Package 'eps'

June 14, 2022

Title Helper functions for my analysis

Version 0.1.3

Date 2021-07-27

Author person(given = ``Elena",
family = ``Priego",
role = c(``aut", ``cre"),
email = ``epriego@cnic.com",
comment = c(ORCID = ``0000-0002-7560-0620"))

Maintainer Elena Priego Saiz <elena.priego.saiz@gmail.com>

Description R package with miscellaneous R functions that are useful to me.

Depends R (>= 3.5.0)

Suggests knitr,
rmarkdown,
pzfx,
rstatix,
scales,
CytoML,
broom,
flowWorkspace

Imports tidyverse,
readxl,
here,
ggtext,
ggthemes

Encoding UTF-8

License GPL-3

LazyData true

Roxygen list(markdown = TRUE)

RoxygenNote 7.1.2

VignetteBuilder knitr

R topics documented:

`CFU2tidy_genotype` *CFU to tidy*

Description

Function to use when the dilution is already calculated. Standard output. Can read multiple csv at the same time, but is better to do it separately inicating the different times. When multiple, write *M*. When no colonies, write 0.

Usage

```
CFU2tidy_genotype(
  file = c("^CFU", "$csv"),
  path_file = path_raw,
  animalario_file = c("^animalario", "$csv"),
  path_mice = path_raw,
  micecode = micecode,
```

```
  animalario_sep = ",",
  multiple = "100",
  marker = "CFU",
  cell = "AM",
  time = "0h",
  treatment = "lp moi"
)
```

Arguments

file	.csv with CFU counts. Header should be label with Code for mice column followed by the different dilutions included in the experiment written written in the format "Dil-dilution". Example: in dil 1/100 (in 2mL) will be 200 Write NA in raw file when can no count
path_file	path where file is located. Usually path_output from path_builder()
animalario_file	raw csv downloaded from animalario with mice used in the experiment
path_mice	path where animalario file to obtain the genotypes is located. usually path_raw from path_builder.
micecode	named list with the replacement for the genotypes. Load from micecode data included in the package.
animalario_sep	separator for the animalario csv file. Default to ","
multiple	Number to replace when the CFU where incontable. Represented by M in the original csv
marker	usually CFU (by deffault)
cell	Am. Indicate if they are from lung, BAL, ex vivo...
time	Time after infection. Default to 0h
treatment	Moi of infection

Value

a tibble with the tidy format of the CFU

Examples

```
data(micecode)
CFU_tidytable_genotype("CFU.csv", path_file = path_raw, animalario_file = "animalario.csv",
    gate_pattern = gate_pattern, micecode = micecode)
```

CFU_boxplot *CFU_boxplot*

Description

CFU_boxplot

Usage

```
CFU_boxplot(
  table,
  x_lab = "genotype",
  y_lab = "L.pneumophila CFU",
  title_lab = "",
  y_trans = "identity",
  x_angle = NULL,
  x_hjust = NULL,
 color_values = (ggthemes::tableau_color_pal("Classic Green-Orange 12"))(12)[1:12],
  color_breaks = waiver(),
  color_labels = waiver(),
  path_output = NULL,
  w = 10,
  h = 5,
  save_plot = FALSE,
  print_plot = FALSE
)
```

Arguments

table	tidy table coming form CFU_tidytable_genotype
x_lab	x-axis label
y_lab	y-axis label
title_lab	title label
y_trans	transformation for the y axis ("asn", "atanh", "boxcox", "date", "exp", "hms", "identity", "log", "log10", "log1p", "log2", "logit", "modulus", "probability", "probit", "pseudo_log", "reciprocal", "reverse", "sqrt" and "time")
x_angle	angle of the labels of the x-axis. NULL for horizontal, 45 for inclination
x_hjust	horizontal justification of the labels of the x-axis
color_values	a set of aesthetic values to map data values to. The values will be matched in order (usually alphabetical).
color_breaks	takes the limits as input and returns breaks as output
color_labels	takes the breaks as input and returns labels as output
path_output	ful name of the generated plot including the path (recommended path_output from path_builder())
w	width of the output plot
h	high of the output plot
save_plot	boolean indicating if the plot is saved or not. Default to TRUE.
print_plot	boolean indicating if the plot is printed or not. Default to FALSE.

Value

plot file in data folder

Examples

```
CFU_boxplot(table)
```

CFU_tidytable_genotype *CFU_tidytable_genotype*

Description

DEPRECATED

Usage

```
CFU_tidytable_genotype(
  file = c("^CFU", "$csv"),
  path_file = path_raw,
  animalario_file = c("^animalario", "$csv"),
  path_mice = path_raw,
  micecode = micecode,
  animalario_sep = ","
)
```

Arguments

file	.csv with CFU counts. Header should be label with Code for mice column followed by the different dilutions included in the experiment written written in the format "Dil-1/dilution"
path_file	path where file is located. Usually path_output from path_builder()
animalario_file	raw csv downloaded from animalario with mice used in the experiment
path_mice	path where animalario file to obtain the genotypes is located. usually path_raw from path_builder.
micecode	named list with the replacement for the genotypes. Load from micecode data included in the package.
animalario_sep	separator for the animalario csv file. Default to ","

