Package 'CRISPRball'

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Title Shiny Application for Interactive CRISPR Screen Visualization, Exploration, Comparison, and Filtering

Version 1.8.0

Description A Shiny application for visualization, exploration, comparison, and filtering of CRISPR screens analyzed with MAGeCK RRA or MLE. Features include interactive plots with on-click labeling, full customization of plot aesthetics, data upload and/or download, and much more. Quickly and easily explore your CRISPR screen results and generate publication-quality figures in seconds.

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`CRISPRball-package` *CRISPRball: Shiny Application for Interactive CRISPR Screen Visualization, Exploration, Comparison, and Filtering*

Description

A Shiny application for visualization, exploration, comparison, and filtering of CRISPR screens analyzed with MAGeCK RRA or MLE. Features include interactive plots with on-click labeling, full customization of plot aesthetics, data upload and/or download, and much more. Quickly and easily explore your CRISPR screen results and generate publication-quality figures in seconds.

Author(s)

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See Also

Useful links:

- https://github.com/j-andrews7/CRISPRball
- Report bugs at https://support.bioconductor.org/

`build_depmap_db` *Build SQLite database of DepMap data*

Description

Build SQLite database of DepMap data

Usage

```
build_depmap_db(
  retrieve = c("rnai", "crispr", "dependency", "cn", "ccle_tpm", "meta", "drug",
    "gene.summary", "release"),
  file = "depmap_db.sqlite"
)
```

Arguments

`retrieve`	Character vector of data to retrieve from DepMap. Options include: • `rnai`: RNAi screen data from `depmap_rnai`. • `crispr`: CRISPR screen data from `depmap_crispr`. • `cn`: Copy number data from `depmap_copyNumber`. • `ccle_tpm`: TPM data from `depmap_TPM`. • `meta`: Cell line metadata from `depmap_metadata`. • `drug`: Drug sensitivity data from `depmap_drug_sensitivity`. • `gene.summary`: Gene summary data from `depmap_gene_summary`. • `release`: DepMap release information from from `depmap_release`.
`file`	Name of SQLite database file to create.

Value

Name of SQLite database containing DepMap data.

Author(s)

Jared Andrews

See Also

depmap_rnai, depmap_crispr, depmap_copyNumber, depmap_TPM, depmap_metadata, depmap_gene_summary, depmap_drug_sensitivity, depmap_release dbPool, dbWriteTable

Examples

```
library(CRISPRball)
build_depmap_db(retrieve = "release")
```

`CRISPRball` *Create an interactive Shiny app for visualization & exploration of CRISPR analyses*

Description

Create an interactive Shiny app for visualization & exploration of CRISPR analyses

Usage

```
CRISPRball(
  gene.data = NULL,
  sgrna.data = NULL,
  count.summary = NULL,
  norm.counts = NULL,
  h.id = "mag1",
  positive.ctrl.genes = NULL,
  essential.genes = NULL,
  depmap.db = NULL,
  genesets = NULL,
  return.app = TRUE
)
```

Arguments

`gene.data`	A named list containing `gene_summary.txt` tables as data.frames. Multiple data.frames may be provided, one per element of the list. Users will be able to swap between them within the app. List element names should match names of `sgrna.data` list elements.
`sgrna.data`	A named list containing `sgrna_summary.txt` tables as data.frames. Multiple data.frames may be provided, one per element of the list. Users will be able to swap between them within the app. List element names should match names of `gene.data` list elements.

`count.summary` Matrix or dataframe containing count summary (`countsummary.txt`) as generated by `mageck count`.

`norm.counts` Matrix or dataframe containing normalized counts (`count_normalized.txt`) as generated by `mageck count`.

`h.id` String indicating unique ID for interactive plots. Required if multiple apps are run within the same Rmd file.

`positive.ctrl.genes` Optional character vector of gene identifiers for positive control genes from the screen so that they can be easily filtered.

`essential.genes` Optional character vector of gene identifiers of common essential genes (i.e. pan-lethal) so that they can be easily filtered. If provided, overrides the depmap essential genes.

`depmap.db` Optional character scalar for name of SQLite database returned by `build_depmap_db`.

`genesets` Optional named list containing genesets that can be interactively highlighted on the plots. The elements of the list should each be a geneset with gene identifiers matching those used in the results.

`return.app` Optional boolean indicating whether a Shiny app should be returned. `TRUE` by default. If `FALSE`, a named list of app elements (ui and server) will be returned instead. Useful for deploying as a standalone shiny app.

Details

Features with no variation will be removed prior to `pca` being run for the PCA visualization. Gene labels can be added to the MAplot and volcano plot by clicking a point. The labels can also be dragged around, though adding labels will reset the positions, so it's recommended to add all labels prior to re-positioning them.

Value

A Shiny app containing interactive visualizations of CRISPR analysis results.

