

# Package ‘SimplyAgree’

March 14, 2022

**Type** Package

**Title** Flexible and Robust Agreement and Reliability Analyses

**Version** 0.0.3

**Maintainer** Aaron Caldwell <arcaldwell149@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.

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

**License** GPL (>= 3)

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.1.2

**Imports** ggplot2, emmeans, lme4, boot, stats, dplyr, magrittr, tidyselect, tidyr, stringr, jmvcore

**Suggests** knitr, rmarkdown, testthat, tidyverse, readr, ggpubr, covr, cccrm

**VignetteBuilder** knitr

**Depends** R (>= 3.5)

**NeedsCompilation** no

**Author** Aaron Caldwell [aut, cre]

**Repository** CRAN

**Date/Publication** 2022-03-14 14:20:10 UTC

## R topics documented:

agree_nest . . . . .	2
agree_reps . . . . .	3
agree_test . . . . .	5
blandPowerCurve . . . . .	6
jmvagree . . . . .	7
jmvagreemulti . . . . .	8
jmvreli . . . . .	9
loa_mixed . . . . .	10
loa_mixed_bs-methods . . . . .	12
powerCurve-methods . . . . .	12
reli_stats . . . . .	13
reps . . . . .	14
simple_agree-methods . . . . .	15
simple_reli-methods . . . . .	15
temps . . . . .	16
<b>Index</b>	<b>17</b>

---

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)
```

### 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  $h_0$ ', 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**

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\_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)
```

**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**

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	<i>Tests for Absolute Agreement</i>
------------	-------------------------------------

---

**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 also provided.

**Usage**

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

**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. 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%. 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

- 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
```

---

jmvagree

*Simple Agreement Analysis*

---

### Description

Simple Agreement Analysis

### Usage

```
jmvagree(
  data,
  method1,
  method2,
  ciWidth = 95,
  agreeWidth = 95,
  testValue = 2,
  CCC = TRUE,
```

```

    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:

```

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
  )

```

### 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\$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\_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

<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**

<code>x</code>	object of class <code>powerCurve</code>
<code>power</code>	Level of power (value between 0 and 1) for <code>find_n</code> to find the sample size.
<code>...</code>	further arguments passed through, see description of return value for details. <a href="#">blandPowerCurve</a> .

**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

---

<code>reli_stats</code>	<i>Reliability Statistics</i>
-------------------------	-------------------------------

---

**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**

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

**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 <code>col.names</code> is a list of the column names containing the measurements for reliability analysis.
<code>conf.level</code>	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**

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.

**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

---

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. <a href="#">agree_test</a> .
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, ...)
```

**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

---

<code>temps</code>	<i>Data</i>
--------------------	-------------

---

**Description**

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

**Usage**

`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**

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.



# Index

- \* **datasets**
  - reps, [14](#)
  - temps, [16](#)
- agree\_nest, [2](#)
- agree\_reps, [3](#)
- agree\_test, [5](#), [15](#)
- as.data.frame, [8–10](#)
- blandPowerCurve, [6](#), [13](#)
- find\_n (powerCurve-methods), [12](#)
- jmvagree, [7](#)
- jmvagreemulti, [8](#)
- jmvreli, [9](#)
- loa\_mixed, [10](#), [12](#)
- loa\_mixed\_bs-methods, [12](#)
- plot.loa\_mixed\_bs
  - (loa\_mixed\_bs-methods), [12](#)
- plot.powerCurve (powerCurve-methods), [12](#)
- plot.simple\_agree
  - (simple\_agree-methods), [15](#)
- plot.simple\_reli (simple\_reli-methods),  
[15](#)
- powerCurve-methods, [12](#)
- print.loa\_mixed\_bs
  - (loa\_mixed\_bs-methods), [12](#)
- print.simple\_agree
  - (simple\_agree-methods), [15](#)
- print.simple\_reli
  - (simple\_reli-methods), [15](#)
- recpre\_long (temps), [16](#)
- reli\_stats, [13](#), [16](#)
- reps, [14](#)
- simple\_agree-methods, [15](#)
- simple\_reli-methods, [15](#)
- temps, [16](#)