Package ‘WebPower’

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Title Basic and Advanced Statistical Power Analysis

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Author Zhiyong Zhang [aut, cre],
        Yujiao Mai [aut],
        Miao Yang [ctb],
        Ziqian Xu [ctb],
        Conor McNamara [ctb]

Maintainer Zhiyong Zhang <johnnyzhz@gmail.com>

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Description This is a collection of tools for conducting both basic and advanced statistical power analysis including correlation, proportion, t-test, one-way ANOVA, two-way ANOVA, linear regression, logistic regression, Poisson regression, mediation analysis, longitudinal data analysis, structural equation modeling and multilevel modeling. It also serves as the engine for conducting power analysis online at <https://webpower.psychstat.org>.

URL https://webpower.psychstat.org

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Description

This is a collection of tools for conducting both basic and advanced statistical power analysis including correlation, proportion, t-test, one-way ANOVA, two-way ANOVA, linear regression, logistic regression, Poisson regression, mediation analysis, longitudinal data analysis, structural equation modeling and multilevel modeling. It also serves as the engineer for conducting power analysis online at https://webpower.psychstat.org.

Details

This is a collection of tools for conducting both basic and advanced statistical power analysis including correlation, proportion, t-test, one-way ANOVA, two-way ANOVA, linear regression, logistic regression, Poisson regression, mediation analysis, longitudinal data analysis, structural equation modeling and multilevel modeling. It also serves as the engineer for conducting power analysis online at https://webpower.psychstat.org.

References


Example Data For CRT With 2 Arms

Description

- ID. The identification number of the subjects.
- cluster. The cluster number.
- score. The score of the subject.
- group. The group number.

Usage

CRT2

Format

An object of class data.frame with 8 rows and 4 columns.
Examples

# ID cluster score group
# 1 1 6 0
# 2 1 2 0
# 3 2 6 1
# 4 2 5 1
# 5 3 1 0
# 6 3 4 0
# 7 4 6 1
# 8 4 4 1

title('Example Data For CRT With 3 Arms', size=10)

description()
"• ID. The identification number of the subjects.
• cluster. The cluster number.
• score. The score of the subject.
• group. The group number.

Usage

CRT3

Format

An object of class \texttt{data.frame} with 30 rows and 4 columns.

Examples

# id cluster score group
# 1 1 1.93 0
# 2 1 1.51 0
# 3 1 2.13 0
# 4 1 2.96 0
# 5 1 3.84 0
# 6 2 3.36 1
# 7 2 3.13 1
# 8 2 1.71 1
# 9 2 3.1 1
# 10 2 2.53 1
# 11 3 2.01 2
# 12 3 4.73 2
# 13 3 3.34 2
# 14 3 0.11 2
# 15 3 3.6 2
# 16 4 2 0
# 17 4 1.99 0
# 18 4 1.89 0
# 19 4 2.25 0
# 20 4 1.83 0
# 21 5 3.03 1
# 22 5 2.08 1
# 23 5 1.5 1
# 24 5 3.18 1
# 25 5 1.92 1
# 26 6 3.49 2
# 27 6 3.08 2
# 28 6 4.54 2
# 29 6 2.34 2
# 30 6 4.33 2

estCRT2arm

Estimate multilevel effect size from data

Description

Estimate multilevel effect size from data

Usage

estCRT2arm(file)
estCRT3arm(file)
estMRT2arm(file)
estMRT3arm(file)

Arguments

file a data file

MRT2

Example Data For MRT With 2 Arms

Description

- ID. The identification number of the subjects.
- cluster. The cluster number.
- score. The score of the subject.
- group. The group number.

Usage

MRT2
Format

An object of class data.frame with 16 rows and 4 columns.

Examples

# Example data for MRT with 2 arms
# id cluster score group
# 1  1  6  0
# 2  1  2  0
# 3  1  3  1
# 4  1  3  1
# 5  2  6  0
# 6  2  10 0
# 7  2  7  1
# 8  2  6  1
# 9  3  6  0
# 10 3  5  0
# 11 3  4  1
# 12 3  4  1
# 13 4  1  0
# 14 4  8  0
# 15 4 10  1
# 16 4 -2  1

Description

- ID. The identification number of the subjects.
- cluster. The cluster number.
- score. The score of the subject.
- group. The group number.