Value

a tibble with the tidy format of the CFU

Examples

```
data(micecode)
CFU_tidytable_genotype("CFU.csv", path_file = path_raw, animalario_file = "animalario.csv",
    gate_pattern = gate_pattern, micecode = micecode)
```

`cover_init` *Generation of the experiment cover in Rmd*

Description

Creation of the cover page in an Rmd to write the protocol and the analysis. Should be used directly in the console within the project folder

Usage

```
cover_init(experiment_name)
```

Arguments

`experiment_name`
: Full name of the experiment. Should have the following structure: project, "hash", year, experiment number, "underscore", experiment title

Examples

```
cover_init("VHL-2101_experiment")
```

`elisa_tidytable` *Make tidytable from ELISA Function to calculate the concentrations of ELISA experiments giving two files as input, one coming from the spectrometer with the raw OD data and other with a template of the plate used. In the template is expected to be at least 1 point of blank_0 that will be subtracted to all values and two or more values from a standard curve labelled as standard_0, standard_10 ... For samples well the format is name_concentration as proportion of samples (for example a sample diluted 1/2 would be 0.5)*

Description

Make tidytable from ELISA Function to calculate the concentrations of ELISA experiments giving two files as input, one coming from the spectrometer with the raw OD data and other with a template of the plate used. In the template is expected to be at least 1 point of blank_0 that will be subtracted to all values and two or more values from a standard curve labelled as standard_0, standard_10 ... For samples well the format is name_concentration as proportion of samples (for example a sample diluted 1/2 would be 0.5)

Usage

```
elisa_tidytable(
  data_file = "elisa.txt",
  template_file = "plate.csv",
  path_file = path_raw,
  sep_data = "\t",
```

```
  sep_template = ",",
  model = "log-log",
  max_value = Inf,
  plot_curve = TRUE
)
```

Arguments

data_file	txt file with the OD data.
template_file	csv file with the template of the experiment. Format will be sample-type_concentration with standard and blank as required keyword
path_file	path where data_file and template_file are located. Usually path_raw
sep_data	separator character from data_file. Frequently tab
sep_template	separator character from template_file. Frequently sep
model	model to fit the analysis: either linear ("lm") or 4-parameter log-logistic ("log-log")
max_value	to restrict the standard curve to a maximal value
plot_curve	print the fitted plot

Examples

```
elisa_tidytable(
  data_file = "elisa-IFNg.txt",
  template_file = "IFNg-plate.csv",
  path_file = path_raw,
  model = "lm",
  max_value = 50,
  plot_curve = FALSE
)
```

---

experiment_init *Initialize the experiment*

Description

Generate the folders associated to the experiment in data, raw and output and creation of the cover page in an Rmd to write the protocol and the analysis. Should be used directly in the console within the project folder

Usage

```
experiment_init(experiment_name)
```

Arguments

experiment_name	Full name of the experiment. Should have the following structure: project, "hash", year, experiment number, "underscore", experiment title

Examples

```
experiment_init("VHL-2101_experiment")
```

`facs_boxplot` *Boxplot creation for cytometry data*

Description

Boxplot generation for data created with facs_tidytable. Design to work inside an apply function with all the possible combinations of parameters in order to generate multiple plots (see examples).

Usage

```
facs_boxplot(
  table = "",
  organ.i = NULL,
  stat.i = NULL,
  time.i = NULL,
  marker.i = NULL,
  cell.i = NULL,
  treatment.i = NULL,
  x_value = "cell",
  title.i = "",
  x_lab = "",
  y_lab = "",
  y_limit = 0,
  x_angle = 45,
  x_hjust = 1,
 color_values = (ggthemes::tableau_color_pal("Classic Green-Orange 12"))(12)[1:12],
  color_breaks = waiver(),
  color_labels = waiver(),
  path_output = NULL,
  w = 10,
  h = 5,
  print_plot = FALSE
)
```

Arguments

`table`	tidy table coming form facs_tidytable
`organ.i`	optional organ selected to plot (specimen in .fcs file)
`stat.i`	optional statistic selected to plot
`time.i`	optional time selected to plot
`marker.i`	optional marker selected to plot
`treatment.i`	optional treatment selected to plot
`title.i`	title of the plot
`x_lab`	x-axis label

y_lab	y-axis label
y_limit	inferior limit for y-axis
x_angle	angle of the labels of the x-axis. NULL for horizontal, 45 for inclination
x_hjust	horizontal justification of the labels of the x-axis
color_values	a set of aesthetic values to map data values to. The values will be matched in order (usually alphabetical).
color_breaks	takes the limits as input and returns breaks as output
color_labels	takes the breaks as input and returns labels as output
path_output	Optional. Full file name desired (e.g. here(path_output, "plot.pdf"))
w	width of the output plot
h	high of the output plot
print_plot	boolean indicating if the plot is printed or not. Default to FALSE.