Author(s)

Jared Andrews, Jacob Steele

Examples

```
library(CRISPRball)
# Create app with no data loaded.
app <- CRISPRball()
if (interactive()) {
    shiny::runApp(app)
}

# Create app with data loaded.
# Create lists of results summaries for each dataset.
d1.genes <- read.delim(system.file("extdata", "esc1.gene_summary.txt",
```

```
    package = "CRISPRball"
), check.names = FALSE)
d2.genes <- read.delim(system.file("extdata", "plasmid.gene_summary.txt",
    package = "CRISPRball"
), check.names = FALSE)

d1.sgrnas <- read.delim(system.file("extdata", "esc1.sgrna_summary.txt",
    package = "CRISPRball"
), check.names = FALSE)
d2.sgrnas <- read.delim(system.file("extdata", "plasmid.sgrna_summary.txt",
    package = "CRISPRball"
), check.names = FALSE)

count.summ <- read.delim(system.file("extdata", "escneg.countsummary.txt",
    package = "CRISPRball"
), check.names = FALSE)
norm.counts <- read.delim(system.file("extdata", "escneg.count_normalized.txt",
    package = "CRISPRball"
), check.names = FALSE)

genes <- list(ESC = d1.genes, plasmid = d2.genes)
sgrnas <- list(ESC = d1.sgrnas, plasmid = d2.sgrnas)

app <- CRISPRball(
    gene.data = genes, sgrna.data = sgrnas,
    count.summary = count.summ, norm.counts = norm.counts
)
if (interactive()) {
    shiny::runApp(app)
}
```

---

depmap_22q1_cn *DepMap copy number data*

Description

The DepMap copy number data for CDK2.

Usage

```
data(depmap_22q1_cn)
```

Format

depmap_22q1_TPM**:**

A dataframe with 1754 rows and 9 columns:

depmap_id Depmap cell line ID

log_copy_number log2 copy number

entrez_id Numeric entrez gene ID

gene_name Gene symbol
dataset Screen type, either CRISPR or RNAi
cell_line_name Cell line name
primary_disease Cell line disease origin
lineage Cell line lineage
lineage_subtype Cell line lineage subtype, usually a malignancy
hover.string String for hover text when plotting

Value

A dataframe containing DepMap 22Q1 copy number data.

Source

https://depmap.org/portal/download/all/
https://bioconductor.org/packages/release/data/experiment/html/depmap.html

---

`depmap_22q1_crispr` *DepMap CRISPR screen data*

Description

The DepMap CRISPR screen data for CDK2.

Usage

```
data(depmap_22q1_crispr)
```

Format

`depmap_22q1_crispr`**:**
A dataframe with 1070 rows and 9 columns:
depmap_id Depmap cell line ID
dependency Depmap dependency score
entrez_id Numeric entrez gene ID
gene_name Gene symbol
cell_line_name Cell line name
primary_disease Cell line disease origin
lineage Cell line lineage
lineage_subtype Cell line lineage subtype, usually a malignancy
hover.string String for hover text when plotting

Value

A dataframe containing DepMap 22Q1 CRISPR screen data.

Source

https://depmap.org/portal/download/all/

https://bioconductor.org/packages/release/data/experiment/html/depmap.html

---

depmap_22q1_crispr_rnai

DepMap CRISPR & RNAi screen data

Description

The DepMap CRISPR & RNAi screen data for CDK2.

Usage

```
data(depmap_22q1_crispr_rnai)
```

Format

depmap_22q1_crispr_rnai:

A dataframe with 1782 rows and 9 columns:

depmap_id Depmap cell line ID

dependency Depmap dependency score

entrez_id Numeric entrez gene ID

gene_name Gene symbol

dataset Screen type, either CRISPR or RNAi

cell_line_name Cell line name

primary_disease Cell line disease origin

lineage Cell line lineage

lineage_subtype Cell line lineage subtype, usually a malignancy

hover.string String for hover text when plotting

Value

A dataframe containing DepMap 22Q1 CRISPR and RNAi data.

Source

https://depmap.org/portal/download/all/

https://bioconductor.org/packages/release/data/experiment/html/depmap.html

depmap_22q1_rnai *DepMap RNAi screen data*

Description

The DepMap RNAi screen data for CDK2.

Usage

```
data(depmap_22q1_rnai)
```

Format

depmap_22q1_rnai:
A dataframe with 712 rows and 9 columns:

dependency Depmap dependency score
entrez_id Numeric entrez gene ID
gene_name Gene symbol
depmap_id Depmap cell line ID
cell_line_name Cell line name
primary_disease Cell line disease origin
lineage Cell line lineage
lineage_subtype Cell line lineage subtype, usually a malignancy
hover.string String for hover text when plotting

Value

A dataframe containing DepMap 22Q1 RNAi screen data.

Source

https://depmap.org/portal/download/all/
https://bioconductor.org/packages/release/data/experiment/html/depmap.html

depmap_22q1_TPM *DepMap expression data*

Description

The DepMap expression data for CDK2.

Usage

```
data(depmap_22q1_TPM)
```

Format

depmap_22q1_TPM:

A dataframe with 1393 rows and 9 columns:

depmap_id Depmap cell line ID

rna_expression log2(TPM+1) expression

entrez_id Numeric entrez gene ID

gene_name Gene symbol

dataset Screen type, either CRISPR or RNAi

cell_line_name Cell line name

primary_disease Cell line disease origin

lineage Cell line lineage

lineage_subtype Cell line lineage subtype, usually a malignancy

hover.string String for hover text when plotting

Value

A dataframe containing DepMap 22Q1 expression data.

