

# Package ‘agRee’

July 2, 2014

**Title** Various Methods for Measuring Agreement.

**Version** 0.3-1

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**Description** Plots for visualization and point and interval estimates for different metrics of agreement.

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**Depends** R (>= 3.0.2), miscF (>= 0.1-2), lme4 (>= 1.0-4)

**Imports** R2jags (>= 0.03-11),

**License** GPL

**NeedsCompilation** no

**Repository** CRAN

**Date/Publication** 2014-06-04 17:57:14

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agree.ccc

*Concordance Correlation Coefficient***Description**

Obtain confidence interval and point estimate of the concordance correlation coefficient (CCC) proposed in Lin (1989).

**Usage**

```
agree.ccc(ratings, conf.level=0.95,
          method=c("jackknifeZ", "jackknife",
                  "bootstrap", "bootstrapBC",
                  "mvn.jeffreys", "mvn.conjugate",
                  "mvt", "lognormalNormal"),
          nboot=999, nmcmc=10000,
          mvt.para=list(prior=list(lower.v=4, upper.v=25,
                                   Mu0=rep(0, ncol(ratings)),
                                   Sigma0=diag(10000, ncol(ratings)),
                                   p=ncol(ratings),
                                   V=diag(1, ncol(ratings))),
                       initial=list(v=NULL, Sigma=NULL)),
          NAaction=c("fail", "omit"))
```

**Arguments**

ratings	a matrix of observations with one subject per row and one rater per column.
conf.level	confidence level of the interval. The default is 0.95.
method	a character string specifying the method used to obtain the estimate of the CCC. It must be one of "jackknifeZ", "jackknife", "bootstrap", "bootstrapBC", "mvn.jeffreys", "mvn.conjugate", "mvt", and "lognormalNormal", and may be abbreviated. The default is "jackknifeZ".
nboot	number of bootstrap replicates. The default value is 999.
nmcmc	number of iterations used in the Bayesian approach. The default value is 10000.
mvt.para	values of hyper-parameters and initial values of parameters for multivariate t (MVT) distribution. lower.v is the lower bound of degrees of freedom (df) of the MVT. upper.v is the upper bound of df of the MVT. Mu0 is the mean vector of multivariate normal prior of the location of the MVT. The default value is 0. Sigma0 is the variance matrix of multivariate normal prior of the location of the MVT. The default value is a diagonal matrix with diagonal entries equal to 10000. p is the df of wishart prior of inverse of the scale matrix of the MVT. The default value is the number of raters. V is the scale matrix of wishart prior of inverse of the scale matrix of the MVT. The default value is identity matrix. v is the initial value of the df of the MVT. The default is NULL. For the default, the value will be generated by using the ECME Algorithm. Sigma is the initial

value of the scale matrix of the MVT. The default is NULL. For the default, the value will be generated by using the ECME Algorithm.

**NAaction** a character string specifying what should happen when the data contain NAs. It must be one of "fail" and "omit" and may be abbreviated. The default is "fail" that causes the function to print an error message and terminate if there are any incomplete observations. If it is "omit", then the entire row(s) containing incomplete observation(s) will be deleted.

## Details

To obtain point estimate and confidence interval, the methods available include the jackknife method with and without Z-transformation, the bootstrap, and the Bayesian approach for the multivariate t, multivariate normal and lognormal-normal distributions.

## Value

Point estimate and lower and upper bounds of the confidence interval of the CCC.

## References

Dai Feng, Richard Baumgartner and Vladimir Svetnik (2014) A Bayesian estimate of the concordance correlation coefficient with skewed data. *under review*

Dai Feng, Richard Baumgartner and Vladimir Svetnik (2013) A robust Bayesian estimate of the concordance correlation coefficient. *Journal of Biopharmaceutical Statistics (in press)*

Dai Feng, Vladimir Svetnik, Alexandre Coimbra and Richard Baumgartner (2014) A comparison of confidence interval methods for the concordance correlation coefficient and intraclass correlation coefficient with small number of raters. *Journal of Biopharmaceutical Statistics* **24(2)** 272-293, doi: 10.1080/10543406.2013.863780.

