Description

iMediate is a collection of methods developed by our group for mediation analysis. It contains methods built upon likelihoods. Use \texttt{?iMediate} to see an introduction.

Details

Package: iMediate
Type: Package
Version: 0.5
Date: 2018-08-29
License: GPL (>=2)
LazyLoad: yes

Author(s)

Kai Wang <kai-wang@uiowa.edu>

References


Examples

data("jobs", package = "mediation")
fit.M <- lm(job_seek ~ treat + econ_hard + sex + age, data=jobs)
fit.Y <- lm(depress2 ~ treat * job_seek + econ_hard + sex + age, data=jobs)
mdn(fit.M, fit.Y, "treat")
Contour Plot of Joint Probabilities related to Mediated Effect

Description
Contour plot of joint probability of mediated effect and total effect in the absence of direct effect and joint probability of mediated effect and direct effect assuming $ab = c'$. 

Usage
```r
figure.joint.prob(prob = "mediated.main", n = 100, sig.level = 0.05, grid.size = 0.01)
```

Arguments
- **prob**: a character string specifying the probability to be plotted. One of "mediated.main" (default) and "mediated.direct". "mediated.main" requests the probability of the mediated effect and the main effect assuming there is no direct effect ($c' = 0$). "mediated.direct" requests the probability of the mediated effect and the direct effect assuming $ab = c'$.
- **n**: sample size
- **sig.level**: significance level used for the test of the mediated effect
- **grid.size**: grid size for $a^2$ and $b^2$

Details
Basic three-factor mediation model is assumed. Coefficients are standardized such that the variances of treatment, mediator, and outcome are equal to 1. Note that the y-axis is $a^2$ and the x-axis is $b^2$. The default axes labels from R function `plot_ly` are switched in order to make them correct.

Value
A plot generated using package `plotly`

Author(s)
Kai Wang <kai-wang@uiowa.edu>

References

Examples
```r
## figure.joint.prob()  # Figure 4 of Wang (2018)
## figure.joint.prob(prob="mediated.direct")  # Figure 5 of Wang (2018)
```
Contour plot of relative power of mediated effect versus total effect in the absence of direct effect and relative power of mediated effect versus direct effect when $ab = c'$. 

Usage

```r
figure.relative.power(comparison = "mediated2main", n = 100,
                      sig.level = 0.05, grid.size = 0.01)
```

Arguments

- `comparison`: a character string specifying the relative power to be plotted. One of "mediated2main" (default) and "mediated2direct". "mediated2main" requests the log of power ratio for the mediated effect versus the main effect assuming there is no direct effect ($c' = 0$). "mediated2direct" requests the log of power ratio for the mediated effect versus the direct effect assuming $ab = c'$.
- `n`: sample size
- `sig.level`: significance level used for the test of the mediated effect
- `grid.size`: grid size for $a^2$ and $b^2$

Details

Basic three-factor mediation model is assumed. Coefficients are standardized such that the variances of treatment, mediator, and outcome are equal to 1. Note that the y-axis is $a^2$ and the x-axis is $b^2$. The default axes labels from R function `plot_ly` are switched in order to make them correct.

Value

A plot generated using package `plotly`.

Author(s)

Kai Wang <kai-wang@uiowa.edu>

References

Examples

```r
## figureNrelativeNpower()  # Figure 2 of Wang (201X)
## figureNrelativeNpower(comparison="mediated2direct")  # Figure 3 of Wang (201X)
```

### fimle.lnl

**Full Information Maximum Likelihood Estimates in Linear M-model and Linear Y-model**

#### Description

Parameter estimates in system of correlated linear M-model and linear Y-model with treatment-mediator interaction using the full information maximum likelihood method.

#### Usage

```r
fimle.lnl(fit.M, fit.Y, treatment, rho = 0, t0 = 0, t1 = 1, m = 1)
```

#### Arguments

- `fit.M`: a fitted model object for mediator. It must be an object generated by function “lm”
- `fit.Y`: a fitted model object for outcome. It must be an object generated by function “lm”. It can contain treatment-mediator interaction
- `treatment`: a character string of the name of the treatment variable. This variable takes numerical values
- `rho`: a numerical variable specifying the correlation coefficient between the residual of the M-model and the residual of the Y-model. Its range is between $-1$ and $1$
- `t0`: a reference value for the treatment
- `t1`: another value for the treatment
- `m`: a value specifying the level of the mediator. Used for CDE computation between the residual of the M-model and the residual of the Y-model. Its range is between $-1$ and $1$

#### Details

P-values are computed from normal distribution.

#### Value

A list containing the following components:

- `M.model`: a data frame containing the results for the M-model
- `Y.model`: a data frame containing the results for the Y-model
- `Effects`: a data frame containing estimated ACME, ADE, Total Effect, and CDE for treatment values `t1` and `t0`
- `Variance`: a matrix of variances and covariances of the parameters estimates
mdn

Mediation Analysis via Likelihood

Description

mdn conducts mediation analysis in terms of likelihood.