Source

https://depmap.org/portal/download/all/

https://bioconductor.org/packages/release/data/experiment/html/depmap.html

---

gene_ingress *Parse gene summary data for easier plotting and display*

Description

Parse gene summary data for easier plotting and display

Usage

```
gene_ingress(
  df,
  sig.thresh,
  es.thresh,
  es.col,
  sig.col,
  positive.ctrl.genes = NULL,
  essential.genes = NULL,
  depmap.genes = NULL
)
```

Arguments

df	data.frame of gene summary data. Gene IDs should be in the first column.
sig.thresh	Numeric scalar for significance threshold to consider a gene a hit.
es.thresh	Numeric scalar for absolute log fold change threshold to consider a gene a hit.
es.col	Character scalar for the column name of the effect size value.
sig.col	Character scalar for the column name of the significance value.
positive.ctrl.genes	Character vector of gene identifiers to label as positive controls.
essential.genes	Character vector of gene identifiers to label as essential genes.
depmap.genes	data.frame of DepMap gene summary data.

Value

A data.frame of gene summary with additional, easier to plot, columns added.

Author(s)

Jared Andrews

Examples

```
library(CRISPRball)
d1.genes <- read.delim(system.file("extdata", "esc1.gene_summary.txt",
    package = "CRISPRball"
), check.names = FALSE)
out.df <- gene_ingress(d1.genes, 0.05, 0.5, es.col = "LFC", sig.col = "fdr")
```

---

get_depmap_essentiality

Get essential/selective gene information from DepMap summary table.

Description

Get essential/selective gene information from DepMap summary table.

Usage

```
get_depmap_essentiality(gene, depmap.summary)
```

Arguments

gene	Character scalar for gene symbol.
depmap.summary	data.frame containing DepMap gene summary information.

Value

Named list containing RNAi and CRISPR named lists containing dataset information for the provided gene, if available. If the gene is not found in the summary data.frame, the `avail` element for the RNAi and CRISPR lists will be set to `FALSE`.

Author(s)

Jared Andrews

Examples

```
library(CRISPRball)
build_depmap_db(retrieve = "gene.summary")
pool <- pool::dbPool(RSQLite::SQLite(), dbname = "depmap_db.sqlite")
depmap.gene <- pool::dbGetQuery(pool, "SELECT * FROM 'gene.summary'")

essentials <- get_depmap_essentiality(gene = "CDK2", depmap.summary = depmap.gene)
```

`get_depmap_plot_data` *Create DepMap dataframe for plotting*

Description

Based on the requested data type, this function will create a dataframe from the DepMap database that can be used for plotting.

Usage

```
get_depmap_plot_data(gene, data.type, depmap.meta, depmap.pool)
```

Arguments

`gene`	Character scalar of gene name.
`data.type`	Character scalar of data type to retrieve. One of "dependency", "crispr", "rnai", "cn", or "ccle_tpm".
`depmap.meta`	data.frame of DepMap cell line metadata, as stored in the 'meta' table of the SQLite database built by `build_depmap_db`.
`depmap.pool`	pool connection to DepMap SQLite database built with `build_depmap_db`.

Value

data.frame containing appropriate DepMap data for plotting.

Author(s)

Jared Andrews

See Also

plot_depmap_lineages

Examples

```
## Not run:
library(CRISPRball)
build_depmap_db(retrieve = c("meta", "crispr"))
pool <- pool::dbPool(RSQLite::SQLite(), dbname = "depmap_db.sqlite")
depmap.meta <- pool::dbGetQuery(pool, "SELECT * FROM 'meta'")

df <- get_depmap_plot_data(
    gene = "CDK2", data.type = "crispr",
    depmap.meta = depmap.meta, depmap.pool = pool
)

## End(Not run)
```

---

plot_bar *Create interactive bar plot*

Description

Create an interactive bar plot for specific summary information for each sample in the dataset.

Usage

```
plot_bar(
  count.summary,
  x = "Label",
  y = "GiniIndex",
  title = "sgRNA Read Distribution",
  xlab = NULL,
  ylab = "Gini Index",
  fill = "#E69F00",
  yaxis.addition = 0.05
)
```

Arguments

count.summary	data.frame containing the count summary information for each sample.
x	Character scalar for column of count.summary to plot along the x-axis.
y	Character scalar for column of count.summary to plot along the y-axis.
title	Character scalar for title of the plot.
xlab	Character scalar for label of the x-axis.
ylab	Character scalar for label of the y-axis.
fill	Character scalar for bar fill color in hex.
yaxis.addition	Numeric scalar for additional space to add to the y-axis.

Value

An interactive bar chart showing the specified summary information for each sample. The axis and plot title are editable.

