

Package ‘SimplyAgree’

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Type Package

Title Flexible and Robust Agreement and Reliability Analyses

Version 0.1.2

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Description Reliability and agreement analyses often have limited software support. Therefore, this package was created to make agreement and reliability analyses easier for the average researcher. The functions within this package include simple tests of agreement, agreement analysis for nested and replicate data, and provide robust analyses of reliability. In addition, this package contains a set of functions to help when planning studies looking to assess measurement agreement. For robust analyses of agreement, limits of agreement through a bootstrap method can also be calculated.

URL <https://aaroncaldwell.us/SimplyAgree/>

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agree_coef	<i>Agreement Coefficients</i>
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Description

agree_coef produces inter-rater reliability or "agreement coefficients" as described by Gwet.

Usage

```
agree_coef(
  wide = TRUE,
  col.names = NULL,
  measure,
  item,
  id,
  data,
  weighted = FALSE,
  conf.level = 0.95
)
```

Arguments

wide	Logical value (TRUE or FALSE) indicating if data is in a "wide" format. Default is TRUE.
col.names	If wide is equal to TRUE then col.names is a list of the column names containing the measurements for reliability analysis.
measure	Name of column containing the measurement of interest.
item	Name of column containing the items. If this is an inter-rater reliability study then this would indicate the rater (e.g., rater1, rater2, rater3, etc).
id	Column with subject identifier.
data	Data frame with all data.
weighted	Logical value (TRUE or FALSE) indicating whether to weight the responses. If TRUE (default is FALSE) then quadratic weights are utilized. This option should be set to TRUE for ordinal or continuous responses.
conf.level	the confidence level required. Default is 95%.

Value

Returns single data frame of inter-rater reliability coefficients.

References

Gwet, K.L. (2014, ISBN:978-0970806284). "Handbook of Inter-Rater Reliability," 4th Edition. Advanced Analytics, LLC. Gwet, K. L. (2008). "Computing inter-rater reliability and its variance in the presence of high agreement," British Journal of Mathematical and Statistical Psychology, 61, 29-48.

Examples

```
data('reps')
agree_coef(data = reps, wide = TRUE, col.names = c("x","y"), weighted = TRUE)
```

agree_nest

Tests for Absolute Agreement with Nested Data

Description

agree_nest produces an absolute agreement analysis for data where there is multiple observations per subject but the mean varies within subjects as described by Zou (2013). Output mirrors that of agree_test but CCC is calculated via U-statistics.

Usage

```
agree_nest(
  x,
  y,
  id,
  data,
  delta,
  agree.level = 0.95,
  conf.level = 0.95,
  TOST = TRUE,
  prop_bias = FALSE
)
```

Arguments

x	Name of column with first measurement
y	Name of other column with the other measurement to compare to the first.
id	Column with subject identifier
data	Data frame with all data
delta	The threshold below which methods agree/can be considered equivalent, can be in any units. Equivalence Bound for Agreement.
agree.level	the agreement level required. Default is 95%. The proportion of data that should lie between the thresholds, for 95% limits of agreement this should be 0.95.
conf.level	the confidence level required. Default is 95%.
TOST	Logical indicator (TRUE/FALSE) of whether to use two one-tailed tests for the limits of agreement. Default is TRUE.
prop_bias	Logical indicator (TRUE/FALSE) of whether proportional bias should be considered for the limits of agreement calculations.

Value

Returns single simple_agree class object with the results of the agreement analysis.

"loa" A data frame of the limits of agreement including the average difference between the two sets of measurements, the standard deviation of the difference between the two sets of measurements and the lower and upper confidence limits of the difference between the two sets of measurements.

"h0_test" Decision from hypothesis test.

"ccc.xy" Lin's concordance correlation coefficient and confidence intervals using U-statistics.
Warning: if underlying value varies this estimate will be inaccurate.

"call" the matched call

"var_comp" Table of Variance Components

"class" The type of simple_agree analysis

References

Zou, G. Y. (2013). Confidence interval estimation for the Bland–Altman limits of agreement with multiple observations per individual. *Statistical methods in medical research*, 22(6), 630-642.

King, TS and Chinchilli, VM. (2001). A generalized concordance correlation coefficient for continuous and categorical data. *Statistics in Medicine*, 20, 2131:2147.

King, TS; Chinchilli, VM; Carrasco, JL. (2007). A repeated measures concordance correlation coefficient. *Statistics in Medicine*, 26, 3095:3113.

