

Package ‘Agreement’

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Type Package

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Author Yue Yu AND Lawrence Lin

Maintainer Yue Yu <yyu@imyy.net>

Description This package computes several statistics for measuring agreement, for example, mean square deviation (MSD), total deviation index (TDI) or concordance correlation coefficient (CCC). It can be used for both continuous data and categorical data for multiple raters and multiple readings cases.

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Agreement-package	<i>Statistical Tools for Measuring Agreement</i>
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Description

This package computes several statistics for measuring agreement, for example, mean square deviation (MSD), total deviation index (TDI) or concordance correlation coefficient (CCC). It can be used for both continuous data and categorical data for multiple raters and multiple readings cases.

Details

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LazyLoad: yes

Author(s)

Yue Yu AND Lawrence Lin
Maintainer: Yue Yu <yyu@imyy.net>

agreement	<i>Assessment of Agreement</i>
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Description

Compute the concordance correlation coefficient (CCC), precision, accuracy, total deviation index (TDI), coverage probability (CP) and relative biased square (RBS) for the paired observations (test and target) based on the model proposed by Lin, Hedayat, Sinha and Yang (2002).

Usage

```
agreement(x, y, error, target, CCC_a = 0.95, TDI_a, alpha = 0.05, CP_a = 0.9, H_label = "x", V_label = "y", min, max, by, dec)
```

Arguments

x	A vector of the readings for the target assay or rater, it will be shown in the horizontal axis of the agreement plot
y	A vector of the readings for the test assay or rater, it will be shown in the vertical axis of the agreement plot
error	Constant or proportional error structure. Use error="const" if the error structure is constant. Then, TDI is expressed as an absolute difference with the same measurement unit as the original data. Use error="prop" if the error structure is proportional. Then, TDI is expressed as a percent change. The natural log transformation to the data will be applied.
target	target="random" or "fixed".
CCC_a	A CCC allowance, the default if CCC_a=0.95.
TDI_a	A TDI allowance which must be specified for computing CP, must be a percent value when error="prop" is specified or an absolute difference when error="const" is specified.
alpha	100(1-alpha)
CP_a	A CP allowance which must be specified for computing TDI. The default is CP_a=0.9.
H_label	Label for the horizontal axis (target) of the agreement plot. The default is H_label="x".
V_label	Label for the vertical axis (test) of the agreement plot. The default is V_label="y".
min	Minimum of the plotting range, if it is not specified, a range will be chosen automatically to show all the data point.
max	Maximum of the plotting range, if it is not specified, a range will be chosen automatically to show all the data point.
by	The increment of the plotting range. If error="const" is specified, it is the value of increment, for example, by=5. If error="prop" is specified, it is the log scale increments in between min and max. For example, if min=1 and max=64, then by=c(2, 4, 8, 16, 32). If by is not specified, it will be chosen automatically based on the error structure.
dec	Significant digits for the output. The default is dec=2.

Details

The functions `summary` and `plot` can be used to print a summary of the results and plot the observations.

Value

An object of class `report` is returned, which contains all the estimated statistics and their confidence limits.

Author(s)

Yue Yu <yyu@imyy.net>

References

Lawrence Lin, A. S Hedayat, Bikas Sinha, Min Yang. Journal of the American Statistical Association. March 1, 2002, 97(457): 257-270.

See Also

[summary.agreement](#), [summary.report](#), [plot.report](#), [html.report](#)

Examples

```
data(DCLHb);
HemocueAve <- apply(DCLHb[,c("HEMOCUE1", "HEMOCUE2")], 1, mean);
SigmaAve <- apply(DCLHb[,c("SIGMA1", "SIGMA2")], 1, mean);

agr=agreement(y=HemocueAve, x=SigmaAve, V_label="Hemacue", H_label="Sigma", min=0, max=2000, by=250, CCC_a=0.9775, CP_
summary(agr);
plot(agr);
```

DCLHb

DCLHb dataset

Description

DCLHb is a treatment solution contain oxygen carrying hemoglobin. The DCLHb level is routinely measured by the Sigma method, and the simpler HemoCue method was modified to reproduce the DCLHb values of the Sigma method. The DCLHb values of each sample were measured by both methods twice.

