

# Package ‘AgreementInterval’

October 25, 2018

**Type** Package

**Title** Agreement Interval of Two Measurement Methods

**Version** 0.1.1

**Description** A tool for calculating agreement interval of two measurement methods (Jason Liao (2015) <DOI:10.1515/ijb-2014-0030>) and present results in plots with discordance rate and/or clinically meaningful limit to quantify agreement quality.

**Depends** R (>= 3.5.0), psych

**License** MIT + file LICENSE

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 6.1.0

**Suggests** testthat, MASS, Matrix, lme4

**NeedsCompilation** no

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**Repository** CRAN

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agrInt2alpha	<i>agrInt2alpha</i>
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**Description**

Function agrInt2alpha calculates discordance rate (alpha) using clinically meaningful limit.

**Usage**

```
agrInt2alpha(clin.limit, n, sigmae)
```

**Arguments**

clin.limit	Clinically meaningful lower and upper limit
n	Sample size
sigmae	Variance estimate of residual from measurement error model

**Details**

Function agrInt2alpha calculates discordance rate (alpha) using clinically meaningful limit.

**Value**

Discordance rate

**Author(s)**

Jialin Xu, Jason Liao

**References**

Jason J. Z. Liao, Quantifying an Agreement Study, Int. J. Biostat. 2015; 11(1): 125-133

**Examples**

```
agrInt2alpha(clin.limit=c(-15, 15), n=52, sigmae=46.09245)
```

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ai	<i>ai</i>
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## Description

Calculate Agreement Interval of Two Measurement Methods and quantify the agreement

## Usage

```
ai(x, y, lambda = 1, alpha = 0.05, clin.limit = NA)
```

## Arguments

x	A continuous numeric vector from measurement method 1
y	A continuous numeric vector from measurement method 2, the same length as x.
lambda	Reliability ratio of x vs y. default 1.
alpha	Discordance rate to estimate confidence interval
clin.limit	Clinically meaningful limit (optional)

## Details

This is the function to calculate agreement interval (confidence interval) of two continuous numerical vectors from two measurement methods on the same samples. Note that this function only works for scenario with two evaluators, for example, comparing the concordance between two evaluators. We are working on the scenario with more than two evaluators. The two numerical vectors are x and y. It also provides commonly used measures based on index approaches, for example, Pearson's correlation coefficient, the intraclass correlation coefficient (ICC), the concordance correlation coefficient (Lin's CCC), and improved CCC (Liao's ICC).

## Value

Function ai returns an object of class "ai".

An object of class "ai" is a list containing the following components:

- alpha: Alpha input for confidence interval estimates
- n: Sample size
- conf.level: Confidence level calculated from alpha
- lambda: Reliability ratio input of x vs y
- summaryStat: Summary statistics of input data
- sigma.e: Random error estimates
- indexEst: Agreement estimates (CI.) based on index approaches
- intervalEst: Agreement estimates (CI.) based on interval approaches
- biasEst: Bias estimate
- intercept: Intercept of linear regression line from measure error model

slope: Slope of linear regression line from measure error model  
 x.name: x variable name extracted from input, used for plotting  
 y.name: y variable name extracted from input, used for plotting  
 tolProb.cl: Tolerance probability calculated based on optional clinically meaningful limit  
 k.cl: Number of discordance pairs based on optional clinically meaningful limit  
 alpha.cl: Discordance rate based on clinically meaningful limit

### Author(s)

Jialin Xu, Jason Liao

### References

Luiz RR, Costa AJL, Kale PL, Werneck GL. Assessment of agreement of a quantitative variable: a new graphical approach. *J Clin Epidemiol* 2003; 56:963-7.  
 Jason J. Z. Liao, Quantifying an Agreement Study, *Int. J. Biostat.* 2015; 11(1): 125-133  
 Shrout, Patrick E. and Fleiss, Joseph L. Intraclass correlations: uses in assessing rater reliability. *Psychological Bulletin*, 1979, 86, 420-3428.  
 Lin L-K., A Concordance Correlation Coefficient to Evaluate Reproducibility. *Biometrics* 1989; 45:255-68  
 Liao JJ. An Improved Concordance Correlation Coefficient. *Pharm Stat* 2003; 2:253-61  
 Nicole Jill-Marie Blackman, Reproducibility of Clinical Data I: Continuous Outcomes, *Pharm Stat* 2004; 3:99-108

### Examples

```
ai(x=1:4, y=c(1, 1, 2, 4))
a <- c(1, 2, 3, 4, 7)
b <- c(1, 3, 2, 5, 3)
ai(x=a, y=b)
ai(x=IPIA$Tomography, y=IPIA$Urography)
ai(x=IPIA$Tomography, y=IPIA$Urography, clin.limit=c(-15, 15))
```

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aiAdj

*aiAdj*

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### Description

Function aiAdj calculates bias-adjusted average interval from ai object

### Usage

```
aiAdj(object, x)
```

**Arguments**

object	ai object from ai function
x	A numeric value or a vector of numeric values to calculate bias-adjusted average interval for

**Details**

Function aiAdj uses proportional bias per x unit, Liao's average interval, Liao's average interval adjusted for fixed bias to calculate bias-adjusted and total-adjusted average interval.