Value

plot file in data folder

Examples

```
comb <- as_tibble(unique(paste(table$organ, table$stat, table$marker,
                               sep = "_-_"))) %>%
        separate(value, into = c("organ", "stat", "marker"), sep = "_-_") %>%
        mutate(output = here(path_output,
                             paste0(organ, "_", stat, "_", marker, ".png")),
               y_lab = paste0(marker, " (", stat, ")")) %>% as.data.frame()

apply(comb, 1, function(x) facs_boxplot(table, organ.i = x[1], stat.i = x[2],
  marker.i = x[3], path_output = x[4], y_lab = x[5],
  title.i = x[1]))
```

---

facs_tidytable *Prepare the data in a tidy format from the data obtained in Flowjo*

Description

Generation of a tidytable from the .xls generated from Flowjo. It's important to have the tubes correctly labelled: specimen should have a descriptive name without using "_" and each tube should be named using ONLY the full name of the mice. Generate standard columns: Time, mice, genotype, treatment, marker, stat, value, experiment, cell

Usage

```
facs_tidytable(
  file = c("^Table"),
  path_file = path_output,
  time = "0h",
  gate_pattern
)
```

Arguments

file	.xls generated from Flowjo with cell percentages and fluorescent intensities
path_file	path where file is located. Usually path_output from path_builder()
gate_pattern	named list with the replacements desired for the gates. Load from gate_pattern data included in the package. Common ones are: c("Freq. of Parent" = "Freq.", "Freq. of Grandparent" = "Freq.", "Geometric Mean" = "GMFI", "Median" = "MdFI", "\)" = "")

Value

a tibble with the tidy format

Examples

```
data(gate_pattern)
facs_tidytable("table.xls", path_file = path_output,
    gate_pattern = gate_pattern)
```

---

facs_tidytable_genotype

Prepare the data in a tidy format from the data obtained in Flowjo

---

Description

Generation of a tidytable from the .xls generated from Flowjo. It's important to have the tubes correctly labelled: specimen should have a descriptive name without using "_" and each tube should be named using ONLY the full name of the mice.

Usage

```
facs_tidytable_genotype(
  file = c("^Table", "$csv"),
  path_file = path_output,
  time = "0h",
  animalario_file = c("^animalario", "$csv"),
  gate_pattern,
  path_mice = path_raw,
  micecode,
  animalario_sep = ","
)
```

Arguments

file	.xls generated from Flowjo with cell percentages and fluorescent intensities
path_file	path where file is located. Usually path_output from path_builder()
animalario_file	raw csv downloaded from animalario with mice used in the experiment

gate_pattern	named list with the replacements desired for the gates. Load from gate_pattern data included in the package. Common ones are: c("Freq. of Parent" = "Freq.", "Freq. of Grandparent" = "Freq.", "Geometric Mean" = "GMFI", "Median" = "MdFI", "\)" = "")
path_mice	path where animalario file to obtain the genotypes is located. usually path_raw from path_builder.
micecode	named list with the replacement for the genotypes. Load from micecode data included in the package.
animalario_sep	separator for the animalario csv file. Default to ","

Value

a tibble with the tidy format

Examples

```
data(gate_pattern)
data(micecode)
facs_tidytable_genotype("table.xls", path_data, "animalario.csv",
    gate_pattern = gate_pattern, micecode = micecode)
```

---

facs_tree *Generate a gatting tree from a FlowJo Analysis*

Description

Plot showing the gatting hierarchy

Usage

```
facs_tree(file_pattern = "*.wsp", path_data = path_data, group = "All Samples")
```

Arguments

file_pattern	Name of the .wps file. As default all the analysis are taken
path_data	Path where the .wsp file locates.
group	analysis group to be plotted. As defaul all Samples (gate 1)

Examples

```
facs_tree("C:/Users/elena/Desktop/working on", "analysis.wps")
```

`facs_ttest` *t-test analysis for facs data*

Description

DEPRECATED- use ggpubr::compare_means() instead. Later ggplot+stat_compare_means(label = "p.signif", label.x = 1.5))

Usage

```
facs_ttest(
  table,
  path_output = path_output,
  file1 = "t-test.csv",
  file2 = "significant-t-test.csv"
)
```

Arguments

`table`	name of the table to be analyzed. Filter to make that genotype column contains only 2 factors
`path_output`	path were the output will be stored
`file1`	name of the file containing all the analysis
`file2`	name of the file containing only the significant analysis

Details

t-test analysis for data coming in a tidy format from facs_tidytable function.

Value

print in the screen the significant values

significant_values data table with the significant samples and their p-value

t-test.csv file with the whole analysis in output folder

significant-t-test.csv file with the samples that show a p-value lower than 0.05 in output folder

Examples

```
table1 <- filter(genotype %in% c("VHL-HIF1a-KO  ", "VHL-HIF1a-WT  "))
facs_ttest(table1,
           path_output = path_output,
           file1 = "HIF1a-DKO-t.test.csv",
           file2 = "HIF1a-DKO-significant-t-test.csv")
```

FC_bar *Bar plot representing FC Plot by column showing FC (KO/WT)*

Description

Bar plot representing FC Plot by column showing FC (KO/WT)

Usage

```
FC_bar(
  table,
  genotype_levels = c("WT", "KO"),
  strain_levels = c("VHL", "VHL-HIF1a", "VHL-HIF2a", "VHL-HIF1a-HIF2a"),
  group_diff = "-WT|-KO",
  group_control = "WT",
  group_plot = "KO",
  identity_bar = "dodge",
  x_lab = "",
  y_lab = "FC (WT/KO)",
  title_lab = "",
  y_trans = "identity",
  y_label = waiver(),
  color_values = hue_pal()(200),
  shape_values = rep(21, 200),
  fill_values = hue_pal()(200),
  plot_stat = TRUE,
  path_output,
  w = 10,
  h = 5,
  save_plot = FALSE,
  print_plot = FALSE
)
```

