

Package ‘negligible’

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Type Package

Title A Collection of Functions for Negligible Effect/Equivalence Testing

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Description Researchers often want to evaluate whether there is a negligible relationship among variables. The 'negligible' package provides functions that are useful for conducting negligible effect testing (also called equivalence testing). For example, there are functions for evaluating the equivalence of means or the presence of a negligible association (correlation or regression). Beribisky, N., Mara, C., & Cribbie, R. A. (2020) <[doi:10.20982/tqmp.16.4.p424](https://doi.org/10.20982/tqmp.16.4.p424)>. Beribisky, N., Davidson, H., Cribbie, R. A. (2019) <[doi:10.7717/peerj.6853](https://doi.org/10.7717/peerj.6853)>. Shiskina, T., Farmus, L., & Cribbie, R. A. (2018) <[doi:10.20982/tqmp.14.3.p167](https://doi.org/10.20982/tqmp.14.3.p167)>. Mara, C. & Cribbie, R. A. (2017) <[doi:10.1080/00220973.2017.1301356](https://doi.org/10.1080/00220973.2017.1301356)>. Counsell, A. & Cribbie, R. A. (2015) <[doi:10.1111/bmsp.12045](https://doi.org/10.1111/bmsp.12045)>. van Wieringen, K. & Cribbie, R. A. (2014) <[doi:10.1111/bmsp.12015](https://doi.org/10.1111/bmsp.12015)>. Goertzen, J. R. & Cribbie, R. A. (2010) <[doi:10.1348/000711009x475853](https://doi.org/10.1348/000711009x475853)>. Cribbie, R. A., Gruman, J. & Arpin-Cribbie, C. (2004) <[doi:10.1002/jclp.10217](https://doi.org/10.1002/jclp.10217)>.

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neg.cat	<i>Equivalence Testing for Categorical Variables</i>
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Description

Testing for the presence of a negligible association between two categorical variables

Usage

```
neg.cat(  
  v1 = NULL,  
  v2 = NULL,  
  tab = NULL,  
  eiU = 0.2,  
  data = NULL,  
  plot = TRUE,  
  save = FALSE,  
  nbootpd = 1000,
```

```

    alpha = 0.05
)

## S3 method for class 'neg.cat'
print(x, ...)
```

Arguments

v1	first categorical variable
v2	second categorical variable
tab	contingency table for the two predictor variables
eiU	upper limit of equivalence interval
data	optional data file containing the categorical variables
plot	logical; should a plot be printed out with the effect and the proportional distance
save	should the plot be saved to 'jpg' or 'png'
nbootpd	number of bootstrap samples for calculating the CI for the proportional distance
alpha	nominal acceptable Type I error rate level
x	Data frame from neg.cat
...	extra arguments

Details

This function evaluates whether a negligible relationship exists among two categorical variables.

The statistical test is based on the Cramer's V statistic; namely addressing the question of whether the upper limit of the confidence interval for Cramer's V falls below the upper bound of the negligible effect (equivalence) interval (eiU).

If the upper bound of the CI for Cramer's V falls below eiU, we can reject Ho: The relationship is nonnegligible ($V \geq eiU$).

eiU is set to .2 by default, but should be set based on the context of the research. Since Cramer's V statistic is in a correlation metric, setting eiU is a matter of determining what correlation is the minimally meaningful effect size (MMES) given the context of the research.

Users can input either the names of the categorical variables (v1, v2) or a frequency (contingency) table (tab).

The proportional distance (V/eiU) estimates the proportional distance of the effect from 0 to eiU, and acts as an alternative effect size measure.

Value

A list containing the following:

- cramv Cramer's V statistic
- propvar Proportion of variance explained (V^2)
- cil Lower bound of the confidence interval for Cramer's V
- ciu Upper bound of the confidence interval for Cramer's V

- eiU Upper bound of the negligible effect (equivalence) interval
- decis NHST decision
- PD Proportional distance
- CI95L Lower bound of the 1-alpha CI for the PD
- CI95U Upper bound of the 1-alpha CI for the PD
- alpha Nominal Type I error rate

Author(s)

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The confidence interval for the proportional distance is computed via bootstrapping (percentile bootstrap).

Examples

```
sex<-rep(c("m", "f"), c(12, 22))
haircol<-rep(c("bld", "brn", "bld", "brn"), c(9, 7, 11, 7))
d <- data.frame(sex, haircol)
tab<-table(sex, haircol)
neg.cat(tab=tab, alpha=.05, nbootpd=5)
neg.cat(v1=sex, v2=haircol, data=d, nbootpd=5)
```

neg.cfi

Equivalence Tests for CFI

Description

Function performs one of six equivalence tests for CFI fit index.

Usage

```
neg.cfi(
  mod,
  alpha = 0.05,
  eq.bound,
  modif.eq.bound = FALSE,
  ci.method = "equiv",
  nbootpd = 50,
  nboot = 250L,
  round = 3,
  plot = TRUE,
  saveplot = TRUE
)

## S3 method for class 'neg.cfi'
print(x, ...)
```

Arguments

<code>mod</code>	lavaan model object
<code>alpha</code>	desired alpha level (default = .05)
<code>eq.bound</code>	lower end of equivalence interval for comparison; must be .99, .95, .92 or .90 if <code>modif.eq.bound = TRUE</code>
<code>modif.eq.bound</code>	should the lower end of the equivalence interval be modified (default = FALSE)
<code>ci.method</code>	method used to calculate confidence interval; options are "yuan", "equiv" or "yhy.boot"; "yuan" corresponds to (1-alpha) percent CI, "equiv" corresponds to (1-2alpha) percent CI, "yhy.boot" corresponds to (1-2alpha) percent boot CI (default = "equiv")
<code>nbootpd</code>	number of bootstrap samples by "yhy.boot" for pd function
<code>nboot</code>	number of bootstrap samples if "yhy.boot" is selected as <code>ci.method</code> (default = 250L)
<code>round</code>	number of digits to round equivalence bound and confidence interval bounds (default = 3)
<code>plot</code>	logical, plotting the results (default = TRUE)
<code>saveplot</code>	saving plots (default = FALSE)
<code>x</code>	object of class <code>neg.cfi</code>
<code>...</code>	extra arguments

Details

#' The user specifies the lavaan fitted model object, the desired equivalence bound, and method of confidence interval computation. By default, the function does not modify the equivalence bounds according to Yuan et al. (2016). The user can also choose to instead run an equivalence test using a modified equivalence bound if the equivalence bound to be modified is .01, .05, .08, or .10. Alpha level can also be modified.

For information on modified equivalence bounds see Yuan, K. H., Chan, W., Marcoulides, G. A., & Bentler, P. M. (2016). Assessing structural equation models by equivalence testing with adjusted fit indexes. *Structural Equation Modeling: A Multidisciplinary Journal*, 23(3), 319-330. doi: <https://doi.org/10.1080/10705511.2015.1065414>.

The proportional distance quantifies the proportional distance from 0 to the nearest negligible effect (equivalence) interval (here, `eiU`). As values get farther from 0 the relationship becomes more substantial, with values greater than 1 indicating that the effect falls outside of the negligible effect (equivalence) interval.

Value

returns a list containing analysis and respective statistics and decision.

- `title1` The title of the CFI equivalence test. The appropriate title of the test will be displayed depending on the `ci.method` chosen and whether `modif.eq.bound` is TRUE or FALSE.
- `cfi_index` The CFI index.
- `ci.method` The method for confidence interval calculation.

- `cfi_eq` The lower end of the confidence interval for the CFI index.
- `eq.bound` The equivalence bound.
- `PD` Proportional distance (PD).
- `cilpd` Lower bound of the 1-alpha CI for the PD.
- `ciupd` Upper bound of the 1-alpha CI for the PD.

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Examples

```
d <- lavaan::HolzingerSwineford1939
hs.mod <- 'visual =~ x1 + x2 + x3
textual =~ x4 + x5 + x6
speed =~ x7 + x8 + x9'
fit1 <- lavaan::cfa(hs.mod, data = d)
neg.cfi(mod = fit1, alpha = .05, eq.bound = .95, modif.eq.bound = FALSE, ci.method = "equiv",
round = 3, plot = TRUE)
```

neg.cor

Test for Lack of Association between Two Continuous Normally Distributed Variables: Equivalence-based correlation tests

Description

Function performs an equivalence based test of lack of association with resampling.