Usage

mdn(fit.M, fit.Y, X, sig.level = 0.05, B = 0)

Arguments

fit.M  a fitted model object for mediator. It is an object from which the function logLik can extract the log-likelihood. Examples include those from “lm”, “glm”, etc.

fit.Y  a fitted model object for outcome. It can be of a class different from the model for the mediator

X  a character string of the name of the treatment variable.

sig.level  a numerical variable specifying the significance level for the test of the mediated effect.

B  an integer specifying the number of replicates used in the bootstrapping method for the confidence interval. Default value is 0 and bootstrapping is not conducted.
Details

Necessary log-likelihoods are extracted from the two fitted models. Various effects are then calculated. Significance of the mediated effect is known up to whether it is larger or smaller than sig.level. If it is larger, a 1 is reported; otherwise a 0 is reported. There is no p-value.

Value

A list with class "mdn" containing the following components:

- result: a data frame containing the results of the mediation analysis. The are five variables. They include estimates of various effects and lower and upper bounds of the bootstrap confidence interval at level (1-sig.level) followed by test statistics and their respective p-values.
- test: a character string specifying the test statistic used for the mediated effect
- Test: a numerical value of 0 or 1. If the specified test statistic is significant, its value is 1; otherwise its value is 0
- sig.level: a numerical variable specifying the significance level for the test of the mediated effect.
- Sample.size: number of subjects in the data
- B: an integer specifying the number of replicates used for the bootstrapping

Author(s)

Kai Wang <kai-wang@uiowa.edu>

References


Examples

data("jobs", package = "mediation")

fit.M <- lm(job_seek ~ treat + econ_hard + sex + age, data=jobs)
fit.Y <- lm(depress2 ~ treat + job_seek + econ_hard + sex + age, data=jobs)
mdn(fit.M, fit.Y)
mdn(fit.M, fit.Y, "treat")
mdn(fit.M, fit.Y, "treat", B=100)
Description

\texttt{print.mdn} is the print utility for the output from function \texttt{mdn}.

Usage

```r
## S3 method for class 'mdn'
print(x, ...)
```

Arguments

- \texttt{x}: an output from function \texttt{mdn}
- \texttt{...}: not used.

Details

The p-value for the mediated effect is displayed as greater or smaller than \texttt{sig.level}. For instance, if it is not significant at level 0.05, then "\texttt{> 0.05}" is displayed.

Author(s)

Kai Wang \(<\text{kai-wang@uiowa.edu}>\)

Examples

```r
data("jobs", package = "mediation")
fit.M <- lm(job_seek ~ treat + econ_hard + sex + age, data=jobs)
fit.Y <- lm(depress2 ~ treat + job_seek + econ_hard + sex + age, data=jobs)
mdn(fit.M, fit.Y, "treat")
```

Description

\texttt{pwr.mdn} Compute power of tests related to mediation analysis or sample size to achieve desired power.

Usage

```r
pwr.mdn(a, b, c.p, tau1, tau2, n = NULL, power = NULL, alpha = 0.05)
```
Arguments

- `a`: specified value for coefficient $a$
- `b`: specified value for coefficient $b$
- `c.p`: specified value for coefficient $c'$
- `tau1`: specified value of the ratio of residual variance of mediator $M$ to the variance of the treatment $X$
- `tau2`: specified value of the ratio of residual variance of outcome $Y$ to the variance of the treatment $X$
- `n`: the sample size available. Either "n" or "power" must be provided
- `power`: a value specifying the desired power. Either "n" or "power" must be provided
- `alpha`: specified significance level

Details

This model is for the basic three-factor model. If coefficients are standardized, then $\tau_1 = 1 - a^2$ and $\tau_2 = 1 - (c')^2 - b^2 - 2abc'$.

Value

A $2 \times 5$ matrix

Author(s)

Kai Wang <kai-wang@uiowa.edu>

References


Examples

```r
n = 100
X = rnorm(n)
s2X = mean((X-mean(X))^2)
a=0.3
b=0.3
c.p = a*b

pwr.mdn(a, b, c.p, 1/s2X, 1/s2X, alpha=0.05, power=0.8)
pwr.mdn(a, b, c.p, 1/s2X, 1/s2X, alpha=0.05, n=200)
```

```r
## using standardized coefficients
pwr.mdn(a, b, c.p, 1-a^2, 1-c.p^2-b^2-2*a*b*c.p, alpha=0.05, power=0.8)
pwr.mdn(a, b, c.p, 1-a^2, 1-c.p^2-b^2-2*a*b*c.p, alpha=0.05, n=200)
```
**S.test**

*S test of Berger (1996)*

**Description**

S.test conducts the S test proposed in Berger (1996)

**Usage**

S.test(u1, u2, alpha)

**Arguments**

- u1: a numerical value between 0 and 1.
- u2: a numerical value between 0 and 1.
- alpha: a numerical variable specifying the significance level for the test.

**Value**

If (u1, u2) falls in the rejection region of the S test, a 1 is returned; otherwise a 0 is returned.

**Author(s)**

Kai Wang <kai-wang@uiowa.edu>

**References**


**Examples**

S.test(0.1, 0.4, 0.05)
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