Carrasco, JL; Phillips, BR; Puig-Martinez, J; King, TS; Chinchilli, VM. (2013). Estimation of the concordance correlation coefficient for repeated measures using SAS and R. *Computer Methods and Programs in Biomedicine*, 109, 293-304.

Examples

```
data('reps')
agree_nest(x = "x", y = "y", id = "id", data = reps, delta = 2)
```

agree_np

Nonparametric Test for Limits of Agreement

Description

agree_np A non-parametric approach to limits of agreement. The hypothesis test is based on binomial proportions within the maximal allowable differences, and the limits are calculated with quantile regression.

Usage

```
agree_np(
  x,
  y,
  id = NULL,
  data,
  delta = NULL,
  prop_bias = FALSE,
  TOST = TRUE,
  agree.level = 0.95,
  conf.level = 0.95
)
```

Arguments

x	Name of column with first measurement.
y	Name of other column with the other measurement to compare to the first.
id	Column with subject identifier with samples are taken in replicates.
data	Data frame with all data.

delta	The threshold below which methods agree/can be considered equivalent and this argument is required. Equivalence Bound for Agreement or Maximal Allowable Difference.
prop_bias	Logical indicator (TRUE/FALSE) of whether proportional bias should be considered for the limits of agreement calculations.
TOST	Logical indicator (TRUE/FALSE) of whether to use two one-tailed tests for the limits of agreement. Default is TRUE.
agree.level	the agreement level required. Default is 95%. The proportion of data that should lie between the thresholds, for 95% limits of agreement this should be 0.95.
conf.level	the confidence level required. Default is 95%.

Value

Returns simple_agree object with the results of the agreement analysis.

"loa" A data frame of the limits of agreement.

"agee" A data frame of the binomial proportion of results in agreement.

"h0_test" Decision from hypothesis test.

"qr_mod" The quantile regression model.

"call" The matched call

References

Bland, J. M., & Altman, D. G. (1999). Measuring agreement in method comparison studies. In *Statistical Methods in Medical Research* (Vol. 8, Issue 2, pp. 135–160). SAGE Publications. <<https://doi.org/10.1177/096228029900800204>>

Examples

```
data('reps')
agree_np(x = "x", y = "y", id = "id", data = reps, delta = 2)
```

agree_reps

Tests for Absolute Agreement with Replicates

Description

agree_nest produces an absolute agreement analysis for data where there is multiple observations per subject but the mean does not vary within subjects as described by Zou (2013). Output mirrors that of agree_test but CCC is calculated via U-statistics.

Usage

```
agree_reps(
  x,
  y,
  id,
  data,
  delta,
  agree.level = 0.95,
  conf.level = 0.95,
  prop_bias = FALSE,
  TOST = TRUE
)
```

Arguments

x	Name of column with first measurement
y	Name of other column with first measurement
id	Column with subject identifier
data	Data frame with all data
delta	The threshold below which methods agree/can be considered equivalent, can be in any units. Equivalence Bound for Agreement.
agree.level	the agreement level required. Default is 95%. The proportion of data that should lie between the thresholds, for 95% limits of agreement this should be 0.95.
conf.level	the confidence level required. Default is 95%.
prop_bias	Logical indicator (TRUE/FALSE) of whether proportional bias should be considered for the limits of agreement calculations.
TOST	Logical indicator (TRUE/FALSE) of whether to use two one-tailed tests for the limits of agreement. Default is TRUE.

Value

Returns single list with the results of the agreement analysis.

"loa" a data frame of the limits of agreement including the average difference between the two sets of measurements, the standard deviation of the difference between the two sets of measurements and the lower and upper confidence limits of the difference between the two sets of measurements.

"h0_test" Decision from hypothesis test.

"ccc.xy" Lin's concordance correlation coefficient and confidence intervals using U-statistics.

"call" The matched call.

"var_comp" Table of Variance Components.

"class" The type of simple_agree analysis.

References

Zou, G. Y. (2013). Confidence interval estimation for the Bland–Altman limits of agreement with multiple observations per individual. *Statistical methods in medical research*, 22(6), 630-642.

King, TS and Chinchilli, VM. (2001). A generalized concordance correlation coefficient for continuous and categorical data. *Statistics in Medicine*, 20, 2131:2147.

King, TS; Chinchilli, VM; Carrasco, JL. (2007). A repeated measures concordance correlation coefficient. *Statistics in Medicine*, 26, 3095:3113.

Carrasco, JL; Phillips, BR; Puig-Martinez, J; King, TS; Chinchilli, VM. (2013). Estimation of the concordance correlation coefficient for repeated measures using SAS and R. *Computer Methods and Programs in Biomedicine*, 109, 293-304.