Usage

MRT3

Format

An object of class data.frame with 24 rows and 4 columns.
nuniroot

Examples

```none
# id cluster score group
# 1 1 2 0
# 2 1 3 0
# 3 1 2 1
# 4 1 0 1
# 5 1 3 2
# 6 1 2 2
# 7 2 1 0
# 8 2 4 0
# 9 2 2 1
# 10 2 3 1
# 11 2 3 2
# 12 2 1 2
# 13 3 1 0
# 14 3 4 0
# 15 3 1 1
# 16 3 1 1
# 17 3 2 2
# 18 3 0 2
# 19 4 4 0
# 20 4 3 0
# 21 4 1 1
# 22 4 3 1
# 23 4 3 2
# 24 4 3 2
```

nuniroot  Solve A Single Equation

Description

The function searches in an interval for a root (i.e., zero) of the function f with respect to its first argument. The argument interval is for the input of x, the corresponding outcome interval will be used as the interval to be searched in.

Usage

nuniroot(f, interval, maxlength = 100)

Arguments

- **f**: Function for which the root is sought.
- **interval**: A vector containing the end-points of the interval to be searched for the root.
- **maxlength**: The number of value points in the interval to be searched. It is 100 by default.
Value

A list with at least four components: root and f.root give the location of the root and the value of the function evaluated at that point. iter and estim.prec give the number of iterations used and an approximate estimated precision for root. (If the root occurs at one of the endpoints, the estimated precision is NA.)

Examples

```r
f <- function(x) 1+x-0.5*x^2
interval <- c(-3,6)
nuniroot(f,interval)
```

plot.lcs.power

Plot the power curve for Latent Change Score Models

Description

This function is used to plot the power analysis results for Latent Change Score Models.

Usage

```r
## S3 method for class 'lcs.power'
plot(x, parameter, ...)
```

Arguments

- `x` : Data to plot.
- `parameter` : Parameters for features of the plot.
- `...` : Extra arguments. It is not required.

References


plot.webpower

To plot Statistical Power Curve

Description

This function is used to plot the power curves generated by webpower.

Usage

## S3 method for class 'webpower'
plot(x, xvar = NULL, yvar = NULL, xlab = NULL, ylab = NULL, ...)

Arguments

x
Objects of power analysis.

xvar
The variable name used as the x (horizontal) axis. It is not required.

yvar
The variable name used as the y (vertical) axis. It is not required.

xlab
The label for the x axis. It is not required.

ylab
The label for the y axis. It is not required.

...
Extra arguments. It is not required.

Value

The plot.

Examples

res <- wp.correlation(n=seq(50,100,10),r=0.3, alternative="two.sided")
plot(res)

print.webpower

To Print Statistical Power Analysis Results

Description

This function is used to summary the power analysis results.

Usage

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

Examples

res <- wp.correlation(n=seq(50,100,10),r=0.3, alternative="two.sided")
print(res)
sem.effect.size

**Arguments**

- `x` Object of power analysis. It is an object returned by a webpower function such as `wp.anova()`.
- `...` Extra arguments. It is not required.

**Value**

The printing of the input object of power analysis.

**Examples**

```r
res <- wp.correlation(n=50, r=0.3, alternative="two.sided")
print(res)
```

---

**Description**

This function is for calculating SEM effect size.

**Usage**

```r
sem.effect.size(full.model.pop, reduced.model)
```

**Arguments**

- `full.model.pop` Full model (under the alternative hypothesis) with population parameters.
- `reduced.model` Reduced model (under the null hypothesis) lavaan specification.

**Value**

An object of the power analysis.

- `delta` Effect size.
- `df` Degrees of freedom
- `RMSEA` RMSEA

**References**


Examples

```r
full.model.pop <-'
  y1 ~ 0.4*x
  y2 ~ 0.5*x + 0.2*y1
  y3 ~ 0.4*x
  y4 ~ 0.4*y1 + 0.4*y2 + 0.4*y3
  y1 ~~ 0.84*y1
  y2 ~~ 0.61*y2
  y3 ~~ 0.84*y3
  y4 ~~ 0.27*y4
',

reduced.model <-'
  y1 ~ x
  y2 ~ x
  y3 ~ x
  y4 ~ y1 + y3
',

sem.effect.size(full.model.pop, reduced.model)
```

---

### Description

This function is used to summary the power analysis results.

#### Usage

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

#### Arguments

- `object` Object of power analysis. It is an object returned by a webpower function for SEM based on Monte Carlo methods with class = 'power'.
- `...` Extra arguments. It is not required.

#### Value

The summary of the input object of power analysis.
**Description**

One-way analysis of variance (one-way ANOVA) is a technique used to compare means of two or more groups (e.g., Maxwell & Delaney, 2003). The ANOVA tests the null hypothesis that samples in two or more groups are drawn from populations with the same mean values. The ANOVA analysis typically produces an F-statistic, the ratio of the between-group variance to the within-group variance.