Author(s)

Jared Andrews

Examples

```
library(CRISPRball)
count.summ <- read.delim(system.file("extdata", "escneg.countsummary.txt",
    package = "CRISPRball"
), check.names = FALSE)
# Gini Index plot
plot_bar(count.summ)

# Zero count sgRNAs plot
plot_bar(count.summ,
    x = "Label", y = "Zerocounts", title = "Fully Depleted sgRNAs",
    fill = "#394E80", ylab = "Zero Count sgRNAs", yaxis.addition = 10
)
```

---

plot_correlation_heatmap

Plot a Correlation Heatmap

Description

This function creates a heatmap using ComplexHeatmap to display the correlation values in a matrix. The color of each cell in the heatmap is determined by the corresponding correlation value, using a color ramp that ranges from the minimum value color to a maximum value color.

Usage

```
plot_correlation_heatmap(
  mat,
  min.color = "#FF0000",
  max.color = "#0000FF",
  legend.title = "Pearson Corr.",
  plot.title = "Correlation Matrix"
)
```

Arguments

mat	A matrix containing the correlation values.
min.color	Character scalar for the hexadecimal color code for the minimum values in the heatmap.

max.color	Character scalar for the hexadecimal color code for the maximum values in the heatmap.
legend.title	Character scalar for title of the legend.
plot.title	Character scalar for title of the plot.

Value

A Heatmap object.

Author(s)

Jared Andrews

Examples

```
library(CRISPRball)
norm.counts <- read.delim(system.file("extdata", "escneg.count_normalized.txt",
    package = "CRISPRball"
), check.names = FALSE)
norm.counts <- as.matrix(norm.counts[, c(-1, -2)])
norm.counts.log <- log2(norm.counts + 1)
cor.mat <- cor(norm.counts.log)
plot_correlation_heatmap(cor.mat)
```

---

plot_depmap_cn *Plot gene copy number information from DepMap*

Description

Plot gene copy number information from DepMap

Usage

```
plot_depmap_cn(df, color = "#CEA3CB", plot.grid = FALSE)
```

Arguments

df	data.frame containing information for a single gene as returned by get_depmap_plot_data.
color	Character scalar for trace color.
plot.grid	Boolean indicating whether to plot gridlines.

Value

plotly object

Author(s)

Jared Andrews

See Also

get_depmap_plot_data

Examples

```
library(CRISPRball)
data(depmap_22q1_cn)
plot_depmap_cn(depmap_22q1_cn)
```

---

plot_depmap_dependency

Plot gene dependency information from DepMap CRISPR and RNAi tables

---

Description

Plot gene dependency information from DepMap CRISPR and RNAi tables

Usage

```
plot_depmap_dependency(
  df,
  crispr.color = "#3584B5",
  rnai.color = "#52288E",
  depline = TRUE,
  plot.grid = FALSE
)
```

Arguments

df	data.frame containing information for a single gene as returned by get_depmap_plot_data.
crispr.color	Character scalar for CRISPR trace color as hexcode.
rnai.color	Character scalar for RNAi trace color as hexcode.
depline	Boolean indicating whether to show the dependency threshold line.
plot.grid	Boolean indicating whether to plot gridlines.

Value

plotly object

Author(s)

Jared Andrews

See Also

get_depmap_plot_data

Examples

```
library(CRISPRball)
data(depmap_22q1_crispr_rnai)
plot_depmap_dependency(depmap_22q1_crispr_rnai)
```

`plot_depmap_expression` *Plot gene expression information from DepMap, mostly from CCLE*

Description

Plot gene expression information from DepMap, mostly from CCLE

Usage

```
plot_depmap_expression(df, color = "#7B8CB2", plot.grid = FALSE)
```

Arguments

`df`	data.frame containing information for a single gene as returned by `get_depmap_plot_data`.
`color`	Character scalar for trace color.
`plot.grid`	Boolean indicating whether to plot gridlines.

Value

plotly object

Author(s)

Jared Andrews

See Also

`get_depmap_plot_data`

Examples

```
library(CRISPRball)
data(depmap_22q1_TPM)
plot_depmap_expression(depmap_22q1_TPM)
```

`plot_depmap_lineages` *Plot selected information across lineages from DepMap.*

Description

Plot selected information across lineages from DepMap.

Usage

```
plot_depmap_lineages(
  df,
  plot.val,
  group.by,
  lineage = NULL,
  depline = TRUE,
  label.size = 12,
  pt.size = 5,
  pt.color = "#56B4E9",
  boxplot.fill = "#E2E2E2",
  boxplot.line.color = "#000000"
)
```

Arguments

`df`	data.frame containing information for a single gene as returned by `get_depmap_plot_data`.
`plot.val`	Character scalar of column name to plot values from.
`group.by`	Character scalar of column name to group by.
`lineage`	Character scalar of lineage for which to plot sub-lineage data.
`depline`	Boolean indicating whether to show the dependency threshold line.
`label.size`	Numeric scaler for axis label size.
`pt.size`	Numeric scalar for point size.
`pt.color`	Character scalar for point color.
`boxplot.fill`	Character scalar for boxplot fill color.
`boxplot.line.color`	Character scalar for boxplot line color.

