

Package ‘dabestr’

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Type Package

Title Data Analysis using Bootstrap-Coupled Estimation

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Description Data Analysis using Bootstrap-Coupled ESTimation. Estimation statistics is a simple framework that avoids the pitfalls of significance testing. It uses familiar statistical concepts: means, mean differences, and error bars. More importantly, it focuses on the effect size of one's experiment/intervention, as opposed to a false dichotomy engendered by P values. An estimation plot has two key features: 1. It presents all datapoints as a swarmplot, which orders each point to display the underlying distribution. 2. It presents the effect size as a bootstrap 95% confidence interval on a separate but aligned axes. Estimation plots are introduced in Ho et al., Nature Methods 2019, 1548-7105. <doi:10.1038/s41592-019-0470-3>. The free-to-view PDF is located at <https://www.nature.com/articles/s41592-019-0470-3.epdf?author_access_token=Euy6APITxsYA3huBKOFBvNRgN0jAjWe19jnR3ZoTv0Pr6zJiJ3AA5aH4989g0JS_dajtNr1Wt17D0fh-t4GFcvqwMYN03qb8C33na_UrCUcGrt-Z0J9aPL6TPSb0xIC-pbHWKUD02XsUOr3hQm1Rew%3D%3D>.

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URL <https://github.com/ACCLAB/dabestr>,
<https://acclab.github.io/dabestr/>

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dabest_plot	<i>Producing an estimation plot</i>
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Description

Produces a Gardner-Altman estimation plot or a Cumming estimation plot depending on whether float_contrast is TRUE. The plot presents all datapoints as a swarmplot, which orders each point to display the underlying distribution. It also presents the effect size as a bootstrap 95% confidence interval (95% CI) on a separate but aligned axes.

Usage

dabest_plot(dabest_effectsize_obj, float_contrast = TRUE, ...)

Arguments

- `dabest_effectsize_obj` A `dabest_effectsize_obj` created by loading in a `dabest_obj` along with other specified parameters with the `effect_size()` function.
- `float_contrast` Default TRUE. If TRUE, a Gardner-Altman plot will be produced. If FALSE, a Cumming estimation plot will be produced.
- ... Adjustment parameters to control and adjust the appearance of the plot. (list of all possible adjustment parameters can be found under `plot_kwargs`)

Examples

```
# Loading of the dataset
data(twogroup_data)

# Preparing the data to be plotted
dabest_obj <- load(non_proportional_data,
  x = Group, y = Measurement,
  idx = c("Control 1", "Test 1")
)
dabest_obj.mean_diff <- mean_diff(dabest_obj)

# Plotting an estimation plot
dabest_plot(dabest_obj.mean_diff, TRUE)
```

effect_size

Calculating effect sizes

Description

Computes the effect size for each control-test group pairing in `idx`. The resampling bootstrap distribution of the effect size is then subjected to Bias-corrected and accelerated bootstrap (BCa) correction.

The following effect sizes `mean_diff`, `median_diff`, `cohens_d`, `hedges_g` and `cliffs_delta` are used for most plot types.

Usage

```
mean_diff(dabest_obj, perm_count = 5000)

median_diff(dabest_obj, perm_count = 5000)

cohens_d(dabest_obj, perm_count = 5000)

hedges_g(dabest_obj, perm_count = 5000)

cliffs_delta(dabest_obj, perm_count = 5000)

cohens_h(dabest_obj, perm_count = 5000)
```

Arguments

dabest_obj	A dabest_obj created by loading in dataset along with other specified parameters with the <code>load()</code> function.
perm_count	The number of reshuffles of control and test labels to be performed for each p-value.

Details

The plot types listed under here are limited to use only the following effect sizes.

- Proportion plots offers only mean_diff and cohens_h.
- Mini-Meta Delta plots offers only mean_diff.

The other plots are able to use all given basic effect sizes as listed in the Description.