Dai Feng, Richard Baumgartner and Vladimir Svetnik (2014) A short note on jackknifing the concordance correlation coefficient. *Statistics in Medicine* **33(3)** 514-516, doi: 10.1002/sim.5931

Lawrence I-Kuei Lin (1989) A concordance correlation coefficient to evaluate reproducibility. *Biometrics* **45** 255-268

## See Also

[epi.ccc](#), [cccvc](#), [agreement](#), [mvt.ecme](#)

## Examples

```
data(judgeRatings)
agree.ccc(judgeRatings[,2:3])
```

---

`agree.plot`*Visualize the Agreement of Ratings among Different Raters*

---

**Description**

Draw Bland-Altman plot(s) and scatter plot(s) with identity line.

**Usage**

```
agree.plot(ratings, NAaction=c("fail", "omit"))
```

**Arguments**

<code>ratings</code>	a matrix of ratings from different raters, one rater per column.
<code>NAaction</code>	a character string specifying what should happen when the data contain NAs. It must be one of "fail" and "omit" and may be abbreviated. The default is "fail" that causes the function to print an error message and terminate if there are any incomplete observations. If it is "omit", then the entire row(s) containing incomplete observation(s) will be deleted.

**Details**

The function produces a matrix of plots. The upper panel consists of scatter plot(s) with identity line. The lower panel consists of the Bland-Altman plot(s) with confidence bounds and bias using dotted line in red color and the horizontal line passing through the origin in black.

**Value**

NULL

**Note**

The confidence bounds are mean of the difference between two raters plus or minus twice of the SD of difference.

**References**

J. Martin Bland and Douglas G. Altman (1986) Statistical methods for assessing agreement between two methods of clinical measurement. *Lancet* **1** 307-310

**Examples**

```
data(judgeRatings)
agree.plot(judgeRatings)
```

---

agree.wscv                      *Within-subject Coefficient of Variation*

---

### Description

Obtain confidence interval and point estimate of the within-subject coefficient of variation (WSCV).

### Usage

```
agree.wscv(ratings, conf.level=0.95, method=c("vst", "delta"),
           NAaction=c("fail", "omit"))
```

### Arguments

ratings	a matrix of observations with one subject per row and one rater per column.
conf.level	confidence level of the interval. The default is 0.95.
method	a character string specifying the method used to obtain confidence interval of the WSCV. It must be one of "vst" and "delta" and may be abbreviated. The default is "vst".
NAaction	a character string specifying what should happen when the data contain NAs. It must be one of "fail" and "omit" and may be abbreviated. The default is "fail" that causes the function to print an error message and terminate if there are any incomplete observations. If it is "omit", then the entire row(s) containing incomplete observation(s) will be deleted.

### Details

The point estimate is based on what proposed in Quan and Shih (1996). To obtain confidence interval, the methods available include the delta method proposed in Quan and Shih (1996) and the variance stabilizing transformation in Shoukri et al. (2006).

### Value

Point estimate of the WSCV and lower and upper bounds of the confidence interval.

### References

Hui Quan and Weichung J. Shih (1996) Assessing reproducibility by the within-subject coefficient of variation with random effects models. *Biometrics* **52** 1195-1203

Mohamed M Shoukri, Nasser Elkum and Stephen D Walter (2006) Interval estimation and optimal design for the within-subject coefficient of variation for continuous and binary variables. *BMC Medical Research Methodology* **6** 24

### Examples

```
data(lesionBurden)
agree.wscv(lesionBurden.M)
```

---

 judgeRatings

*Ratings of Different Judges*


---

**Description**

The ratings of judges on a specific characteristic.

**Usage**

judgeRatings

**Format**

A matrix presenting the ratings of four judges on six people.

**Source**

B. J. Winer (1971) *Statistical principles in experimental design*, (2nd ed.). McGraw-Hill, New York

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lesionBurden

*Total Lesion Burden*


---

**Description**

The total lesion volumes measured manually and by an automated technique known as Geometrically Constrained Region Growth.

**Usage**

lesionBurden

**Format**

lesionBurden.M is a matrix presenting the manually measured volumes on three patients each with ten replicates.

lesionBurden.G is a matrix presenting the automatically measured volumes on three patients each with ten replicates.

**Source**

Mohamed M Shoukri, Nasser Elkum and Stephen D Walter (2006) Interval estimation and optimal design for the within-subject coefficient of variation for continuous and binary variables. *BMC Medical Research Methodology* 6 24

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