean should the missing cell lines not in the molecular data object be filled in with missing values?
summarize A flag which when set to FALSE (defaults to TRUE) disables summarizing and returns the data unchanged as a ExpressionSet
verbose boolean should messages be printed
binarize.threshold numeric A value on which the molecular data is binarized. If NA, no binarization is done.
binarize.direction character One of "less" or "greater", the direction of binarization on binarize.threshold, if it is not NA.
removeTreated logical If treated/perturbation experiments are present, should they be removed? Defaults to yes.

Value

matrix An updated PharmacoSet with the molecular data summarized per cell line.
summarizeSensitivityProfiles,PharmacoSet-method

Examples

data(GDSCsmall)
GDSCsmall <- summarizeMolecularProfiles(GDSCsmall, mDataType = "rna", cell.lines=sampleNames(GDSCsmall), summary.stat = 'median', fill.missing = TRUE, verbose=TRUE)
GDSCsmall

summarizeSensitivityProfiles,PharmacoSet-method

Takes the sensitivity data from a PharmacoSet, and summarises them into a drug vs cell line table

Description

This function creates a table with cell lines as rows and drugs as columns, summarising the drug sensitivity data of a PharmacoSet into drug-cell line pairs

Usage

## S4 method for signature 'PharmacoSet'
summarizeSensitivityProfiles(
  object,
  sensitivity.measure = "auc_recomputed",
  cell.lines,
  drugs,
  summary.stat = c("mean", "median", "first", "last", "max", "min"),
  fill.missing = TRUE,
  verbose = TRUE
)

Arguments

object PharmacoSet The PharmacoSet from which to extract the data
sensitivity.measure character which sensitivity measure to use? Use the sensitivityMeasures function to find out what measures are available for each object.
cell.lines character The cell lines to be summarized. If any cell lines has no data, it will be filled with missing values
drugs character The drugs to be summarized. If any drugs has no data, it will be filled with missing values
summary.stat character which summary method to use if there are repeated cell line-drug experiments? Choices are "mean", "median", "first", or "last"
fill.missing boolean should the missing cell lines not in the molecular data object be filled in with missing values?
verbose Should the function print progress messages?
Value

matrix A matrix with cell lines going down the rows, drugs across the columns, with the selected sensitivity statistic for each pair.

Examples

```r
data(GDScsmall)
GDSCauc <- summarizeSensitivityProfiles(GDScsmall,
  sensitivity.measure='auc_published')
```

Description

Update the PharmacoSet class after changes in its structure or API

Usage

## S4 method for signature 'PharmacoSet'
updateObject(object)

Arguments

object A PharmacoSet object to update the class structure for.

Value

PharmacoSet with update class structure.

Usage

## S4 method for signature 'PharmacoSet,ANY,ANY,ANY'
x[i, j, ..., drop = FALSE]
Arguments

- `x` object
- `i` Cell lines to keep in object
- `j` Drugs to keep in object
- `...` further arguments
- `drop` A boolean flag of whether to drop single dimensions or not

Value

Returns the subsetted object

Examples

```r
data(CCLEsmall)
CCLEsmall["WM1799", "Sorafenib"]
```
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