Arguments

table	tidy table with data coming from the analysis. Columns: genotype, value and experiment (time, mice, treatment, marker, stat, cell)
genotype_levels	vector will all the genotypes all the analysis
strain_levels	ordered levels to plot. Default to VHL groups
group_diff	text to remove from the genotype column to generate the strain by which the relativation groups will be generated. Default to "-WT|-KO"
group_control	text that identify the group to relativize. Should be included inside group_diff. Default to "WT"
group_plot	text that identify the group to plot. Should be included inside group_diff. Default to "KO"
x_lab	X-axis label
y_lab	y-axis label
title_lab	title label

y_trans	transformation of the y axis
y_label	default to waiver. Could be scientific_format()
color_values	color to be ploted. Same number as levels have genotype . For VHL paper table$VHL_palette_color
shape_values	shape to be ploted. Same number as levels have genotype. For VHL paper table$VHL_palette_shape
fill_values	fill color to be ploted. Same number as levels have genotype. For VHL paper table$VHL_palette_fill
plot_stat	Boolean indicating if include the stat. Default to TRUE.
path_output	ful name of the generated plot including the path (recommended path_output from path_builder())
w	width of the output plot
h	high of the output plot
save_plot	Boolean indicating if the plot is saved or not. Default to FALSE.
print_plot	Boolean indicating if the plot is printed or not. Default to TRUE.

Value

plot file in data folder

Examples

```
plot %>%
FC_bar(genotype_levels = VHL_table$genotypes,
color_values = VHL_table$palette_color,
shape_values = VHL_table$palette_shape,
fill_values = VHL_table$palette_fill)
```

---

gate_pattern *List of replacements for facs analysis*

Description

Named list containing common replacement for facs analysis

Usage

```
gate_pattern
```

Format

Named list with the desired replacements

genotype_mean_violin *Violin plot of mean data by genotype*

Description

Violin plot of mean data by genotype

Usage

```
genotype_mean_violin(
  table,
  genotype_levels = c("WT", "KO"),
  x_lab = "",
  y_lab = "",
  title_lab = "",
  y_trans = "identity",
  y_label = waiver(),
  x_angle = NULL,
  x_hjust = NULL,
  color_values = hue_pal()(200),
  shape_values = rep(21, 200),
  fill_values = hue_pal()(200),
  path_output,
  w = 10,
  h = 5,
  save_plot = FALSE,
  print_plot = FALSE
)
```

Arguments

table	tidy table with data comming from the analysis. Columns: genotype, value (and experiment)
genotype_levels	vector will all the genotypes all the analysis
x_lab	X-axis label
y_lab	y-axis label
title_lab	title label
y_trans	transformation of the y axis
y_label	default to waiver. Could be scientific_format()
x_angle	Angle to display the x axis
x_hjust	Justificacion of the x axis
color_values	color to be ploted. Same number as levels have genotype . For VHL paper table$VHL_palette_color
shape_values	shape to be ploted. Same number as levels have genotype. For VHL paper table$VHL_palette_shape
fill_values	fill color to be ploted. Same number as levels have genotype. For VHL paper table$VHL_palette_fill

path_output	ful name of the generated plot including the path (recommended path_output from path_builder())
w	width of the output plot
h	high of the output plot
save_plot	Boolean indicating if the plot is saved or not. Default to FALSE.
print_plot	Boolean indicating if the plot is printed or not. Default to TRUE.

Value

plot file in data folder

Examples

```
genotype_mean_violin(genotype_levels = VHL_table$genotypes,
color_values = VHL_table$palette_color,
shape_values = VHL_table$palette_shape,
fill_values = VHL_table$palette_fill)
```

---

genotype_paired_violin

Paired violin plot by genotype

Description

Paired violin plot by genotype

Usage

```
genotype_paired_violin(
  table,
  genotype_levels = c("WT", "KO"),
  genotype_labels = genotype_levels,
  y_value = value,
  x_lab = "",
  y_lab = "",
  title_lab = "",
  color_values = hue_pal()(200),
  shape_values = rep(21, 200),
  fill_values = hue_pal()(200),
  path_output,
  w = 10,
  h = 5,
  save_plot = FALSE,
  print_plot = FALSE
)
```

Arguments

table	tidy table with at least the following columns: genotype, value and experiment
genotype_levels	vector will all the genotypes all the analysis
genotype_labels	name to be display in the legend
x_lab	X-axis label
y_lab	y-axis label
title_lab	title label
color_values	color to be ploted. Same number as levels have genotype . For VHL paper table$VHL_palette_color
shape_values	shape to be ploted. Same number as levels have genotype. For VHL paper table$VHL_palette_shape
fill_values	fill color to be ploted. Same number as levels have genotype. For VHL paper table$VHL_palette_fill
path_output	full name of the generated plot including the path (recommended path_output from path_builder())
w	width of the output plot
h	high of the output plot
save_plot	Boolean indicating if the plot is saved or not. Default to FALSE.
print_plot	Boolean indicating if the plot is printed or not. Default to TRUE.