Examples

```
data('reps')
agree_reps(x = "x", y = "y", id = "id", data = reps, delta = 2)
```

agree_test

Tests for Absolute Agreement

Description

The `agree_test` function calculates a variety of agreement statistics. The hypothesis test of agreement is calculated by the method described by Shieh (2019). Bland-Altman limits of agreement, and confidence intervals, are also provided (Bland & Altman 1999; Bland & Altman 1986). In addition, the concordance correlation coefficient (CCC; Lin 1989) is additional part of the output.

Usage

```
agree_test(
  x,
  y,
  delta,
  conf.level = 0.95,
  agree.level = 0.95,
  TOST = TRUE,
  prop_bias = FALSE
)
```

Arguments

<code>x</code>	Vector with first measurement
<code>y</code>	Vector with second measurement
<code>delta</code>	The threshold below which methods agree/can be considered equivalent, can be in any units. Often referred to as the "Equivalence Bound for Agreement" or "Maximal Allowable Difference".

conf.level	the confidence level required. Default is 95%.
agree.level	the agreement level required. Default is 95%. The proportion of data that should lie between the thresholds, for 95% limits of agreement this should be 0.95.
TOST	Logical indicator (TRUE/FALSE) of whether to use two one-tailed tests for the limits of agreement. Default is TRUE.
prop_bias	Logical indicator (TRUE/FALSE) of whether proportional bias should be considered for the limits of agreement calculations.

Value

Returns single list with the results of the agreement analysis.

"shieh_test" The TOST hypothesis test as described by Shieh.

"ccc.xy" Lin's concordance correlation coefficient and confidence intervals.

"s.shift" Scale shift from x to y.

"l.shift" Location shift from x to y.

"bias" a bias correction factor that measures how far the best-fit line deviates from a line at 45 degrees. No deviation from the 45 degree line occurs when bias = 1. See Lin 1989, page 258.

"loa" Data frame containing the limits of agreement calculations

"h0_test" Decision from hypothesis test.

"call" the matched call

References

Shieh (2019). Assessing Agreement Between Two Methods of Quantitative Measurements: Exact Test Procedure and Sample Size Calculation, *Statistics in Biopharmaceutical Research*, <<https://doi.org/10.1080/19466315.2019.1644444>>

Bland, J. M., & Altman, D. G. (1999). Measuring agreement in method comparison studies. *Statistical methods in medical research*, 8(2), 135-160.

Bland, J. M., & Altman, D. (1986). Statistical methods for assessing agreement between two methods of clinical measurement. *The lancet*, 327(8476), 307-310.

Lawrence, I., & Lin, K. (1989). A concordance correlation coefficient to evaluate reproducibility. *Biometrics*, 255-268.

Examples

```
data('reps')
agree_test(x=reps$x, y=reps$y, delta = 2)
```

blandPowerCurve *Estimate power curve for Bland-Altman limits of agreement*

Description

This function calculates the power for the Bland-Altman method under varying parameter settings and for a range of sample sizes.

Usage

```
blandPowerCurve(  
  samplesizes = seq(10, 100, 1),  
  mu = 0,  
  SD,  
  delta,  
  conf.level = 0.95,  
  agree.level = 0.95  
)
```

Arguments

samplesizes	vector of samples sizes at which to estimate power.
mu	mean of differences
SD	standard deviation of differences
delta	The threshold below which methods agree/can be considered equivalent, can be in any units. Equivalence Bound for Agreement. More than one delta can be provided.
conf.level	the confidence level(s) required. Default is 95%. More than one confidence level can be provided.
agree.level	the agreement level(s) required. Default is 95%. The proportion of data that should lie between the thresholds, for 95% limits of agreement this should be 0.95. More than one confidence level can be provided.

Value

A dataframe is returned containing the power analysis results. The results can then be plotted with the plot.powerCurve function.

references

Lu, M. J., et al. (2016). Sample Size for Assessing Agreement between Two Methods of Measurement by Bland-Altman Method. The international journal of biostatistics, 12(2), <<https://doi.org/10.1515/ijb-2015-0039>>

Examples

```

powerCurve <- blandPowerCurve(samplesizes = seq(10, 200, 1),
mu = 0,
SD = 3.3,
delta = 8,
conf.level = .95,
agree.level = .95)
# Plot the power curve
plot(powerCurve, type = 1)
# Find at what N power of .8 is achieved
find_n(powerCurve, power = .8)

# If the desired power is not found then
## Sample size range must be expanded

```

dem_reg

*Deming Regression***Description**

A function for fitting a straight line to two-dimensional data (i.e., X and Y) are measured with error.