**Usage**

```r
wp.anova(k = NULL, n = NULL, f = NULL, alpha = 0.05, power = NULL, type = c("overall", "two.sided", "greater", "less"))
```

**Arguments**

- `k`: Number of groups.
- `n`: Sample size.
- `f`: Effect size. We use the statistic $f$ as the measure of effect size for one-way ANOVA as in Cohen (1988). Cohen defined the size of effect as: small 0.1, medium 0.25, and large 0.4.
- `alpha`: Significance level chose for the test. It equals 0.05 by default.
- `power`: Statistical power.
- `type`: Type of test ("overall" or "two.sided" or "greater" or "less"). The default is "two.sided". The option "overall" is for the overall test of anova; "two.sided" is for a contrast anova; "greater" is testing the between-group variance greater than the within-group, while "less" is vis versus.

**Value**

An object of the power analysis.

**References**


Examples

#To calculate the statistical power for the overall test of one-way ANOVA:
wp.anova(f=0.25,k=4, n=100, alpha=0.05)
# Power for One-way ANOVA
#
# k  n  f  alpha  power
# 4  100  0.25  0.05  0.5181755
#
# NOTE: n is the total sample size (overall)
# URL: http://psychstat.org/anova

#To calculate the power curve with a sequence of sample sizes:
res <- wp.anova(f=0.25, k=4, n=seq(100,200,10), alpha=0.05)
res
# Power for One-way ANOVA
#
# k  n  f  alpha  power
# 4  100  0.25  0.05  0.5181755
# 4  110  0.25  0.05  0.5636701
# 4  120  0.25  0.05  0.6065228
# 4  130  0.25  0.05  0.6465721
# 4  140  0.25  0.05  0.6837365
# 4  150  0.25  0.05  0.7180010
# 4  160  0.25  0.05  0.7494045
# 4  170  0.25  0.05  0.7780286
# 4  180  0.25  0.05  0.8039869
# 4  190  0.25  0.05  0.8274169
# 4  200  0.25  0.05  0.8484718
#
# NOTE: n is the total sample size (overall)
# URL: http://psychstat.org/anova

#To plot the power curve:
plot(res, type='b')

#To estimate the sample size with a given power:
wp.anova(f=0.25,k=4, n=NULL, alpha=0.05, power=0.8)
# Power for One-way ANOVA
#
# k  n  f  alpha  power
# 4  178.3971  0.25  0.05  0.8
#
# NOTE: n is the total sample size (overall)
# URL: http://psychstat.org/anova

#To estimate the minimum detectable effect size with a given power:
wp.anova(f=NULL,k=4, n=100, alpha=0.05, power=0.8)
# Power for One-way ANOVA
#
# k  n  f  alpha  power
# 4  100  0.3369881  0.05  0.8
# Statistical Power Analysis for One-way ANOVA with Binary Data

## Description

The power analysis procedure for one-way ANOVA with binary data is introduced by Mai and Zhang (2017). One-way ANOVA with binary data is used for comparing means of three or more groups of binary data. Its outcome variable is supposed to follow Bernoulli distribution. And its overall test uses a likelihood ratio test statistics.

## Usage

```r
wp.anova.binary(k = NULL, n = NULL, V = NULL, alpha = 0.05, power = NULL)
```

## Arguments

- **k**: Number of groups.
wp.anova.binary

n  Sample size.
V  Effect size. See the research by Mai and Zhang (2017) for details.
alpha  Significance level chosen for the test. It equals 0.05 by default.
power  Statistical power.

Value
An object of the power analysis.

References

Examples
#To calculate the statistical power for one-way ANOVA (overall test) with binary data:
wp.anova.binary(k=4,n=100,V=0.15,alpha=0.05)
# One-way Analogous ANOVA with Binary Data
#
# k  n  V  alpha  power
# 4 100 0.15 0.05 0.5723443
#
# NOTE: n is the total sample size
# URL: http://psychstat.org/anovabinary

#To generate a power curve given a sequence of sample sizes:
res <- wp.anova.binary(k=4,n=seq(100,200,10),V=0.15,alpha=0.05,power=NULL)
res
# One-way Analogous ANOVA with Binary Data
#
# k  n  V  alpha  power
# 4 100 0.15 0.05 0.5723443
# 4 110 0.15 0.05 0.6179014
# 4 120 0.15 0.05 0.6601594
# 4 130 0.15 0.05 0.6990429
# 4 140 0.15 0.05 0.7345606
# 4 150 0.15 0.05 0.7667880
# 4 160 0.15 0.05 0.7958511
# 4 170 0.15 0.05 0.8219126
# 4 180 0.15 0.05 0.8451603
# 4 190 0.15 0.05 0.8657970
# 4 200 0.15 0.05 0.8840327
#
# NOTE: n is the total sample size
# URL: http://psychstat.org/anovabinary
#To plot the power curve:
plot(res)

