Package ‘synlet’

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Type Package

Title Hits Selection for Synthetic Lethal RNAi Screen Data

Version 2.2.0

Description Select hits from synthetic lethal RNAi screen data. For example, there are two identical cell lines except one gene is knocked-down in one cell line. The interest is to find genes that lead to stronger lethal effect when they are knocked-down further by siRNA. Quality control and various visualisation tools are implemented. Four different algorithms could be used to pick up the interesting hits. This package is designed based on 384 wells plates, but may apply to other platforms with proper configuration.

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biocViews ImmunoOncology, CellBasedAssays, QualityControl, Preprocessing, Visualization, FeatureExtraction

Imports data.table, ggplot2, grDevices, magrittr, methods, patchwork, RankProd, RColorBrewer, stats, utils

Suggests BiocStyle, knitr, testthat, rmarkdown

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Author Chunxuan Shao [aut, cre]

Maintainer Chunxuan Shao <chunxuan@outlook.com>
### bScore

**Calculate B-score**

**Description**

Calculate the B-score for plates belonging to the same master plate. Positive / negative controls are removed from the calculation.

**Usage**

```r
bScore(masterPlate, dta, treatment, control, outFile = FALSE)
```

**Arguments**

- `masterPlate` a master plate to be normalized.
- `dta` synthetic lethal RNAi screen data.
- `treatment` the treatment experiment condition in `EXPERIMENT_MODIFICATION`.
- `control` the control experiment condition in `EXPERIMENT_MODIFICATION`.
- `outFile` should calculated B-score files be written to the current folder? File names is `(masterPlate).bscore.csv`.

**Value**

A list contains B-score for each master plate, treatment plates are the first columns, followed by control plates.

**References**

Examples
data(example_dt)
res <- sapply(unique(example_dt$MASTER_PLATE), bScore, example_dt,
             treatment = "treatment", control = "control", simplify = FALSE)

Example_dt Synthetif lethal RNAi screen example data.

Description
A dataset containing synthetic lethal RNAi screen data to show how functions work. The variables
are as follows (all are character except READOUT):

Usage
data(example_dt)

Format
A data.table with 4320 rows and 8 variables

Details
- PLATE. plate names.
- MASTER_PLATE. master plate names.
- WELL_CONTENT_NAME. siRNA targets of wells.
- EXPERIMENT_TYPE. sample, negative/positive controls.
- EXPERIMENT_MODIFICATION. experiment conditions, "treatment" or "control".
- ROW_NAME. row names of plates.
- COL_NAME. column names of plates.
- READOUT. screen results.

Value
A data.table containing RNAi screen data, the READOUT value has no real biological meaning.
madSelect

Select hits basing on median + k*MAD

Description
Select hits basing on median + k*MAD, by default k is three.

Usage
madSelect(
  masterPlate,
  dat,
  k = 3,
  treatment,
  control,
  outFile = FALSE,
  normMethod = "PLATE"
)

Arguments
- masterPlate: the master plate to analysis
- dat: synthetic lethal RNAi screen data
- k: cutoff for selecting hits, default is three
- treatment: the treatment condition in EXPERIMENT_MODIFICATION
- control: the control condition in EXPERIMENT_MODIFICATION
- outFile: whether or not write the median normalized results
- normMethod: normalization methods to be used. If "PLATE", the raw readouts are normalized by plate median, otherwise use median provided control siRNA.

Value
A data.frame contains the hits selection results.
- MASTER_PLATE: location of siRNA
- treat_cont_ratio: ratio of treatment / control
- treat_median: median value of treatment plates
- control_median: median value of control plates
- Hits: Is this siRNA a hit?

References
Examples

```r
data(example_dt)
res <- sapply(unique(example_dt$MASTER_PLATE),
               madSelect,
               example_dt,
               control = "control",
               treatment = "treatment",
               simplify = FALSE)

plateHeatmap(res)
```

Description

Put all individual plates in one graph, values are the readout in experiments.