Usage

```

dem_reg(
  x,
  y,
  id = NULL,
  data,
  conf.level = 0.95,
  weighted = FALSE,
  weights = NULL,
  error.ratio = 1,
  keep_data = FALSE
)

```

Arguments

x	Name of column with first measurement
y	Name of other column with the other measurement to compare to the first.
id	Column with subject identifier
data	Data frame with all data
conf.level	The confidence level required. Default is 95%.
weighted	Logical indicator (TRUE/FALSE) for whether to use weighted Deming regression. Default is FALSE.

weights	an optional vector of weights to be used in the fitting process. Should be NULL or a numeric vector.
error.ratio	Ratio of the two error variances. Default is 1. This argument is ignored if subject identifiers are provided.
keep_data	Logical indicator (TRUE/FALSE). If TRUE the jackknife samples are returned; default is FALSE.

Details

This function provides a Deming regression analysis wherein the sum of distances in both x and y direction is minimized. Deming is useful in situations where both X & Y are measured with error. The use of Deming regression is beneficial when comparing to methods for measuring the same continuous variable.

Currently, the dem_reg function covers simple Deming regression and weighted Deming regression. Weighted Deming regression can be used by setting weighted to TRUE. The weights can be provided by the user or can be calculated within function.

If the data are measured in replicates, then the measurement error can be directly derived from the data. This can be accomplished by indicating the subject identifier with the id argument. When the replicates are not available in the data, then the ratio of error variances (y/x) can be provided with the error.ratio argument.

Value

The function returns a simple_eiv (eiv meaning "error in variables") object.

"call" The matched call.

"model" Data frame presenting the results from the Deming regression analysis.

"resamples" List containing resamples from jackknife procedure.

References

Linnet, K. (1990) Estimation of the linear relationship between the measurements of two methods with proportional errors. *Statistics in Medicine*, 9, 1463-1473.

Linnet, K. (1993). Evaluation of regression procedures for methods comparison studies. *Clinical chemistry*, 39, 424-432.

Description

Simple Agreement Analysis

Usage

```
jmvagree(
  data,
  method1,
  method2,
  ciWidth = 95,
  agreeWidth = 95,
  testValue = 2,
  CCC = TRUE,
  plotbland = TRUE,
  plotcon = FALSE,
  plotcheck = FALSE,
  prop_bias = FALSE,
  xlabel = "Average of Both Methods",
  ylabel = "Difference between Methods"
)
```

Arguments

data	Data
method1	Name of column containing 1st Vector of data
method2	Name of column containing Vector of data
ciWidth	a number between 50 and 99.9 (default: 95), the width of confidence intervals
agreeWidth	a number between 50 and 99.9 (default: 95), the width of agreement limits
testValue	a number specifying the limit of agreement
CCC	TRUE or FALSE (default), produce CCC table
plotbland	TRUE or FALSE (default), for Bland-Altman plot
plotcon	TRUE or FALSE (default), for Bland-Altman plot
plotcheck	TRUE or FALSE (default), assumptions plots
prop_bias	TRUE or FALSE
xlabel	The label for the x-axis on the BA plot
ylabel	The label for the y-axis on the BA plot

Value

A results object containing:

results\$text	a html
results\$blandtab	a table
results\$ccctab	a table
results\$plotba	an image
results\$plotcon	an image
results\$plotcheck	an image

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

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

jmvagreemulti

Nested/Replicate Data Agreement Analysis

Description

Nested/Replicate Data Agreement Analysis

Usage

```
jmvagreemulti(
  data,
  method1,
  method2,
  id,
  ciWidth = 95,
  agreeWidth = 95,
  testValue = 2,
  CCC = TRUE,
  valEq = FALSE,
  plotbland = FALSE,
  plotcon = FALSE,
  prop_bias = FALSE,
  xlabel = "Average of Both Methods",
  ylabel = "Difference between Methods"
)
```