#To calculate the required sample size for one-way ANOVA (overall test) with binary data:
wp.anova.binary(k=4,n=NULL,V=0.15,power=0.8, alpha=0.05)
# One-way Analogous ANOVA with Binary Data
#
# k   n   V  alpha  power
# 4  161.5195  0.15  0.05  0.8
#
# NOTE: n is the total sample size
# URL: http://psychstat.org/anovabinary

#To calculate the minimum detectable effect size for one-way ANOVA (overall test) with binary data:
wp.anova.binary(k=4,n=100,V=NULL,power=0.8, alpha=0.05)
# One-way Analogous ANOVA with Binary Data
#
# k   n   V  alpha  power
# 4  100  0.1906373  0.05  0.8
#
# NOTE: n is the total sample size
# URL: http://psychstat.org/anovabinary

#To generate a power curve given a sequence of effect sizes:
wp.anova.binary(k=4,n=100,V=seq(0.1,0.5,0.05),alpha=0.05,power=NULL)
# One-way Analogous ANOVA with Binary Data
#
# k   n   V  alpha  power
# 4  100  0.10  0.05  0.2746396
# 4  100  0.15  0.05  0.5723443
# 4  100  0.20  0.05  0.8402271
# 4  100  0.25  0.05  0.9659434
# 4  100  0.30  0.05  0.9961203
# 4  100  0.35  0.05  0.9997729
# 4  100  0.40  0.05  0.9999933
# 4  100  0.45  0.05  0.9999999
# 4  100  0.50  0.05  1.0000000
#
# NOTE: n is the total sample size
# URL: http://psychstat.org/anovabinary

---

**wp.anova.count**  
*Statistical Power Analysis for One-way ANOVA with Count Data*

**Description**

The power analysis procedure for one-way ANOVA with count data is introduced by *Mai and Zhang (2017)*. One-way ANOVA with count data is used for comparing means of three or more groups of binary data. Its outcome variable is supposed to follow Poisson distribution. And its overall test uses a likelihood ratio test statistics.
wp.anova.count

Usage

wp.anova.count(k = NULL, n = NULL, V = NULL, alpha = 0.05, power = NULL)

Arguments

k Number of groups.

n Sample size.

V Effect size. See the research by Mai and Zhang (2017) for details.

alpha Significance level chose for the test. It equals 0.05 by default.

power Statistical power.

Value

An object of the power analysis.

References


Examples

#To calculate the statistical power for one-way ANOVA (overall test) with count data:
wp.anova.count(k=4,n=100,V=0.148,alpha=0.05)
# One-way Analogous ANOVA with Count Data
#
# k  n  V  alpha  power
# 4  100 0.148 0.05 0.5597441
#
# NOTE: n is the total sample size
# URL: http://psychstat.org/anovacount

#To generate a power curve given sequence of sample sizes:
res <- wp.anova.count(k=4,n=seq(100,200,10),V=0.148,alpha=0.05,power=NULL)
res
# One-way Analogous ANOVA with Count Data
#
# k  n  V  alpha  power
# 4  100 0.148 0.05 0.5597441
# 4  110 0.148 0.05 0.6049618
# 4  120 0.148 0.05 0.6470911
# 4  130 0.148 0.05 0.6860351
# 4  140 0.148 0.05 0.7217782
# To plot the power curve:
plot(res)

# To calculate the required sample size for one-way ANOVA (overall test) with count data:
wp.anova.count(k=4,n=NULL,V=0.148,power=0.8, alpha=0.05)
# One-way Analogous ANOVA with Count Data
#
# k  n  V  alpha  power
# 4  165.9143 0.148 0.05 0.8
#
# NOTE: n is the total sample size
# URL: http://psychstat.org/anovacount

# To calculate the minimum detectable effect size for one-way ANOVA (overall test) with count data:
wp.anova.count(k=4,n=100,V=NULL,power=0.8, alpha=0.05)
# One-way Analogous ANOVA with Count Data
#
# k  n  V  alpha  power
# 4  100 0.1906373 0.05 0.8
#
# NOTE: n is the total sample size
# URL: http://psychstat.org/anovacount

# To generate a power curve given a sequence of effect sizes:
res <- wp.anova.count(k=5,n=100,V=seq(0.1,0.5,0.05),alpha=0.05,power=NULL)
res
# One-way Analogous ANOVA with Count Data
#
# k  n  V  alpha  power
# 5  100 0.10 0.05 0.3200744
# 5  100 0.15 0.05 0.6634861
# 5  100 0.20 0.05 0.9118531
# 5  100 0.25 0.05 0.9893643
# 5  100 0.30 0.05 0.9994549
# 5  100 0.35 0.05 0.9999887
# 5  100 0.40 0.05 0.9999999
# 5  100 0.45 0.05 1.0000000
# 5  100 0.50 0.05 1.0000000
#
# NOTE: n is the total sample size
# URL: http://psychstat.org/anovacount
Description