Usage

```
neg.cor(
  v1,
  v2,
  eiU,
  eiL,
  alpha = 0.05,
  na.rm = TRUE,
  plot = TRUE,
  data = NULL,
  saveplot = FALSE,
  seed = NA,
  ...
)

## S3 method for class 'neg.cor'
print(x, ...)
```

Arguments

v1	the first variable of interest
v2	the second variable of interest
eiU	the upper bound of the equivalence interval, in terms of the magnitude of a correlation
eiL	the lower bound of the equivalence interval, in terms of the magnitude of a correlation
alpha	desired alpha level
na.rm	logical; remove missing values?
plot	whether or not to print graphics of the results (default = TRUE)
data	data frame where two variables (v1 and y) are contained - optional
saveplot	saving plots (default = FALSE)
seed	optional argument to set seed
...	additional arguments to be passed
x	object of class neg.cor

Details

From Goertzen, J. R., & Cribbie, R. A. (2010). Detecting a lack of association. *British Journal of Mathematical and Statistical Psychology*, 63(3), 527–537

This function evaluates whether a negligible relationship exists among two continuous variables.

The statistical test is based on a bootstrap-generated $1-2*\alpha$ CI for the correlation; in other words, does the $1-2*\alpha$ CI for the falls completely within the negligible effect (equivalence) interval.

The user needs to specify the lower and upper bounds of the negligible effect (equivalence) interval (eiL,eiU). Since we working in a correlation magnitude, setting these bounds requires estimating the minimally meaningful effect size (MMES); in this case, the minimally meaningful correlation (e.g., eiL = - .3, eiU = .3).

The 'plot' argument, if TRUE, will generate a plot of the observed effect (correlation) with the associated $1-2*\alpha$ CI, along with a plot of the PD and the associated $1-\alpha$ CI.

Value

A list including the following:

- corxy Sample correlation value
- eiL Lower bound of the negligible effect (equivalence) interval
- eiU Upper bound of the negligible effect (equivalence) interval
- nresamples Number of resamples for the bootstrapping procedure
- q1 Lower bound of the confidence interval for the correlation
- q2 Upper bound of the confidence interval for the correlation
- PD Proportional distance
- CIPDL Lower bound of the $1-\alpha$ CI for the PD
- CIPDU Upper bound of the $1-\alpha$ CI for the PD
- alpha Nominal Type I error rate

Author(s)

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Examples

```
#Negligible correlation test between v1 and v2
#with an interval of ei=(-.2.2)
v1 <- rnorm(50)
v2 <- rnorm(50)
cor(v1, v2)
neg.cor(v1 = v1, v2 = v2, eiU = .2, eiL = -.2)
```

neg.esm

Test for Evaluating Substantial Mediation

Description

Function computes the equivalence testing method (total effect) for evaluating substantial mediation and Kenny method for full mediation.

Usage

```
neg.esm(
  X,
  Y,
  M,
  alpha = 0.05,
  minc = 0.15,
  eil = -0.15,
  eiu = 0.15,
  nboot = 1000L,
  data = NULL,
  plot = TRUE,
  saveplot = FALSE,
  seed = NA
)

## S3 method for class 'neg.esm'
print(x, ...)
```

Arguments

X	predictor variable
Y	outcome variable
M	mediator variable

alpha	alpha level (default = .05)
minc	minimum correlation between x and Y (default is .15)
eil	lower bound of equivalence interval in standardized units (default is -.15)
eiU	upper bound of equivalence interval in standardized units (default is .15)
nboot	number of bootstraps (default = 500L)
data	optional data argument
plot	logical, plotting the results (default = TRUE)
saveplot	saving plots (default = FALSE)
seed	optional argument to set seed
x	object of class neg.esm
...	extra arguments

Details

This function evaluates whether a negligible direct effect of X on Y exists after controlling for the mediator. Another way to word this is that the indirect effect accounts for a substantial proportion of the variability in X-Y relationship. See Beribisky, Mara, and Cribbie (<https://doi.org/10.20982/tqmp.16.4.p424>)

The user specifies the IV (X), DV (Y) and mediator (M). The user can also specify the alpha level, the lower/upper bound of the negligible effect interval (eiL, eiU), the number of bootstrap samples (nboot), as well as the minimum correlation between X and Y that is permitted for a valid test of substantial mediation.

The variables X, Y and M can be specified as stand-alone, or a data argument can be used if the data reside in an R dataset.

For the Kenny method see: <https://davidakenny.net/cm/mediate.htm>

The proportional distance quantifies the proportional distance from 0 to the nearest negligible effect (equivalence) interval (eiL, eiU). As values get farther from 0 the relationship becomes more substantial, with values greater than 1 indicating that the effect falls outside of the negligible effect (equivalence) interval.

Note that the number of bootstrap samples (nboot) are low for the example since the example has a time limit of 5 seconds to pass CRAN testing; we recommend running a much higher number of bootstrap samples for analyses.

Value

A list including the following:

- minc Minimum correlation between X and Y for a valid negligible effect (equivalence) test
- corxy Sample correlation between the IV (X) and DV (Y)
- dir_eff Sample standardized direct effect between the IV (X) and DV (Y) after controlling for the mediator (M)
- eiL Lower bound of the negligible effect (equivalence) interval
- eiU Upper bound of the negligible effect (equivalence) interval
- cil Lower bound of the 1-2*alpha CI for the standardized direct effect of X on Y

- ciu Upper bound of the $1-2*\alpha$ CI for the standardized direct effect of X on Y
- PD Proportional distance (PD)
- cilpd Lower bound of the $1-\alpha$ CI for the PD
- ciupd Upper bound of the $1-\alpha$ CI for the PD
- ab_par Standardized indirect effect
- abdivc_k Proportion mediated: Standardized indirect effect divided by the standardized total effect
- alpha Nominal Type I error rate

Author(s)

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Examples

```
#equivalence test for substantial mediation
#with an equivalence interval of -.15 to .15
X<-rnorm(100,sd=2)
M<-.5*X + rnorm(100)
Y<-.5*M + rnorm(100)
neg.esm(X,Y,M, eil = -.15, eiu = .15, nboot = 5)
```

neg.indvars

Negligible Effect Test for Variances of Independent Populations

Description

This function allows researchers to test whether the difference in the variances of independent populations is negligible, where negligible represents the smallest meaningful effect size (MMES, where in this case the effect is the difference in population variances)

Usage

```
neg.indvars(dv, iv, eps = 0.5, alpha = 0.05, na.rm = TRUE, data = NULL, ...)
```

```
## S3 method for class 'neg.indvars'
print(x, ...)
```

Arguments

dv	Outcome Variable
iv	Independent Variable
eps	Used to Establish the Equivalence Bound (Conservative: .25; Liberal: .50, according to Wellek, 2010)
alpha	Nominal Type I Error Rate

na.rm	Missing Data Treatment
data	Dataset containing dv and iv
...	Extra arguments
x	object of class neg.indvars

Details

This function evaluates whether the difference in the population variances of J independent groups can be considered negligible (i.e., the population variances can be considered equivalent).

The user provides the name of the outcome/dependent variable (should be continuous) and the name of Independent Variable (predictor, should be a factor), as well as the epsilon value (eps) which determines the smallest difference in variances that can be considered non-negligible.

Wellek (2010) suggests liberal and conservative values of $\text{eps} = .50$ and $\text{eps} = .25$, respectively. See Wellek, 2010, pp. 16, 17, 22, for details.

See Mara & Cribbie (2018): <https://doi.org/10.1080/00220973.2017.1301356>

Value

A list including the following:

- vars Sample variances
- sds Sample standard deviations
- mads Sample median absolute deviations
- ratio Ratio of the largest to smallest variance
- eps Epsilon (e) can be described as the maximum difference in the variances that one would consider to be unimportant (see Details).
- LWW_md Levene-Wellek-Welch statistic based on the median.
- crit_LWW_md Critical value for the Levene-Wellek-Welch statistic based on the median.
- alpha Nominal Type I error rate

Author(s)

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Examples

```
#Two Group Example
indvar<-rep(c("a","b"),c(10,12))
depvar<-rnorm(22)
d<-data.frame(indvar,depvar)
neg.indvars(depvar,indvar)
neg.indvars(dv=depvar,iv=indvar,eps=.25,data=d)
neg.indvars(dv=depvar,iv=indvar,eps=.5)

#Four Group Example
indvar<-rep(c("a","b","c","d"),c(10,12,15,13))
depvar<-rnorm(50)
```

```
d<-data.frame(indvar,depvar)
neg.indvars(dv=depvar,iv=indvar,eps=.25,data=d)
neg.indvars(dv=depvar,iv=indvar)
```

neg.intcat	<i>Test for Negligible Interaction between Two Categorical Variables with a Continuous Outcome</i>
------------	--

Description

This function allows researchers to test whether the interaction effect among two categorical independent variables, with a continuous outcome variable, is negligible.