Usage

```
data(DCLHb)
```

Format

A data frame with 299 observations on 4 variables, 2 variables for Sigma method and 2 variables for HemoCue method.

References

Lawrence Lin, A. S Hedayat, Bikas Sinha, Min Yang. Journal of the American Statistical Association. March 1, 2002, 97(457): 257-270.

Examples

```
data(DCLHb);
HemocueAve <- apply(DCLHb[,c("HEMOCUE1","HEMOCUE2")],1,mean);
SigmaAve <- apply(DCLHb[,c("SIGMA1","SIGMA2")],1,mean);

agr=agreement(y=HemocueAve,x=SigmaAve,V_label="Hemacue",H_label="Sigma",min=0,max=2000,by=250,CCC_a=0.9775,CP_
summary(agr);
```

html.report

Generate a HTML Report for Agreement Statistics

Description

Generate a HTML report for an agreement object class report. Contain the plot of data and all agreement statistics and confidence limits. Require package R2HTML.

Usage

```
## S3 method for class 'report'
html(result, dir = getwd(), file = "report", CSS = "R2HTML", ...)
```

Arguments

result	The name of an object of class report, which can be get from function agreement.
dir	Directory to store the output file. The default is the current working directory.
file	File name.
CSS	Name of CSS file used. The default is R2HTML.
...	Arguments passed to the HTMLInitFile method.

Details

In order to use the CSS style, the CSS file has to be placed in the same directory as the report file. The default is to use the simple CSS file R2HTML.CSS included in the package R2HTML.

Author(s)

Yue Yu <yyu@imyy.net>

See Also

[agreement](#)

html.unified_agreement

Generate a HTML Report for Unified Agreement Statistics

Description

Generate a HTML report for an agreement object class unified_agreement. Contain the plot of data and all agreement statistics. Require package R2HTML.

Usage

```
## S3 method for class 'unified_agreement'
html(result, dir = getwd(), file = "report", CSS = "R2HTML", ...)
```

Arguments

result	The name of an object of class unified_agreement, which can be get from function unified.agreement.
dir	Directory to store the output file. The default is the current working directory.
file	File name.
CSS	Name of CSS file used. The default is R2HTML.
...	Arguments passed to the HTMLInitFile method.

Details

In order to use the CSS style, the CSS file has to be placed in the same directory as the report file. The default is to use the simple CSS file R2HTML.CSS included in the package R2HTML.

Author(s)

Yue Yu <yyu@imyy.net>

See Also

[unified.agreement](#)

Examples

```
data(DCLHb);
ua <- unified.agreement(dataset=DCLHb, var=c("HEMOCUE1", "HEMOCUE2", "SIGMA1", "SIGMA2"), k=2, m=2, CCC_a_intra=0)
html.unified_agreement(ua);
```

IIR

*Intra-Intra Ratio (IIR)***Description**

Intra-Intra Ratio (IIR) compares the intra-rater precision among selected raters.

Usage

```
IIR(data, k, m, testindex, refindex, error, alpha = 0.05)
```

Arguments

data	Name of your dataset.
k	Number of methods/raters/instruments/assay, etc.
m	Number of replications for each methods/raters/instruments/assay, etc.
testindex	The index for the test raters, it must be a numerical vector. For example, if $k=3$ and $\text{testindex}=c(1, 2)$, the first and second rater are selected as the test raters for calculating IIR.
refindex	The index for the reference raters, it must be a numerical vector. For example, if $k=3$ and $\text{refindex}=3$, the third rater is selected as the reference raters for calculating TIR.
error	$\text{error}=\text{"const"}$ for the constant error structure for continuous data. $\text{error}=\text{"prop"}$ for the proportional error structure for continuous data. Here, log transformation to data will be applied for the continuous data. For categorical data, use $\text{error}=\text{"const"}$.
alpha	$100(1-\alpha)$

Value

Return a list of values

IIR	The estimator of IIR.
IIR_upper	The upper $1-\alpha/2$ confidence limit for IIR.
IIR_lower	The lower $1-\alpha/2$ confidence limit for IIR.

