Package 'MethodCompare'

July 21, 2025

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.

License GPL (>= 3)

Encoding UTF-8

RoxygenNote 7.3.1

Imports estimatr, graphics, lme4, Matrix, mfp, rockchalk, stats

Depends R (>= 2.10)

LazyData true

URL https://github.com/UBERLULU/MethodCompare

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

NeedsCompilation no

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Repository CRAN

Date/Publication 2025-02-09 14:00:02 UTC

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agreement0   *Plot the agreement before recalibration*

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 y1-y2 (difference of the methods) versus the
BLUP of the latent trait, x, along with the bias and 95% limits of agreement with their 95% simulta-
neous 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 y1-y2 (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 y1 (new method) and y2 (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 esti-
                            mating 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 *Simulated dataset 1*

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 measuremment method

y2 values from the reference method

Dataset 1 was created based on the following equations:

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

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

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

for $i = 1, \ldots, 100$ 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 measuremment method

y2 values from the reference method

Dataset 1 was created based on the following equations:

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

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

$$x_i \sim Uniform[20 - 100]$$

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

y2 values from the reference method

Dataset 1 was created based on the following equations:

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

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

$$x_i \sim Uniform[20 - 100]$$

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

---

measure_compare	*Estimation of the amount of bias of the new measurement method relative to the reference method*

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 >= if_value && y2 >= 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 y1 (new method) and y2 (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 *Plot the precision of the methods*

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 *Plot the square root of the mean squared errors*

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 *Plot total bias*

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)
```

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