Package ‘blandr’

October 12, 2022

Title Bland-Altman Method Comparison

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Description Carries out Bland Altman analyses (also known as a Tukey mean-difference plot) as described by JM Bland and DG Altman in 1986 <doi:10.1016/S0140-6736(86)90837-8>. This package was created in 2015 as existing Bland-Altman analysis functions did not calculate confidence intervals. This package was created to rectify this, and create reproducible plots. This package is also available as a module for the ‘jamovi’ statistical spreadsheet (see <https://www.jamovi.org> for more information).

Depends R (>= 3.2.0)

License GPL-3

Encoding UTF-8

LazyData true

URL https://github.com/deepankardatta/blandr/

BugReports https://github.com/deepankardatta/blandr/issues

Imports ggplot2, knitr, stringr, jmvcore (>= 0.8.5), R6, rmarkdown

Suggests testthat

SystemRequirements pandoc (>=1.12.3)

VignetteBuilder knitr

Collate 'blandr.data.preparation.r' 'blandr.dataset.fibre.r' 'blandr.dataset.sbp.r' 'blandr.dataset.o2sats.r' 'blandr.dataset.pefr.r' 'blandr.dataset.load.r' 'blandr.plot.ggplot.r' 'blandr.plot.rplot.r' 'blandr.plot.limits.r' 'blandr.statistics.r' 'blandr.draw.r' 'blandr.output.text.r' 'blandr.display.and.draw.r' 'blandr.display.and.plot.r' 'blandr.method.comparison.r' 'blandr.output.report.r' 'blandr.plot.normality.r' 'blandr.plot.qq.r' 'blandr.plot.r' 'jamovibaanalysis.b.R' 'jamovibaanalysis.h.R' 'jamovibaplothistogram.b.R'
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Sample PEFR comparison data from Bland-Altman (1986)

Description
This is the sample PEFR data set from the 1986 Lancet paper written by Bland and Altman. I do not claim any copyright on the data - this is meant to allow testing of the function. I encourage future package authors to use the .rda file if they so wish.

Usage
```r
data("bland.altman.PEFR.1986")
```

Format
A data frame with 17 observations on the following 4 variables.

- `WrightFirst` a numeric vector
- `WrightSecond` a numeric vector
- `MiniWrightFirst` a numeric vector
- `MiniWrightSecond` a numeric vector

References

Examples
```r
data(bland.altman.PEFR.1986)
```

---

Data preparation for method comparison analysis

Description
Prepares the data and runs error checks before the calling function runs whatever method analysis mode is wants.

Usage
```r
blandr.data.preparation(method1, method2, sig.level)
```
blandr.dataset.fibre

**Arguments**

- `method1` A list of numbers.
- `method2` A list of numbers.
- `sig.level` Significance level. Is not optional in this function, as the calling package should have a default value to pass if needed.

**Value**

- `method.comparison` A data frame of paired values. These have been data checked, and empty rows omitted, from the originally supplied data.

**Author(s)**

Deeprankar Datta <deepankardatta@nhs.net>

**Examples**

```r
# Generates two random measurements
measurement1 <- rnorm(100)
measurement2 <- rnorm(100)

# Calls the function - do note that this function was really meant to be called from other functions and not a stand-alone function
blandr.data.preparation( measurement1 , measurement2, sig.level=0.95 )
```

---

**blandr.dataset.fibre**  *Function to load D’arbela mean velocity of circumferential fibre shortening dataset from internet*

**Description**

Loads the D’arbela mean velocity of circumferential fibre shortening dataset from Martin Bland’s website.

**Usage**

```r
blandr.dataset.fibre()
```

**Value**

- `converted.from.dct` A data frame containing the dataset

**Note**

The function converts the STATA DCT data format into a data frame that R can process.
blandr.dataset.load

Author(s)

Deepankar Datta <deepankardatta@nhs.net>

References

https://www-users.york.ac.uk/~mb55/datasets/pefr.dct - The D’arbela mean velocity of circumferential fibre shortening dataset from Martin Bland’s website
https://www-users.york.ac.uk/~mb55/datasets/datasets.htm - Martin Bland’s example data-set webpage

Examples

blandr.dataset.fibre()
pefr.data <- blandr.dataset.fibre()

blandr.dataset.load  Function to load example data sets

Description

Loads example data sets from the internet.