Note

The selected two sets of test and reference raters should be mutually exclusive.

Author(s)

Yue Yu <yyu@imyy.net>

See Also[TIR_IIR](#), [TIR](#)**Examples**

```
data(DCLHb);
IIR(DCLHb, k=2,m=2,testindex=1,refindex=2,error="const",alpha=0.05);
```

plot.report

Plotting an Agreement Object

Description

Perform the x-y plot for the agreement data. The x, y label, plotting range and axis increments are in the report object.

Usage

```
## S3 method for class 'report'
plot(x, ...)
```

Arguments

x The name of an object of class report. It can be get from function agreement.

... Arguments passed to the plot.method.

Author(s)

Yue Yu <yyu@imyy.net>

See Also[agreement](#)**Examples**

```
data(DCLHb);
HemocueAve=apply(DCLHb[,c("HEMOCUE1","HEMOCUE2")],1,mean);
SigmaAve=apply(DCLHb[,c("SIGMA1","SIGMA2")],1,mean);

agr=agreement(y=HemocueAve,x=SigmaAve,V_label="Hemacue",H_label="Sigma",min=0,max=2000,by=250,CCC_a=0.9775,CP_
plot(agr);
```

summary.agreement	<i>Summarize an Agreement Object</i>
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Description

This function is a method for summary for an agreement object class agreement.

Usage

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

Arguments

object	The name of an object of class agreement.
dec	Significant digits.
...	Arguments passed to the print method.

Author(s)

Yue Yu <yyu@imyy.net>

See Also

[summary.report](#)

summary.report	<i>Summarize an Agreement Object</i>
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Description

This function is a method for summary for a unified agreement object class report, which can be get from function agreement.

Usage

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

Arguments

object	The name of an object of class report.
...	Arguments passed to the print method.

Author(s)

Yue Yu <yyu@imyy.net>

See Also

[summary.agreement](#), [agreement](#)

Examples

```
data(DCLHb);
HemocueAve <- apply(DCLHb[,c("HEMOCUE1", "HEMOCUE2")], 1, mean);
SigmaAve <- apply(DCLHb[,c("SIGMA1", "SIGMA2")], 1, mean);
```

```
agr=agreement(y=HemocueAve, x=SigmaAve, V_label="Hemacue", H_label="Sigma", min=0, max=2000, by=250, CCC_a=0.9775, CP_
summary(agr);
```

summary.tir_iir

Summarize an TIR and IIR Object

Description

This function is a method for summary for a unified agreement object class `tir_iir`, which can be get from function `TIR_IIR`.

Usage

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

Arguments

<code>object</code>	The name of an object of class <code>tir_iir</code> .
<code>...</code>	Arguments passed to the print method.

Author(s)

Yue Yu <yyu@imyy.net>

See Also

[TIR_IIR](#)

Examples

```
data(DCLHb);
```

```
TI <- TIR_IIR(dataset=DCLHb, var=c("HEMOCUE1", "HEMOCUE2", "SIGMA1", "SIGMA2"), k=2, m=2, TIR_test="1,2", TIR_ref=
summary(TI);
```

summary.unified_agreement	<i>Summarize a Unified Agreement Object</i>
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Description

This function is a method for summary for a unified agreement object class unified_agreement, which can be get from function unified_agreement.

Usage

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

Arguments

object The name of an object of class unified_agreement.
... Arguments passed to the print method.