Arguments

<code>data</code>	Data
<code>method1</code>	Name of column containing 1st Vector of data
<code>method2</code>	Name of column containing Vector of data
<code>id</code>	Name of column containing subject identifier
<code>ciWidth</code>	a number between 50 and 99.9 (default: 95), the width of confidence intervals
<code>agreeWidth</code>	a number between 50 and 99.9 (default: 95), the width of agreement limits
<code>testValue</code>	a number specifying the limit of agreement
<code>CCC</code>	TRUE or FALSE (default), produce CCC table
<code>valEq</code>	.
<code>plotbland</code>	TRUE or FALSE (default), for Bland-Altman plot
<code>plotcon</code>	TRUE or FALSE (default), for Line of identity plot
<code>prop_bias</code>	TRUE or FALSE
<code>xlabel</code>	The label for the x-axis on the BA plot
<code>ylabel</code>	The label for the y-axis on the BA plot

Value

A results object containing:

results\$text	a preformatted
results\$blandtab	a table
results\$ccctab	a table
results\$plotba	an image
results\$plotcon	an image

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

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

jmvdeming

Deming Regression

Description

Deming Regression

Usage

```
jmvdeming(
  data,
  method1,
  method2,
  ciWidth = 95,
  testValue = 1,
  plotcon = FALSE,
  plotcheck = FALSE,
  weighted = FALSE,
  xlabel = "Method: 1",
  ylabel = "Method: 2"
)
```

Arguments

data	Data
method1	Name of column containing 1st Vector of data
method2	Name of column containing Vector of data
ciWidth	a number between 50 and 99.9 (default: 95), the width of confidence intervals
testValue	Ratio of the two error variances. Default is 1.
plotcon	TRUE or FALSE (default), for Bland-Altman plot

plotcheck	TRUE or FALSE (default), assumptions plots
weighted	TRUE or FALSE
xlabel	The label for the x-axis
ylabel	The label for the y-axis

Value

A results object containing:

results\$text	a html
results\$demtab	a table
results\$plotcon	an image
results\$plotcheck	an image

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

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

jmvreli

Reliability Analysis

Description

Reliability Analysis

Usage

```
jmvreli(data, vars, ciWidth = 95, desc = FALSE, plots = FALSE)
```

Arguments

data	the data as a data frame
vars	a list of the column names containing the measurements for reliability analysis.
ciWidth	a number between 50 and 99.9 (default: 95), the width of confidence intervals
desc	TRUE or FALSE (default), provide table of variance components
plots	TRUE or FALSE (default), plot data

Value

A results object containing:

results\$text	a html
results\$icctab	a table
results\$varstab	a table
results\$plots	an image

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

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

loa_lme

Limits of Agreement with Linear Mixed Effects

Description

This function allows for the calculation of (parametric) bootstrapped limits of agreement when there are multiple observations per subject.

Usage

```
loa_lme(
  diff,
  avg,
  condition = NULL,
  id,
  data,
  type = c("perc", "norm", "basic"),
  conf.level = 0.95,
  agree.level = 0.95,
  replicates = 999,
  prop_bias = FALSE,
  het_var = FALSE
)
```

Arguments

<code>diff</code>	Column name of the data frame that includes the difference between the 2 measurements of interest.
<code>avg</code>	Column name of the data frame that includes the average of the 2 measurements of interest.
<code>condition</code>	Column name indicating different conditions subjects were tested under. This can be left missing if there are no differing conditions to be tested.
<code>id</code>	Column name indicating the subject/participant identifier
<code>data</code>	A data frame containing the variables within the model.
<code>type</code>	A character string representing the type of bootstrap confidence intervals. Only "norm", "basic", and "perc" currently supported. Bias-corrected and accelerated, bca, is the default. See <code>?boot::boot.ci</code> for more details.
<code>conf.level</code>	The confidence level required. Default is 95%.
<code>agree.level</code>	The agreement level required. Default is 95%.

replicates	The number of bootstrap replicates. Passed on to the boot function. Default is 999.
prop_bias	Logical indicator (default is FALSE) of whether proportional bias should be considered for the limits of agreement calculations.
het_var	Logical indicator (default is FALSE) of whether to assume homogeneity of variance in each condition.

Value

Returns single list with the results of the agreement analysis.

"var_comp" Table of variance components

"loa" A data frame of the limits of agreement including the average difference between the two sets of measurements, the standard deviation of the difference between the two sets of measurements and the lower and upper confidence limits of the difference between the two sets of measurements.

"call" The matched call.

References

Parker, R. A., Weir, C. J., Rubio, N., Rabinovich, R., Pinnock, H., Hanley, J., McLoughan, L., Drost, E.M., Mantoani, L.C., MacNee, W., & McKinstry, B. (2016). "Application of mixed effects limits of agreement in the presence of multiple sources of variability: exemplar from the comparison of several devices to measure respiratory rate in COPD patients". PLOS One, 11(12), e0168321. <<https://doi.org/10.1371/journal.pone.0168321>>

loa_mermod-methods *Methods for loa_mermod objects*

Description

Methods defined for objects returned from the loa_lme.