Value

plotly object

Author(s)

Jared Andrews

See Also

get_depmap_plot_data

Examples

```
library(CRISPRball)
data("depmap_22q1_rnai")
plot_depmap_lineages(df = depmap_22q1_rnai, plot.val = "dependency", group.by = "lineage")
```

---

plot_hist *Create a plotly plot from a distribution of values*

Description

This function creates a plotly plot with the distribution of values for each column in the `mat` matrix, using different colors for each column. The legend will show the column names from `mat`, and the plot will have the title "Distribution of read counts".

Usage

```
plot_hist(
  mat,
  title = NULL,
  xlab = "Values",
  ylab = "Frequency",
  show.grid = FALSE
)
```

Arguments

`mat`	A matrix with the data to plot.
`title`	A character scalar for the title of the plot.
`xlab`	Character scalar for label of the x-axis.
`ylab`	Character scalar for label of the y-axis.
`show.grid`	A boolean for whether to show the grid lines.

Value

A plotly plot with the distribution of read counts.

Author(s)

Jared Andrews

Examples

```
library(CRISPRball)
cts <- read.delim(system.file("extdata", "escneg.count_normalized.txt",
    package = "CRISPRball"
), check.names = FALSE)
cts.log <- as.matrix(log2(cts[, c(-1, -2)] + 1))
colnames(cts.log) <- colnames(cts)[c(-1, -2)]

plot_hist(cts.log,
    title = "Distribution of read counts",
    xlab = "log2(counts + 1)", ylab = "Frequency"
)
```

`plot_lawn` *Create an interactive lawn plot*

Description

Create an interactive lawn plot for data with significance values. Typically, this plot is randomly ordered along the x-axis, but the user is free to order it by any term in `res` that they'd like.

Usage

```
plot_lawn(
  res,
  ylim = 5,
  fc.thresh = 0.5,
  hover.info = NULL,
  sig.line = TRUE,
  h.id = "crispr",
  feat.term = "rows",
  x.term = "RandomIndex",
  sig.term = "fdr",
  lfc.term = "LFC",
  down.color = "#0026ff",
  up.color = "#ff0000",
  insig.color = "#A6A6A6",
  sig.thresh = 0.05,
  fs = NULL,
  sig.size = 6,
  insig.size = 5,
  sig.opacity = 1,
  insig.opacity = 0.5,
  label.size = 10,
  webgl = TRUE,
  webgl.ratio = 7,
  show.counts = TRUE,
```

```
  show.hl.counts = TRUE,
  counts.size = TRUE,
  highlight.featsets = NULL,
  highlight.feats = NULL,
  featsets = NULL,
  highlight.feats.color = "#E69F00",
  highlight.feats.size = 7,
  highlight.feats.opac = 1,
  highlight.feats.linecolor = "#000000",
  highlight.feats.linewidth = 1,
  highlight.feats.label = TRUE,
  highlight.featsets.color = "#009E73",
  highlight.featsets.size = 7,
  highlight.featsets.opac = 1,
  highlight.featsets.linecolor = "#000000",
  highlight.featsets.linewidth = 1,
  highlight.featsets.label = FALSE,
  h.id.suffix = "_lawn"
)
```

Arguments

`res`	Dataframe containing, at minimum, significance values and a term by which the x-axis can be ordered.
`ylim`	Positive numeric scalar indicating y-axis limits. The negative value will be used for the lower limit.
`fc.thresh`	Numeric scalar indicating the fold change threshold for coloring significant features.
`hover.info`	Character vector indicating which additional columns from `res` to include in the hover info.
`sig.line`	Logical indicating whether to add a significance threshold line to the plot.
`h.id`	Character scalar indicating the unique ID of the plotly object. Can usually be ignored, but should be used if multiple plots are being created in the same R session (e.g. Shiny app).
`feat.term`	Character scalar indicating the column name of the feature IDs in `res`.
`x.term`	Character scalar for the x-axis term from `res` to be plotted.
`sig.term`	Character scalar indicating the column name of the significance values in `res`.
`lfc.term`	Character scalar indicating the column name of the log fold change values in `res`.
`down.color`	Character scalar indicating the color of down-regulated features.
`up.color`	Character scalar indicating the color of up-regulated features.
`insig.color`	Character scalar indicating the color of insignificant features.
`sig.thresh`	Numeric scalar indicating the significance threshold for coloring significant features.

`fs` Dataframe containing coordinates and label information for points that should be labeled. Columns should be:

- `x` - x coordinate of the point
- `y` - y coordinate of the point
- `customdata` - label to be displayed

`sig.size` Numeric scalar indicating the size of significant feature points.

`insig.size` Numeric scalar indicating the size of insignificant feature points.

`sig.opacity` Numeric scalar indicating the opacity of significant feature points.

`insig.opacity` Numeric scalar indicating the opacity of insignificant feature points.

`label.size` Numeric scalar indicating the size of feature labels.

`webgl` Logical indicating whether to use WebGL for rendering the plot.

`webgl.ratio` Numeric scalar indicating the ratio of WebGL to HTML5 canvas rendering, increases resolution of saved plot when WebGL plotting is not used.

`show.counts` Logical indicating whether to show annotations for the number of features in the plot.

`show.hl.counts` Logical indicating whether to show annotations for the number of highlighted features in the plot.