Usage

blandr.dataset.load(dataset.name)

Arguments

dataset.name  Loads the requisite data set. See the description for further details.

Value

dataset.name  A data frame containing the requisite dataset

Note

Dataset 1 ("1","PEFR","pefr") - Bland Altman PEFR dataset (from blandr.dataset.pefr)
Dataset 2 ("2","o2sats","sealey") - Selaey oxygen saturations dataset (from blandr.dataset.o2sats)
Dataset 3 ("3","fibre","darbela") - D’arbela mean velocity of circumferential fibre shortening dataset (from blandr.dataset.fibre)
Dataset 4 ("4","sbp","close") - Close systolic blood pressure dataset (from blandr.dataset.sbp)
Author(s)

Deepankar Datta <deepankardatta@nhs.net>

Examples

blandr.dataset.load("pefr")
pefr.data <- blandr.dataset.load("pefr")

blandr.dataset.o2sats Function to load Bland-Altman oxygen saturation dataset from internet

Description

Loads the Bland-Altman oxygen saturation dataset from Martin Bland’s website.

Usage

blandr.dataset.o2sats()

Value

converted.from.dct A data frame containing the dataset

Note

The function converts the STATA DCT data format into a data frame that R can process.

Author(s)

Deepankar Datta <deepankardatta@nhs.net>

References

https://www-users.york.ac.uk/~mb55/datasets/sealey.dct - The oxygen saturation dataset from Martin Bland’s website
https://www-users.york.ac.uk/~mb55/datasets/datasets.htm - Martin Bland’s example data-set web-page

Examples

blandr.dataset.o2sats()
pefr.data <- blandr.dataset.o2sats()
blandr.dataset.pefr  

Function to load Bland-Altman PEFR dataset from internet

Description

Loads the Bland-Altman PEFR dataset from Martin Bland’s website.

Usage

blandr.dataset.pefr()

Value

converted.from.dct A data frame containing the dataset

Note

The function converts the STATA DCT data format into a data frame that R can process.

Author(s)

Deepankar Datta <deepankardatta@nhs.net>

References

https://www-users.york.ac.uk/~mb55/datasets/pefr.dct - The PEFR dataset from Martin Bland’s website
https://www-users.york.ac.uk/~mb55/datasets/datasets.htm - Martin Bland’s example data-set webpage

Examples

blandr.dataset.pefr()
pefr.data <- blandr.dataset.pefr()
blandr.dataset.sbp

*Function to load Close systolic blood pressure dataset from internet*

**Description**

Loads the Close systolic blood pressure dataset from Martin Bland’s website.

**Usage**

blandr.dataset.sbp()

**Value**

converted.from.dct A data frame containing the dataset

**Note**

The function converts the STATA DCT data format into a data frame that R can process.

**Author(s)**

Deepankar Datta <deepankardatta@nhs.net>

**References**

https://www-users.york.ac.uk/~mb55/datasets/pefr.dct - The Close systolic blood pressure dataset from Martin Bland’s website

https://www-users.york.ac.uk/~mb55/datasets/datasets.htm - Martin Bland’s example data-set webpage


**Examples**

blandr.dataset.sbp()
pefr.data <- blandr.dataset.sbp()
blandr.display.and.draw

_Bland-Altman display and draw for R_

**Description**

Stub function: calls both the display and plots functions (in that order). Uses the same parameters as the plot and display functions to allow easy all-in-one use.

This function may be deprecated in future, as you really can use the functions easily separately.

**Usage**

```r
blandr.display.and.draw(method1, method2, plotter = "ggplot",
method1name = "Method 1", method2name = "Method 2",
plotTitle = "Bland-Altman plot for comparison of 2 methods",
sig.level = 0.95, annotate = FALSE, ciDisplay = TRUE,
ciShading = FALSE, normalLow = FALSE, normalHigh = FALSE,
lowest_y_axis = FALSE, highest_y_axis = FALSE, point_size = 0.8)
```