Usage

```
neg.intcat(
  iv1 = NULL,
  iv2 = NULL,
  dv = NULL,
  neiL,
  neiU,
  nboot = 50,
  alpha = 0.05,
  data = NULL
)

## S3 method for class 'neg.intcat'
print(x, ...)
```

Arguments

iv1	Levels of the first independent variable
iv2	Levels of the second independent variable
dv	Score on the continuous dependent/outcome variable
neiL	Lower bound of the negligible effect interval
neiU	Upper bound of the negligible effect interval
nboot	Number of bootstrap samples for calculating CIs
alpha	Nominal Type I Error rate
data	Dataset containing iv1, iv2 and dv
x	object of class neg.twointcat
...	extra arguments

Details

This function allows researchers to test whether the interaction effect among two categorical independent variables, with a continuous outcome variable, is negligible. In this case, 'negligible' represents the minimum meaningful interaction effect.

This test uses an intersection union approach, where a decision regarding the omnibus interaction effect is inferred from the decision regarding all simple (2 x 2) interaction effects; in other words, if all simple interaction effects are deemed negligible, then the omnibus interaction is also deemed negligible.

The test also uses the percentile bootstrap to determine confidence intervals, an approach that has been found to be robust to violations of normality and variance homogeneity.

See Cribbie, R. A., Ragoonanan, C., & Counsell, A. (2016). Testing for negligible interaction: A coherent and robust approach. *British Journal of Mathematical and Statistical Psychology*, 69, 159-174.

Value

A list including the following:

- meanx Sample mean of the first population/group.
- meany Sample mean of the second population/group.
- trmeanx Sample trimmed mean of the first population/group.
- trmeanx Sample trimmed mean of the second population/group.
- sdx Sample standard deviation of the first population/group.
- sdy Sample standard deviation of the second population/group.
- madx Sample median absolute deviation of the first population/group.
- mady Sample median absolute deviation of the second population/group.
- eiL Lower bound of the negligible effect (equivalence) interval.
- eiU Upper bound of the negligible effect (equivalence) interval.
- effsizerau Simple difference in the means (or trimmed means if normality = FALSE)
- cilraw2 Lower bound of the 1-alpha CI for the raw mean difference.
- ciuraw2 Upper bound of the 1-alpha CI for the raw mean difference.
- cilraw Lower bound of the 1-2*alpha CI for the raw mean difference.
- ciuraw Upper bound of the 1-2*alpha CI for the raw mean difference.
- effsized Standardized mean (or trimmed mean if normality = FALSE) difference.
- cild Lower bound of the 1-alpha CI for the standardized mean (or trimmed mean if normality = FALSE) difference.
- ciud Upper bound of the 1-alpha CI for the standardized mean (or trimmed mean if normality = FALSE) difference.
- effsizepd Proportional distance statistic.
- cilpd Lower bound of the 1-alpha CI for the proportional distance statistic.
- ciupd Upper bound of the 1-alpha CI for the proportional distance statistic.

- t1 First t-statistic from the TOST procedure.
- t2 Second t-statistic from the TOST procedure.
- df1 Degrees of freedom for the first t-statistic from the TOST procedure.
- df2 Degrees of freedom for the second t-statistic from the TOST procedure.
- p1 p value associated with the first t-statistic from the TOST procedure.
- p2 p value associated with the second t-statistic from the TOST procedure.
- alpha Nominal Type I error rate

Author(s)

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Examples

```
outcome<-rnorm(60,mean=50,sd=10)
iv_1<-rep(c("male","female"),each=30)
iv_2<-rep(c("young","middle","old"),each=10,times=2)
d<-data.frame(iv_1,iv_2,outcome)
neg.intcat(iv1=iv_1,iv2=iv_2,dv=outcome,neiL=-15,neiU=15,nboot=10)
neg.intcat(iv1=iv_1,iv2=iv_2,dv=outcome,neiL=-15,neiU=15,nboot=10,data=d)
```

neg.intcont

Negligible Interaction Test for Continuous Predictors

Description

Testing for the presence of a negligible interaction between two continuous predictor variables

Usage

```
neg.intcont(
  outcome = NULL,
  pred1 = NULL,
  pred2 = NULL,
  eiL,
  eiU,
  standardized = TRUE,
  nbootpd = 1000,
  data = NULL,
  alpha = 0.05,
  plot = TRUE,
  save = FALSE
)

## S3 method for class 'neg.intcont'
print(x, ...)
```

Arguments

outcome	continuous outcome variable
pred1	first continuous predictor variable
pred2	second continuous predictor variable
eiL	lower limit of the negligible effect (equivalence) interval
eiU	upper limit of the negligible effect (equivalence) interval
standardized	logical; should the solution be based on standardized variables (and eiL/eiU)
nbootpd	number of bootstrap samples for the calculation of the CI for the proportional distance
data	optional data file containing the categorical variables
alpha	nominal acceptable Type I error rate level
plot	logical; should a plot be printed out with the effect and the proportional distance
save	logical; should the plot be saved
x	object of class neg.intcont
...	extra arguments

Details

This function evaluates whether the interaction between two continuous predictor variables is negligible. This can be important for deciding whether to remove an interaction term from a model or to evaluate a hypothesis related to negligible interaction.

eiL/eiU represent the bounds of the negligible effect (equivalence) interval (i.e., the minimally meaningful effect size, MMES) and should be set based on the context of the research. When `standardized = TRUE`, Acock (2014) suggests that the MMES for correlations can also be applied to standardized effects - Acock, A. C. (2014). *A Gentle Introduction to Stata* (4th ed.). Texas: Stata Press.

User can input the outcome variable and two predictor variable names directly (i.e., without a data statement), or can use the data statement to indicate the dataset in which the variables can be found.

The advantage of this approach when `standardized = TRUE` and there are only two predictors is that the Delta method is adopted. However, for general cases researchers can also use the `neg.reg` function.

The proportional distance (interaction coefficient/negligible effect bound) estimates the proportional distance of the effect from 0 to negligible effect bound, and acts as an alternative effect size measure.

The confidence interval for the proportional distance is computed via bootstrapping (percentile bootstrap).

Value

A list containing the following:

- `intcoef` Interaction coefficient
- `intcil` Lower bound of the 1-alpha CI for the interaction coefficient

- intciu Upper bound of the 1-alpha CI for the interaction coefficient
- eiL Lower bound of the negligible effect (equivalence) interval
- eiU Upper bound of the negligible effect (equivalence) interval
- sprs Semi-partial correlation squared for the interaction term
- PD Proportional distance
- CI95L Lower bound of the 1-alpha CI for the PD
- CI95U Upper bound of the 1-alpha CI for the PD
- alpha Nominal Type I error rate

Author(s)

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Examples

```
y<-rnorm(25)
x1<-rnorm(25)
x2<-rnorm(25)
d<-data.frame(y,x1,x2)
neg.intcont(outcome = y, pred1 = x1, pred2 = x2, data = d,
eiL = -.25, eiU = .25, standardized = TRUE, nbootpd = 100)
```

neg.normal

Negligible Effect Test for Normality of a Univariate Distribution

Description

This function allows researchers to test whether the distribution of scores in a distribution has a Shapiro-Wilk W statistic that is negligibly different from 1.

Usage

```
neg.normal(x, eiL = 0.95, nboot = 1000, plot = TRUE, alpha = 0.05, data = NULL)
```

```
## S3 method for class 'neg.normal'
print(x, ...)
```

Arguments

x	object of class neg.normal
eiL	Lower Bound of the Negligible Effect Interval for W
nboot	Number of Bootstrap Samples for computing the CIs
plot	If the user prefers plots to be generated
alpha	Nominal Type I Error Rate
data	Dataset containing x
...	Extra arguments

Details

#' This function allows researchers to test whether the distribution of scores in a distribution has a Shapiro-Wilk W statistic that is negligibly different from 1. I.e., we are testing the null hypothesis that W is less than or equal to some prespecified lower bound for W (i.e., the least extreme value of W that is non-negligibly different from 1). We recommend .95 and .975 as liberal and conservative bounds, respectively

Value

A list including the following:

- sw Sample Shapiro-Wilk W statistic
- sskew Sample skewness
- skurt Sample kurtosis
- sddiff_mn_mdn Standardized difference between the sample mean and median
- sddiff_mn_trmn Standardized difference between the sample mean and trimmed mean
- lb Lower bound of 1-alpha CI for W
- eiL Maximum W for which the degree of nonnormality is considered extreme

Author(s)

Rob Cribbie <cribbie@yorku.ca> and Linda Farmus <lifarm@yorku.ca>

Examples

```
#Normal Distribution
xx<-stats::rnorm(200)
neg.normal(xx)
#Positive Skewed Distribution
xx<-stats::rchisq(200, df=3)
neg.normal(xx)
```

neg.paired	<i>Negligible Effect Test on the Difference between the Means of Dependent Populations</i>
------------	--

Description

This function allows researchers to test whether the difference between the means of two dependent populations is negligible, where negligible represents the smallest meaningful effect size (MMES)