Author(s)

Yue Yu <yyu@imyy.net>

See Also

[unified_agreement](#)

Examples

```
data(DCLHb);  
ua <- unified_agreement(dataset=DCLHb, var=c("HEMOCUE1", "HEMOCUE2", "SIGMA1", "SIGMA2"), k=2, m=2, CCC_a_intra=0  
summary(ua);
```

TIR	<i>Total-Intra Ratio (TIR)</i>
-----	--------------------------------

Description

Total-Intra Ratio (TIR) is the ratio of MSD(total) and MSD(intra), it compares the total-rater agreement to intra-rater precision.

Usage

```
TIR(data, k, m, testindex, reindex, error, alpha = 0.05)
```

Arguments

<code>data</code>	Name of your dataset.
<code>k</code>	Number of methods/raters/instruments/assay, etc.
<code>m</code>	Number of replications for each methods/raters/instruments/assay, etc.
<code>testindex</code>	The index for the test raters, it can be a numerical vector or a character value "all". For example, if <code>testindex=c(1,2)</code> , the first and second rater are selected as the test raters for calculating TIR.
<code>refindex</code>	The index for the reference raters, it can be a numerical vector or a character value "all". For example, if <code>refindex="all"</code> , all raters are selected as the reference raters for calculating TIR.
<code>error</code>	<code>error="const"</code> for the constant error structure for continuous data. <code>error="prop"</code> for the proportional error structure for continuous data. Here, log transformation to data will be applied for the continuous data. For categorical data, use <code>error="const"</code> .
<code>alpha</code>	$100(1-\alpha)$

Value

Return a list of values

<code>TIR</code>	The estimator of TIR.
<code>TIR_upper</code>	The upper $1-\alpha$ confidence limit for TIR.
<code>TIR_lower</code>	The lower $1-\alpha$ confidence limit for TIR.

Author(s)

Yue Yu <yyu@imyy.net>

See Also

[TIR_IIR](#), [IIR](#)

Examples

```
data(DCLHb);
TIR(DCLHb, k=2,m=2,testindex=c(1,2),refindex="all",error="const",alpha=0.05);
```

TIR_IIR

*A Comparative Model***Description**

This function is used for comparing the total-rater agreement to intra-rater precision, and for comparing intra-rater precision among selected raters.

Usage

```
TIR_IIR(dataset, var, k, m, TIR_test, TIR_ref, IIR_test, IIR_ref, error = "const", alpha = 0.05, TI
```

Arguments

dataset	Name of your dataset.
var	Name of the dependent variables used in the dataset. The variables should be sorted by methods. For example, var=c("Method1_Rep1", "Method1_Rep2", "Method2_Rep1", "Method2_Rep2").
k	Number of methods/raters/instruments/assay, etc.
m	Number of replications for each methods/raters/instruments/assay, etc.
TIR_test	The selected test raters for calculating TIR, and must input in the format of a string "1, 2, ..., k", where 1 represents rater 1, 2 represents rater 2, and k represents for rater k, etc. For example, TIR_test="1, 2" means the selected test raters for calculating TIR are the first and second rater. When calculating multiple TIRs, the test raters for calculating each TIR must be written in a vector. For example, when k=3, we could specify TIR_test=c("1, 3", "1, 2, 3", "3", "2", "1, 2").
TIR_ref	The selected reference raters for calculating TIR that correspond to the TIR_test. It has the same format as TIR_test. If TIR_ref="all" is specified, then the intra-raters of all raters will be used as the denominator.
IIR_test	The selected test raters for calculating IIR. It has the same format as TIR_test, but can not be "all".
IIR_ref	The selected reference raters for calculating IIR. It has the same format as TIR_test, but can not be "all".
error	error="const" for the constant error structure for continuous data. error="prop" for the proportional error structure for continuous data. Here, log transformation to data will be applied for the continuous data. For categorical data, use error="const".
alpha	1-alpha one-tailed upper confidence limit for TIR or two-tailed confidence interval for IIR. The default is alpha=0.05.
TIR_a	Allowance for TIR.

