

Package ‘negligible’

March 14, 2022

Type Package

Title A Collection of Functions for Negligible Effect/Equivalence Testing

Version 0.1.0

Maintainer Robert Cribbie <cribbie@yorku.ca>

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/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)>.

License GPL-3

Encoding UTF-8

LazyData true

Imports DescTools, lavaan, WRS2, ggplot2, nptest, dplyr

RoxygenNote 7.1.2

Depends R (>= 2.10)

NeedsCompilation no

Author Robert Cribbie [aut, cre],
Udi Alter [aut],
Nataly Beribisky [aut],
Phil Chalmers [aut],
Alyssa Counsell [aut],
Linda Farmus [aut],
Naomi Martinez Gutierrez [aut],
Victoria Ng [ctb]

Repository CRAN

Date/Publication 2022-03-14 08:50:05 UTC

R topics documented:

neg.cat	2
neg.cor	3
neg.esm	5
neg.indvars	6
neg.pd	7
neg.reg	8
neg.twoindmeans	10
perfectionism	11
print.neg.reg	13

Index **16**

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

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	data file containing the categorical variables
plot	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

Value

returns a list containing each analysis and their respective statistics and decision

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=50)
neg.cat(v1=sex, v2=haircol, data=d, nbootpd=50)
```

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
ei.u	the upper bound of the equivalence interval, in terms of the magnitude of a correlation
ei.l	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

Value

returns a list containing each analysis and their respective statistics and decision

Author(s)

Rob Cribbie <cribbie@yorku.ca> Phil Chalmers <rphilip.chalmers@gmail.com> and Nataly Beribisky <natalyb1@yorku.ca>

Examples

```
#Negligible correlation test between v1 and v2
#with an interval of ei=(-.2,.2)
v1 <- rnorm(50)
v2 <- rnorm(50)
plot(v1, v2)
cor(v1, v2)
neg.cor(v1 = v1, v2 = v2, ei.u = .2, ei.l = -.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 = 500L,
  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

Value

returns a list containing each analysis and their respective statistics and decision

Author(s)

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

Examples

```
#equivalence test for substantial mediation
#with an equivalence interval of -.15 to .15
X<-rnorm(200,sd=2)
M<-.5*X + rnorm(100)
Y<-.5*M + rnorm(100)
neg.esm(X,Y,M, eil = -.15, eiu = .15,nboot=50)
```

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

Value

returns a list containing each analysis and their respective statistics and decision

Author(s)

Rob Cribbie <cribbie@yorku.ca> and Constance Mara <Constance.Mara@cchmc.org>

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.pd

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

Description

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

Usage

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

Arguments

effect	observed effect
PD	proportional distance for effect
EIsign	equivalence interval value of the same sign as the effect
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

Value

nothing is returned

Examples

```
## Not run:  
1+1  
  
## End(Not run)
```

neg.reg

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

Description

This function tests whether a certain predictor variable can be considered statistically and practically negligible according to a predefined interval (i.e., $SESOI/MMES/\delta$) based on the Anderson-Hauck (1983) test of equivalence or Schuirmann's (1987) Two One-Sided Test (TOST)

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,  
  ...  
)
```

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 Data not required
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 Needed for both
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
...	additional arguments to be passed

Value

returns a list containing each analysis and their respective statistics and decision

Author(s)

Udi Alter <udialter@yorku.ca> and Alyssa Counsell <a.counsell@ryerson.ca>

Examples

```
# Negligible Regression Coefficient (equivalence interval: -.1 to .1)
pr1 <- stats::rnorm(20)
pr2 <- stats::rnorm(20)
dp <- stats::rnorm(20)
dat <- data.frame(pr1,pr2,dp)
# dataset available (unstandardized coefficients, AH procedure):
neg.reg(formula=dp~pr1+pr2,data=dat,predictor=pr1,eil=-.1,eiu=.1,nboot=50)
# end
```

neg.twoindmeans *Negligible Effect Test on the Difference between the Means of Independent Populations*

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

Value

returns a list containing each analysis and their respective statistics and decision

Author(s)

Rob Cribbie <cribbie@yorku.ca> R. Philip Chalmers <chalmp@yorku.ca> Naomi Martinez Gutierrez <naomimg@yorku.ca>

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

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

mpsfpre.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/>

`print.neg.reg`*Test for Evaluating Negligible Effects of Two Independent or Dependent Correlation Coefficients: Based on Counsell & Cribbie (2015)*

Description

This function tests whether two correlation coefficients can be considered equivalent according to a predefined interval (i.e., SESOI/MMES/delta) based on the Anderson-Hauck (1983) test of equivalence

Usage

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

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

<code>x</code>	object of class <code>neg.twocors</code>
<code>...</code>	additional arguments to be passed

<code>data</code>	a data.frame or matrix which includes the variables in <code>r1</code> and <code>r2</code>
<code>r1v1</code>	the name of the 1st variable included in the 1st correlation coefficient (<code>r1</code> , variable 1)
<code>r1v2</code>	the name of the 2nd variable included in the 1st correlation coefficient (<code>r1</code> , variable 2)
<code>r2v1</code>	the name of the 1st variable included in the 2nd correlation coefficient (<code>r2</code> , variable 1)
<code>r2v2</code>	the name of the 2nd variable included in the 2nd correlation coefficient (<code>r2</code> , variable 2)
<code>r1</code>	entered 1st correlation coefficient manually, without a dataset
<code>n1</code>	entered sample size associated with <code>r1</code> manually, without a dataset
<code>r2</code>	entered 2nd correlation coefficient manually, without a dataset
<code>n2</code>	entered sample size associated with <code>r2</code> manually, without a dataset
<code>dep</code>	are the correlation coefficients dependent (overlapping)?
<code>r3</code>	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 $r3 = r23$)
<code>test</code>	'AH' is the default based on recommendation in Counsell & Cribbie (2015), 'TOST' is an additional (albeit, more conservative) option.
<code>uiu</code>	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
<code>uil</code>	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
<code>alpha</code>	desired alpha level, default is .05
<code>bootstrap</code>	logical, default is TRUE, incorporating bootstrapping when calculating regression coefficients, SE, and CIs
<code>nboot</code>	1000 is the default. indicate if other number of bootstrapping iterations is desired
<code>seed</code>	to reproduce previous analyses using bootstrapping, the user can set their seed of choice
<code>plots</code>	logical, plotting the results. TRUE is set as default
<code>saveplots</code>	FALSE for no, "png" and "jpeg" for different formats

Value

returns a list containing each analysis and their respective statistics and decision

Author(s)

Rob Cribbie <cribbie@yorku.ca> and Alyssa Counsell <a.counsell@ryerson.ca>

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=-0.15,nboot=50)
# end
```

Index

* datasets

- perfectionism, 11
- available (neg.reg), 8
- data (neg.reg), 8
- equiv.reg (neg.reg), 8
- is (neg.reg), 8
- neg.cat, 2
- neg.cor, 3
- neg.esm, 5
- neg.indvars, 6
- neg.pd, 7
- neg.reg, 8
- neg.twocors (print.neg.reg), 13
- neg.twoindmeans, 10
- perfectionism, 11
- print.neg.cat (neg.cat), 2
- print.neg.cor (neg.cor), 3
- print.neg.esm (neg.esm), 5
- print.neg.indvars (neg.indvars), 6
- print.neg.reg, 13
- print.neg.twocors (print.neg.reg), 13
- print.neg.twoindmeans
(neg.twoindmeans), 10
- When (neg.reg), 8