Usage

```
## S3 method for class 'loa_mermod'
print(x, ...)

## S3 method for class 'loa_mermod'
plot(
  x,
  x_label = "Average of Both Methods",
  y_label = "Difference Between Methods",
  geom = "geom_point",
  smooth_method = NULL,
  smooth_se = TRUE,
```

```

    ...
  )

  ## S3 method for class 'loa_mermod'
  check(x)

```

Arguments

x	object of class loa_mermod.
...	further arguments passed through, see description of return value for details. loa_mixed .
x_label	Label for x-axis.
y_label	Label for y-axis.
geom	String naming the type of geometry to display the data points. Default is "geom_point". Other options include: "geom_bin2d", "geom_density_2d", "geom_density_2d_filled", and "stat_density_2d".
smooth_method	Smoothing method (function) to use, accepts either NULL or a character vector, e.g. "lm", "glm", "gam", "loess" or a function. Default is NULL, which will not include a trend line.
smooth_se	Display confidence interval around smooth?

Value

print Prints short summary of the Limits of Agreement
 plot Returns a plot of the limits of agreement

loa_mixed	<i>Mixed Effects Limits of Agreement</i>
-----------	--

Description

This function allows for the calculation of bootstrapped limits of agreement when there are multiple observations per subject.

Usage

```

loa_mixed(
  diff,
  condition,
  id,
  data,
  plot.xaxis = NULL,
  delta,
  conf.level = 0.95,
  agree.level = 0.95,
  replicates = 1999,
  type = "bca"
)

```

Arguments

<code>diff</code>	column name of the data frame that includes the continuous measurement of interest.
<code>condition</code>	column name indicating different conditions subjects were tested under.
<code>id</code>	column name indicating the subject/participant identifier
<code>data</code>	A data frame containing the variables within the model.
<code>plot.xaxis</code>	column name indicating what to plot on the x.axis for the Bland-Altman plots. If this argument is missing or set to NULL then no plot will be produced.
<code>delta</code>	The threshold below which methods agree/can be considered equivalent, can be in any units. Equivalence Bound for Agreement.
<code>conf.level</code>	the confidence level required. Default is 95%.
<code>agree.level</code>	the agreement level required. Default is 95%.
<code>replicates</code>	the number of bootstrap replicates. Passed on to the boot function. Default is 500.
<code>type</code>	A character string representing the type of bootstrap confidence intervals. Only "norm", "basic", "bca", and "perc" currently supported. Bias-corrected and accelerated, bca, is the default. See <code>?boot::boot.ci</code> for more details.

Value

Returns single list with the results of the agreement analysis.

`"var_comp"` Table of variance components

`"loa"` a data frame of the limits of agreement including the average difference between the two sets of measurements, the standard deviation of the difference between the two sets of measurements and the lower and upper confidence limits of the difference between the two sets of measurements.

`"h0_test"` Decision from hypothesis test.

`"bland_alt.plot"` Simple Bland-Altman plot. Red line are the upper and lower bounds for shieh test; grey box is the acceptable limits (delta). If the red lines are within the grey box then the shieh test should indicate 'reject h0', or to reject the null hypothesis that this not acceptable agreement between x & y.

`"conf.level"` Returned as input.

`"agree.level"` Returned as input.

References

Parker, R. A., Weir, C. J., Rubio, N., Rabinovich, R., Pinnock, H., Hanley, J., McLoughan, L., Drost, E.M., Mantoani, L.C., MacNee, W., & McKinstry, B. (2016). "Application of mixed effects limits of agreement in the presence of multiple sources of variability: exemplar from the comparison of several devices to measure respiratory rate in COPD patients". *Plos One*, 11(12), e0168321. <<https://doi.org/10.1371/journal.pone.0168321>>

 loa_mixed_bs-methods *Methods for loa_mixed_bs objects*

Description

Methods defined for objects returned from the loa_mixed functions.

Usage

```
## S3 method for class 'loa_mixed_bs'
print(x, ...)
```

```
## S3 method for class 'loa_mixed_bs'
plot(x, ...)
```

Arguments

x object of class loa_mixed_bs as returned from loa_mixed
 ... further arguments passed through, see description of return value for details.
 [loa_mixed](#).

Value

print Prints short summary of the Limits of Agreement
 plot Returns a plot of the limits of agreement

 powerCurve-methods *Methods for powerCurve objects*

Description

Methods defined for objects returned from the powerCurve function.