Value

plot file in data folder

Examples

```
genotype_violin(genotype_levels = VHL_table$genotypes,
color_values = VHL_table$palette_color,
shape_values = VHL_table$palette_shape,
fill_values = VHL_table$palette_fill)
```

---

genotype_violin *Violin plot by genotype*

Description

Violin plot by genotype

Usage

```
genotype_violin(
  table,
  genotype_levels = c("WT", "KO"),
  genotype_labels = genotype_levels,
  x_lab = "",
  y_lab = "",
  title_lab = "",
  y_trans = "identity",
  y_label = waiver(),
  color_values = hue_pal()(200),
  shape_values = rep(21, 200),
  fill_values = hue_pal()(200),
  path_output,
  w = 10,
  h = 5,
  save_plot = FALSE,
  print_plot = FALSE
)
```

Arguments

table	tidy table with data comming from the analysis. Columns: genotype, value (and experiment)
genotype_levels	vector will all the genotypes all the analysis
genotype_labels	name to be display in the legend
x_lab	X-axis label
y_lab	y-axis label
title_lab	title label
y_trans	transformation of the y axis
y_label	default to waiver. Could be scientific_format()
color_values	color to be ploted. Same number as levels have genotype . For VHL paper table$VHL_palette_color
shape_values	shape to be ploted. Same number as levels have genotype. For VHL paper table$VHL_palette_shape
fill_values	fill color to be ploted. Same number as levels have genotype. For VHL paper table$VHL_palette_fill
path_output	ful name of the generated plot including the path (recommended path_output from path_builder())
w	width of the output plot
h	high of the output plot
save_plot	Boolean indicating if the plot is saved or not. Default to FALSE.
print_plot	Boolean indicating if the plot is printed or not. Default to TRUE.
x_angle	Angle to display the x axis
x_hjust	Justificacion of the x axis

Value

plot file in data folder

Examples

```
genotype_violin(genotype_levels = VHL_table$genotypes,
color_values = VHL_table$palette_color,
shape_values = VHL_table$palette_shape,
fill_values = VHL_table$palette_fill)
```

---

get_genotype *Generate an object matching miceID with their genotype*

Description

Extract mice number and genotype from multiple files animalario*.csv pattern as default download in english layout NOTE: take a look to determine if the first row is indicating sep=";" and remove in that case. NOTE: if an error ocurrs remove the accent mark. micecode as union from Nickname with Genotyping -> stored in data Return a data.table with two column: one for the miceID and the other with their genotype

Usage

```
get_genotype(
  file_name = c("^animalario", "$csv"),
  path_raw,
  micecode,
  csv_sep = ","
)
```

Arguments

file_name	Input file
path_raw	path were the file is located. Usually in the experiment subfolder inside raw
micecode	Named chr list containing the replacement chr for the genotype. BBV, CCT, DCX and DCW strains can be loaded with data(micecode)
csv_sep	separator for the csv file. Default to ","

Examples

```
data(micecode)
get_genotype("Animalario-VHL2101.csv", micecode)
```

graphpad_column *graphpad_column*

Description

read a pzfx file containing column displayed data and convert it into a tidy table for further representation. Generate a csv file into data folder

Usage

```
graphpad_column(
  name_graphpad = "pzfx",
  sheet_n = 1,
  to_pivot = c(1, 2),
  folder = "",
  output_name = "table"
)
```

Arguments

name_graphpad	name of the file to be open. By default select the files with pzfx extension
sheet_n	number of the sheet to be read
to_pivot	columns selected to pivot
folder	folder to look in. Partial pathway from here()
output_name	name to be written the tidy_file. In folder data

Value

tidy table

Examples

```
table <- graphpad_column(file)
```

graphpad_grouped *graphpad_grouped*

Description

Return a csv file into data folder

Usage

```
graphpad_grouped(
  name_graphpad = "pzfx",
  sheet_n = 1,
  folder = "",
  save = FALSE,
  output_name = "table"
)
```

Arguments

name_graphpad	name of the file to be open. By default select the files with pzfx extension
sheet_n	number of the sheet to be read
folder	folder to look in. Partial pathway from here()
save	conditional to decide if save the file
output_name	name to be written the tidy_file. In folder data

Value

tidy table

Examples

```
table <- graphpad_grouped(file)
```

---

micecode *Mice genotypes list*

Description

Named list with the genotypes of the mice I am working with

Usage

```
data(micecode)
```

Format

Named chr

Examples

```
data(micecode)
get_genotype("Animalario-VHL2101.csv", micecode)
```

path_builder *Initialize the experiment creating the needed pathways*

Description

Generate the pathways to save the files of the projects and create specific folders in data, raw and output. The pathways are saved in R environment to be used along the analysis

Usage

```
path_builder(experiment_name)
```

Arguments

experiment_name	Full name of the experiment

Examples

```
path_builder("VHL-2101_experiment")
```

qPCR_ttest *ttest analysis form qPCR*

Description

ttest analysis form qPCR

Usage

```
qPCR_ttest(
  table,
  genotype_levels,
  name,
  excluded_genes = c("Actin", "empty", "H2O")
)
```