`counts.size` Numeric scalar indicating the size of the feature counts labels.

`highlight.featsets`
Character vector indicating which feature sets should be highlighted.

`highlight.feats`
Character vector indicating which features should be highlighted.

`featsets` Named list of feature sets to be used for highlighting.

`highlight.feats.color`
Character scalar indicating the color of highlighted features.

`highlight.feats.size`
Numeric scalar indicating the size of highlighted features.

`highlight.feats.opac`
Numeric scalar indicating the opacity of highlighted features.

`highlight.feats.linecolor`
Character scalar indicating the line color of highlighted features.

`highlight.feats.linewidth`
Numeric scalar indicating the line width of highlighted features.

`highlight.feats.label`
Logical indicating whether to label highlighted features.

`highlight.featsets.color`
Character scalar indicating the color of highlighted feature sets.

`highlight.featsets.size`
Numeric scalar indicating the point size of highlighted feature sets.

`highlight.featsets.opac`
Numeric scalar indicating the opacity of highlighted feature sets.

highlight.featsets.linecolor
: Character scalar indicating the line color of highlighted feature sets.

highlight.featsets.linewidth
: Numeric scalar indicating the line width of highlighted feature sets.

highlight.featsets.label
: Logical indicating whether to label highlighted feature sets.

h.id.suffix
: Character scalar indicating the suffix to be added to the plotly object ID.

Value

An interactive plotly rank plot.

Author(s)

Jared Andrews

Examples

```
library(CRISPRball)
d1.genes <- read.delim(system.file("extdata", "esc1.gene_summary.txt",
    package = "CRISPRball"
), check.names = FALSE)
plot.df <- gene_ingress(d1.genes,
    sig.thresh = 0.05, es.thresh = 0.5,
    es.col = "LFC", sig.col = "fdr"
)
plot_lawn(plot.df, feat.term = "id")
```

---

plot_pca_biplot *Plot a biplot from a PCAtools* pca *object*

Description

This function plots a biplot from a PCAtools pca object.

Usage

```
plot_pca_biplot(
  pca.res,
  dim.x = "PC1",
  dim.y = "PC2",
  dim.z = NULL,
  plot.title = "PCA Biplot",
  color.by = NULL,
  shape.by = NULL,
  hover.info = NULL,
  show.loadings = FALSE,
  n.loadings = 3,
  pt.size = 12
)
```

Arguments

pca.res	A pca generated by the PCAtools package.
dim.x	Character scalar for the principal component to plot on the x-axis.
dim.y	Character scalar for the principal component to plot on the y-axis.
dim.z	Character scalar for the principal component to plot on the z-axis.
plot.title	Character scalar for the title of the plot.
color.by	Character scalar for the column name to use for coloring points.
shape.by	Character scalar for the column name to use for shaping points.
hover.info	Character vector of column name(s) to include in the hover info for each point.
show.loadings	Boolean indicating whether to show component loadings on the plot.
n.loadings	Integer for number of loadings to show.
pt.size	Numeric size of the plotted points.

Value

A plotly plot of the PCA biplot, or a text grob indicating no PCA was provided.

Author(s)

Jared Andrews

See Also

pca

Examples

```
library("PCAtools")
library("CRISPRball")
col <- 10
row <- 2000
mat <- matrix(
    rexp(col * row, rate = 0.1),
    ncol = col
)
rownames(mat) <- paste0("gene", seq_len(nrow(mat)))
colnames(mat) <- paste0("sample", seq_len(ncol(mat)))

metadata <- data.frame(row.names = colnames(mat))
metadata$Group <- rep(NA, ncol(mat))
metadata$Group[seq(1, 10, 2)] <- "A"
metadata$Group[seq(2, 10, 2)] <- "B"

p <- pca(mat, metadata = metadata, removeVar = 0.1)
plot_pca_biplot(p, color.by = "Group")
```

plot_rank *Create an interactive rank plot*

Description

Create an interactive rank plot for data with fold change, significance terms, and rank.

Usage

```
plot_rank(
  res,
  ylim = c(-10, 10),
  y.thresh = 0.5,
  y.lines = TRUE,
  hover.info = NULL,
  h.id = "crispr",
  feat.term = "rows",
  sig.term = "fdr",
  rank.term = "LFC",
  rank.ascending = TRUE,
  down.color = "#0026ff",
  up.color = "#ff0000",
  insig.color = "#A6A6A6",
  sig.thresh = 0.05,
  fs = NULL,
  sig.size = 6,
  insig.size = 5,
  sig.opacity = 1,
  insig.opacity = 0.5,
  label.size = 10,
  webgl = TRUE,
  webgl.ratio = 7,
  show.counts = TRUE,
  show.hl.counts = TRUE,
  counts.size = TRUE,
  highlight.featsets = NULL,
  highlight.feats = NULL,
  featsets = NULL,
  highlight.feats.color = "#E69F00",
  highlight.feats.size = 7,
  highlight.feats.opac = 1,
  highlight.feats.linecolor = "#000000",
  highlight.feats.linewidth = 1,
  highlight.feats.label = TRUE,
  highlight.featsets.color = "#009E73",
  highlight.featsets.size = 7,
  highlight.featsets.opac = 1,
```

```
  highlight.featsets.linecolor = "#000000",
  highlight.featsets.linewidth = 1,
  highlight.featsets.label = FALSE,
  h.id.suffix = "_rank"
)
```