Usage

```
find_n(x, power = 0.8)
```

```
## S3 method for class 'powerCurve'
plot(x, ...)
```

Arguments

x object of class powerCurve
 power Level of power (value between 0 and 1) for find_n to find the sample size.
 ... further arguments passed through, see description of return value for details.
 [blandPowerCurve](#).

Value

plot Returns a plot of the limits of agreement (type = 1) or concordance plot (type = 2)

find_n Find sample size at which desired power is achieved

reli_stats

Reliability Statistics

Description

The `reli_stats` and `reli_aov` functions produce reliability statistics described by Weir (2005). This includes intraclass correlation coefficients, the coefficient of variation, and the standard MSE of measurement.

Usage

```
reli_stats(  
  measure,  
  item,  
  id,  
  data,  
  wide = FALSE,  
  col.names = NULL,  
  cv_calc = c("MSE", "residuals", "SEM"),  
  conf.level = 0.95,  
  other_ci = FALSE,  
  type = c("perc", "norm", "basic"),  
  replicates = 1999  
)
```

```
reli_aov(  
  measure,  
  item,  
  id,  
  data,  
  wide = FALSE,  
  col.names = NULL,  
  cv_calc = c("MSE", "residuals", "SEM"),  
  conf.level = 0.95,  
  other_ci = FALSE,  
  type = "perc",  
  replicates = 1999  
)
```

Arguments

<code>measure</code>	Name of column containing the measurement of interest
<code>item</code>	Name of column containing the items. If this is a test-retest reliability study then this would indicate the time point (e.g., time1,time2, time3, etc.)
<code>id</code>	Column with subject identifier
<code>data</code>	Data frame with all data
<code>wide</code>	Logical value (TRUE or FALSE) indicating if data is in a "wide" format. Default is TRUE.
<code>col.names</code>	If wide is equal to TRUE then col.names is a list of the column names containing the measurements for reliability analysis.
<code>cv_calc</code>	Coefficient of variation (CV) calculation. This function allows for 3 versions of the CV. "MSE" is the default.
<code>conf.level</code>	the confidence level required. Default is 95%.
<code>other_ci</code>	Logical value (TRUE or FALSE) indicating whether to calculate confidence intervals for the CV, SEM, SEP, and SEE. Note: this will dramatically increase the computation time.
<code>type</code>	A character string representing the type of bootstrap confidence intervals. Only "norm", "basic", and "perc" currently supported. Bias-corrected and accelerated, bca, is the default. See ?boot::boot.ci for more details.
<code>replicates</code>	The number of bootstrap replicates. Passed on to the boot function. Default is 1999.

Details

These functions return intraclass correlation coefficients and other measures of reliability (CV, SEM, SEE, and SEP). The estimates of variances for any of the measures are derived from linear mixed models. When `other_ci` is set to TRUE, then a parametric bootstrap approach to calculating confidence intervals is used for the CV, SEM, SEE, and SEP.

`reli_stats` uses a linear mixed model to estimate variance components. In some cases there are convergence issues. When this occurs it is prudent to use `reli_aov` which instead utilizes sums of squares approach. The results may differ slightly between the functions. If `reli_aov` is used then rows with missing observations (e.g., if a participant has a missing observation) will be dropped.

The CV calculation has 3 versions. The "MSE" uses the "mean squared error" from the linear mixed model used to calculate the ICCs. The "SEM" option instead uses the SEM calculation and expresses CV as a ratio of the SEM to the overall mean. The "residuals" option uses the model residuals to calculate the root mean square error which is then divided by the grand mean.

Value

Returns single list with the results of the agreement analysis.

"icc" Table of ICC results

"lmer" Linear mixed model from lme4

"anova" Analysis of Variance table

"var_comp" Table of Variance Components
 "n.id" Number of subjects/participants
 "n.items" Number of items/time points
 "cv" Coefficient of Variation
 "SEM" List with Standard MSE of Measurement estimate (est)
 "SEE" List with Standard MSE of the Estimate estimate (est)
 "SEP" List with Standard MSE of Predictions (est)
 "call" the matched call

References

Weir, J. P. (2005). Quantifying test-retest reliability using the intraclass correlation coefficient and the SEM. *The Journal of Strength & Conditioning Research*, 19(1), 231-240.

Shrout, P.E. and Fleiss, J.L. (1976). Intraclass correlations: uses in assessing rater reliability. *Psychological Bulletin*, 86, 420-3428.

