Package ‘blandr’

June 9, 2024

Title  Bland-Altman Method Comparison
Version  0.6.0
Date  2024-06-09

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  glue, ggplot2, knitr, stringr, jmvcore (>= 0.8.5), markdown, rmarkdown
Suggests  testthat

SystemRequirements  pandoc (>=1.12.3)

VignetteBuilder  knitr

Collate  'blandr.data.preparation.r' 'blandr.dataset.fibre.r'
'blandr.data.preparation.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'
RoxygenNote 7.3.1
Language en-GB
NeedsCompilation no
Author Deepankar Datta [aut, cre],
        Jonathon Love [ctb]
Maintainer Deepankar Datta <deepankar.datta@gmail.com>
Repository CRAN
Date/Publication 2024-06-09 20:40:02 UTC

Contents

  blandr.alman.PEFR.1986 ........................................ 3
  blandr.data.preparation ........................................ 3
  blandr.dataset.fibre .......................................... 4
  blandr.dataset.load ........................................... 5
  blandr.dataset.o2sats ........................................ 6
  blandr.dataset.pefr .......................................... 7
  blandr.dataset.sbp ......................................... 8
  blandr.display.and.draw ..................................... 9
  blandr.display.and.plot .................................... 10
  blandr.draw .................................................. 12
  blandr.method.comparison .................................. 14
  blandr.output.report ....................................... 15
  blandr.output.text .......................................... 16
  blandr.plot .................................................. 17
  blandr.plot.ggplot ......................................... 18
  blandr.plot.limits .......................................... 20
  blandr.plot.normality ...................................... 22
  blandr.plot.qq ............................................. 22
  blandr.plot.rplot .......................................... 23
  blandr.statistics ........................................... 24
  blandr.statistics.formula .................................. 26
  giavarina.2015 ............................................... 27
  jamoviBAanalysis .......................................... 28
  jamoviBAplotHistogram ....................................... 29
  jamoviBAplotQQ ............................................. 30
  jamoviBAstats .............................................. 30
  print.blandr ............................................... 31

Index 32
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
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
data(bland.altman.PEFR.1986)

blandr.data.preparation
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
blandr.data.preparation(method1, method2, sig.level)
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)

Deepankar Datta deepankar.datta@gmail.com

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.
Author(s)

Deepankar Datta deepankar.datta@gmail.com

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

element dataset 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)
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 deepankar.datta@gmail.com

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**

```r
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 [deepankar.datta@gmail.com](mailto:deepankar.datta@gmail.com)

**References**

- [https://www-users.york.ac.uk/~mb55/datasets/pefr.dct](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](https://www-users.york.ac.uk/~mb55/datasets/datasets.htm) - Martin Bland’s example data-set webpage

**Examples**

```r
blandr.dataset.pefr()
pefr.data <- blandr.dataset.pefr()
```
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 deepankar.datta@gmail.com

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 web-page


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**

    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.

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 deepankar.datta@gmail.com

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' )

blandr.display.and.plot

(DEPRECATED) Bland-Altman display and plot for R

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
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**

```r
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 vector of numbers corresponding to the results from method 1.
- `method2`: A vector of numbers corresponding to the results from method 2.
- `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
blandr.method.comparison

Bland-Altman method comparison

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)
blandr.output.report

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 deepankar.datta@gmail.com

References

  Based on: (1) Bland, J. M., & Altman, D. (1986). Statistical methods for assessing agreement be-
  tween two methods of clinical measurement. The Lancet, 327(8476), 307-310. http://dx.doi.org/10.1016/S0140-
  6736(86)90837-8

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)

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 rMarkdwon to save the contents. I couldn’t add this to the function as it’s not allowed in CRAN. On the other hand 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 deepankar.datta@gmail.com