A longitudinal design often involves data collection on multiple variables from multiple participants at multiple times. Growth curve models (GCM) are structural equation models for longitudinal data analysis (McArdle & Epstein, 1987; McArdle & Nesselroade, 2014). Latent change score models (LCSM) combine difference equations with growth curves to investigate change in longitudinal studies. LCSM provided an efficient way to model nonlinear trajectory (e.g., McArdle, 2000; McArdle & Hamagami, 2001; Hamagami et al., 2010). This function is used to conduct power analysis for bivariate LCSMs based on a Monte Carlo method (a method also used by Muthén & Muthén, 2002; Thoemmes et al., 2010; Zhang & Wang, 2009; Zhang, 2014). For each Monte Carlo replication, the Maximum likelihood ratio test is used for the model, while the Wald test is used for the parameter test. The method can obtain the power for testing each individual parameter of the models such as the change rate and coupling parameters.

Usage

```r
wp.blcsm(N = 100, T = 5, R = 1000, betay = 0, my0 = 0, mys = 0,
          vary = 1, vary0 = 1, varys = 1, vary0ys = 0, alpha = 0.05,
          betax = 0, mx0 = 0, mxs = 0, varx = 1, varx0 = 1, varxs = 1,
          varx0xs = 0, varx0y0 = 0, varx0ys = 0, vary0xs = 0, varxsys = 0,
          gammax = 0, gammay = 0, ...)
```

Arguments

- **N**: Sample size. It is 100 by default.
- **T**: Number of measurement occasions. It is 5 by default.
- **R**: Number of replications for the Monte Carlo simulation. It is 1000 by default.
- **betay**: Parameter in the model: The compound rate of change for variable y. Its default value is 0.
- **my0**: Parameter in the model: Mean of the initial latent score for variable y. Its default value is 0.
- **mys**: Parameter in the model: Mean of the linear constant effect for variable y. Its default value is 0.
- **varey**: Parameter in the model: Variance of the measurement error/uniqueness score for variable y. Its default value is 1.
- **vary0**: Parameter in the model: Variance of the initial latent score for variable y. Its default value is 0.
- **varys**: Parameter in the model: Variance of the linear constant effect for variable y. Its default value is 0.
- **vary0ys**: Parameter in the model: Covariance of the initial latent score and the linear constant effect for variable y. Its default value is 0.
alpha  

significance level chose for the test. It equals 0.05 by default.

betax  

Parameter in the model: The compound rate of change for variable x. Its default value is 0.

mx0  

Parameter in the model: Mean of the initial latent score for variable x. Its default value is 0.

mxs  

Parameter in the model: Mean of the linear constant effect for variable x. Its default value is 0.

varex  

Parameter in the model: Variance of the measurement error/uniqueness score for variable x. Its default value is 1.

varx0  

Parameter in the model: Variance of the initial latent score for variable x. Its default value is 1.

varxs  

Parameter in the model: Variance of the linear constant effect for variable x. Its default value is 0.

varx0xs  

Parameter in the model: Covariance of the initial latent score and the linear constant effect for variable x. Its default value is 0.

varx0y0  

Parameter in the model: Covariance of the initial latent scores for y and x. Its default value is 0.

varx0ys  

Parameter in the model: Covariance of the initial latent score for x and the linear constant effect for y. Its default value is 0.

vary0xs  

Parameter in the model: Covariance of the initial latent score for y and the linear constant effect for x. Its default value is 0.

varxsys  

Parameter in the model: Covariance of the linear constant effects for y and x. Its default value is 0.

gammax  

Coupling parameter in the model: The effect of variable x on the change score of variable y. Its default value is 0.

gammay  

Coupling parameter in the model: The effect of variable y on the change score of variable x. Its default value is 0.

...  

Extra arguments. It is not required.

Value  

An object of the power analysis. The output of the R function includes 4 main pieces of information for each parameter in the model. The first is the Monte Carlo estimate (mc.est). It is calculated as the mean of the R sets of parameter estimates from the simulated data. Note that the Monte Carlo estimates should be close to the population parameter values used in the model. The second is the Monte Carlo standard deviation (mc.sd), which is calculated as the standard deviation of the R sets of parameter estimates. The third is the Monte Carlo standard error (mc.se), which is obtained as the average of the R sets of standard error estimates of the parameter estimates. Lastly, mc.power is the statistical power for each parameter.

