

Package ‘MethodCompare’

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Title Evaluating Bias and Precision in Method Comparison Studies

Version 1.1.0

Description Evaluate bias and precision in method comparison studies. One provides measurements for each method and it takes care of the estimates. Multiple plots to evaluate bias, precision and compare methods.

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BugReports <https://github.com/UBERLULU/MethodCompare/issues>

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Author Thomas Blomet [aut, cre],
Mingkai Peng [aut],
Patrick Taffé [aut],
Tyler Williamson [aut]

Maintainer Thomas Blomet <thomas.blomet@alumni.epfl.ch>

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Contents

agreement0	2
agreement1	3
bias_plot	3
compare_plot	4
data1	5

data2	6
data3	7
measure_compare	8
mse	9
pct_agreement0	10
pct_agreement1	10
precision_plot	11
sqrt_mse	12
total_bias_plot	12

Index	14
--------------	-----------

agreement0	<i>Plot the agreement before recalibration</i>
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Description

This function draws the "agreement plot" before recalibration, which is used to visually appraise the degree of agreement between the new and reference methods, before recalibration of the new method. It is obtained by graphing a scatter plot of $y_1 - y_2$ (difference of the methods) versus the BLUP of the latent trait, x , along with the bias and 95% limits of agreement with their 95% simultaneous confidence bands. The function adds a second scale on the right axis, showing the percentage of agreement index.

Usage

```
agreement0(object, rarea = FALSE)
```

Arguments

object	list returned by measure_compare function.
rarea	if TRUE, draw the plot with shading areas between the confidence bands.

Examples

```
### Load the data
data(data1)
### Analysis
measure_model <- measure_compare(data1, nb_simul=100)
### Plot the agreement without recalibration
agreement0(measure_model)
```

`agreement1`*Plot the agreement after recalibration*

Description

This function draws the "agreement plot" after recalibration, which is used to visually appraise the degree of agreement between the new and reference methods, before recalibration of the new method. It is obtained by graphing a scatter plot of $y_1 - y_2$ (difference of the methods) versus the BLUP of the latent trait, x , along with the bias and 95% limits of agreement with their 95% simultaneous confidence bands. The function adds a second scale on the right axis, showing the percentage of agreement index.

Usage

```
agreement1(object, rarea = FALSE)
```

Arguments

`object` list returned by `measure_compare` function.
`rarea` if TRUE, draw the plot with shading areas between the confidence bands.

Examples

```
### Load the data
data(data1)
### Analysis
measure_model <- measure_compare(data1, nb_simul=100)
### Plot the agreement after recalibration
agreement0(measure_model)
```

`bias_plot`*Plot the bias and measurements*

Description

This function draws the "bias plot", which is used to visually assess the bias of the new method relative to the reference method. It is obtained by graphing a scatter plot of y_1 (new method) and y_2 (reference method) versus the BLUP of the latent trait, x , along with the two regression lines. The function adds a second scale on the right axis, showing the relationship between the estimated amount of bias and BLUP of the latent trait, x .

Usage

```
bias_plot(object)
```

Arguments

object list returned by [measure_compare](#) function.

Examples

```
### Load the data
data(data1)
### Analysis
measure_model <- measure_compare(data1, nb_simul=100)
### Plot the bias
bias_plot(measure_model)
```

compare_plot *Plot used to visualize the recalibration of the new method after estimating the bias*

Description

This function allows the visualization of the bias-corrected values (i.e. recalibrated values, variable `y1_corr`) of the new measurement method.

Usage

```
compare_plot(object)
```

Arguments

object list returned by [measure_compare](#) function.

Examples

```
### Load the data
data(data1)
### Analysis
measure_model <- measure_compare(data1, nb_simul=100)
### Plot the bias
compare_plot(measure_model)
```

data1	<i>Simulated dataset 1</i>
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Description

In the simulated dataset 1, each subject has 1 to 3 measurement values from the new method and 10 to 20 measurement values from the reference method. Compared to the reference method, the new method has differential bias of 4 and proportional bias of 0.8. Variance of the new method is smaller than that for the reference method.

Usage

```
data1
```

Format

```
data1:
```

An object of class `data.frame` with 1468 rows and 3 columns

Details

A data frame with 3 variables:

`id` identification number for subjects

`y1` values from the new measurement method

`y2` values from the reference method

Dataset 1 was created based on the following equations:

$$y_{1i} = 4 + 0.8x_i + \varepsilon_{1i}, \quad \varepsilon_{1i} | x_i \sim N(0, (0.2x_i)^2)$$

$$y_{2i} = x_i + \varepsilon_{2i}, \quad \varepsilon_{2i} | x_i \sim N(0, (1.75 + 0.08x_i)^2)$$

$$x_i \sim Uniform[25 - 45]$$

for $i = 1, \dots, 100$ and the number of repeated measurements for each subject i from the reference standard was $n_{2i} \sim Uniform[10, 20]$ and $n_{1i} \sim Uniform[1, 3]$ for the new measurement method.

 data2

 Simulated dataset 2

Description

In the simulated dataset 2, each subject has 10 to 20 measurement values from the new method and 10 to 20 measurement values from the reference method. Compared to the reference method, the new method has differential bias of 4 and proportional bias of 0.8. Variance of the new method is smaller than that for the reference method.