Value

Returns a dabest_effectsize_obj list with 22 elements. The following are the elements contained within:

- raw_data The tidy dataset passed to `load()` that was cleaned and altered for plotting.
- idx The list of control-test groupings as initially passed to `load()`.
- delta_x_labels Vector containing labels for the x-axis of the delta plot.
- delta_y_labels String label for the y-axis of the delta plot.
- Ns List of labels for x-axis of the raw plot.
- raw_y_labels Vector containing labels for the y-axis of the raw plot.
- is_paired Boolean value determining if it is a paired plot.
- is_colour Boolean value determining if there is a colour column for the plot.
- paired Paired ("sequential" or "baseline") as initially passed to `load()`.
- resamples The number of resamples to be used to generate the effect size bootstraps.
- control_summary Numeric value for plotting of control summary lines for float_contrast = TRUE.
- test_summary Numeric value for plotting of control summary lines for float_contrast = TRUE.
- ylim Vector containing the y limits for the raw plot.
- enquox Quosure of x as initially passed to `load()`.
- enquoy Quosure of y as initially passed to `load()`.
- enquoidcol Quosure of id_col as initially passed to `load()`.
- enquocolour Quosure of colour as initially passed to `load()`.
- proportional Boolean value as initially passed to `load()`.
- minimeta Boolean value as initially passed to `load()`.
- delta Boolean value as initially passed to `load()`.
- proportional_data List of calculations related to the plotting of proportion plots.

- `boot_result` List containing values related to the calculation of the effect sizes, bootstrapping and BCa correction.
- `baseline_ec_boot_result` List containing values related to the calculation of the effect sizes, bootstrapping and BCa correction for the baseline error curve.
- `permtest_pvals` List containing values related to the calculations of permutation t tests and the corresponding p values, and p values for different types of effect sizes and different statistical tests.

Examples

```
# Loading of the dataset
data(non_proportional_data)

# Applying effect size to the dabest object
dabest_obj <- load(non_proportional_data,
  x = Group, y = Measurement,
  idx = c("Control 1", "Test 1")
)
dabest_obj.mean_diff <- mean_diff(dabest_obj)

# Printing dabest effectsize object
print(dabest_obj.mean_diff)
```

forest_plot	<i>Generates a Forest Plot</i>
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Description

This function creates a forest plot summarizing a list of contrasts.

Usage

```
forest_plot(
  contrasts,
  contrast_labels,
  contrast_type = "delta2",
  effect_size = "mean_diff",
  ylabel = "effect size",
  title = "Delta Delta Forest",
  fontsize = 12,
  title_font_size = 16,
  violin_kwargs = NULL,
  marker_size = 1.1,
  ci_line_width = 1.3,
  custom_palette = NULL,
  rotation_for_xlabels = 0,
  alpha_violin_plot = 0.8
)
```

Arguments

<code>contrasts</code>	A list of contrast objects. These objects should contain the statistical information for each comparison (e.g., estimates, standard errors).
<code>contrast_labels</code>	A list of labels for the contrast objects. E.g., <code>c('Drug1', 'Drug2', 'Drug3')</code> These labels will be used to identify each comparison on the plot.
<code>contrast_type</code>	Select between "delta2" (for delta-delta) or "minimeta" for mini-meta analysis. This determines the type of effect size calculation used in the plot.
<code>effect_size</code>	Character string specifying the effect size metric to display. Valid options include "mean_diff", "median_diff", "cliffs_delta", "cohens_d", "hedges_g", or "delta_g". The default is "mean_diff".
<code>ylabel</code>	Character string specifying the axis label for the dependent variable (Y-axis for vertical layout, X-axis for horizontal layout). The default is "value".
<code>title</code>	Character string specifying the title for the forest plot. The default is "Delta delta Forest".
<code>fontsize</code>	Font size for text elements in the plot. Default is 12.
<code>title_font_size</code>	Font size for text of plot title. Defaults is 16.
<code>violin_kwargs</code>	Additional arguments for violin plot customization. Default is NULL
<code>marker_size</code>	Marker size for plotting mean differences or effect sizes. Default is 20.
<code>ci_line_width</code>	Width of confidence interval lines. Default is 2.5.
<code>custom_palette</code>	A list or key:value pair of colors, one for each contrast object. E.g., <code>c('gray', 'blue', 'green')</code> or <code>c('Drug1'='gray', 'Drug2'='blue', 'Drug3'='green')</code> . Default NULL.
<code>rotation_for_xlabels</code>	Rotation angle for x-axis labels, improving readability. Default is 45.
<code>alpha_violin_plot</code>	Transparency level for violin plots. Default is 0.8