References  

## Examples

```r
## Not run:
# To conduct power analysis for a bivariate LCSM with sample size equal to 100:
wp.blcsm(N=100, T=5, R=1000, betay=0.08, my0=20, mys=1.5, varey=9,
vary0=3, vary0ys=0, alpha=0.05, betax=0.2, mx0=20, mxs=5,
    varex=9, varx0=3, varx0xs=0, varx0y0=1, varx0ys=0,
    vary0xs=0, varxsys=0, gammax=0, gammay=-.1)
# pop.par mc.est mc.sd mc.se mc.power N T
# betax 0.20 0.230 0.260 0.187 0.241 100 5
# betay 0.08 0.164 0.572 0.435 0.081 100 5
# gammax 0.00 -0.033 0.234 0.178 0.112 100 5
# gammay -0.10 -0.175 0.641 0.458 0.075 100 5
# mx0 20.00 20.004 0.336 0.326 1.000 100 5
# mxs 5.00 5.933 7.848 5.615 0.167 100 5
# my0 20.00 20.019 0.346 0.326 1.000 100 5
# mys 1.50 0.451 6.933 5.321 0.156 100 5
# varex 9.00 8.941 0.744 0.732 1.000 100 5
# vary0 3.00 2.951 1.423 1.245 0.684 100 5
# varx0 3.00 3.029 1.243 1.222 0.739 100 5
# varx0xs 0.00 -0.210 0.768 0.767 0.030 100 5
# varx0y0 1.00 1.052 0.840 0.835 0.226 100 5
# varx0ys 0.00 -0.012 0.668 0.601 0.017 100 5
# varxs 0.60 2.343 6.805 2.687 0.090 100 5
# varxsys 0.00 0.072 3.559 1.740 0.226 100 5
# vary0xs 0.00 0.198 2.263 1.629 0.031 100 5
# vary0ys 0.00 -0.371 1.970 1.511 0.106 100 5
# varys 0.05 1.415 3.730 2.096 0.024 100 5

# To conduct power analysis for a bivariate LCSM with sample size equal to 500:
wp.blcsm(N=500, T=5, R=1000, betay=0.08, my0=20, mys=1.5, varey=9,
vary0=3, vary0ys=0, alpha=0.05, betax=0.2, mx0=20,
    varex=9, varx0=3, varx0xs=0, varx0y0=1, varx0ys=0,
    vary0xs=0, varxsys=0, gammax=0, gammay=-.1)
# pop.par mc.est mc.sd mc.se mc.power N T
# betax 0.20 0.2009 0.031 0.031 1.000 500 5
# betay 0.08 0.0830 0.070 0.068 0.199 500 5
# gammax 0.00 -0.0014 0.036 0.036 0.057 500 5
# gammay -0.10 -0.1022 0.072 0.072 0.271 500 5
# mx0 20.00 19.9911 0.145 0.145 1.000 500 5
# mxs 5.00 5.0308 0.939 0.939 1.000 500 5
# my0 20.00 19.9999 0.143 0.143 1.000 500 5
# mys 1.50 1.4684 0.885 0.885 0.420 500 5
# varex 9.00 8.9836 0.340 0.340 1.000 500 5
# vary0 3.00 2.9961 1.341 1.341 1.000 500 5
# varx0 3.00 3.0052 0.524 0.524 1.000 500 5
# varx0xs 0.00 -0.0144 0.222 0.222 0.047 500 5
# varx0y0 1.00 1.0064 0.360 0.360 0.808 500 5
# varx0ys 0.00 -0.0012 0.199 0.201 0.051 500 5
```
### Description

This function is for power analysis for correlation. Correlation measures whether and how a pair of variables are related. The Pearson Product Moment correlation coefficient ($r$) is adopted here. The power calculation for correlation is conducted based on Fisher’s $z$ transformation of Pearson correlation coefficient (Fisher, 1915, 1921).

### Usage

```r
wp.correlation(n = NULL, r = NULL, power = NULL, p = 0, rho0 = 0,
alpha = 0.05, alternative = c("two.sided", "less", "greater"))
```

### Arguments

- `n`: Sample size.
- `r`: Effect size or correlation. According to Cohen (1988), a correlation coefficient of 0.10, 0.30, and 0.50 are considered as an effect size of "small", "medium", and "large", respectively.
- `power`: Statistical power.
- `p`: Number of variables to partial out.
- `rho0`: Null correlation coefficient.
- `alpha`: Significance level chose for the test. It equals 0.05 by default.
- `alternative`: Direction of the alternative hypothesis ("two.sided", "less", or "greater"). The default is "two.sided".