Usage

```
neg.paired(
  var1 = NULL,
  var2 = NULL,
  outcome = NULL,
  group = NULL,
  ID = NULL,
  neiL,
  neiU,
  normality = TRUE,
  nboot = 10000,
  alpha = 0.05,
  plot = TRUE,
  saveplot = FALSE,
  data = NULL,
  seed = NA,
  ...
)

## S3 method for class 'neg.paired'
print(x, ...)
```

Arguments

var1	Data for Group 1 (if outcome, group and ID are omitted)
var2	Data for Group 2 (if outcome, group and ID are omitted)
outcome	Dependent Variable (if var1 and var2 are omitted)
group	Dichotomous Predictor/Independent Variable (if var1 and var2 are omitted)
ID	participant ID (if var1 and var2 are omitted)
neiL	Lower Bound of the Equivalence Interval
neiU	Upper Bound of the Equivalence Interval
normality	Are the population variances (and hence the residuals) assumed to be normally distributed?
nboot	Number of bootstrap samples for calculating CIs
alpha	Nominal Type I Error rate
plot	Should a plot of the results be produced?
saveplot	Should the plot be saved?
data	Dataset containing var1/var2 or outcome/group/ID
seed	Seed number
...	Extra arguments
x	object of class neg.paired

Details

This function evaluates whether the difference in the means of 2 dependent populations can be considered negligible (i.e., the population means can be considered equivalent).

The user specifies either the data associated with the first and second groups/populations (var1, var2, both should be continuous) or specifies the Independent Variable/Predictor (group, should be a factor) and the Dependent Variable (outcome, should be continuous). A 'data' statement can be used if the variables are stored in an R dataset.

The user must also specify the lower and upper bounds of the negligible effect (equivalence) interval. These are specified in the original units of the outcome variable.

Value

A list including the following:

- meanx Sample mean of the first population/group.
- meany Sample mean of the second population/group.
- medx Sample median of the first population/group.
- medy Sample median second population/group.
- sdx Sample standard deviation of the first population/group.
- sdy Sample standard deviation of the second population/group.
- madx Sample median absolute deviation of the first population/group.
- mady Sample median absolute deviation of the second population/group.
- neiL Lower bound of the negligible effect (equivalence) interval.
- neiU Upper bound of the negligible effect (equivalence) interval.
- effsizeraw Simple difference in the means (or medians if normality = FALSE)
- cilraw2 Lower bound of the 1-alpha CI for the raw mean difference.
- ciuraw2 Upper bound of the 1-alpha CI for the raw mean difference.
- cilraw Lower bound of the 1-2*alpha CI for the raw mean difference.
- ciuraw Upper bound of the 1-2*alpha CI for the raw mean difference.
- effsized Standardized mean (or median if normality = FALSE) difference.
- cild Lower bound of the 1-alpha CI for the standardized mean (or median if normality = FALSE) difference.
- ciud Upper bound of the 1-alpha CI for the standardized mean (or median if normality = FALSE) difference.
- effsizepd Proportional distance statistic.
- cilpd Lower bound of the 1-alpha CI for the proportional distance statistic.
- ciupd Upper bound of the 1-alpha CI for the proportional distance statistic.
- t1 First t-statistic from the TOST procedure.
- t1 Second t-statistic from the TOST procedure.
- df1 Degrees of freedom for the first t-statistic from the TOST procedure.

- df2 Degrees of freedom for the second t-statistic from the TOST procedure.
- pval1 p value associated with the first t-statistic from the TOST procedure.
- pval2 p value associated with the second t-statistic from the TOST procedure.
- alpha Nominal Type I error rate
- seed Seed number

Author(s)

Rob Cribbie <cribbie@yorku.ca> Naomi Martinez Gutierrez <naomimg@yorku.ca>

Examples

```
#wide format
ID<-rep(1:20)
control<-rnorm(20)
intervention<-rnorm(20)
d<-data.frame(ID, control, intervention)
head(d)
neg.paired(var1=control,var2=intervention,neiL=-1,neiU=1,plot=TRUE,
            data=d)
neg.paired(var1=d$control,var2=d$intervention,neiL=-1,neiU=1,plot=TRUE)
neg.paired(var1=d$control,var2=d$intervention,neiL=-1,neiU=1,normality=FALSE,
            nboot=10,plot=TRUE)

## Not run:
#long format
sample1<-sample(1:20, 20, replace=FALSE)
sample2<-sample(1:20, 20, replace=FALSE)
ID<-c(sample1, sample2)
group<-rep(c("control","intervention"),c(20,20))
outcome<-c(control,intervention)
d<-data.frame(ID,group,outcome)
neg.paired(outcome=outcome,group=group,ID=ID,neiL=-1,neiU=1,plot=TRUE,data=d)
neg.paired(outcome=d$outcome,group=d$group,ID=d$ID,neiL=-1,neiU=1,plot=TRUE)
neg.paired(outcome=d$outcome,group=d$group,ID=d$ID,neiL=-1,neiU=1,plot=TRUE, normality=FALSE)

#long format with multiple variables
sample1<-sample(1:20, 20, replace=FALSE)
sample2<-sample(1:20, 20, replace=FALSE)
ID<-c(sample1, sample2)
attendance<-sample(1:3, 20, replace=TRUE)
group<-rep(c("control","intervention"),c(20,20))
outcome<-c(control,intervention)
d<-data.frame(ID,group,outcome,attendance)
neg.paired(outcome=outcome,group=group,ID=ID,neiL=-1,neiU=1,plot=TRUE,data=d)
neg.paired(outcome=d$outcome,group=d$group,ID=d$ID,neiL=-1,neiU=1,plot=TRUE)

#open a dataset
library(negligible)
d<-perfectionism
names(d)
```

```

head(d)
neg.paired(var1=atqpre.total,var2=atqpost.total,
           neiL=-10,neiU=10,data=d)

#Dataset with missing data
x<-rnorm(10)
x[c(3,6)]<-NA
y<-rnorm(10)
y[c(7)]<-NA
neg.paired(x,y,neiL=-1,neiU=1, normality=FALSE)

## End(Not run)

```

neg.pd	<i>Proportional Distance Function (post hoc function - not to be used independently)</i>
--------	--

Description

Proportional Distance Function (post hoc function - not to be used independently)

Usage

```
neg.pd(effect, PD, eil, eiu, PDcil, PDciu, cil, ciu, Elevel, Plevel, save, oe)
```

Arguments

effect	observed effect
PD	proportional distance for effect
eil	lower bound of the equivalence interval
eiu	upper bound of the equivalence interval
PDcil	lower bound of the CI for the proportional distance
PDciu	upper bound of the CI for the proportional distance
cil	lower bound of the CI for the effect
ciu	upper bound of the CI for the effect
Elevel	1-2alpha CI for the effect
Plevel	1-alpha CI for the PD
save	Whether to save the plot or not
oe	Name of the original units of the effect of interest

Value

nothing is returned

Examples

```
## Not run:
1+1

## End(Not run)
```

neg.reg

Test for Evaluating Negligible Effect Between a Predictor and Outcome in a Multiple Regression Model

Description

This function evaluates whether a certain predictor variable in a multiple regression model can be considered statistically and practically negligible according to a predefined interval. i.e., minimally meaningful effect size (MMES)/smallest effect size of interest (SESOI). Where the effect tested is the relationship between the predictor of interest and the outcome variable, holding all other predictors constant.

Usage

```
neg.reg(
  data = NULL,
  formula = NULL,
  predictor = NULL,
  b = NULL,
  se = NULL,
  nop = NULL,
  n = NULL,
  eil,
  eiu,
  alpha = 0.05,
  test = "AH",
  std = FALSE,
  bootstrap = TRUE,
  nboot = 1000,
  plots = TRUE,
  saveplots = FALSE,
  seed = NA,
  ...
)

## S3 method for class 'neg.reg'
print(x, ...)
```

Arguments

data	a data.frame or matrix which includes the variables considered in the regression model
formula	an argument of the form $y \sim x_1 + x_2 \dots x_n$ which defines the regression model
predictor	name of the variable/predictor upon which the test will be applied
b	effect size of the regression coefficient of interest, can be in standardized or unstandardized units
se	standard error associated with the above regression coefficient effect size, pay close attention to standardized vs. unstandardized
nop	number of predictors (excluding intercept) in the regression model
n	the sample size used in the regression analysis
eil	lower bound of the equivalence interval measured in the same units as the regression coefficients (can be either standardized or unstandardized)
eiu	upper bound of the equivalence interval measured in the same units as the regression coefficients (can be either standardized or unstandardized)
alpha	desired alpha level, default is .05
test	AH is the default based on recommendation in Alter & Counsell (2020), TOST is an additional option
std	indicate if eil and eiu along with b (when dataset is not entered) are in standardized units
bootstrap	logical, default is TRUE, incorporating bootstrapping when calculating regression coefficients, SE, and CIs
nboot	1000 is the default. indicate if other number of bootstrapping iterations is desired
plots	logical, plotting the results. TRUE is set as default
saveplots	FALSE for no, "png" and "jpeg" for different formats
seed	to reproduce previous analyses using bootstrapping, the user can set their seed of choice
...	extra arguments
x	object of class neg.reg

Details

This function evaluates whether a certain predictor variable in a multiple regression model can be considered statistically and practically negligible according to a predefined interval. i.e., minimally meaningful effect size (MMES)/smallest effect size of interest (SESOI). Where the effect tested is the relationship between the predictor of interest and the outcome variable, holding all other predictors constant.