Arguments

res	Dataframe containing, at minimum, significance values and something to rank by (LFC, RRA score, betas, etc).
ylim	Numeric vector of length two for the y-axis limits.
y.thresh	Numeric scalar used as the y-axis threshold for point coloring. The negative of this value is also used as the threshold.
y.lines	Logical as for whether or not to show horizontal lines at `y.thresh`.
hover.info	Character vector indicating which additional columns from `res` to include in the hover info.
h.id	Character scalar indicating the unique ID of the plotly object. Can usually be ignored, but should be used if multiple plots are being created in the same R session (e.g. Shiny app).
feat.term	Character scalar indicating the column name of the feature IDs in `res`.
sig.term	Character scalar indicating the column name of the significance values in `res`.
rank.term	Character scalar for the term to rank by from `res`. This will be used as the y-axis.
rank.ascending	Boolean indicating whether or not the rank should be ascending.
down.color	Character scalar indicating the color of down-regulated features.
up.color	Character scalar indicating the color of up-regulated features.
insig.color	Character scalar indicating the color of insignificant features.
sig.thresh	Numeric scalar indicating the significance threshold for coloring significant features.
fs	Dataframe containing coordinates and label information for points that should be labeled. Columns should be: • `x` - x coordinate of the point • `y` - y coordinate of the point • `customdata` - label to be displayed
sig.size	Numeric scalar indicating the size of significant feature points.
insig.size	Numeric scalar indicating the size of insignificant feature points.
sig.opacity	Numeric scalar indicating the opacity of significant feature points.
insig.opacity	Numeric scalar indicating the opacity of insignificant feature points.
label.size	Numeric scalar indicating the size of feature labels.
webgl	Logical indicating whether to use WebGL for rendering the plot.
webgl.ratio	Numeric scalar indicating the ratio of WebGL to HTML5 canvas rendering, increases resolution of saved plot when WebGL plotting is not used.

`show.counts` Logical indicating whether to show annotations for the number of features in the plot.

`show.hl.counts` Logical indicating whether to show annotations for the number of highlighted features in the plot.

`counts.size` Numeric scalar indicating the size of the feature counts labels.

`highlight.featsets`
Character vector indicating which feature sets should be highlighted.

`highlight.feats`
Character vector indicating which features should be highlighted.

`featsets` Named list of feature sets to be used for highlighting.

`highlight.feats.color`
Character scalar indicating the color of highlighted features.

`highlight.feats.size`
Numeric scalar indicating the size of highlighted features.

`highlight.feats.opac`
Numeric scalar indicating the opacity of highlighted features.

`highlight.feats.linecolor`
Character scalar indicating the line color of highlighted features.

`highlight.feats.linewidth`
Numeric scalar indicating the line width of highlighted features.

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`highlight.featsets.size`
Numeric scalar indicating the point size of highlighted feature sets.

`highlight.featsets.opac`
Numeric scalar indicating the opacity of highlighted feature sets.

`highlight.featsets.linecolor`
Character scalar indicating the line color of highlighted feature sets.

`highlight.featsets.linewidth`
Numeric scalar indicating the line width of highlighted feature sets.

`highlight.featsets.label`
Logical indicating whether to label highlighted feature sets.

`h.id.suffix` Character scalar indicating the suffix to be added to the plotly object ID.

Value

An interactive plotly rank plot.

Author(s)

Jared Andrews

Examples

```
library(CRISPRball)
d1.genes <- read.delim(system.file("extdata", "esc1.gene_summary.txt",
    package = "CRISPRball"
), check.names = FALSE)
plot.df <- gene_ingress(d1.genes,
    sig.thresh = 0.05, es.thresh = 0.5,
    es.col = "LFC", sig.col = "fdr"
)
plot_rank(plot.df, feat.term = "id")
```

`plot_volcano` *Create an interactive volcano plot*

Description

Create an interactive volcano plot for data with fold change and significance terms.

Usage

```
plot_volcano(
  res,
  xlim = 5,
  ylim = 5,
  fc.thresh = 0.5,
  fc.lines = TRUE,
  hover.info = NULL,
  sig.line = TRUE,
  h.id = "crispr",
  feat.term = "rows",
  sig.term = "fdr",
  lfc.term = "LFC",
  down.color = "#0026ff",
  up.color = "#ff0000",
  insig.color = "#A6A6A6",
  sig.thresh = 0.05,
  fs = NULL,
  sig.size = 6,
  insig.size = 5,
  sig.opacity = 1,
  insig.opacity = 0.5,
  label.size = 10,
  webgl = TRUE,
  webgl.ratio = 7,
  show.counts = TRUE,
  show.hl.counts = TRUE,
  counts.size = 8,
```

```
  highlight.featsets = NULL,
  highlight.feats = NULL,
  featsets = NULL,
  highlight.feats.color = "#E69F00",
  highlight.feats.size = 7,
  highlight.feats.opac = 1,
  highlight.feats.linecolor = "#000000",
  highlight.feats.linewidth = 1,
  highlight.feats.label = TRUE,
  highlight.featsets.color = "#009E73",
  highlight.featsets.size = 7,
  highlight.featsets.opac = 1,
  highlight.featsets.linecolor = "#000000",
  highlight.featsets.linewidth = 1,
  highlight.featsets.label = FALSE,
  h.id.suffix = "_volc"
)
```