### Value

An object of the power analysis.
References


Examples

```r
wp.correlation(n=50,r=0.3, alternative="two.sided")
# Power for correlation
#
# n r alpha power
# 50 0.3 0.05 0.5728731
#
# URL: http://psychstat.org/correlation

#To calculate the power curve with a sequence of sample sizes:
res <- wp.correlation(n=seq(50,100,10),r=0.3, alternative="two.sided")
res
# Power for correlation
#
# n r alpha power
# 50 0.3 0.05 0.5728731
# 60 0.3 0.05 0.6541956
# 70 0.3 0.05 0.7230482
# 80 0.3 0.05 0.7803111
# 90 0.3 0.05 0.8272250
# 100 0.3 0.05 0.8651692
#
# URL: http://psychstat.org/correlation

#To plot the power curve:
plot(res, type='b')

#To estimate the sample size with a given power:
wp.correlation(n=NULL, r=0.3, power=0.8, alternative="two.sided")
# Power for correlation
#
# n r alpha power
# 83.94932 0.3 0.05 0.8
#
# URL: http://psychstat.org/correlation

#To estimate the minimum detectable effect size with a given power:
wp.correlation(n=NULL,r=0.3, power=0.8, alternative="two.sided")
# Power for correlation
```
Statistical Power Analysis for Cluster Randomized Trials with 2 Arms

Description

Cluster randomized trials (CRT) are a type of multilevel design for the situation when the entire cluster is randomly assigned to either a treatment arm or a control arm (Liu, 2013). The data from CRT can be analyzed in a two-level hierarchical linear model, where the indicator variable for treatment assignment is included in second level. If a study contains multiple treatments, then multiple indicators will be used. This function is for designs with 2 arms (i.e., a treatment and a control). Details leading to power calculation can be found in Raudenbush (1997) and Liu (2013).

Usage

```
wp.crt2arm(n = NULL, f = NULL, J = NULL, icc = NULL, power = NULL, alpha = 0.05, alternative = c("two.sided", "one.sided"), interval = NULL)
```
Arguments

- n: Sample size. It is the number of individuals within each cluster.
- f: Effect size. It specifies either the main effect of treatment, or the mean difference between the treatment clusters and the control clusters.
- J: Number of clusters/sides. It tells how many clusters are considered in the study design. At least two clusters are required.
- icc: Intra-class correlation. ICC is calculated as the ratio of between-cluster variance to the total variance. It quantifies the degree to which two randomly drawn observations within a cluster are correlated.
- power: Statistical power.
- alpha: Significance level chosen for the test. It equals 0.05 by default.
- alternative: Type of the alternative hypothesis ("two.sided" or "one.sided"). The default is "two.sided". The option "one.sided" can be either "less" or "greater".
- interval: A vector containing the end-points of the interval to be searched for the root.

Value

An object of the power analysis.

References


Examples

# To calculate the statistical power given sample size and effect size:
wp.crt2arm(f = 0.6, n = 20, J = 10, icc = 0.1, alpha = 0.05, power = NULL)
# Cluster randomized trials with 2 arms
#
# J n f icc power alpha
# 10 20 0.6 0.1 0.5901684 0.05
#
# NOTE: n is the number of subjects per cluster.
# URL: http://psychstat.org/crt2arm

# To generate a power curve given a sequence of sample sizes:
res <- wp.crt2arm(f = 0.6, n = seq(20, 100, 10), J = 10,
                  icc = 0.1, alpha = 0.05, power = NULL)
res
# Cluster randomized trials with 2 arms
#
# J n f icc power alpha
Cluster randomized trials (CRT) are a type of multilevel design for the situation when the entire cluster is randomly assigned to either a treatment arm or a control arm (Liu, 2013). The data from CRT can be analyzed in a two-level hierarchical linear model, where the indicator variable for treatment assignment is included in second level. If a study contains multiple treatments, then multiple indicators will be used. This function is for designs with 3 arms (i.e., two treatments and a control). Details leading to power calculation can be found in Raudenbush (1997) and Liu (2013).

Usage

```r
wp.crt3arm(n = NULL, f = NULL, J = NULL, icc = NULL, power = NULL, alpha = 0.05, alternative = c("two.sided", "one.sided"), type = c("main", "treatment", "omnibus"), interval = NULL)
```

Arguments

- `n`: Sample size. It is the number of individuals within each cluster.
Effect size. It specifies one of the three types of effects: the main effect of treatment, the mean difference between the treatment clusters, and the control clusters.

Number of clusters / sides. It tells how many clusters are considered in the study design. At least two clusters are required.

Intra-class correlation. ICC is calculated as the ratio of between-cluster variance to the total variance. It quantifies the degree to which two randomly drawn observations within a cluster are correlated.