Unlike the most common null hypothesis significance tests looking to detect a difference or the existence of an effect statistically different than zero, in negligible effect testing, the hypotheses are flipped: In essence, H0 states that the effect is non-negligible, whereas H1 states that the effect is in fact statistically and practically negligible.

The statistical tests are based on Anderson-Hauck (1983) and Schuirmann's (1987) Two One-Sided Test (TOST) equivalence testing procedures; namely addressing the question of whether the estimated effect size (and its associated uncertainty) of a predictor variable in a multiple regression model is smaller than the what the user defines as negligible effect size. Defining what is considered negligible effect is done by specifying the negligible (equivalence) interval: its upper (eiu) and lower (eil) bounds.

The negligible (equivalence) interval should be set based on the context of the research. Because the predictor's effect size can be in either standardized or unstandardized units, setting eil and eiu is a matter of determining what magnitude of the relationship between predictor and outcome in either standardized or unstandardized units is the minimally meaningful effect size (MMES) given the context of the research.

It is necessary to be consistent with the units of measurement. For example, unstandardized negligible interval bounds (i.e., eil and eiu) must only be used when `std = FALSE` (default). If the effect size (b), standard error (se), and sample size (n) are entered manually as arguments (i.e., without the dataset), these should also be in the same units of measurements. Whereas if the user prefers to specify eiu and eil in standardized unites, `std = TRUE` should be specified. In which case, any units entered into the function must also be in standardized form. Mixing unstandardized and standardized units would yield inaccurate results and likely lead to invalid conclusions. Thus, users must be cognizant of the measurement units of the negligible interval.

There are two main approaches to using `neg.reg`. The first (and more recommended) is by inserting a dataset ('data' argument) into the function. If the user/s have access to the dataset, they should use the following set of arguments: `data`, `formula`, `predictor`, `bootstrap` (optional), `nboot` (optional), and `seed` (optional). However, this function also accommodates cases where no dataset is available. In this case, users should use the following set of arguments instead: `b`, `se`, `n`, and `nop`. In either situation, users must specify the negligible interval bounds (eiu and eil). Other optional arguments and features include: `alpha`, `std`, `test`, `plots`, and `saveplots`.

The proportional distance (PD; effect size/eiu) estimates the proportional distance of the estimated effect to eiu, and acts as an alternative effect size measure.

The confidence interval for the PD is computed via bootstrapping (percentile bootstrap), unless the user does not insert a dataset. In which case, the PD confidence interval is calculated by dividing the upper and lower CI bounds for the effect size estimate by the absolute value of the negligible interval bounds.

Value

A list containing the following:

- `formula` The regression model
- `effect` Specifying if effect size is in standardized or unstandardized units
- `test` Test type, i.e., Anderson-Hauck (AH) or Two One-Sided Tests (TOST)
- `t.value` t test statistic. If TOST was specified, only the smaller of the t values will be presented
- `df` Degrees of freedom associated with the test statistic
- `n` Sample size
- `p.value` p value associated with the test statistic. If TOST was specified, only the larger of the p values will be presented

- eil Lower bound of the negligible effect (equivalence) interval
- eiu Upper bound of the negligible effect (equivalence) interval
- predictor Variable name of the predictor in question
- b Effect size of the specified predictor
- se Standard error associated with the effect size point estimate (in the same units)
- l.ci Lower bound of the 1-alpha CI for the effect size
- u.ci Upper bound of the 1-alpha CI for the effect size
- pd Proportional distance
- pd.l.ci Lower bound of the 1-alpha CI for the PD
- pd.u.ci Upper bound of the 1-alpha CI for the PD
- seed Seed identity if bootstrapping is used
- decision NHST decision
- alpha Nominal Type I error rate

Author(s)

Udi Alter <udialter@gmail.com> and Alyssa Counsell <a.counsell@torontomu.ca> and Rob Cribbie <cribbie@yorku.ca>

Examples

```
# Negligible Regression Coefficient (equivalence interval: -.1 to .1)
pr1 <- stats::rnorm(20, mean = 0, sd= 1)
pr2 <- stats::rnorm(20, mean = 0, sd= 1)
dp <- stats::rnorm(20, mean = 0, sd= 1)
dat <- data.frame(pr1,pr2,dp)

# dataset available (unstandardized coefficients, AH procedure, using bootstrap-generated CIs):
neg.reg(formula=dp~pr1+pr2,data=dat,predictor=pr1,eil=-.1,eiu=.1,nboot=5)
neg.reg(formula=dat$dp ~ dat$pr1 + dat$pr2, predictor= pr1, eil= -.25, eiu= .25, nboot=5)

# dataset unavailable (standardized coefficients, TOST procedure):
neg.reg(b= .017, se= .025, nop= 3, n= 500, eil=-.1,eiu=.1, std=TRUE, test="TOST")
# end.
```

neg.rmsea

Equivalence Tests for RMSEA

Description

Function performs one of four equivalence tests for RMSEA fit index.

Usage

```

neg.rmsea(
  mod,
  alpha = 0.05,
  eq.bound,
  modif.eq.bound = FALSE,
  ci.method = "not.close",
  nbootpd = 50L,
  nboot = 250L,
  round = 3,
  plot = TRUE,
  saveplot = FALSE
)

## S3 method for class 'neg.rmsea'
print(x, ...)

```

Arguments

<code>mod</code>	lavaan model object
<code>alpha</code>	desired alpha level (default = .05)
<code>eq.bound</code>	upper end of equivalence interval for comparison; must be .01, .05, .08 or .10 if <code>modif.eq.bound = TRUE</code>
<code>modif.eq.bound</code>	should the upper end of the equivalence interval be modified? (default = FALSE)
<code>ci.method</code>	method used to calculate confidence interval; options are "not.close" or "yhy.boot"; "not.close" corresponds to (1-2alpha) percent CI, "yhy.boot" corresponds to (1-2alpha) percent boot CI (default = "not.close")
<code>nbootpd</code>	number of bootstrap samples by "yhy.boot" for pd function
<code>nboot</code>	number of bootstrap samples if "yhy.boot" is selected as <code>ci.method</code> (default = 250L)
<code>round</code>	number of digits to round equivalence bound and confidence interval bounds (default = 3)
<code>plot</code>	logical, plotting the results (default = TRUE)
<code>saveplot</code>	saving plots (default = FALSE)
<code>x</code>	object of class <code>neg.rmsea</code>
<code>...</code>	extra arguments

Details

The user specifies the lavaan fitted model object, the desired equivalence bound, and method of confidence interval computation. By default, the function does not modify the equivalence bounds according to Yuan et al. (2016). The user can also choose to instead run an equivalence test using a modified equivalence bound if the equivalence bound to be modified is .01, .05, .08, or .10. Alpha level can also be modified.

For information on modified equivalence bounds see Yuan, K. H., Chan, W., Marcoulides, G. A., & Bentler, P. M. (2016). Assessing structural equation models by equivalence testing with adjusted fit indexes. *Structural Equation Modeling: A Multidisciplinary Journal*, 23(3), 319-330. doi: <https://doi.org/10.1080/10705511.2015.1065414>.

The proportional distance quantifies the proportional distance from 0 to the nearest negligible effect (equivalence) interval (here, eiU). As values get farther from 0 the relationship becomes more substantial, with values greater than 1 indicating that the effect falls outside of the negligible effect (equivalence) interval.

Value

returns a list including the following:

- `title1` The title of the RMSEA equivalence test. The appropriate title of the test will be displayed depending on the `ci.method` chosen and whether `modif.eq.bound` is TRUE or FALSE.
- `rmsea_index` The RMSEA index.
- `ci.method` The method for confidence interval calculation (direct computation or bootstrap).
- `rmsea_eq` The upper end of the $1-2*\alpha$ confidence interval for the RMSEA index.
- `eq.bound` The equivalence bound.
- `PD` Proportional distance (PD).
- `cilpd` Lower bound of the $1-\alpha$ CI for the PD.
- `ciupd` Upper bound of the $1-\alpha$ CI for the PD.