**Arguments**

- **method1**: A list of numbers.
- **method2**: A list of numbers.
- **plotter**: (Optional- default='ggplot') Selects which graphics engine to use to plot the Bland-Altman charts. 2 options are 'ggplot' or 'rplot'. If unknown parameter sent, will default to 'ggplot'.
- **method1name**: (Optional) Plotting name for 1st method, default 'Method 1'
- **method2name**: (Optional) Plotting name for 2nd method, default 'Method 2'
- **plotTitle**: (Optional) Title name, default 'Bland-Altman plot for comparison of 2 methods'
- **sig.level**: (Optional) Two-tailed significance level. Expressed from 0 to 1. Defaults to 0.95.
- **annotate**: (Optional) TRUE/FALSE switch to provides annotations to plot, default=FALSE
- **ciDisplay**: (Optional) TRUE/FALSE switch to plot confidence intervals for bias and limits of agreement, default=TRUE
- **ciShading**: (Optional) TRUE/FALSE switch to plot confidence interval shading to plot, default=TRUE
- **normalLow**: (Optional) If there is a normal range, entering a continuous variable will plot a vertical line on the plot to indicate its lower boundary
- **normalHigh**: (Optional) If there is a normal range, entering a continuous variable will plot a vertical line on the plot to indicate its higher boundary
- **lowest_y_axis**: (Optional) Defaults to NULL If given a continuous variable will use this as the lower boundary of the y axis. Useful if need multiple plots with equivalent y-axes.
blandr.display.and.plot

(Optional) Defaults to NULL. If given a continuous variable will use this as the upper boundary of the y axis. Useful if need multiple plots with equivalent y-axes.

point_size  
(Optional) Size of marker for each dot. Default is cex=0.8

Author(s)

Deepankar Datta <deepankardatta@nhs.net>

Examples

# Generates two random measurements
measurement1 <- rnorm(100)
measurement2 <- rnorm(100)

# Generates a plot, with no optional arguments
blandr.display.and.draw(measurement1, measurement2)

# Generates a plot, with title
blandr.display.and.draw(measurement1, measurement2, plotTitle = 'Bland-Altman example plot')

Description

(DEPRECATED) Re-directs to blandr.display.and.draw

Usage

blandr.display.and.plot(method1, method2, method1name = "Method 1", method2name = "Method 2", plotTitle = "Bland-Altman plot for comparison of 2 methods", sig.level = 0.95, annotate = FALSE, ciDisplay = TRUE, ciShading = FALSE, normalLow = FALSE, normalHigh = FALSE, lowest_y_axis = FALSE, highest_y_axis = FALSE, point_size = 0.8)

Arguments

method1 A list of numbers.
method2 A list of numbers.
method1name (Optional) Plotting name for 1st method, default 'Method 1'
method2name (Optional) Plotting name for 2nd method, default 'Method 2'
plotTitle (Optional) Title name, default 'Bland-Altman plot for comparison of 2 methods'
sig.level  (Optional) Two-tailed significance level. Expressed from 0 to 1. Defaults to 0.95.
annotate  (Optional) TRUE/FALSE switch to provides annotations to plot, default=FALSE
ciDisplay  (Optional) TRUE/FALSE switch to plot confidence intervals for bias and limits of agreement, default=TRUE
ciShading  (Optional) TRUE/FALSE switch to plot confidence interval shading to plot, default=TRUE
normalLow  (Optional) If there is a normal range, entering a continuous variable will plot a vertical line on the plot to indicate its lower boundary
normalHigh  (Optional) If there is a normal range, entering a continuous variable will plot a vertical line on the plot to indicate its higher boundary
lowest_y_axis  (Optional) Defaults to NULL If given a continuous variable will use this as the lower boundary of the y axis. Useful if need multiple plots with equivalent y-axes.
highest_y_axis  (Optional) Defaults to NULL If given a continuous variable will use this as the upper boundary of the y axis. Useful if need multiple plots with equivalent y-axes.
point_size  (Optional) Size of marker for each dot. Default is cex=0.8

Author(s)
Deepankar Datta <deepankardatta@nhs.net>

blandr.draw  

Bland-Altman drawing function for R

Description
Bland-Altman drawing function. Depends on the blandr.statistics function in the package. Will generate a plot via the standard R plotting functions.