Arguments

res	Dataframe containing, at minimum, fold change and significance values.
xlim	Positive numeric scalar indicating x-axis limits. The negative value will be used for the lower limit.
ylim	Positive numeric scalar indicating y-axis limits. The negative value will be used for the lower limit.
fc.thresh	Numeric scalar indicating the fold change threshold for coloring significant features.
fc.lines	Logical indicating whether to add fold change threshold lines to the plot.
hover.info	Character vector indicating which additional columns from res to include in the hover info.
sig.line	Logical indicating whether to add a significance threshold line to the plot.
h.id	Character scalar indicating the unique ID of the plotly object. Can usually be ignored, but should be used if multiple plots are being created in the same R session (e.g. Shiny app).
feat.term	Character scalar indicating the column name of the feature IDs in res.
sig.term	Character scalar indicating the column name of the significance values in res.
lfc.term	Character scalar indicating the column name of the log fold change values in res.
down.color	Character scalar indicating the color of down-regulated features.
up.color	Character scalar indicating the color of up-regulated features.
insig.color	Character scalar indicating the color of insignificant features.
sig.thresh	Numeric scalar indicating the significance threshold for coloring significant features.
fs	Dataframe containing coordinates and label information for points that should be labeled. Columns should be:

- x - x coordinate of the point
- y - y coordinate of the point
- customdata - label to be displayed

sig.size Numeric scalar indicating the size of significant feature points.

insig.size Numeric scalar indicating the size of insignificant feature points.

sig.opacity Numeric scalar indicating the opacity of significant feature points.

insig.opacity Numeric scalar indicating the opacity of insignificant feature points.

label.size Numeric scalar indicating the size of feature labels.

webgl Logical indicating whether to use WebGL for rendering the plot.

webgl.ratio Numeric scalar indicating the ratio of WebGL to HTML5 canvas rendering, increases resolution of saved plot when WebGL plotting is not used.

show.counts Logical indicating whether to show annotations for the number of features in the plot.

show.hl.counts Logical indicating whether to show annotations for the number of highlighted features in the plot.

counts.size Numeric scalar indicating the size of the feature counts labels.

highlight.featsets
Character vector indicating which feature sets should be highlighted.

highlight.feats
Character vector indicating which features should be highlighted.

featsets Named list of feature sets to be used for highlighting.

highlight.feats.color
Character scalar indicating the color of highlighted features.

highlight.feats.size
Numeric scalar indicating the size of highlighted features.

highlight.feats.opac
Numeric scalar indicating the opacity of highlighted features.

highlight.feats.linecolor
Character scalar indicating the line color of highlighted features.

highlight.feats.linewidth
Numeric scalar indicating the line width of highlighted features.

highlight.feats.label
Logical indicating whether to label highlighted features.

highlight.featsets.color
Character scalar indicating the color of highlighted feature sets.

highlight.featsets.size
Numeric scalar indicating the point size of highlighted feature sets.

highlight.featsets.opac
Numeric scalar indicating the opacity of highlighted feature sets.

highlight.featsets.linecolor
Character scalar indicating the line color of highlighted feature sets.

highlight.featsets.linewidth
: Numeric scalar indicating the line width of highlighted feature sets.

highlight.featsets.label
: Logical indicating whether to label highlighted feature sets.

h.id.suffix
: Character scalar indicating the suffix to be added to the plotly object ID.

Value

An interactive plotly volcano plot.

Author(s)

Jared Andrews

Examples

```
library(CRISPRball)
d1.genes <- read.delim(system.file("extdata", "esc1.gene_summary.txt",
    package = "CRISPRball"
), check.names = FALSE)
plot.df <- gene_ingress(d1.genes,
    sig.thresh = 0.05, es.thresh = 0.5,
    es.col = "LFC", sig.col = "fdr"
)
plot_volcano(plot.df, feat.term = "id")
```

---

read_mle_gene_summary *Read and parse MAGeCK MLE output gene summary file*

Description

This function reads the gene summary file output by `mageck mle` and parses it into a list of data.frames, one for each sample. The sample names are extracted from the column names of the input file and used as the names of the list elements.

Usage

```
read_mle_gene_summary(filepath)
```

Arguments

filepath
: Path to the gene summary file output by `mageck mle`.

Value

A named list of data.frames containing MAGeCK MLE output, one for each sample contained in the file.

Author(s)

Jared Andrews

Examples

```
library(CRISPRball)
mle_gene_summary <- file.path(system.file("extdata", "beta_leukemia.gene_summary.txt",
    package = "CRISPRball"
))
gene_data <- read_mle_gene_summary(mle_gene_summary)
```

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