Arguments

table	table with the information. Should have the columns "Cq", "Target", "mice", "Mean_Cq", "Cq_SD", "genotype", "Delta", "Expression"
genotype_levels	Select 2 levels to perform the t.test
name	name of the output files (before -t-test.CSV)
excluded_genes	name of the genes to be excluded in the analysis #know the present genes in each sample to exclude in the t.test analysis the ones that doesn't appear table_target <- table %>% group_by(Target, genotype) %>% summarise(n=n()) %>% pivot_wider(id_cols=Target, names_from = genotype, values_from = n, values_fill = 0)

Examples

```
qPCR_ttest(table, c("VHL-WT  ", "VHL-KO  "), "VHL")
```

`relative_data` *Make relative data to genotype Make relative data to WT samples from each experiment. representing this as 1.*

Description

Make relative data to genotype Make relative data to WT samples from each experiment. representing this as 1.

Usage

```
relative_data(df, group_diff = "-WT|-KO", group_control = "WT")
```

Arguments

`df`	input dataframe with at least genotype and value
`group_diff`	text to remove from the genotype column to generate the strain by which the relativation groups will be generated. Default to "-WT|-KO"
`group_control`	text that identify the control group to relative by. Should be included inside group_diff. Default to "WT"

Examples

```
my_data %>% relative_data(.) %>% genotype_violin()
```

`save_tidy` *save_tidy*

Description

save_tidy

Usage

```
save_tidy(table, path_output = path_output)
```

Arguments

`table`	final raw table
`path_output`	generated with eps::path_builder()

Examples

```
save_tidy(table, path_output)
```

seahorse_curve *Plot OCR / ECAR profile from a Seahorse analysis*

Description

Plot OCR / ECAR profile from a Seahorse analysis

Usage

```
seahorse_curve(
  table,
  genotype_levels = c("WT", "KO"),
  x_lab = "Time (minutes)",
  y_lab = "Oxygen Consumption Rate (OCR) \n (pmol/min)",
  title_lab = "",
  x_angle = 0,
  x_hjust = 0.5,
  color_values = hue_pal()(200),
  shape_values = rep(21, 200),
  fill_values = hue_pal()(200),
  lty_values = rep("solid", 200),
  path_output = "plot.png",
  w = 10,
  h = 5,
  save_plot = FALSE,
  print_plot = FALSE
)
```

Arguments

table	tidy table with data comming from the analysis. Columns: time, genotype, mice, value
genotype_levels	vector will all the genotypes all the analysis
x_lab	X-axis label
y_lab	y-axis label
x_angle	Angle to display the x axis
x_hjust	Justificacion of the x axis
color_values	color to be ploted. Same number as levels have genotype . For VHL paper table$VHL_palette_color
shape_values	shape to be ploted. Same number as levels have genotype. For VHL paper table$VHL_palette_shape
fill_values	fill color to be ploted. Same number as levels have genotype. For VHL paper table$VHL_palette_fill
lty_values	line structure. to be ploted. Same number as levels have genotype. For VHL paper table$VHL_palette_lty
path_output	ful name of the generated plot including the path (recommended path_output from path_builder())

w	width of the output plot
h	high of the output plot
save_plot	boolean indicating if the plot is saved or not. Default to FALSE.
print_plot	boolean indicating if the plot is printed or not. Default to TRUE.
title.i	title label

Value

plot file in data folder

Examples

```
seahorse_curve(curve, title.i = "GGP Seahorse",
color_values = table$VHL_palette_color,
shape_values = table$VHL_palette_shape,
fill_values = table$VHL_palette_fill,
lty_values = table$VHL_palette_lty)
```

---

strain_bar *Bar plot by strains Plot by column having WT and KO next on the same bar*

Description

Bar plot by strains Plot by column having WT and KO next on the same bar

Usage

```
strain_bar(
  table,
  genotype_levels = c("WT", "KO"),
  strain_levels = c("VHL", "VHL-HIF1a", "VHL-HIF2a", "VHL-HIF1a-HIF2a"),
  group_diff = "-WT|-KO",
  identity_bar = "dodge",
  x_lab = "",
  y_lab = "",
  title_lab = "",
  y_trans = "identity",
  y_label = waiver(),
  color_values = hue_pal()(200),
  shape_values = rep(21, 200),
  fill_values = hue_pal()(200),
  path_output,
  w = 10,
  h = 5,
  save_plot = FALSE,
  print_plot = FALSE
)
```

Arguments

table	tidy table with data comming from the analysis. Columns: genotype, value and experiment (time, mice, treatment, marker, stat, cell)
genotype_levels	vector will all the genotypes all the analysis
strain_levels	ordered levels to plot. Default to VHL groups
group_diff	text to remove from the genotype column to generate the strain by which the relativation groups will be generated. Default to "-WT|-KO"
identity_bar	Position to plot the bar graph. "identity" to pile, "dodge" to put next to each other. Default to dodge. Depending on the value, the points represented are pilled up by strain or not
x_lab	X-axis label
y_lab	y-axis label
title_lab	title label
y_trans	transformation of the y axis
y_label	default to waiver. Could be scientific_format()
color_values	color to be ploted. Same number as levels have genotype . For VHL paper table$VHL_palette_color
shape_values	shape to be ploted. Same number as levels have genotype. For VHL paper table$VHL_palette_shape
fill_values	fill color to be ploted. Same number as levels have genotype. For VHL paper table$VHL_palette_fill
path_output	ful name of the generated plot including the path (recommended path_output from path_builder())
w	width of the output plot
h	high of the output plot
save_plot	Boolean indicating if the plot is saved or not. Default to FALSE.
print_plot	Boolean indicating if the plot is printed or not. Default to TRUE.
x_angle	Angle to display the x axis
x_hjust	Justificacion of the x axis