Usage
blandr.draw(method1, method2, method1name = "Method 1", method2name = "Method 2", plotTitle = "Bland-Altman plot for comparison of 2 methods", sig.level = 0.95, LoA.mode = 1, annotate = FALSE, ciDisplay = TRUE, ciShading = TRUE, normalLow = FALSE, normalHigh = FALSE, lowest_y_axis = FALSE, highest_y_axis = FALSE, point_size = 0.8, overlapping = FALSE, plotter = "ggplot", x.plot.mode = "means", y.plot.mode = "difference", plotProportionalBias = FALSE, plotProportionalBias.se = TRUE, assume.differences.are.normal = TRUE)
**Arguments**

- **method1**: A list of numbers.
- **method2**: A list of numbers.
- **method1name** (Optional) Plotting name for 1st method, default 'Method 1'
- **method2name** (Optional) Plotting name for 2nd method, default 'Method 2'
- **plotTitle** (Optional) Title name, default 'Bland-Altman plot for comparison of 2 methods'
- **sig.level** (Optional) Two-tailed significance level. Expressed from 0 to 1. Defaults to 0.95.
- **LoA.mode** (Optional) Switch to change how accurately the limits of agreement (LoA) are calculated from the bias and its standard deviation. The default is LoA.mode=1 which calculates LoA with the more accurate 1.96x multiplier. LoA.mode=2 uses the 2x multiplier which was used in the original papers. This should really be kept at default, except to double check calculations in older papers.
- **annotate** (Optional) TRUE/FALSE switch to provides annotations to plot, default=FALSE
- **ciDisplay** (Optional) TRUE/FALSE switch to plot confidence intervals for bias and limits of agreement, default=TRUE
- **ciShading** (Optional) TRUE/FALSE switch to plot confidence interval shading to plot, default=TRUE
- **normalLow** (Optional) If there is a normal range, entering a continuous variable will plot a vertical line on the plot to indicate its lower boundary
- **normalHigh** (Optional) If there is a normal range, entering a continuous variable will plot a vertical line on the plot to indicate its higher boundary
- **lowest_y_axis** (Optional) Defaults to NULL If given a continuous variable will use this as the lower boundary of the y axis. Useful if need multiple plots with equivalent y-axes.
- **highest_y_axis** (Optional) Defaults to NULL If given a continuous variable will use this as the upper boundary of the y axis. Useful if need multiple plots with equivalent y-axes.
- **point_size** (Optional) Size of marker for each dot. Default is cex=0.8
- **overlapping** (Optional) TRUE/FALSE switch to increase size of plotted point if multiple values using ggplot's geom_count, default=FALSE. Not currently recommend until I can tweak the graphics to make them better
- **plotter** (Optional- default='ggplot') Selects which graphics engine to use to plot the Bland-Altman charts. 2 options are 'ggplot' or 'rplot'. If unknown parameter sent, will default to 'ggplot'
- **x.plot.mode** (Optional) Switch to change x-axis from being plotted by means (="means") or by either 1st method (="method1") or 2nd method (="method2"). Default is "means". Anything other than "means" will switch to default mode.
- **y.plot.mode** (Optional) Switch to change y-axis from being plotted by difference (="difference") or by proportion magnitude of measurements (="proportion"). Default is "difference". Anything other than "proportional" will switch to default mode.
plotProportionalBias
  (Optional) TRUE/FALSE switch. Plots a proportional bias line. Default is FALSE.
plotProportionalBias.se
  (Optional) TRUE/FALSE switch. If proportional bias line is drawn, switch to plot standard errors. See stat_smooth for details. Default is TRUE.
assume.differences.are.normal
  (Optional, not operationally used currently) Assume the difference of means has a normal distribution. Will be used to build further analyses

Note

Started 2015-11-14
Last update 2015-11-19
Originally designed for LAVAS and CVLA

Author(s)

Deepankar Datta <deepankardatta@nhs.net>

Examples

# Generates two random measurements
measurement1 <- rnorm(100)
measurement2 <- rnorm(100)

# Generates a plot, with no optional arguments
blandr.draw( measurement1 , measurement2 )

# Generates a plot, using the in-built R graphics
blandr.draw( measurement1 , measurement2 , plotter = 'rplot' )

# Generates a plot, with title changed
blandr.draw( measurement1 , measurement2 , plotTitle = 'Bland-Altman example plot' )

# Generates a plot, with title changed, and confidence intervals off
blandr.draw( measurement1 , measurement2 , plotTitle = 'Bland-Altman example plot' ,
  ciDisplay = FALSE , ciShading = FALSE )

Description

Everyone likes graphs, lines and T-tests. This uses the data provided to generate simple tests whilst trying to explain why they should be treated with caution in method comparison studies. This is hopefully the first step in getting people to use the Bland-Altman functions as I suspect everyone will try to do these tests anyway.
Usage

blandr.method.comparison(method1, method2, sig.level = 0.95)

Arguments

method1               A list of numbers.
method2               A list of numbers.
sig.level             (Optional) Two-tailed significance level. Expressed from 0 to 1. Defaults to 0.95.