Value

A ggplot object representing the forest plot.

load

Loading data with dabestr

Description

Processes and converts a tidy dataset into the dabestr format. The output of this function is then used as an input for various procedural functions within dabestr to create estimation plots.

Usage

```
load(
  data,
  x,
  y,
  idx = NULL,
  paired = NULL,
  id_col = NULL,
  ci = 95,
  resamples = 5000,
  colour = NULL,
  proportional = FALSE,
  minimeta = FALSE,
  delta2 = FALSE,
  experiment = NULL,
  experiment_label = NULL,
  x1_level = NULL
)
```

Arguments

data	A tidy dataframe.
x	Column in data that contains the treatment groups.
y	Column in data that contains the measurement values.
idx	List of control-test groupings for which the effect size will be computed for.
paired	Paired ("sequential" or "baseline"). Used for plots for experiments with repeated-measures designs. If "sequential", comparison happens between each measurement to the one directly preceding it. (control vs group i) If "baseline", comparison happens between each group to a shared control. (group i vs group i+1)
id_col	Column in data indicating the identity of the datapoint if the data is tagged. Compulsory parameter if paired is TRUE.
ci	Default 95. Determines the range of the confidence interval for effect size and bootstrap calculations. Only accepts values between 0 to 100 (inclusive).
resamples	The number of resamples to be used to generate the effect size bootstraps.
colour	Column in data that determines the groupings for colour of the swarmplot as opposed to x.
proportional	Boolean value determining if proportion plots are being produced.
minimeta	Boolean value determining if mini-meta analysis is conducted.
delta2	Boolean value determining if delta-delta analysis for 2 by 2 experimental designs is conducted.
experiment	Experiment column name for delta-delta analysis.

`experiment_label` String specifying the experiment label that is used to distinguish the experiment and the factors (being used in the plotting labels).

`x1_level` String setting the first factor level in a 2 by 2 experimental design.

Value

Returns a `dabest_obj` list with 18 elements. The following are the elements contained within:

- `raw_data` The tidy dataset passed to `load()` that was cleaned and altered for plotting.
- `proportional_data` List of calculations related to the plotting of proportion plots.
- `enquo_x` Quosure of `x` as initially passed to `load()`.
- `enquo_y` Quosure of `y` as initially passed to `load()`.
- `enquo_id_col` Quosure of `id_col` as initially passed to `load()`.
- `enquo_colour` Quosure of `colour` as initially passed to `load()`.
- `proportional` Boolean value determining if proportion plots are being produced.
- `minimeta` Boolean value determining if mini-meta analysis is conducted.
- `delta2` Boolean value determining if delta-delta analysis for 2 by 2 experimental designs is conducted.
- `idx` List of control-test groupings for which the effect size will be computed for.
- `resamples` The number of resamples to be used to generate the effect size bootstraps.
- `is_paired` Boolean value determining if it is a paired plot.
- `is_colour` Boolean value determining if there is a specified colour column for the plot.
- `paired` Paired ("sequential" or "baseline") as initially passed to `load()`.
- `ci` Numeric value which determines the range of the confidence interval for effect size and bootstrap calculations. Only accepts values between 0 to 100 (inclusive).
- `Ns` List of labels for x-axis of the rawdata swarm plot.
- `control_summary` Numeric value for plotting of control summary lines for `float_contrast = TRUE`.
- `test_summary` Numeric value for plotting of test summary lines for `float_contrast = TRUE`.
- `ylim` Vector containing the y limits for the rawdata swarm plot.