Value

plot file in data folder

Examples

```
plot %>%
strain_bar(genotype_levels = VHL_table$genotypes,
color_values = VHL_table$palette_color,
shape_values = VHL_table$palette_shape,
fill_values = VHL_table$palette_fill)
```

`treatment_violin` *Violin plot by treatment*

Description

Violin plot by treatment

Usage

```
treatment_violin(
  table,
  genotype_levels = levels(table$genotype),
  x_lab = "",
  y_lab = "",
  title_lab = "",
  y_trans = "identity",
  y_label = waiver(),
  x_angle = NULL,
  x_hjust = NULL,
  color_values = hue_pal()(200),
  shape_values = rep(21, 200),
  fill_values = hue_pal()(200),
  path_output,
  w = 10,
  h = 5,
  save_plot = FALSE,
  print_plot = FALSE
)
```

Arguments

`table`	tidy table with data coming from the analysis. Columns: time, mice, genotype, treatment, marker, stat, value, experiment
`genotype_levels`	vector will all the genotypes all the analysis
`x_lab`	X-axis label
`y_lab`	y-axis label
`title_lab`	title label
`y_trans`	transformation of the y axis
`y_label`	default to waiver. Could be scientific_format()
`x_angle`	Angle to display the x axis
`x_hjust`	Justificacion of the x axis
`color_values`	color to be ploted. Same number as levels have genotype . For VHL paper table$VHL_palette_color
`shape_values`	shape to be ploted. Same number as levels have genotype. For VHL paper table$VHL_palette_shape
`fill_values`	fill color to be ploted. Same number as levels have genotype. For VHL paper table$VHL_palette_fill

path_output	ful name of the generated plot including the path (recommended path_output from path_builder())
w	width of the output plot
h	high of the output plot
save_plot	Boolean indicating if the plot is saved or not. Default to FALSE.
print_plot	Boolean indicating if the plot is printed or not. Default to TRUE.

Value

plot file in data folder

Examples

```
genotype_violin(genotype_levels = VHL_table$genotypes,
color_values = VHL_table$palette_color,
shape_values = VHL_table$palette_shape,
fill_values = VHL_table$palette_fill)
```

---

weight_csv_read

weight_csv_read function to read the csv were the mice weight is storage. Mice are represented in rows whereas days are represented in columns. To use inside weight_tidytable function to also get the genotype and make ID as factors.

Description

weight_csv_read function to read the csv were the mice weight is storage. Mice are represented in rows whereas days are represented in columns. To use inside weight_tidytable function to also get the genotype and make ID as factors.

Usage

```
weight_csv_read(
  csv_file,
  path_csv,
  relative = FALSE,
  csv_sep = ",",
  date_format = "%d.%b"
)
```

Arguments

csv_file	name of the csv file with the introduced weights. Usually "weight-curve.csv"
path_csv	path were csv file is located. Usually path_output
relative	bool indicating if the final output will be raw number or the relative porcentage to day 1
csv_sep	sep parameter for read.delim function. Default ","
date_format	format parameter of strftime function. Character string. The default for the format methods is "%d.%b" that is for format "01.jul". Other common format are %d-%m

Examples

```
weight_csv_read("weight-curve.csv", path_output)
```

`weight_individual_plot`

weight_individual_plot plot a weight-loss curve with the individual value of each mice by day

---

Description

weight_individual_plot plot a weight-loss curve with the individual value of each mice by day

Usage

```
weight_individual_plot(
  table,
  title.i = "",
  x_lab = "",
  y_lab = "",
  y_limit = 0,
  color_values = RColorBrewer::brewer.pal(8, "Paired")[7:8],
  color_breaks = waiver(),
  color_labels = waiver(),
  path_output,
  w = 10,
  h = 5,
  save_plot = TRUE,
  print_plot = FALSE
)
```

Arguments

`table`	tidy table coming form facs_tidytable
`title.i`	title of the plot
`x_lab`	x-axis label
`y_lab`	y-axis label
`y_limit`	inferior limit for y-axis
`color_values`	a set of aesthetic values to map data values to. The values will be matched in order (usually alphabetical).
`color_breaks`	takes the limits as input and returns breaks as output
`color_labels`	takes the breaks as input and returns labels as output
`path_output`	ful name of the generated plot including the path (recommended path_output from path_builder())
`w`	width of the output plot
`h`	high of the output plot
`save_plot`	boolean indicating if the plot is saved or not. Default to TRUE.
`print_plot`	boolean indicating if the plot is printed or not. Default to FALSE.