**Value**

bias-adjusted and total-adjusted average interval for each value in x

**Author(s)**

Jialin Xu, Jason Liao

**References**

Jason J. Z. Liao, Quantifying an Agreement Study, *Int. J. Biostat.* 2015; 11(1): 125-133

**Examples**

```
ans <- ai(x=IPIA$Tomography, y=IPIA$Urography)
aiAdj(object=ans, x=1)
aiAdj(object=ans, x=c(1, 2))
```

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IPIA

*IPIA measures from 52 kidneys*

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**Description**

A dataset containing inferior pelvic infundibular angle (IPIA) dataset measured by urography and tomography on n=52 kidneys. The variables are as follows:

**Usage**

IPIA

**Format**

A data frame with 52 rows and 3 variables:

- id: sample ids
- Urography: IPIA data evaluated by means of computerized urography
- Tomography: IPIA data evaluated by means of computerized tomography

## References

Luiz RR, Costa AJL, Kale PL, Werneck GL. Assessment of agreement of a quantitative variable: a new graphical approach. J Clin Epidemiol 2003; 56:963-7.

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plot.ai

*plot.ai*

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## Description

The plot method for ai objects

## Usage

```
## S3 method for class 'ai'
plot(x, clin.limit = NA, which = 1:4, ...)
```

## Arguments

x	ai object from ai function
clin.limit	Clinically meaningful lower and upper limit
which	Index parameter to control which plot to output, by default, all four plots will be outputed.
...	Additional arguments to be passed to the round function and to control number of decimals in the display.

## Details

The four plots include 1) scatterplot of raw data with regression line from the measurement error model, 2) Difference between two measurement methods with original average interval determined by alpha and clinically meaningful lower and upper limit, 3) Difference between two measurement methods with average interval adjusted for fixed bias, as well as 4) Sorted difference between two measurement methods with average interval adjusted for total bias.

## Value

Function plot.ai returns 2 by 2 plots (See details)

## Author(s)

Jialin Xu, Jason Liao

## References

Jason J. Z. Liao, Quantifying an Agreement Study, Int. J. Biostat. 2015; 11(1): 125-133

**Examples**

```
a <- c(1, 2, 3, 4, 7)
b <- c(1, 3, 2, 5, 3)
ans <- ai(x=a, y=b)
plot(x=ans)
plot(x=ans, clin.limit=c(-5, 5))
```

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summary.ai

*summary.ai*

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**Description**

The summary method for ai objects

**Usage**

```
## S3 method for class 'ai'
summary(object, ...)
```

**Arguments**

object	ai object from ai function
...	additional arguments affecting the summary produced

**Value**

Function summary.ai prints out key summaries on screen

**Author(s)**

Jialin Xu, Jason Liao

**References**

Jason J. Z. Liao, Quantifying an Agreement Study, Int. J. Biostat. 2015; 11(1): 125-133

**Examples**

```
a <- c(1, 2, 3, 4, 7)
b <- c(1, 3, 2, 5, 3)
ans <- ai(x=a, y=b)
summary(ans)
```

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tolProb	<i>tolProb</i>
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### Description

Function tolProb calculates tolerance probability based on sample size (n), number of discordance pairs (k) and discordance rate (alpha).

### Usage

```
tolProb(n, k, alpha = 0.05)
```

### Arguments

n	Sample size
k	Number of discordance pairs, discordance pairs are defined as samples with difference greater than average interval
alpha	Discordance rate, default 0.05.

### Details

Function tolProb calculates tolerance probability based on sample size(n), number of discordance pairs (k) and discordance rate (alpha). Its value is calculated as the largest value such that the following inequality is true:

$$1 - \sum_{i=0}^k \binom{n}{i} * (1 - \alpha)^{n-i} * \alpha^i \geq \beta$$

### Value

tolerance probability

### Author(s)

Jialin Xu, Jason Liao

### References

Jason J. Z. Liao, Quantifying an Agreement Study, Int. J. Biostat. 2015; 11(1): 125-133

### Examples

```
tolProb(n=52, k=5, alpha=0.05)
tolProb(n=52, k=0, alpha=0.05)
```



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