Usage

```r
plateHeatmap(dta, base_size = 12, heatmap_col = NULL)
```

Arguments

- `dta` synthetic lethal RNAi screen data
- `base_size` basic font size used for x/y axis and title for heatmaps
- `heatmap_col` color function generated by colorRampPalette.

Value

a ggplot object

Examples

```r
data(example_dt)
plateHeatmap(example_dt)
```
Select hits by rank product method by comparing treatment and control.

Usage

```r
rankProdHits(masterPlate, dta, treatment, control, normMethod = "PLATE")
```

Arguments

- `masterPlate`: the master plate to be analyzed
- `dta`: synthetic lethal RNAi screen data
- `treatment`: the treatment condition in `EXPERIMENT_MODIFICATION`
- `control`: the control condition in `EXPERIMENT_MODIFICATION`
- `normMethod`: normalization methods to be used. If "PLATE", the raw readouts are normalized by plate median, otherwise use provided control siRNA

Value

A list contains results by the rank product method for each master plate.

- `MASTER_PLATE`: location of siRNA
- `pvalue_treat_lowerthan_cont`: p-value for the hypothesis that treatment has lower normalized readout compared to control
- `FDR_treat_lowerthan_cont`: FDR value
- `treat_cont_log2FC`: log2 fold change of treatment / control

References


Examples

```r
data(example_dt)
res <- sapply(unique(example_dt$MASTER_PLATE),
              rankProdHits,
              example_dt,
              control = "control",
              treatment = "treatment",
              simplify = FALSE)
```
rsaHits

**rsaHits**

*Select hits by RSA*

**Description**

Selected hits by redundant siRNA activity method. Here is a wrapper function of RSA 1.8 by Yingyao Zhou.

**Usage**

```r
rsaHits(
  dta,
  treatment,
  control,
  normMethod = "PLATE",
  LB,
  UB,
  revHits = FALSE,
  Bonferroni = FALSE,
  outputFile = "RSAhits.csv",
  scoreFile = "RSA_score.csv"
)
```

**Arguments**

- `dta`: synthetic lethal RNAi screen data
- `treatment`: the treatment condition in EXPERIMENT_MODIFICATION
- `control`: the control condition in EXPERIMENT_MODIFICATION
- `normMethod`: normalization methods. If "PLATE", then values are normalized by plate median, otherwise use the provided control siRNA
- `LB`: Low bound
- `UB`: up bound
- `revHits`: reverse hit picking, default the lower the score the better
- `Bonferroni`: conceptually useful when there are different number of siRNAs per gene, default FALSE
- `outputFile`: output file name
- `scoreFile`: name of the score file to be written under the current folder

**Value**

A result file written to the current folder.

- Gene_ID,Well_ID,Score: columns from input spreadsheet
- LogP: OPI p-value in log10, i.e., -2 means 0.01
• OPI_Hit: whether the well is a hit, 1 means yes, 0 means no
• #hitWell: number of hit wells for the gene
• #totalWell: total number of wells for the gene. If gene A has three wells w1, w2 and w3, and w1 and w2 are hits, #totalWell should be 3, #hitWell should be 2, w1 and w2 should have OPI_Hit set as 1 and w3 should have OPI_Hit set as 0.
• OPI_Rank: ranking column to sort all wells for hit picking
• Cutoff_Rank: ranking column to sort all wells based on Score in the simple activity-based method

Note: a rank value of 999999 means the well is not a hit

References

Examples
data(example_dt)
rsaHits(example_dt, treatment = "treatment", control = "control",
        normMethod = "PLATE", LB = 0.2, UB = 0.8, revHits = FALSE,
        Bonferroni = FALSE, outputFile = "RSAhits.csv")

scatterPlot  Scatter plot of RNAi screen results

Description
Produce a single plot for readouts of each plate, with the option of highlighting specific signals, like positive/negative controls.