Author(s)

Deepankar Datta <deepankardatta@nhs.net>

References


Examples

# Generates two random measurements
measurement1 <- rnorm(100)
measurement2 <- rnorm(100)

# Call the function
blandr.method.comparison( measurement1 , measurement2 )

blandr.output.report   Bland-Altman report generator

Description

Generates a report for the Bland-Altman statistics using rMarkdown and Shiny.

Usage

blandr.output.report(method1, method2)
blandr.output.text

Arguments

method1 A list of numbers for the first method
method2 A list of numbers for the second method

Note

Use the function to generate a report. You can also take the .Rmd file to customise it and create your own report. Or use rMarkdown to save the contents. I couldn’t add this to the function as it’s not allowed in CRAN. On the otherhand a full Shiny app would take too long. So this is a stop-gap way of creating this function. Hopefully I can improve it in the future

Author(s)

Deepankar Datta <deepankardatta@nhs.net>

Examples

```r
# NOT RUN
# Generates two random measurements
# measurement1 <- rnorm(100)
# measurement2 <- rnorm(100)

# blandr.output.report( measurement1 , measurement2 )
#
# Use this to manually run the rmarkdown template
# However specify where the template is
# Also define your methods as method1 and method2 exactly
# For a reason I can't fathom (or how the list of parameters is constructed)
# not naming them method1 and method2 makes them invisible to the rMarkdown document
#
# rmarkdown::run( file = "blandr_report_template.Rmd" ,
#    render_args = list( runtime = "shiny" ,
#    params = list( method1 = measurement1 ,
#    method2 = measurement2 ) ) )
# END OF NOT RUN
```

blandr.output.text  Bland-Altman summary statistics display function

Description

Displays results of Bland-Altman analysis in a nicer text format. Relies on the blandr.statistics function in the package.
Usage
blandr.output.text(method1, method2, sig.level = 0.95)

Arguments
method1 A list of numbers.
method2 A list of numbers.
sig.level (Optional) Two-tailed significance level. Expressed from 0 to 1. Defaults to 0.95.

Author(s)
Deepankar Datta <deepankardatta@nhs.net>

Examples
# Generates two random measurements
measurement1 <- rnorm(100)
measurement2 <- rnorm(100)

# Displays basic statistics for the two measurements in a readable form
blandr.output.text(measurement1, measurement2)

blandr.plot (DEPRECATED) Bland-Altman drawing function for R

Description
(DEPRECATED) Re-directs to blandr.draw.r

Usage
blandr.plot(method1, method2, plotter = "ggplot", method1name = "Method 1",
method2name = "Method 2",
plotTitle = "Bland-Altman plot for comparison of 2 methods",
sig.level = 0.95, annotate = FALSE, ciDisplay = TRUE,
ciShading = TRUE, normallow = FALSE, normalHigh = FALSE,
lowest_y_axis = FALSE, highest_y_axis = FALSE, point_size = 0.8)

Arguments
method1 A list of numbers.
method2 A list of numbers.
plotter (Optional- default='ggplot') Selects which graphics engine to use to plot the Bland-Altman charts. 2 options are 'ggplot' or 'rplot'. If unknown parameter sent, will default to 'ggplot'
**blandr.plot.ggplot**

**Bland-Altman plotting function, using ggplot2**

### Description

Draws a Bland-Altman plot using data calculated using the other functions, using ggplot2