Usage

data2

Format

data2:

An object of class `data.frame` with 1680 rows and 3 columns

Details

A data frame with 3 variables:

id identification number for subjects

y1 values from the new measurement method

y2 values from the reference method

Dataset 1 was created based on the following equations:

$$y_{1i} = 4 + 0.8x_i + \varepsilon_{1i}, \quad \varepsilon_{1i} \mid x_i \sim N(0, (0.2x_i)^2)$$

$$y_{2i} = x_i + \varepsilon_{2i}, \quad \varepsilon_{2i} \mid x_i \sim N(0, (1.75 + 0.08x_i)^2)$$

$$x_i \sim \text{Uniform}[20 - 100]$$

for $i = 1, \dots, 100$ and the number of repeated measurements for each subject i from the reference standard was $n_{2i} \sim \text{Uniform}[10, 20]$ and $n_{1i} \sim \text{Uniform}[10, 20]$ for the new measurement method.

 data3

 Simulated dataset 3

Description

In the simulated dataset 3, each subject has 10 to 20 measurement values from the new method and 10 to 20 measurement values from the reference method. Compared to the reference method, the new method has differential bias of 1 and proportional bias of 0.9. Variance of the new method is smaller than that for the reference method.

Usage

data3

Format

data3:

An object of class `data.frame` with 1682 rows and 3 columns

Details

A data frame with 3 variables:

id identification number for subjects

y1 values from the new measurement method

y2 values from the reference method

Dataset 1 was created based on the following equations:

$$y_{1i} = 1 + 0.9x_i + \varepsilon_{1i}, \quad \varepsilon_{1i} \mid x_i \sim N(0, (1 + 0.04x_i)^2)$$

$$y_{2i} = x_i + \varepsilon_{2i}, \quad \varepsilon_{2i} \mid x_i \sim N(0, (1.75 + 0.08x_i)^2)$$

$$x_i \sim \text{Uniform}[20 - 100]$$

for $i = 1, \dots, 100$ and the number of repeated measurements for each subject i from the reference standard was $n_{2i} \sim \text{Uniform}[10, 20]$ and $n_{1i} \sim \text{Uniform}[10, 20]$ for the new measurement method.

measure_compare	<i>Estimation of the amount of bias of the new measurement method relative to the reference method</i>
-----------------	--

Description

measure_compare() implements the methodology reported in the paper: Taffé P. Effective plots to assess bias and precision in method comparison studies. *Stat Methods Med Res* 2018;27:1650-1660. Other relevant references: Taffé P, Peng M, Stagg V, Williamson T. Biasplot: A package to effective plots to assess bias and precision in method comparison studies. *Stata J* 2017;17:208-221. Taffé P, Peng M, Stagg V, Williamson T. MethodCompare: An R package to assess bias and precision in method comparison studies. *Stat Methods Med Res* 2019;28:2557-2565. Taffé P, Halfon P, Halfon M. A new statistical methodology to assess bias and precision overcomes the defects of the Bland & Altman method. *J Clin Epidemiol* 2020;124:1-7. Taffé P. Assessing bias, precision, and agreement in method comparison studies. *Stat Methods Med Res* 2020;29:778-796. Taffé P. When can the Bland-Altman limits of agreement method be used and when it should not be used. *J Clin Epidemiol* 2021; 137:176-181.

Usage

```
measure_compare(
  data,
  new = "y1",
  ref = "y2",
  id = "id",
  nb_simul = 1000,
  if_value = NULL
)
```

Arguments

data	a required data frame containing the identification number of the subject (id), the measurement values from the new method (y1) and those from the reference method (y2).
new	an optional string. The column name containing the measurements of the new measurement method.
ref	an optional string. The column name containing the measurements of the reference method (at least two measurements per subject).
id	an optional string. The column name containing the subject identification numbers.
nb_simul	an optional number. The number of simulations used for simultaneous confidence bands.
if_value	an optional number. Restrict the study to observed measurement greater than the provided value, i.e., $y1 \geq \text{if_value} \ \&\& \ y2 \geq \text{if_value}$.

Value

The function returns a list with the following items:

- `models`: a list of models fitted in estimation procedure
- `data`: the original data frame with renamed columns and additional computed data
- `sim_params`: estimated model coefficients used afterward
- `nb_simul`: the number of simulations used for confidence bands simulations
- `bias`: differential and proportional biases for new method and the associated 95 percent confidence intervals
- `methods`: a list of methods names provided by the user

Examples

```
### Load the data
data(data1)
### Analysis
measure_model <- measure_compare(data1, nb_simul=100)
```

mse

Plot the mean squared errors

Description

This function draws the "MSE plot", which is used to compare the precision of the two measurement methods without recalibrating the new method. It is obtained by graphing the mean squared errors of y_1 (new method) and y_2 (reference method) versus the BLUP of the latent trait, x , along with their 95% simultaneous confidence bands.