Author(s)

Rob Cribbie <cribbie@yorku.ca> and Nataly Beribisky <natalyb1@yorku.ca>

@export neg.rmsea

Examples

```
d <- lavaan::HolzingerSwineford1939
hs.mod <- 'visual =~ x1 + x2 + x3
textual =~ x4 + x5 + x6
speed =~ x7 + x8 + x9'
fit1 <- lavaan::cfa(hs.mod, data = d)
neg.rmsea(alpha = .05, mod = fit1, eq.bound = .05, ci.method = "not.close", modif.eq.bound = FALSE,
round = 5, nboot = 50)
```

neg.semfit

*Equivalence Tests for Fit Indices***Description**

Function performs equivalence tests for RMSEA, CFI, and SRMR.

Usage

```
neg.semfit(
  mod,
  alpha = 0.05,
  round = 3,
  rmsea.eq.bound = 0.05,
  rmsea.modif.eq.bound = FALSE,
  rmsea.ci.method = "not.close",
  rmsea.nboot = 250L,
  cfi.eq.bound = 0.95,
  cfi.modif.eq.bound = FALSE,
  cfi.ci.method = "yhy.boot",
  cfi.nboot = 250L,
  srmr.eq.bound = 0.08,
  srmr.modif.eq.bound = FALSE,
  srmr.ci.method = "M0",
  usrmr = TRUE,
  srmr.nboot = 250L
)
```

Arguments

mod	lavaan model object
alpha	desired alpha level (default = .05)
round	number of digits to round equivalence bound and confidence interval bounds (default = 3)
rmsea.eq.bound	upper bound of the equivalence interval for RMSEA for comparison; must be .01, .05, .08, or .10 if rmsea.modif.eq.bound = TRUE
rmsea.modif.eq.bound	should the upper bound of the equivalence interval for RMSEA be modified (default = FALSE)
rmsea.ci.method	method used to calculate confidence interval for RMSEA; options are "not.close" or "yhy.boot"; "not.close" corresponds to (1-2alpha) percent CI, "yhy.boot" corresponds to (1-2alpha) percent boot CI (default = "not.close")
rmsea.nboot	number of bootstrap samples if "yhy.boot" is selected as rmsea.ci.method (default = 250L)

<code>cfi.eq.bound</code>	lower bound of equivalence interval for CFI for comparison; must be .99, .95, .92 or .90 if <code>cfi.modif.eq.bound = TRUE</code>
<code>cfi.modif.eq.bound</code>	should the lower bound of the equivalence interval for CFI be modified (default = FALSE)
<code>cfi.ci.method</code>	method used to calculate confidence interval for CFI; options are "yuan", "equiv" or "yhy.boot"; "yuan" corresponds to (1-alpha) percent CI, "equiv" corresponds to (1-2alpha) percent CI, "yhy.boot" corresponds to (1-2alpha) percent boot CI (default = "equiv")
<code>cfi.nboot</code>	number of bootstrap samples if "yhy.boot" is selected as <code>cfi.ci.method</code> (default = 250L)
<code>srmr.eq.bound</code>	upper bound of equivalence interval for SRMR for comparison; must be .05 or .10 if <code>modif.eq.bound = TRUE</code>
<code>srmr.modif.eq.bound</code>	should the upper bound of the equivalence interval for SRMR be modified? (default = FALSE)
<code>srmr.ci.method</code>	method used to calculate confidence interval for SRMR; options are "MO" or "yhy.boot"; "MO" corresponds to (1-2alpha) percent CI, "yhy.boot" corresponds to (1-2alpha) percent boot CI (default = "MO")
<code>usrmr</code>	fit index around which equivalence test should be structured (<code>usrmr = TRUE</code> which is the default states that <code>usrmr</code> from Maydeu-Olivares, 2017 will be used, otherwise <code>srmr</code> from <code>fitmeasures()</code> output in lavaan will be used)
<code>srmr.nboot</code>	number of bootstrap samples if "yhy.boot" is selected as <code>srmr.ci.method</code> (default = 250L)

Details

#' The user specifies the lavaan fitted model object, the desired equivalence bound, and method of confidence interval computation for RMSEA, CFI, and SRMR. By default, the function does not modify the equivalence bounds according to Yuan et al. (2016) or according to Shi et al. (2018). The user can also choose to instead run an equivalence test using a modified equivalence bound if the equivalence bound to be modified is .01, .05, .08, or .10 for RMSEA, .99, .95, .92 or .90 for CFI, .05 or .10 for SRMR. Alpha level can also be modified.

For information on modified equivalence bounds for CFI and RMSEA see Yuan, K. H., Chan, W., Marcoulides, G. A., & Bentler, P. M. (2016). Assessing structural equation models by equivalence testing with adjusted fit indexes. *Structural Equation Modeling: A Multidisciplinary Journal*, 23(3), 319-330. doi: <https://doi.org/10.1080/10705511.2015.1065414>. For information on uSRMR and modified cut-offs for SRMR see: Maydeu-Olivares, A. (2017). Maximum likelihood estimation of structural equation models for continuous data: Standard errors and goodness of fit. *Structural Equation Modeling: A Multidisciplinary Journal*, 24(3), 383-394. Shi, D., Maydeu-Olivares, A., & DiStefano, C. (2018). The relationship between the standardized root mean square residual and model misspecification in factor analysis models. *Multivariate Behavioral Research*, 53(5), 676-694.

Value

returns a list containing analysis and respective statistics and decision.

- `title1` The appropriate title of the test will be displayed depending on the `ci.method` chosen and whether `modif.eq.bound` is TRUE or FALSE.
- `cfi_index` The CFI index.
- `ci.method` The method for confidence interval calculation.
- `cfi_eq` The lower end of the confidence interval for the CFI index.
- `eq.bound` The equivalence bound.

Author(s)

Rob Cribbie <cribbie@yorku.ca> and Nataly Beribisky <natalyb1@yorku.ca>

Examples

```
d <- lavaan::HolzingerSwineford1939
hs.mod <- 'visual =~ x1 + x2 + x3
textual =~ x4 + x5 + x6
speed =~ x7 + x8 + x9'
fit1 <- lavaan::cfa(hs.mod, data = d)
neg.cfi(mod = fit1, alpha = .05, eq.bound = .95, modif.eq.bound = FALSE, ci.method = "equiv",
round = 3, plot = TRUE)
```

neg.srmr

Equivalence Tests for SRMR

Description

Function performs one of four equivalence tests for SRMR fit index.

Usage

```
neg.srmr(
  mod,
  alpha = 0.05,
  eq.bound,
  modif.eq.bound = FALSE,
  ci.method = "MO",
  usrmr = TRUE,
  nboot = 250L,
  round = 3
)

## S3 method for class 'neg.srmr'
print(x, ...)
```

Arguments

<code>mod</code>	lavaan model object
<code>alpha</code>	desired alpha level (default = .05)
<code>eq.bound</code>	upper bound of equivalence interval for comparison; must be .05 or .10 if <code>modif.eq.bound = TRUE</code>
<code>modif.eq.bound</code>	should the upper bound of the equivalence interval be modified? (default = FALSE)
<code>ci.method</code>	method used to calculate confidence interval; options are "MO" or "yhy.boot"; "MO" corresponds to (1-2alpha) percent CI, "yhy.boot" corresponds to (1-2alpha) percent boot CI (default = "MO")
<code>usrmr</code>	fit index around which equivalence test should be structured (<code>usrmr = TRUE</code> which is the default states that <code>usrmr</code> from Maydeu-Olivares, 2017 will be used, otherwise <code>srmr</code> from <code>fitmeasures()</code> output in lavaan will be used)
<code>nboot</code>	number of bootstrap samples if "yhy.boot" is selected as <code>ci.method</code> (default = 250L)
<code>round</code>	number of digits to round equivalence bound and confidence interval bounds (default = 3)
<code>x</code>	object of class <code>neg.srmr</code>
<code>...</code>	extra arguments

Details

The user specifies the lavaan fitted model object, the desired equivalence bound, the method of confidence interval computation, and whether unbiased SRMR or original SRMR should be used. By default, the function does not modify the equivalence bounds. The user can also choose to instead run an equivalence test using a modified equivalence bound of .05 or .10 multiplied by the average communality of the observed indicators. Alpha level can also be modified.