### Usage

```r
blandr.plot.ggplot(statistics.results, method1name = "Method 1",
                   method2name = "Method 2",
                   plotTitle = "Bland-Altman plot for comparison of 2 methods",
                   ciDisplay = TRUE, ciShading = TRUE, normalLow = FALSE,
                   normalHigh = FALSE, overlapping = FALSE, x.plot.mode = "means",
                   y.plot.mode = "difference", plotProportionalBias = FALSE,
                   plotProportionalBias.se = TRUE, assume.differences.are.normal = TRUE)
```
Arguments

statistics.results
A list of statistics generated by the blandr.statistics function: see the function’s return list to see what variables are passed to this function

method1name (Optional) Plotting name for 1st method, default "Method 1"

method2name (Optional) Plotting name for 2nd method, default "Method 2"

plotTitle (Optional) Title name, default "Bland-Altman plot for comparison of 2 methods"

ciDisplay (Optional) TRUE/FALSE switch to plot confidence intervals for bias and limits of agreement, default is TRUE

ciShading (Optional) TRUE/FALSE switch to plot confidence interval shading to plot, default is TRUE

normalLow (Optional) If there is a normal range, entering a continuous variable will plot a vertical line on the plot to indicate its lower boundary

normalHigh (Optional) If there is a normal range, entering a continuous variable will plot a vertical line on the plot to indicate its higher boundary

overlapping (Optional) TRUE/FALSE switch to increase size of plotted point if multiple values using ggplot’s geom_count, default=FALSE. Not currently recommend until I can tweak the graphics to make them better

x.plot.mode (Optional) Switch to change x-axis from being plotted by means ("means") or by either 1st method ("method1") or 2nd method ("method2"). Default is "means". Anything other than "means" will switch to default mode.

y.plot.mode (Optional) Switch to change y-axis from being plotted by difference ("difference") or by proportion magnitude of measurements ("proportion"). Default is "difference". Anything other than "proportional" will switch to default mode.

plotProportionalBias (Optional) TRUE/FALSE switch. Plots a proportional bias line. Default is FALSE.

plotProportionalBias.se (Optional) TRUE/FALSE switch. If proportional bias line is drawn, switch to plot standard errors. See stat_smooth for details. Default is TRUE.

assume.differences.are.normal (Optional, not operationally used currently) Assume the difference of means has a normal distribution. Will be used to build further analyses

Value

ba.plot Returns a ggplot data set that can then be plotted

Author(s)

Deepankar Datta <deepankardatta@nhs.net>
Examples

# Generates two random measurements
measurement1 <- rnorm(100)
measurement2 <- rnorm(100)

# Generates a ggplot
# Do note the ggplot function wasn't meant to be used on it's own
# and is generally called via the bland.altman.display.and.draw function

# Passes data to the blandr.statistics function to generate Bland-Altman statistics
statistics.results <- blandr.statistics( measurement1, measurement2 )

# Generates a ggplot, with no optional arguments
blandr.plot.ggplot( statistics.results )

# Generates a ggplot, with title changed
blandr.plot.ggplot( statistics.results, plotTitle = "Bland-Altman example plot" )

# Generates a ggplot, with title changed, and confidence intervals off
blandr.plot.ggplot( statistics.results, plotTitle = "Bland-Altman example plot", ciDisplay = FALSE, ciShading = FALSE )

blandr.plot.limits

Bland-Altman plot limits for R

Description

Works out plot limits for the Bland-Altman plots. Depends on the blandr.statistics function in the package.

Usage

blandr.plot.limits(statistics.results, lowest_y_axis = FALSE, highest_y_axis = FALSE)

Arguments

statistics.results
A list of statistics generated by the blandr.statistics function: see the function’s return list to see what variables are passed to this function

lowest_y_axis
(Optional) Defaults to NULL If given a continuous variable will use this as the lower boundary of the y axis. Useful if need multiple plots with equivalent y-axes.

highest_y_axis
(Optional) Defaults to NULL If given a continuous variable will use this as the upper boundary of the y axis. Useful if need multiple plots with equivalent y-axes.
Value

- `x_upper` The upper limit of the X-axis
- `x_lower` The lower limit of the X-axis
- `y_upper` The upper limit of the Y-axis
- `y_lower` The lower limit of the Y-axis

Author(s)

Deepankar Datta <deepankardatta@nhs.net>

Examples

```r
# Generates two random measurements
measurement1 <- rnorm(100)
measurement2 <- rnorm(100)

# Passes data to the blandr.statistics function to generate Bland-Altman statistics
statistics.results <- blandr.statistics(measurement1, measurement2)

# Calls the function
blandr.plot.limits(statistics.results)
```