Usage

```
mse(object, rarea = FALSE)
```

Arguments

`object` list returned by `measure_compare` function.

`rarea` if TRUE, draw the plot with shading areas between the confidence bands.

Examples

```
### Load the data
data(data1)
### Analysis
measure_model <- measure_compare(data1, nb_simul=100)
### Plot the mean squared errors
mse(measure_model)
```

pct_agreement0 *Plot the percentage agreement before recalibration*

Description

This function draws the "percentage agreement plot" before recalibration, which shows the amount of percentage agreement. It is obtained by graphing the percentage agreement index before recalibration versus the BLUP of the latent trait, x , along with its 95% simultaneous confidence bands.

Usage

```
pct_agreement0(object)
```

Arguments

object list returned by [measure_compare](#) function.

Examples

```
### Load the data
data(data1)
### Analysis
measure_model <- measure_compare(data1, nb_simul=100)
### Plot the percentage agreement without recalibration
pct_agreement0(measure_model)
```

pct_agreement1 *Plot the percentage agreement after recalibration*

Description

This function draws the "percentage agreement plot" after recalibration, which shows the amount of percentage agreement. It is obtained by graphing the percentage agreement index after recalibration versus the BLUP of the latent trait, x , along with its 95% simultaneous confidence bands.

Usage

```
pct_agreement1(object)
```

Arguments

object list returned by [measure_compare](#) function.

Examples

```
### Load the data
data(data1)
### Analysis
measure_model <- measure_compare(data1, nb_simul=100)
### Plot the percentage agreement after recalibration
pct_agreement0(measure_model)
```

precision_plot	<i>Plot the precision of the methods</i>
----------------	--

Description

This function draws the "precision plot", which allows the visual comparison of the precision (i.e. standard deviation) of the new measurement method with the reference standard by creating a scatter plot of the estimated standard deviations, along with their 95% simultaneous confidence bands, against the best linear prediction (BLUP) of the true latent trait, x .

Usage

```
precision_plot(object, object2 = NULL, log = FALSE, rarea = FALSE)
```

Arguments

object	list returned by measure_compare function.
object2	(optional) returned by measure_compare function. If provided, will plot a second precision estimate.
log	if TRUE, guarantee the simultaneous confidence bands around the standard deviation of measurement errors to be strictly positive.
rarea	if TRUE, draw the plot with shading areas between the confidence bands.

Examples

```
### Load the data
data(data1)
### Analysis
measure_model <- measure_compare(data1, nb_simul=100)
### Plot the precision of the two methods
precision_plot(measure_model)
```

sqrt_mse	<i>Plot the square root of the mean squared errors</i>
----------	--

Description

This function draws the "sqrt(MSE) plot", which is used to compare the precision of the two measurement methods without recalibrating the new method. It is obtained by graphing the square root mean squared errors of y1 (new method) and y2 (reference method) versus the BLUP of the latent trait, x, along with their 95% simultaneous confidence bands.

Usage

```
sqrt_mse(object, rarea = FALSE)
```

Arguments

object	list returned by measure_compare function.
rarea	if TRUE, draw the plot with shading areas between the confidence bands.

Examples

```
### Load the data
data(data1)
### Analysis
measure_model <- measure_compare(data1, nb_simul=100)
### Plot the square root mean squared errors
sqrt_mse(measure_model)
```

total_bias_plot	<i>Plot total bias</i>
-----------------	------------------------

Description

This function draws the "total bias plot", which is used to visually assess the amount of bias. It is obtained by graphing the bias versus the BLUP of the latent trait, x, along with the 95% simultaneous confidence bands.

Usage

```
total_bias_plot(object, object2 = NULL, rarea = FALSE)
```

Arguments

object	list returned by measure_compare function.
object2	(optional) returned by measure_compare function. If provided, will plot a second total bias estimate.
rarea	if TRUE, draw the plot with shading areas between the confidence bands.

Examples

```
### Load the data
data(data1)
### Analysis
measure_model <- measure_compare(data1, nb_simul=100)
### Plot the total bias
total_bias_plot(measure_model)
```

Index

* datasets

data1, [5](#)

data2, [6](#)

data3, [7](#)

agreement0, [2](#)

agreement1, [3](#)

bias_plot, [3](#)

compare_plot, [4](#)

data1, [5](#)

data2, [6](#)

data3, [7](#)

measure_compare, [2-4](#), [8](#), [9-12](#)

mse, [9](#)

pct_agreement0, [10](#)

pct_agreement1, [10](#)

precision_plot, [11](#)

sqrt_mse, [12](#)

total_bias_plot, [12](#)