For information on unbiased SRMR and its confidence interval computation see Maydeu-Olivares, A. (2017). Maximum likelihood estimation of structural equation models for continuous data: Standard errors and goodness of fit. *Structural Equation Modeling: A Multidisciplinary Journal*, 24(3), 383-394. <https://doi.org/10.1080/10705511.2016.1269606>

Value

returns a list including the following:

- `title1` The title of the SRMR equivalence test. The appropriate title of the test will be displayed depending on the `ci.method` chosen whether `usrmr` and `modif.eq.bound` are TRUE or FALSE.
- `srmr_index` The SRMR index.
- `ci.method` The method for confidence interval calculation (direct computation or bootstrap).
- `srmr_ci` The upper bound of the 1-2*alpha confidence interval for the RMSEA index.
- `eq.bound` The equivalence bound.
- `PD` Proportional distance (PD).
- `ci1pd` Lower bound of the 1-alpha CI for the PD.
- `ciupd` Upper bound of the 1-alpha CI for the PD.

Author(s)

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Examples

```
d <- lavaan::HolzingerSwineford1939
hs.mod <- 'visual =~ x1 + x2 + x3
textual =~ x4 + x5 + x6
speed =~ x7 + x8 + x9'
fit1 <- lavaan::cfa(hs.mod, data = d)
neg.srmr(mod=fit1,alpha=.05,eq.bound=.08,usrmr = TRUE)
```

neg.twocors

Test for Evaluating Negligible Effects of Two Independent or Dependent Correlation Coefficients: Based on Counsell & Cribbie (2015)

Description

This function evaluates whether the difference between two correlation coefficients can be considered statistically and practically negligible

Usage

```
neg.twocors(
  data = NULL,
  r1v1 = NULL,
  r1v2 = NULL,
  r2v1 = NULL,
  r2v2 = NULL,
  r1 = NULL,
  n1 = NULL,
  r2 = NULL,
  n2 = NULL,
  dep = FALSE,
  r3 = NA,
  test = "AH",
  eiu,
  eil,
  alpha = 0.05,
  bootstrap = TRUE,
  nboot = 1000,
  seed = NA,
  plots = TRUE,
  saveplots = FALSE,
  ...
)
```



```
## S3 method for class 'neg.twocors'
print(x, ...)
```

Arguments

data	a data.frame or matrix which includes the variables in r1 and r2
r1v1	the name of the 1st variable included in the 1st correlation coefficient (r1, variable 1)
r1v2	the name of the 2nd variable included in the 1st correlation coefficient (r1, variable 2)
r2v1	the name of the 1st variable included in the 2nd correlation coefficient (r2, variable 1)
r2v2	the name of the 2nd variable included in the 2nd correlation coefficient (r2, variable 2)
r1	entered 1st correlation coefficient manually, without a dataset
n1	entered sample size associated with r1 manually, without a dataset
r2	entered 2nd correlation coefficient manually, without a dataset
n2	entered sample size associated with r2 manually, without a dataset
dep	are the correlation coefficients dependent (overlapping)?
r3	if the correlation coefficients are dependent and no datasets were entered, specify the correlation between the two, non-intersecting variables (e.g. if r1 = r12 and r2 = r13, then r3 = r23)
test	'AH' is the default based on recommendation in Counsell & Cribbie (2015), 'TOST' is an additional (albeit, more conservative) option.
eiU	upper bound of the equivalence interval measured as the largest difference between the two correlations for which the two coefficients would still be considered equivalent
eiL	lower bound of the equivalence interval measured as the largest difference between the two correlations for which the two coefficients would still be considered equivalent
alpha	desired alpha level, default is .05
bootstrap	logical, default is TRUE, incorporating bootstrapping when calculating regression coefficients, SE, and CIs
nboot	1000 is the default. indicate if other number of bootstrapping iterations is desired
seed	to reproduce previous analyses using bootstrapping, the user can set their seed of choice
plots	logical, plotting the results. TRUE is set as default
saveplots	FALSE for no, "png" and "jpeg" for different formats
...	extra arguments
x	object of class neg.twocors

Details

This function evaluates whether the difference between two correlation coefficients can be considered statistically and practically negligible according to a predefined interval. i.e., minimally meaningful effect size (MMES)/smallest effect size of interest (SESOI). The effect size tested is the difference between two correlation coefficients (i.e., $r_1 - r_2$).

Unlike the most common null hypothesis significance tests looking to detect a difference or the existence of an effect statistically different than zero, in negligible effect testing, the hypotheses are flipped: In essence, H_0 states that the effect is non-negligible, whereas H_1 states that the effect is in fact statistically and practically negligible.

The statistical tests are based on Anderson-Hauck (1983) and Schuirmann's (1987) Two One-Sided Test (TOST) equivalence testing procedures; namely addressing the question of whether the estimated effect size (and its associated uncertainty) of a difference between two correlation coefficients (i.e., r_1 and r_2) is smaller than the what the user defines as negligible effect size. Defining what is considered negligible effect is done by specifying the negligible (equivalence) interval: its upper (eiu) and lower (eil) bounds.

The negligible (equivalence) interval should be set based on the context of the research. Because the two correlations (and, therefore their difference) are in standardized units, setting eil and eiu is a matter of determining what is the smallest difference between the two correlations that can be considered of practical significance. For example, if the user determines that the smallest effect of interest is 0.1 – that is, any difference between the two correlation coefficient larger than 0.1 is meaningful in this context - then eil will be set to -0.1 and eiu to 0.1. Therefore, any observable difference that is larger than -0.1 AND smaller than 0.1, will be considered practically negligible.

There are two main approaches to using neg.twocors. The first (and more recommended) is by inserting a dataset ('data' argument) into the function. If the user/s have access to the dataset, they should use the following set of arguments: data, formula, r1v1, r1v2, r2v1, r2v2, dep (if applicable), bootstrap (optional), nboot (optional), and seed (optional). However, this function also accommodates cases where no dataset is available. In this case, users should use the following set of arguments instead: r1, n1, r2, n2, and r3 (if applicable). In either situation, users must specify the negligible interval bounds (eiu and eil). Other optional arguments and features include: alpha, test, plots, and saveplots.

This function accommodates both independent and dependent correlations. A user might want to compare two independent correlations. For example, the correlation between X and Y in one group (e.g., Control group; rXYc) with the correlation between X and Y in a different, independent group (e.g., Treatment group; rXYt). The 'independent correlations' setting (i.e., dep=FALSE) is the default in this function. However, in other cases, a user might want to compare two dependent correlation coefficients. That is, the two correlations share a common variable (i.e., same variable values). For example, the correlation between X and Y in one group (e.g., Treatment group; rXYt) with the correlation between X and B in the same group (e.g., Treatment group; rXBt). Because values in variable X are shared among the two correlations, the two correlations (e.g., rXYt and rXBt) are not independent from one another, but, in fact, dependent. To compare two dependent correlation coefficients, users need only to specify dep=TRUE. If no dataset is entered into the function, users should also use the argument r3, which will hold the correlation between the two non-shared variables. In the example above (i.e., rXYt and rXBt), the two non-shared variables are Y and B. In this case, $r_3 = r_{YBt}$. If dep=TRUE is entered into the function, test statistics and p values will be calculated differently to account for the shared variable. The negligible testing methods for comparing dependent correlations in this function are based on Williams's (1959) modification to

Hotelling's (1931) test for comparing overlapping dependent correlations. For more details see Counsell and Cribbie (2015).

The proportional distance (PD; effect size/eiu) estimates the proportional distance of the estimated effect to eiu, and acts as an alternative effect size measure.

The confidence interval for the PD is computed via bootstrapping (percentile bootstrap), unless the user does not insert a dataset. In which case, the PD confidence interval is calculated by dividing the upper and lower CI bounds for the effect size estimate by the absolute value of the negligible interval bounds.

