Package ‘SimplyAgree’

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Type Package
Title Flexible and Robust Agreement and Reliability Analyses
Version 0.0.2
Maintainer Aaron Caldwell <arcaldwell49@gmail.com>
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.

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R topics documented:

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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)
```

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%.
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.

"identity.plot" Plot of x and y with a line of identity with a linear regression line

"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.

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

"conf.level" Returned as input.

"agree.level" Returned as input.

References


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)
Usage

agree_reps(x, y, id, data, delta, agree.level = 0.95, conf.level = 0.95)

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%.

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.
"identity.plot" Plot of x and y with a line of identity with a linear regression line
"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.
"ccc.xy" Lin's concordance correlation coefficient and confidence intervals using U-statistics.
"conf.level" Returned as input.
"agree.level" Returned as input.

References

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.
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 also provided.

### Usage

```r
agree_test(x, y, delta, conf.level = 0.95, agree.level = 0.95)
```

### Arguments

- **x**: Vector with first measurement
- **y**: Vector with second measurement
- **delta**: The threshold below which methods agree/can be considered equivalent, can be in any units. Equivalence Bound for Agreement.
- **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.

### 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.
- "identity.plot" Plot of x and y with a line of identity with a linear regression line
- "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.
References


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


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


```r
jmvagreemulti(data,
method1,
method2,
plotbland = FALSE,
plotcon = FALSE)
```

**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

**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:

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

---

**jmvagreemulti**  
 Nested/Replicate Data Agreement Analysis

**Description**

Nested/Replicate Data Agreement Analysis

**Usage**

```r
jmvagreemulti(data,
method1,
method2,
plotbland = FALSE,
plotcon = FALSE)
```
id,  
ciWidth = 95,  
agreeWidth = 95,  
testValue = 2,  
CCC = TRUE,  
valEq = FALSE,  
plotbland = FALSE,  
plotcon = FALSE  
)

Arguments

data Data
method1 Name of column containing 1st Vector of data
method2 Name of column containing Vector of data
id Name of column containing subject identifier
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
valEq .
plotbland TRUE or FALSE (default), for Bland-Altman plot
plotcon TRUE or FALSE (default), for Line of identity 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)
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$text a preformatted
- results$icctab a table
- results$vartab a table
- results$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_mixed Mixed Effects Limits of Agreement

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

diff column name of the data frame that includes the continuous measurement of interest.

column name indicating different conditions subjects were tested under.

id column name indicating the subject/participant identifier

data A data frame containing the variables within the model.

plot.xaxis 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.

delta The threshold below which methods agree/can be considered equivalent, can be in any units. Equivalence Bound for Agreement.

conf.level the confidence level required. Default is 95%.

agree.level the agreement level required. Default is 95%.

replicates the number of bootstrap replicates. Passed on to the boot function. Default is 500.

type 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 ?boot::boot.ci 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


---

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.

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**

`reli_stats` produces reliability statistics described by Weir (2005). This includes intraclass correlation coefficients, the coefficient of variation, and the standard error of measurement.

**Usage**

```r
reli_stats(
  measure,
  item,
  id,
  data,
  wide = FALSE,
  col.names = NULL,
  conf.level = 0.95
)
```

**Arguments**

- `measure` Name of column containing the measurement of interest
- `item` 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.)
- `id` Column with subject identifier
- `data` Data frame with all data
- `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.
- `conf.level` the confidence level required. Default is 95%.
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" Standard Error of Measurement
"SEE" Standard Error of the Estimate
"SEP" Standard Error of Predictions
"plot.reliability" Plot of data points within subjects across items

References


Examples

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

<table>
<thead>
<tr>
<th>reps</th>
<th>reps</th>
</tr>
</thead>
</table>

Description

A fake data set of an 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
simple_agree-methods  Methods for simple_agree objects

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, ...)

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.

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)

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, ...)

temps

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.

Value

print  Prints short summary of the Limits of Agreement

plot  Returns a plot of the data points used in the reliability analysis

Description

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

Usage

temps

temps

recpre_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

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