Value

plot file in data folder

Examples

```
weight_individual_plot(table_raw, y_limit = 10,
path_output = here(path_output, "individual_raw.png"))
```

`weight_mean_plot` *weight_mean_plot plot a weight-loss curve with the mean value of each genotype by day*

Description

weight_mean_plot plot a weight-loss curve with the mean value of each genotype by day

Usage

```
weight_mean_plot(
  table,
  title.i = "",
  x_lab = "",
  y_lab = "",
  y_limit = 0,
  color_values = RColorBrewer::brewer.pal(8, "Paired")[7:8],
  color_breaks = waiver(),
  color_labels = waiver(),
  path_output,
  w = 10,
  h = 5,
  save_plot = TRUE,
  print_plot = FALSE
)
```

Arguments

`table`	tidy table coming form facs_tidytable
`title.i`	title of the plot
`x_lab`	x-axis label
`y_lab`	y-axis label
`y_limit`	inferior limit for y-axis
`color_values`	a set of aesthetic values to map data values to. The values will be matched in order (usually alphabetical).
`color_breaks`	takes the limits as input and returns breaks as output
`color_labels`	takes the breaks as input and returns labels as output
`path_output`	ful name of the generated plot including the path (recommended path_output from path_builder())
`w`	width of the output plot

h	high of the output plot
save_plot	boolean indicating if the plot is saved or not. Default to TRUE.
print_plot	boolean indicating if the plot is printed or not. Default to FALSE.

Value

plot file in data folder

Examples

```
weight_mean_plot(table_raw, y_limit = 10,
path_output = here(path_output, "mean_raw.png"))
```

---

weight_relative_curve *Plot of relative weight by mice*

Description

Plot of relative weight by mice

Usage

```
weight_relative_curve(
  table,
  genotype_levels = c("WT", "KO"),
  x_lab = "Time (days)",
  y_lab = "Relative weight",
  title_lab = "",
  x_angle = 0,
  x_hjust = 0.5,
  color_values = hue_pal()(200),
  shape_values = rep(21, 200),
  fill_values = hue_pal()(200),
  lty_values = rep("solid", 200),
  path_output = "plot.png",
  w = 10,
  h = 5,
  save_plot = FALSE,
  print_plot = FALSE
)
```

Arguments

table	tidy table with data comming from the analysis. Columns: time, mice, genotype, value, experiment
genotype_levels	vector will all the genotypes all the analysis
x_lab	X-axis label
y_lab	y-axis label

title_lab	title label
x_angle	Angle to display the x axis
x_hjust	Justificacion of the x axis
color_values	color to be ploted. Same number as levels have genotype . For VHL paper table$VHL_palette_color
shape_values	shape to be ploted. Same number as levels have genotype. For VHL paper table$VHL_palette_shape
fill_values	fill color to be ploted. Same number as levels have genotype. For VHL paper table$VHL_palette_fill
lty_values	line structure. to be ploted. Same number as levels have genotype. For VHL paper table$VHL_palette_lty
path_output	ful name of the generated plot including the path (recommended path_output from path_builder())
w	width of the output plot
h	high of the output plot
save_plot	boolean indicating if the plot is saved or not. Default to FALSE.
print_plot	boolean indicating if the plot is printed or not. Default to TRUE.

Value

plot file in data folder

Examples

```
weight_relative_curve(table, title_lab = "GGP Seahorse",
color_values = table$VHL_palette_color,
shape_values = table$VHL_palette_shape,
fill_values = table$VHL_palette_fill,
lty_values = table$VHL_palette_lty)
```

---

weight_statistics *weight_statistics Function to perform the statistic analysis of the weight-loss curve experiments.*

Description

weight_statistics Function to perform the statistic analysis of the weight-loss curve experiments.

Usage

```
weight_statistics(
  table_tidy,
  path_to_save = path_output,
  file_name = "statistic.txt"
)
```

Arguments

table_tidy	input table in tidy format with columns for genotype, day, value and mice.
path_to_save	path where the output txt will be saved (path_output from the path_builder function).
file_name	Name of the output file. "statistic.txt" by default.

Examples

```
weight_statistics(table_raw, path_to_save = path_output)
```

---

weight_tidytable *weight_tidytable*

Description

weight_tidytable

Usage

```
weight_tidytable(
  csv_file,
  path_csv,
  animalario_file,
  path_mice,
  micecode,
  mice_genotype,
  relative = FALSE,
  csv_sep = ",",
  date_format = "%d.%b"
)
```

Arguments

csv_file	name of the csv file with the introduced weights. Usually "weight-curve.csv"
path_csv	path were csv file is located. Usually path_output
animalario_file	raw csv downloaded from animalario with mice used in the experiment
path_mice	path where animalario file to obtain the genotypes is located. usually path_raw from path_builder.
micecode	Named chr list containing the replacement chr for the genotype. BBV, CCT, DCX and DCW strains can be loaded with data(micecode)
mice_genotype	ordered list containing the levels of the mice to be included. Can be obtain from micecode data (followed by /t). For example c("VHL-HIF2a-WT ", "VHL-HIF2a-KO ")
relative	bool indicating if the final output will be raw number or the relative porcentage to day 1
csv_sep	sep parameter for read.delim function. Default ","
date_format	format parameter of strftime function. Character string. The default for the format methods is "%d.%b" that is for format "01.jul". Other common format are %d-%m

Examples

```
data(micecode)
weight_tidytable("weight-curve.csv", path_output,
"Animalario-VHL2101.csv", micecode)
```

Index