Examples

```
# Loading in of the dataset
data(non_proportional_data)

# Creating a dabest object
dabest_obj <- load(
  data = non_proportional_data, x = Group, y = Measurement,
  idx = c("Control 1", "Test 1")
)

# Printing dabest object
print(dabest_obj)
```

Description

These are the available plot kwarg for adjusting the plot aesthetics of your estimation plot:

- `swarm_label` Default "value" or "proportion of success" for proportion plots. Label for the y-axis of the swarm plot.
- `contrast_label` Default "effect size", based on the effect sizes as given in `effect_size()`. Label for the y-axis of the contrast plot.
- `delta2_label` Default NULL. Label for the y-label for the delta-delta plot.
- `swarm_x_text` Default 11. Numeric value determining the font size of the x-axis of the swarm plot.
- `swarm_y_text` Default 15. Numeric value determining the font size of the y-axis of the swarm plot.
- `contrast_x_text` Default 11. Numeric value determining the font size of the x-axis of the delta plot.
- `contrast_y_text` Default 15. Numeric value determining the font size of the y-axis of the delta plot.
- `swarm_ylim` Default NULL. Vector containing the y limits for the swarm plot
- `contrast_ylim` Default NULL. Vector containing the y limits for the delta plot.
- `delta2_ylim` Default NULL. Vector containing the y limits for the delta-delta plot.
- `raw_marker_size` Default 1.5. Numeric value determining the size of the points used in the swarm plot.
- `tufte_size` Default 0.8. Numeric value determining the size of the tufte line in the swarm plot.
- `es_marker_size` Default 0.5. Numeric value determining the size of the points used in the delta plot.
- `es_line_size` Default 0.8. Numeric value determining the size of the ci line in the delta plot.
- `raw_marker_alpha` Default 1. Numeric value determining the transparency of the points in the swarm plot.
- `raw_bar_width` Default 0.3. Numeric value determining the width of the bar in the sankey diagram.
- `raw_marker_spread` Default 2. The distance between the points if it is a swarm plot.
- `raw_marker_side_shift` Default 0. The horizontal distance that the swarm plot points are moved in the direction of the `asymmetric_side`.
- `asymmetric_side` Default "right". Can be either "right" or "left". Controls which side the swarm points are shown.
- `show_delta2` Default FALSE. Boolean value determining if the delta-delta plot is shown.

- `show_mini_meta` Default FALSE. Boolean value determining if the weighted average plot is shown. If False, the resulting graph would be identical to a multiple two-groups plot.
- `show_zero_dot` Default TRUE. Boolean value determining if there is a dot on the zero line of the effect size for the control-control group.
- `show_baseline_ec` Default FALSE. Boolean value determining whether the baseline curve is shown.
- `show_legend` Default TRUE. If TRUE, legend will be shown. If FALSE, legend will not be shown.
- `sankey` Default TRUE. Boolean value determining if the flows between the bar charts will be plotted.
- `raw_flow_alpha` Default 0.5. Numeric value determining the transparency of the sankey flows in a paired proportion plot.
- `flow` Default TRUE. Boolean value determining whether the bars will be plotted in pairs.
- `custom_palette` Default "d3". String. The following palettes are available for use: `npg`, `aaas`, `nejm`, `lancet`, `jama`, `jco`, `ucscgb`, `d3`, `locuszoom`, `igv`, `cosmic`, `uchicago`, `brewer`, `ordinal`, `viridis_d`.
- `contrast_bars` Default TRUE. Whether or not to display the contrast bars at the delta plot.
- `params_contrast_bars`. Default value: `list(color = NULL, alpha = 0.3)`. Pass relevant keyword arguments to the contrast bars.
- `swarm_bars` Default TRUE. Whether or not to display the swarm bars.
- `params_swarm_bars`. Default value: `list(color = NULL, alpha = 0.3)`. Pass relevant keyword arguments to the swarm bars.

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