Value

A list containing the following:

- r1v1 Name of the 1st variable included in the 1st correlation coefficient (r1, variable 1 ; if applicable)
- r1v2 Name of the 2nd variable included in the 1st correlation coefficient (r1, variable 2; if applicable)
- r2v1 Name of the 1st variable included in the 2nd correlation coefficient (r2, variable 1; if applicable)
- r2v2 Name of the 2nd variable included in the 2nd correlation coefficient (r2, variable 2; if applicable)
- r1 Effect size of the first bivariate relationship (1st correlation coefficient)
- n1 Sample size in each variable included in the first correlation (r1)
- r2 Effect size of the second bivariate relationship (2nd correlation coefficient)
- n2 Sample size in each variable included in the second correlation (r2)
- r3 If the correlation coefficients (r1 and r2) are dependent, r3 is then the correlation coefficient of the two, non-intersecting variables (e.g. if $r1 = r12$ and $r2 = r13$, then $r3 = r23$; if applicable)
- rsdiff The difference between the two correlation coefficients. Specifically, $r1 - r2$.
- se Standard error associated with the effect size point estimate (the difference between r1 and r2). The SE calculations are based on Kraatz (2007) and can be found in Counsell & Cribbie (2015)
- dep Logical. TRUE if r1 and r2 are dependent, otherwise FALSE
- eil Lower bound of the negligible effect (equivalence) interval
- eiu Upper bound of the negligible effect (equivalence) interval
- u.ci.a Upper bound of the 1-alpha CI for the effect size
- l.ci.a Lower bound of the 1-alpha CI for the effect size
- pd Proportional distance
- pd.l.ci Lower bound of the 1-alpha CI for the PD
- pd.u.ci Upper bound of the 1-alpha CI for the PD
- seed Seed identity if bootstrapping is used (if applicable)
- nboot Number of bootstrapping iterations, if bootstrapping was used (if applicable)

- which.test Test type, e.g., AH-rho-D, KTOST-rho etc. See Counsell & Cribbie (2015) for details
- degfree Degrees of freedom associated with the test statistic
- pv p value associated with the test statistic. If TOST was specified, only the larger of the p values will be presented
- NHSTdecision NHST decision
- alpha Nominal Type I error rate

Author(s)

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Examples

```
# Negligible difference between two correlation coefficients
# Equivalence interval: -.15 to .15
v1a<-stats::rnorm(10)
v2a<-stats::rnorm(10)
v1b <- stats::rnorm(10)
v2b <- stats::rnorm(10)
dat<-data.frame(v1a, v2a, v1b, v2b)
# dataset available (independent correlation coefficients):
neg.twocors(r1v1=v1a,r1v2=v2a,r2v1=v1b,r2v2=v2b,data=dat,eiu=.15,eil=-.15,nboot=50, dep=FALSE)
neg.twocors(r1=0.5,n1=300,r2=0.6,n2=500,eiu=.15,eil=-0.15, dep=TRUE, r3=0.51)
# end.
```

neg.twoindmeans	<i>Negligible Effect Test on the Difference between the Means of Independent Populations</i>
-----------------	--

Description

This function allows researchers to test whether the difference between the means of two independent populations is negligible, where negligible represents the smallest meaningful effect size (MMES, which in this case the effect is the mean difference)

Usage

```
neg.twoindmeans(
  v1 = NULL,
  v2 = NULL,
  dv = NULL,
```

```

    iv = NULL,
    eiL,
    eiU,
    varequiv = FALSE,
    normality = FALSE,
    tr = 0.2,
    nboot = 500,
    alpha = 0.05,
    plot = TRUE,
    saveplot = FALSE,
    data = NULL
)

## S3 method for class 'neg.twoindmeans'
print(x, ...)

```

Arguments

v1	Data for Group 1 (if dv and iv are omitted)
v2	Data for Group 2 (if dv and iv are omitted)
dv	Dependent Variable (if v1 and v2 are omitted)
iv	Dichotomous Predictor/Independent Variable (if v1 and v2 are omitted)
eiL	Lower Bound of the Equivalence Interval
eiU	Upper Bound of the Equivalence Interval
varequiv	Are the population variances assumed to be equal? Population variances are assumed to be unequal if normality=FALSE.
normality	Are the population variances (and hence the residuals) assumed to be normally distributed?
tr	Proportion of trimming from each tail (relevant if normality = FALSE)
nboot	Number of bootstrap samples for calculating CIs
alpha	Nominal Type I Error rate
plot	Should a plot of the results be produced?
saveplot	Should the plot be saved?
data	Dataset containing v1/v2 or iv/dv
x	object of class neg.twoindmeans
...	extra arguments

Details

This function evaluates whether the difference in the means of 2 independent populations can be considered negligible (i.e., the population means can be considered equivalent).

The user specifies either the data associated with the first and second groups/populations (iv1, iv2, both should be continuous) or specifies the Independent Variable/Predictor (iv, should be a factor)

and the Dependent Variable (outcome, should be continuous). A 'data' statement can be used if the variables are stored in an R dataset.

The user must also specify the lower and upper bounds of the negligible effect (equivalence) interval. These are specified in the original units of the outcome variable.

The arguments 'varequiv' and 'normality' control what test statistic is adopted. If varequiv = TRUE and normality = TRUE the ordinary Student t statistic is adopted. If varequiv = FALSE and normality = TRUE the Welch t statistic is adopted. If normality = FALSE the ordinary Student t statistic is adopted. d

Value

A list including the following:

- meanx Sample mean of the first population/group.
- meany Sample mean of the second population/group.
- trmeanx Sample trimmed mean of the first population/group.
- trmeany Sample trimmed mean of the second population/group.
- sdx Sample standard deviation of the first population/group.
- sdy Sample standard deviation of the second population/group.
- madx Sample median absolute deviation of the first population/group.
- mady Sample median absolute deviation of the second population/group.
- eiL Lower bound of the negligible effect (equivalence) interval.
- eiU Upper bound of the negligible effect (equivalence) interval.
- effsizeraW Simple difference in the means (or trimmed means if normality = FALSE)
- cilraw2 Lower bound of the 1-alpha CI for the raw mean difference.
- ciuraw2 Upper bound of the 1-alpha CI for the raw mean difference.
- cilraw Lower bound of the 1-2*alpha CI for the raw mean difference.
- ciuraw Upper bound of the 1-2*alpha CI for the raw mean difference.
- effsized Standardized mean (or trimmed mean if normality = FALSE) difference.
- cild Lower bound of the 1-alpha CI for the standardized mean (or trimmed mean if normality = FALSE) difference.
- ciud Upper bound of the 1-alpha CI for the standardized mean (or trimmed mean if normality = FALSE) difference.
- effsizepd Proportional distance statistic.
- cilpd Lower bound of the 1-alpha CI for the proportional distance statistic.
- ciupd Upper bound of the 1-alpha CI for the proportional distance statistic.
- t1 First t-statistic from the TOST procedure.
- t2 Second t-statistic from the TOST procedure.
- df1 Degrees of freedom for the first t-statistic from the TOST procedure.
- df2 Degrees of freedom for the second t-statistic from the TOST procedure.
- p1 p value associated with the first t-statistic from the TOST procedure.
- p2 p value associated with the second t-statistic from the TOST procedure.
- alpha Nominal Type I error rate

Author(s)

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Examples

```
indvar<-rep(c("a","b"),c(10,12))
depvar<-rnorm(22)
d<-data.frame(indvar,depvar)
neg.twoindmeans(dv=depvar,iv=indvar,eil=-1,eiU=1,plot=TRUE,data=d)
neg.twoindmeans(dv=depvar,iv=indvar,eil=-1,eiU=1)
neg.twoindmeans(v1=depvar[indvar=="a"],v2=depvar[indvar=="b"],eil=-1,eiU=1)
xx<-neg.twoindmeans(dv=depvar,iv=indvar,eil=-1,eiU=1)
xx$decis
```

perfectionism

Perfectionism Data

Description

This dataset comes from the dissertation of Chantal Arpin-Cribbie. The study was an RCT looking at the effect of an online CBT therapy on perfectionism (and related variables) in a sample of undergraduate students with extreme perfectionism. This dataset has missing data imputed with a single stochastic regression imputation.

Usage

```
data(perfectionism)
```

Format

A data frame with 83 rows and 17 variables:

group whether the participants received the CBT therapy, a general stress reduction protocol, or no treatment

mpshfpre.sop Pretest Score, Self-oriented Perfectionism, Hewitt & Flett Multidimensional Perfectionism Scale

mpshfpre.spp Pretest Score, Socially-prescribed Perfectionism, Hewitt & Flett Multidimensional Perfectionism Scale

pcipre.total Pretest Score, Perfection Cognitions Inventory

baipre.total Pretest Score, Beck Anxiety Inventory

cesdpre.total Pretest Score, CESD Depression Scale

mpsfpres.cm Pretest Score, Concern Over Mistakes subscale, Frost Multidimensional Perfectionism Scale

mpshfpost.sop Posttest Score, Self-oriented Perfectionism, Hewitt & Flett Multidimensional Perfectionism Scale

mpshfpost.spp Posttest Score, Self-prescribed Perfectionism, Hewitt & Flett Multidimensional Perfectionism Scale

pcipost.total Posttest Score, Perfection Cognitions Inventory

baipost.total Posttest Score, Beck Anxiety Inventory

cesdpost.total Posttest Score, CESD Depression Scale

mpsfpost.cm Posttest Score, Concern Over Mistakes subscale, Frost Multidimensional Perfectionism Scale

atqpre.total Pretest Score, Automatic Thoughts Questionnaire

atqpost.total Posttest Score, Automatic Thoughts Questionnaire

mpshfpre.oop Pretest score, Other Oriented Perfectionism, Hewitt & Flett Multidimensional Perfectionism Scale

mpshfpost.oop Posttest Score, Other Oriented Perfectionism, Hewitt & Flett Multidimensional Perfectionism Scale ...

Source

<https://pubmed.ncbi.nlm.nih.gov/22122217/>

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