Details

When `TIR_ref` is not specified as "all", each TIR is computed as the total MSD of test vs selected reference raters relative to the intra MSD of the selected reference raters. When `TIR_ref` is specified as "all", the function would assess the average of the total MSD of all raters relative to the average of intra MSD of all raters. For example, if `TIR_test=c("1,3","1,2,3","3","2","1,2")` and `TIR_ref=c("2","all","1,2","1","1,2")`. For the first pair in `TIR_test` and `TIR_ref`, the function would assess the average of the total MSD of "raters 1 vs 2 and raters 3 vs 2" relative to the intra MSD of "rater 2". For the second pair, the function would assess the average of the total MSD of all raters relative to the average of intra MSD of all raters. For the third pair, the function would assess the average of the total MSD of "raters 3 vs 1 and raters 3 vs 2" relative to the average of intra MSD of "raters 1 and 2". For the fourth pair, the function would assess the total MSD of "raters 2 and 1" relative to the intra MSD of "rater 1". For the fifth pair, the function would assess the total MSD of "raters 1 and 2" relative to the average of intra MSD of "raters 1 and 2".

Value

An object of class `tir_iir` is returned, which contains all the estimated statistics and their confidence limits.

Author(s)

Yue Yu <yyu@imyy.net>

See Also

[summary.tir_iir](#), [TIR](#), [IIR](#)

Examples

```
data(DCLHb);
```

```
TI <- TIR_IIR(dataset=DCLHb, var=c("HEMOCUE1","HEMOCUE2","SIGMA1","SIGMA2"), k=2, m=2, TIR_test="1,2", TIR_ref="all",
summary(TI);
```

unified.agreement

A Unified Approach for Assessment of Agreement

Description

The unified approach calculates the agreement statistics for both continuous and categorical data to cover multiple readings from each of the n subjects.

Usage

```
unified.agreement(dataset, var = NA, k, m, CCC_a = 0.9775, CCC_a_intra = 0.995, CCC_a_inter = 0.9775)
```

Arguments

dataset	Name of your dataset.
var	Name of the dependent variables used in the dataset, if it is not specified, all the variables in the dataset will be used.
k	Number of methods/raters/instruments/assay, etc.
m	Number of replications for each methods/raters/instruments/assay, etc.
CCC_a	CCC allowance when there is no replications, the default is CCC_a=0.9775.
CCC_a_intra	Intra CCC allowance.
CCC_a_inter	Inter CCC allowance.
CCC_a_total	Total CCC allowance.
CP_a	CP allowance for continuous data.
TDI_a	TDI allowance when there is no replications for continuous data. The default is TDI_a=150.
TDI_a_intra	Intra TDI allowance for continuous data.
TDI_a_inter	Inter TDI allowance for continuous data.
TDI_a_total	Total TDI allowance for continuous data.
tran	If transformation is used for the dataset. tran=0: no transformation will be used for statistical inference. tran=1 transformation such as Z, logit and log will be used for statistical inference. tran=1 can be used for categorical data but the TDI and CP outputs would become irrelevant. Therefore, tran=0 is recommended for all categorical data and tran=1 is recommended for all continuous data.
error	error="const": constant error structure for continuous data. When error="const", TDI is an absolute difference with the same measurement unit as for the original data. error="prop": proportional error structure for continuous data. When error="prop", TDI is the percent change. Log transformation will be applied to original data. For categorical data, use error="const".
dec	Significant digits after the decimal point printed for TDI when the error="const" is specified. The default is dec=2.
alpha	100(1-alpha)
iter	Number of iterations in the GEE step. The default is iter=35.
toe	The error tolerance of the GEE iteration. The default is toe = 1e-10.

Value

An object of class unified_agreement is returned, which contains all the estimated statistics and their confidence limits.

Author(s)

Yue Yu <yyu@imyy.net>

See Also

[agreement](#), [summary.unified_agreement](#), [html.unified_agreement](#)

Examples

```
data(DCLHb);  
ua <- unified.agreement(dataset=DCLHb, var=c("HEMOCUE1", "HEMOCUE2", "SIGMA1", "SIGMA2"), k=2, m=2, CCC_a_intra=0  
summary(ua);
```


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