Description

Generates a combined histogram and density curve for Bland-Altman differences

Usage

```r
blandr.plot.normality(statistics.results)
```

Arguments

- `statistics.results`,
  A list of statistics generated by the `blandr.statistics` function: see the function’s return list to see what variables are passed to this function

Author(s)

Deepankar Datta <deepankardatta@nhs.net>
**blandr.plot.qq**

*Bland-Altman differences QQ plot*

**Description**
Generates a QQ plot for Bland-Altman differences

**Usage**

```r
blandr.plot.qq(statistics.results)
```

**Arguments**

- `statistics.results`
  
  A list of statistics generated by the `blandr.statistics` function: see the function’s return list to see what variables are passed to this function

**Author(s)**

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**blandr.plot.rplot**

*Bland-Altman plotting function, using basic R drawing functions*

**Description**

Draws a Bland-Altman plot using data calculated using the other functions, using the in-built R graphics

**Usage**

```r
blandr.plot.rplot(statistics.results, plot.limits, method1name = "Method 1", method2name = "Method 2", plotTitle = "Bland-Altman plot for comparison of 2 methods", annotate = FALSE, ciDisplay = TRUE, ciShading = TRUE, normalLow = FALSE, normalHigh = FALSE, point_size = 0.8)
```

**Arguments**

- `statistics.results`
  
  A list of statistics generated by the `blandr.statistics` function: see the function’s return list to see what variables are passed to this function

- `plot.limits`
  
  A list of statistics generated by the `blandr.plot.limits` function to define the extent of the x- and y- axes: see the function’s return list to see what variables are passed to this function
method1name  (Optional) Plotting name for 1st method, default 'Method 1'
method2name  (Optional) Plotting name for 2nd method, default 'Method 2'
plotTitle    (Optional) Title name, default 'Bland-Altman plot for comparison of 2 methods'
annotate     (Optional) TRUE/FALSE switch to provides annotations to plot, default=FALSE
ciDisplay    (Optional) TRUE/FALSE switch to plot confidence intervals for bias and limits of agreement, default=TRUE
ciShading    (Optional) TRUE/FALSE switch to plot confidence interval shading to plot, default=TRUE
normalLow    (Optional) If there is a normal range, entering a continuous variable will plot a vertical line on the plot to indicate its lower boundary
normalHigh   (Optional) If there is a normal range, entering a continuous variable will plot a vertical line on the plot to indicate its higher boundary
point_size   (Optional) Size of marker for each dot. Default is cex=0.8

Author(s)

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Examples

# Generates two random measurements
measurement1 <- rnorm(100)
measurement2 <- rnorm(100)

# Generates a basic plot
# Do note the blandr.plot.rplot function wasn't meant to be used on it's own
# and is generally called via the bland.altman.display.and.draw function

# Passes data to the blandr.statistics function to generate Bland-Altman statistics
statistics.results <- blandr.statistics(measurement1, measurement2)

# Passed data to the blandr.plot.limits function to generate plot limits
plot.limits <- blandr.plot.limits(statistics.results)

# Generates a basic plot, with no optional arguments
blandr.plot.rplot(statistics.results, plot.limits)

# Generates a basic plot, with title changed
blandr.plot.rplot(statistics.results, plot.limits, plotTitle = 'Bland-Altman example plot')

# Generates a basic plot, with title changed, and confidence intervals off
blandr.plot.rplot(statistics.results, plot.limits, plotTitle = 'Bland-Altman example plot',
                 ciDisplay = FALSE, ciShading = FALSE)
Description

Bland-Altman analysis function for R. Package created as existing functions don’t suit my needs, and don’t generate 95% confidence intervals for bias and limits of agreement. This base function calculates the basic statistics, and generates return values which can be used in the related blandr.display and bland.altmann.plot functions. However the return results can be used to generate a custom chart if desired.

Usage

blandr.statistics(method1, method2, sig.level = 0.95, LoA.mode = 1)

Arguments

method1 A list of numbers.
method2 A list of numbers.
sig.level (Optional) Two-tailed significance level. Expressed from 0 to 1. Defaults to 0.95.
LoA.mode (Optional) Switch to change how accurately the limits of agreement (LoA) are calculated from the bias and its standard deviation. The default is LoA.mode=1 which calculates LoA with the more accurate 1.96x multiplier. LoA.mode=2 uses the 2x multiplier which was used in the original papers. This should really be kept at default, except to double check calculations in older papers.

