Package: agRee (via r-universe)

September 16, 2024

Title Various Methods for Measuring Agreement

Version 0.5-3

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Description Bland-Altman plot and scatter plot with identity line for visualization and point and interval estimates for different metrics related to reproducibility/repeatability/agreement including the concordance correlation coefficient, intraclass correlation coefficient, within-subject coefficient of variation, smallest detectable difference, and mean normalized smallest detectable difference.

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

Imports R2jags (>= 0.03-11), coda (>= 0.16-1)

License GPL

NeedsCompilation no

LazyData true

Date/Publication 2020-04-03 14:10:34 UTC

Repository https://daifengstat.r-universe.dev

RemoteUrl https://github.com/cran/agRee

RemoteRef HEAD

RemoteSha c2be14f241c8514bbf0b5801933d7e6aef1418d2

Contents

`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", "mvsn", "mvst"),
          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", "lognormalNormal", "mvsn", and "mvst". It can 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 and the default value is 0. `Sigma0` is the variance matrix of multivariate normal prior of the location of the MVT and 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 and 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 and the default value is identity matrix. `v` is the initial value of the df of the MVT. Its default is `NULL` and 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. Its default is `NULL` and 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 `NA`s. 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 normal, multivariate t, lognormal-normal, multivariate skew normal, and multivariate skew t distributions.

Value

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

References

Dai Feng, Richard Baumgartner and Vladimir Svetnik (2016) Estimating the concordance correlation coefficient using a unified Bayesian framework *under review*

Dai Feng, Richard Baumgartner and Vladimir Svetnik (2015) A Bayesian estimate of the concordance correlation coefficient with skewed data. *Pharmaceutical Statistics*, DOI: 10.1002/pst.1692

Dai Feng, Richard Baumgartner and Vladimir Svetnik (2015) A robust Bayesian estimate of the concordance correlation coefficient. *Journal of Biopharmaceutical Statistics* **25(3)** 490-507, DOI: 10.1080/10543406.2014.920342

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`, `mvt.ecme`

Examples

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

`agree.icc1` *Intraclass correlation coefficient for one-way random anova model*

Description

Obtain confidence interval and point estimate of the intraclass correlation coefficient for one-way random anova model (ICC1).

Usage

```
agree.icc1(ratings, conf.level=0.95, method=c("sf"),
           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 ICC1. Now only the "sf" method is supported.
`NAaction`	a character string specifying what should happen when the data contain `NA`s. 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 and confidence interval are based on a one-way random anova model as proposed in Shrout and Fleiss (1979).

Value

Point estimate of the ICC1 and lower and upper bounds of the confidence interval.

References

Patrick E Shrout and Joseph L Fleiss (1979). Intraclass correlations: uses in assessing rater reliability. *Psychological Bulletin* **86** 420-428

Examples

```
data(lesionBurden)
agree.icc1(lesionBurden.M)
```

`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

`ratings`	a matrix of ratings from different raters, one rater per column.
`NAaction`	a character string specifying what should happen when the data contain `NA`s. 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, respectively.

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.sdd` *Smallest Detectable Difference*

Description

Obtain confidence interval and point estimate of the smallest detectable difference (SDD).

Usage

```
agree.sdd(ratings, conf.level=0.95, 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.
`NAaction`	a character string specifying what should happen when the data contain `NA`s. 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 calculation is based on one-way random-effects ANOVA and the details can be found in Baumgartner et al. (2015).

Value

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

References

Richard Baumgartner, Dai Feng and Aniket Joshi (2015) Determination of smallest detectable difference for PET tracers using test-retest data: application in receptor occupancy studies (*under review*)

Examples

```
data(petVT)
agree.sdd(petVT$cerebellum)
```

`agree.sddm` *Mean Normalized Smallest Detectable Difference*

Description

Obtain confidence interval and point estimate of the mean normalized smallest detectable difference (SDDm).

Usage

```
agree.sddm(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, based on what the SDDm is calculated. 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 `NA`s. 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 calculation is based on the relationship with the WSCV and the details can be found in Baumgartner et al. (2015).

Value

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

References

Richard Baumgartner, Dai Feng and Aniket Joshi (2015) Determination of smallest detectable difference for PET tracers using test-retest data: application in receptor occupancy studies (*under review*)

Examples

```
data(petVT)
agree.sddm(petVT$cerebellum)
```

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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 `NA`s. 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

`petVT` *PET Total Volume of Distribution*

Description

Test/retest data for total volume of distribution (VT) from three published PET studies.

Usage

```
petVT
```

Format

A list presenting the VT from three studies. The first component is the data from Table 6 of Ogden et al. (2007). The second component is the data from Table 3 of Hostetler et al. (2013). The third component is the data from Table II of Gunn et al. (2011).

Source

R Todd Ogden et al. (2007) In vivo quantification of serotonin transporters using [11C]DASB and positron emission tomography in humans: modeling considerations *Journal of Cerbral Blood Flow & Metabolism* **27** 205-217

Eric D. Hostetler et al. (2013) In vivo quantification of calcitonin gene-related peptide receptor occupancy by telcagepant in rhesus monkey and human brain using the positron emission tomography tracer [11C]MK-4232 *The Journal of Pharmacology and Experimental Therapeutics* **347** 478-486

Roger N. Gunn et al. (2011) Translational characterization of [11C]GSK931145, a PET ligand for the Glycine transporter type 1 *SYNAPSE* **65** 1319-1332

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