Usage
scatterPlot(
  dta,
  scatter_colour = rainbow(10),
  controlOnly = FALSE,
  control_name = NULL
)

Arguments
dta        synthetic lethal RNAi screen data
scatter_colour colour for different signals
controlOnly  whether or not to plot control wells only
control_name  names of control siRNAs.
siRNAPlot

Value

a ggplot object

Examples

data(example_dt)
scatterPlot(example_dt, control_name = c("PLK1 si1", "scrambled control si1", "lipid only"))

---

siRNAPlot  
Plot siRNA data and quality metrics.

Description

Plot the normalized RNAi screen data, row data, control signals and Z' factor.

Usage

siRNAPlot(
  gene,
  dta,
  controlsiRNA,
  FILEPATH = ".",
  colour = rainbow(10),
  zPrimeMed,
  zPrimeMean,
  treatment,
  control,
  normMethod = c("PLATE"),
  save_plot = FALSE,
  width = 15,
  height = 14
)

Arguments

gene  
gene symbol, case sensitive
dta  
synthetic lethal RNAi screen data
controlsRNA  
controlsRNA could be a vector of several siRNA, including postive/negative control
FILEPATH  
path to store the figure
colour  
colour used in graphs
zPrimeMed  
zPrime factor basing on median
zPrimeMean  
zPrime factor basing on mean
treatment  
the treatment condition in EXPERIMENT_MODIFICATION
control the control condition in EXPERIMENT_MODIFICATION
normMethod could be a PLATE and negative controls
save_plot whether save a png file in the working directory.
width width of the plot
height height of the plot

Value
Return the ggplot2 objects in a list, which could be plotted individually.

Examples
```r
data(example_dt)
ZF_mean <- zFactor(example_dt, negativeCon = "scrambled control si1", positiveCon = "PLK1 si1")
ZF_med <- zFactor(example_dt, negativeCon = "scrambled control si1", positiveCon = "PLK1 si1", useMean = FALSE)
p01 <- siRNAPlot("AAK1", example_dt, controlsRNA = c("lipid only", "scrambled control si1"), FILEPATH = ".", zPrimeMed = ZF_med, zPrimeMean = ZF_mean, treatment = "treatment", control = "control", normMethod = c("PLATE", "lipid only", "scrambled control si1"))
```

dtTest  

Description
Select hits by student's t-test using B-score from treatment and control plates.

Usage
tTest(mtx, n_treat, n_cont)

Arguments

ntxt b-score matrix.
n_treat number of treatment plates
n_cont number of control plates

Value
A list containing student's t-test for each master plate
- pvalue: p-value of the t-test
- Treat_Cont: difference in bscore: treatment - control
- p_adj: BH adjusted p-value

```r
data(example_dt)
zF_mean <- zFactor(example_dt, negativeCon = "scrambled control si1", positiveCon = "PLK1 si1")
zF_med <- zFactor(example_dt, negativeCon = "scrambled control si1", positiveCon = "PLK1 si1", useMean = FALSE)
p01 <- siRNAPlot("AAK1", example_dt, controlsRNA = c("lipid only", "scrambled control si1"), FILEPATH = ".", zPrimeMed = ZF_med, zPrimeMean = ZF_mean, treatment = "treatment", control = "control", normMethod = c("PLATE", "lipid only", "scrambled control si1"))
```
**zFactor**

References


Examples

data(example_dt)
bscore_res <- sapply(unique(example_dt$MASTER_PLATE), bScore,
  example_dt, control = "control", treatment = "treatment", simplify = FALSE)
tTest(bscore_res$P001, 3, 3)

---

**zFactor**

Calculate the Z and Z' factor

Description

calculate the Z and Z' factor for each plate.

Usage

zFactor(dta, negativeCon, positiveCon, useMean = TRUE)

Arguments

dta  synthetic lethal RNAi screen data.
negativeCon the negative control used in the WELL_CONTENT_NAME.
positiveCon the positive control used in the WELL_CONTENT_NAME.
useMean use mean to calculate z factor and z' factor by default; otherwise use median.

Value

A data.frame contains z factor and z' factor

References


Examples

data(example_dt)
res <- zFactor(example_dt, negativeCon = "scrambled control si1", positiveCon = "PLK1 si1")
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