McGraw, K. O. and Wong, S. P. (1996). Forming inferences about some intraclass correlation coefficients. *Psychological Methods*, 1, 30-46. See errata on page 390 of same volume.

Examples

```
data('reps')
reli_stats(data = reps, wide = TRUE, col.names = c("x","y"))
```

reps

reps

Description

A fake data set of a agreement study where both measures have replicates.

Usage

```
reps
```

Format

A data frame with 20 rows with 3 variables

id Subject identifier
x X measurement
y Y measurement

Description

Methods defined for objects returned from the agree functions.

Usage

```
## S3 method for class 'simple_agree'
print(x, ...)

## S3 method for class 'simple_agree'
plot(
  x,
  type = 1,
  x_name = "x",
  y_name = "y",
  geom = c("geom_point", "geom_bin2d", "geom_density_2d", "geom_density_2d_filled",
           "stat_density_2d"),
  smooth_method = NULL,
  smooth_se = TRUE,
  ...
)

check(x)

## S3 method for class 'simple_agree'
check(x)
```

Arguments

x	object of class simple_agree as returned from a function starting with 'agree'
...	further arguments passed through, see description of return value for details. agree_test .
type	Type of plot to output. Default (1) is Bland-Altman plot while type=2 will produce a line-of-identity plot.
x_name	Name/label for x values (first measurement)
y_name	Name/label for y values (second measurement)
geom	String naming the type of geometry to display the data points. Default is "geom_point". Other options include: "geom_bin2d", "geom_density_2d", "geom_density_2d_filled", and "stat_density_2d".
smooth_method	Smoothing method (function) to use, accepts either NULL or a character vector, e.g. "lm", "glm", "gam", "loess" or a function. Default is NULL, which will not include a trend line.
smooth_se	Display confidence interval around smooth?

Value

`print` Prints short summary of the Limits of Agreement

`plot` Returns a plot of the limits of agreement (type = 1) or concordance plot (type = 2)

`check` Returns 2 plots, `p_norm` and `p_het`, testing the assumptions of a Bland-Altman analysis. P-values for the normality and heteroskedascity tests are provided as captions to the plot.

simple_eiv-methods *Methods for simple_eiv objects*

Description

Methods defined for objects returned from the error-in-variables models (e.g., `dem_reg`).

Usage

```
## S3 method for class 'simple_eiv'
print(x, ...)

## S3 method for class 'simple_eiv'
plot(x, x_name = "x", y_name = "y", ...)

## S3 method for class 'simple_eiv'
check(x)
```

Arguments

<code>x</code>	object of class <code>simple_eiv</code> from the <code>dem_reg</code> function.
<code>...</code>	further arguments passed through, see description of return value. for details. agree_test .
<code>x_name</code>	Name/label for x values (first measurement)
<code>y_name</code>	Name/label for y values (second measurement)

Value

`print` Prints short summary of the error-in-variables (e.g., Deming) regression model.

`plot` Returns a plot of the deming regression line, the line-of-identity, and the raw data.

`check` Returns plots of the optimized residuals.

simple_reli-methods *Methods for simple_reli objects*

Description

Methods defined for objects returned from the agree functions.

Usage

```
## S3 method for class 'simple_reli'
print(x, ...)

## S3 method for class 'simple_reli'
plot(x, ...)

## S3 method for class 'simple_reli'
check(x)
```

Arguments

x object of class simple_reli as returned from the reli_stats function
... further arguments passed through, see description of return value for details.
 [reli_stats](#).

Value

print Prints short summary of the Limits of Agreement
plot Returns a plot of the data points used in the reliability analysis

temps *Data*

Description

A dataset from a study on the reliability of human body temperature at different times of day before and after exercise.

Usage

```
temps

repre_long
```

Format

A data frame with 60 rows and 10 variables:

id Subject identifier

trial_num order in which the experimental trial was completed

trial_condition Environmental condition and metabolic heat production

tod Time of Day

trec_pre Rectal temperature before the beginning of the trial

trec_post Rectal temperature at the end of the trial

trec_delta Change in rectal temperature

teso_pre Esophageal temperature before the beginning of the trial

teso_post Esophageal temperature at the end of the trial

teso_delta Change in esophageal temperature

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 30 rows and 6 columns.

Source

Ravanelli N, Jay O. The Change in Core Temperature and Sweating Response during Exercise Are Unaffected by Time of Day within the Wake Period. *Med Sci Sports Exerc.* 2020 Dec 1. doi: 10.1249/MSS.0000000000002575. Epub ahead of print. PMID: 33273272.

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