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 rMarkdwon document
#
# rmarkdown::run( file = "blandr_report_template.Rmd" ,
# render_args = list( runtime = "shiny" ,
# params = list( method1 = method1 ,
#               method2 = method2 ) ) )
# END OF NOT RUN
```

blandr.output.text (DEPRECATED) Bland-Altman summary statistics display function

Description

(DEPRECATED) 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)
blandr.plot

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 deepankar.datta@gmail.com

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 vector of numbers corresponding to the results from method 1.
- **method2**: A vector of numbers corresponding to the results from method 2.
- **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.
- **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 deepankar.datta@gmail.com

---

**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

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 deepankar.datta@gmail.com

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 deepankar.datta@gmail.com

Examples

# 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 )
blandr.plot.normality  \textit{Bland-Altman histogram and density plot}

\textbf{Description}

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

\textbf{Usage}

\begin{verbatim}
  blandr.plot.normality(statistics.results)
\end{verbatim}

\textbf{Arguments}

\begin{verbatim}
  statistics.results
\end{verbatim}

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

\textbf{Author(s)}

Deepankar Datta \texttt{deepankar.datta@gmail.com}

\hline
\hline
blandr.plot.qq  \textit{Bland-Altman differences QQ plot}

\textbf{Description}

Generates a QQ plot for Bland-Altman differences

\textbf{Usage}

\begin{verbatim}
  blandr.plot.qq(statistics.results)
\end{verbatim}

\textbf{Arguments}

\begin{verbatim}
  statistics.results
\end{verbatim}

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

\textbf{Author(s)}

Deepankar Datta \texttt{deepankar.datta@gmail.com}
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

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
blandr.statistics

Author(s)
Deepankar Datta deepankar.datta@gmail.com

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 )

blandr.statistics      Bland-Altman statistics for R

Description

Bland-Altman analysis function for R. Package created as existing functions don’t suit my needs,
and don’t generate 95\% for bias and limits of agreement. This base function calculates the ba-
sic 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  Either a formula, or a vector of numbers corresponding to the results from
          method 1.
method2  A vector of numbers corresponding to the results from method 2. Only needed
          if X is a vector.
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

An object of class 'blandr' is returned. This is a list with the following elements:

- 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: Standard deviation for the bias
- 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%

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

Started 2015-11-14

Last update 2016-02-04

Originally designed for LAVAS and CVLA

Author(s)

Deepankar Datta deepankar.datta@gmail.com

References


Examples

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

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

---

**blandr.statistics.formula**

*Bland-Altman statistics for R - submitting data as a formula*

**Description**

If data is supplied as a formula, the function interprets it and then passes it through to the main blandr.statistics function.

**Usage**

```r
blandr.statistics.formula(formula, data = parent.frame(), ...)
```
Arguments

- formula: A formula, to be eventually passed to the blandr.statistics function
- data: A data frame
- ... other arguments.

Note

This was initially packaged in the same file as the blandr.statistics function. Changes to R package checks made it easier to separate it out, but functionally it has not changed.

Author(s)

Deepankar Datta deepankar.datta@gmail.com

Examples

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

# Generates Bland-Altman statistics data of the two measurements using the formula interface
blandr.statistics.formula( measurement2 ~ measurement1 )

# Example with a real data set

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.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 .
jamoviBAplotHistogram

Value

A results object containing:

\[
\begin{align*}
\text{results$table} & \quad \text{a table} \\
\text{results$plot} & \quad \text{an image}
\end{align*}
\]

Tables can be converted to data frames with asDF or \texttt{as.data.frame}. For example:

\[
\begin{align*}
\text{results$table$asDF} \\
\text{as.data.frame(results$table)}
\end{align*}
\]

jamoviBAplotHistogram \quad \text{Differences Histogram and Density Curve}

Description

Differences Histogram and Density Curve

Usage

jamoviBAplotHistogram(data, method1, method2)

Arguments

\begin{itemize}
  \item \texttt{data} .
  \item \texttt{method1} .
  \item \texttt{method2} .
\end{itemize}

Value

A results object containing:

\[
\begin{align*}
\text{results$plot} & \quad \text{an image}
\end{align*}
\]
jamoviBAPlotQQ  

**Differences Q-Q Plot**

**Description**
Differences Q-Q Plot

**Usage**
jamoviBAPlotQQ(data, method1, method2)

**Arguments**
- **data** .
- **method1** .
- **method2** .

**Value**
A results object containing:

\[
\text{results$plot} \quad \text{an image}
\]

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
```

preformatted

Description

Compactly print the statistics used to construct a Bland-Altman plot

Usage

```r
## S3 method for class 'blandr'
print(x, digits = getOption("digits"), ...)
```

Arguments

- `x`: the results from `blandr.statistics`
- `digits`: number of significant digits to be used.
- `...`: other arguments.

Author(s)

Deepankar Datta [deepankar.datta@gmail.com](mailto:deepankar.datta@gmail.com)

Examples

```r
results
```
Index

* datasets
  - bland.altman.PEFR.1986, 3
  - giavarina.2015, 27
  - as.data.frame, 29
  - bland.altman.PEFR.1986, 3
  - blandr.data.preparation, 3
  - blandr.dataset.fibre, 4
  - blandr.dataset.load, 5
  - blandr.dataset.o2sats, 6
  - blandr.dataset.pefr, 7
  - blandr.dataset.sbp, 8
  - blandr.display.and.draw, 9
  - blandr.display.and.plot, 10
  - blandr.draw, 12
  - blandr.method.comparison, 14
  - blandr.output.report, 15
  - blandr.output.text, 16
  - blandr.plot, 17
  - blandr.plot.ggplot, 18
  - blandr.plot.limits, 20
  - blandr.plot.normality, 22
  - blandr.plot.qq, 22
  - blandr.plot.rplot, 23
  - blandr.statistics, 24
  - blandr.statistics.formula, 26

  giavarina.2015, 27

  jamoviBAanalysis, 28
  jamoviBAPlotHistogram, 29
  jamoviBAPlotQQ, 30
  jamoviBASTATS, 30

  print.blandr, 31