Package ‘negligible’

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Type Package

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### Description

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

### Usage

```r
neg.cat(
  v1 = NULL,
  v2 = NULL,
  tab = NULL,
  eiU = 0.2,
  data = NULL,
  plot = TRUE,
  save = FALSE,
  nbootpd = 1000,
  alpha = 0.05
)
```

```r
# 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
### Description

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

### Usage

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

```r
## 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


Value

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

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)
plot(v1, v2)
cor(v1, v2)
neg.cor(v1 = v1, v2 = v2, eiu = .2, eil = -.2)
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)

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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)
eg.esm(X, Y, M, eil = -.15, eiu = .15, n.boot = 50)

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

neg.indvars  Negligible Effect Test for Variances of Independent Populations
neg.pd

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

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.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
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

```r
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 \(y = x_1 + x_2 \ldots x_n\) 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)
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Examples
# Negligible Regression Coefficient (equivalence interval: -.1 to .1)
pr1 <- stats::rnorm(20)
pr2 <- stats::rnorm(20)
ep <- stats::rnorm(20)
dat <- data.frame(pr1, pr2, ep)
# dataset available (unstandardized coefficients, AH procedure):
egreg(formula=ep-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)
perfectionism

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)
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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
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

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

x object of class neg.twocors

... additional arguments to be passed
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 2st 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

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
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