Value

means List of arithmetic mean of the two methods
differences List of differences of the two methods
method1 Returns the ‘method1’ list in the data frame if further evaluation is needed
method2 Returns the ‘method2’ list in the data frame if further evaluation is needed
sig.level Significance level supplied to the function
sig.level.convert.to.z Significance level convert to Z value
bias Bias of the two methods
biasUpperCI Upper confidence interval of the bias (based on significance level)
biasLowerCI Lower confidence interval of the bias (based on significance level)
biasStdDev
biasSEM Standard error for the bias
LOA_SEM Standard error for the limits of agreement
upperLOA Upper limit of agreement
upperLOA_upperCI Upper confidence interval of the upper limit of agreement
upperLOA_lowerCI Lower confidence interval of the upper limit of agreement
lowerLOA Lower limit of agreement
lowerLOA_upperCI Upper confidence interval of the lower limit of agreement
lowerLOA_lowerCI Lower confidence interval of the lower limit of agreement
proportion Differences/means*100
no.of.observations Number of observations
regression.equation A regression equation to help determine if there is any proportional bias
regression.fixed.slope The slope value of the regression equation
regression.fixed.intercept The intercept value of the regression equation

Note

The function will give similar answers when used on the original Bland-Altman PEFR data sets. They won't be exactly the same as (a) for 95% limits of agreement I have used +/-1.96, rather than 2, and (b) the computerised calculation means that the rounding that is present in each step of the original examples does not occur. This will give a more accurate answer, although I can understand why in 1986 rounding would occur at each step for ease of calculation.

The function depends on paired values.

It currently only can currently work out fixed bias.

Improvements for the future: proportional bias charts will need further work

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Last update 2016-02-04
Originally designed for LAVAS and CVLA

Author(s)

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References


Examples

# Generates two random measurements
measurement1 <- rnorm(100)
measurement2 <- rnorm(100)

# Generates Bland-Altman statistics data of the two measurements
blandr.statistics( measurement1 , measurement2 )

Sample comparison data from Giavarina (2015)

Description

This is sample comparison data, taken from Giavarina’s 2015 paper on Bland-Altman analysis. The data is from table 1 of the paper. I do not claim any copyright on the data - this is meant to allow testing of the function. I encourage future package authors to use the .rda file if they so wish.

Usage

data("giavarina.2015")

Format

A data frame with 30 observations on the following 5 variables.

Method.A a numeric vector
Method.B a numeric vector
Mean a numeric vector
Difference a numeric vector
Diff.Mean.Proportion a factor with levels

References


Examples

data(giavarina.2015)
jamoviBAanalysis  

_Bland-Altman Analysis_

**Description**

Bland-Altman Analysis

**Usage**

`jamoviBAanalysis(data, method1, method2, ciDisplay = TRUE, ciShading = TRUE, plotProportionalBias = FALSE, plotProportionalBias.se = TRUE, overlapping = FALSE)`

**Arguments**

- `data`
- `method1`
- `method2`
- `ciDisplay`
- `ciShading`
- `plotProportionalBias`
- `plotProportionalBias.se`
- `overlapping`

**Value**

A results object containing:

- `results$table` a table
- `results$plot` an image

Tables can be converted to data frames with `asDF` or `as.data.frame`. For example:

```
results$table$asDF
as.data.frame(results$table)
```

jamoviBAplotHistogram  

_Differences Histogram and Density Curve_
jamoviBAplotQQ

Description
Differences Histogram and Density Curve

Usage
jamoviBAplotHistogram(data, method1, method2)

Arguments
data
method1
method2

Value
A results object containing:

```
results$plot an image
```

jamoviBAplotQQ

Description
Differences Q-Q Plot

Usage
jamoviBAplotQQ(data, method1, method2)

Arguments
data
method1
method2

Value
A results object containing:

```
results$plot an image
```
jamoviBAstats  

**Bland-Altman Raw Statistics**

**Description**

Bland-Altman Raw Statistics

**Usage**

jamoviBAstats(data, method1, method2)

**Arguments**

- data
- method1
- method2

**Value**

A results object containing:

```r
results$text
```

a preformatted
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