

Package: BoxDensityPlot (via r-universe)

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Type Package

Title Multi-Trait Density and Boxplot Visualization

Version 0.1.0

Description Reads wide-format phenotypic data (one row per genotype or sample, one column per trait) from CSV or 'Excel' files, reshapes it to long format, and produces faceted figures that combine a mirrored density curve with a boxplot for each trait. Density curves can be drawn on the left, right, or both sides of the box, and figures can be saved automatically at publication resolution.

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Depends R (>= 4.1.0)

Imports ggplot2 (>= 3.4.0), dplyr (>= 1.1.0), tidyr (>= 1.3.0), rlang, readxl, stats, utils, grid, tools

Suggests testthat (>= 3.0.0)

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example_trait_data	<i>Path to the bundled example trait data set</i>
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Description

Returns the file path to a small example CSV bundled with the package, containing genotype-level values for six traits. Useful for examples, tests, and trying out [plot_trait_density_box](#).

Usage

```
example_trait_data()
```

Value

A file path (character string).

Examples

```
f <- example_trait_data()
dat <- read_trait_data(f)
head(dat)
```

make_density_boxplot	<i>Build a density + boxplot figure for multiple traits</i>
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Description

Creates a faceted **ggplot2** figure that overlays a mirrored density curve (violin-style) with a boxplot for each trait found in `long_data`. This is the low-level plot builder used internally by [plot_trait_density_box](#); call it directly if you already have data prepared in the expected long format.

Usage

```
make_density_boxplot(
  long_data,
  density_data,
  ncol_plot,
  density_position = c("both", "left", "right"),
  density_colour = "#4DBBD5",
  plot_title = NULL,
  density_width = 0.45,
  density_alpha = 0.3,
  boxplot_width = 0.25,
  box_colour = "#006D6F",
  mean_colour = "#E31A1C"
)
```

Arguments

<code>long_data</code>	Long-format data frame with (at least) columns Trait and Value.
<code>density_data</code>	Long-format data frame with columns Trait, Value, and Density_scaled, one row per point on each trait's estimated density curve.
<code>ncol_plot</code>	Number of facet columns.
<code>density_position</code>	One of "both", "left", or "right": which side(s) of the boxplot show the density curve.
<code>density_colour</code>	Fill colour for the density ribbon.
<code>plot_title</code>	Title shown above the figure. Use NULL for no title.
<code>density_width</code>	Numeric half-width of the density curve.
<code>density_alpha</code>	Fill transparency (0-1) of the density ribbon.
<code>boxplot_width</code>	Numeric width of the boxplot.
<code>box_colour</code>	Fill colour of the boxplot.
<code>mean_colour</code>	Fill colour of the mean point marker.

Value

A ggplot object.

plot_trait_density_box

Read trait data and generate density + boxplot figure(s)

Description

High-level, one-call wrapper that reads a wide-format CSV or Excel file of multi-trait data (one row per genotype/sample, one column per trait), reshapes it, builds one or more density + boxplot figures (see [make_density_boxplot](#)), and optionally saves each one to disk at publication resolution.

Usage

```
plot_trait_density_box(
  file,
  genotype_col = "Genotype",
  density_position = c("both", "left", "right"),
  save = FALSE,
  out_dir = NULL,
  prefix = "Multiple_Traits_Boxplot_Density",
  format = "jpg",
  dpi = 600,
  width = NULL,
  height = NULL,
  ...
)
```

Arguments

<code>file</code>	Path to a .csv, .xls, or .xlsx file, or a data frame already in wide format (one identifier column plus one column per trait).
<code>genotype_col</code>	Name of the identifier column (e.g. "Genotype").
<code>density_position</code>	Which figure(s) to build: any combination of "both", "left", "right". Defaults to all three.
<code>save</code>	Logical; if TRUE each figure is saved with ggsave .
<code>out_dir</code>	Directory to save figures into. Must be supplied explicitly when <code>save = TRUE</code> ; no output directory is assumed by default.
<code>prefix</code>	File name prefix for saved figures.
<code>format</code>	Image format passed to <code>ggsave</code> (e.g. "jpg", "png", "pdf", "tiff").
<code>dpi</code>	Resolution (dots per inch) for saved figures.
<code>width, height</code>	Figure size in inches. If NULL (default) a size is chosen automatically from the number of traits, matching the original script's behaviour.
<code>...</code>	Additional styling arguments forwarded to make_density_boxplot : <code>density_width</code> , <code>density_alpha</code> , <code>boxplot_width</code> , <code>box_colour</code> , <code>mean_colour</code> , plus the per-position ribbon colours <code>both_colour</code> , <code>left_colour</code> , <code>right_colour</code> .

Value

A named list of ggplot objects (one per requested `density_position`), returned invisibly.

Examples

```
f <- example_trait_data()
plots <- plot_trait_density_box(f, save = FALSE)
plots$both
```

read_trait_data	<i>Read multi-trait phenotypic data from CSV or Excel</i>
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Description

Reads a wide-format data set (one row per genotype/sample, one column per trait) from a .csv, .xls, or .xlsx file.

Usage

```
read_trait_data(file, sheet = 1, genotype_col = "Genotype")
```

Arguments

file	Path to the input file. The file extension (.csv, .xls, .xlsx) determines how the file is parsed.
sheet	Sheet name or index to read when file is an Excel file. Ignored for CSV files. Defaults to the first sheet.
genotype_col	Name of the identifier column (genotype, sample, accession, etc.). Defaults to "Genotype".

Value

A data frame in wide format with the identifier column plus one column per trait.

Examples

```
f <- example_trait_data()
dat <- read_trait_data(f)
head(dat)
```

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