Statistical power.

significance level chosen for the test. It equals 0.05 by default.

Type of the alternative hypothesis ("two.sided" or "one.sided"). The default is "two.sided". The option "one.sided" can be either "less" or "greater".

Type of effect ("main" or "treatment" or "omnibus") with "main" as default. The type "main" tests the difference between the average treatment arms and the control arm; Type "treatment" tests the difference between the two treatment arms; and Type "omnibus" tests whether the tree arms are all equivalent.

A vector containing the end-points of the interval to be searched for the root.

An object of the power analysis.


# To calculate the statistical power given sample size and effect size:
res <- wp.crt3arm(f = 0.5, n = seq(20, 100, 10), J = 10, icc = 0.1, alpha = 0.05, power = NULL)
res
# Cluster randomized trials with 3 arms
#
#  J  n  f  icc  power alpha
# 10 20 0.5 0.1 0.3940027 0.05
#
# NOTE: n is the number of subjects per cluster.
# URL: http://psychstat.org/crt3arm

# To generate a power curve given a sequence of sample sizes:
res <- wp.crt3arm(f = 0.5, n = seq(20, 100, 10), J = 10, icc = 0.1, alpha = 0.05, power = NULL)
res
# Cluster randomized trials with 3 arms
wp.effect.CRT2arm

Effect size calculator based on raw data for Cluster Randomized Trials with 2 Arms

Description

This function is for effect size and ICC calculation for CRT with 2 arms based on empirical data. Cluster randomized trials (CRT) are a type of multilevel design for the situation when the entire cluster is randomly assigned to either a treatment arm or a control arm (Liu, 2013). The data from CRT can be analyzed in a two-level hierarchical linear model, where the indicator variable for treatment assignment is included in second level. If a study contains multiple treatments, then multiple indicators will be used. This function is for designs with 3 arms (i.e., two treatments and a control). Details leading to power calculation can be found in Raudenbush (1997) and Liu (2013). The Effect size $f$ specifies the main effect of treatment, the mean difference between the treatment clusters and the control clusters. This function is used to calculate the effect size with a input data set.

Usage

wp.effect.CRT2arm(file)
Arguments

file  The input data set. The first column of the data is the ID variable, the second column represents cluster, the third column is the outcome variable, and the fourth column is the condition variable (0 for control, 1 for condition).

Value

A list including effect size $f$ and ICC.

References


Examples

#Empirical data set CRT2:
CRT2
#ID cluster score group
#1 1 6 0
#2 1 2 0
#3 2 6 1
#4 2 5 1
#5 3 1 0
#6 3 4 0
#7 4 6 1
#8 4 4 1

#To calculate the effect size and ICC based on empirical data
wp.effect.CRT2arm (CRT2)
# Effect size for CRT2arm
#
# f ICC
# 1.264911 -0.5
#
# NOTE: f is the effect size.
# URL: http://psychstat.org/crt2arm
Description

This function is for effect size and ICC calculation for Cluster randomized trials (CRT) with 3 arms based on empirical data. CRT are a type of multilevel design for the situation when the entire cluster is randomly assigned to either a treatment arm or a control arm (Liu, 2013). The data from CRT can be analyzed in a two-level hierarchical linear model, where the indicator variable for treatment assignment is included in second level. If a study contains multiple treatments, then multiple indicators will be used. This function is for designs with 3 arms (i.e., two treatments and a control). Details leading to power calculation can be found in Raudenbush (1997) and Liu (2013). The Effect size $f$ specifies the main effect of treatment, the mean difference between the treatment clusters and the control clusters. This function is used to calculate the effect size with a input data set.

Usage

wp.effect.CRT3arm(file)

Arguments

file  The input data set. The first column of the data is the ID variable, the second column represents cluster, the third column is the outcome variable, and the fourth column is the condition variable (0 for control, 1 for treatment1, 2 for treatment2).

Value

A list including effect size $f_1$, $f_2$, $f_3$, and ICC.

References


Examples

# To calculate the effect sizes based on empirical data
wp.effect.CRT3arm (CRT3)
# Effect size for CRT3arm
#
# f1    f2    f3    ICC
# 0.6389258 -0.6189113  0.3931397 -0.019794
#
# NOTE: f1 for treatment main effect;
#        f2 for difference between two treatments;
#        f3 for effect size of omnibus test.
# URL: http://psychstat.org/crt3arm
Effect size calculator based on raw data for Multisite Randomized Trials with 2 Arms

Description

This function is for effect size calculation for Multisite randomized trials (MRT) with 2 arms based on empirical data. MRTs are a type of multilevel design for the situation when the entire cluster is randomly assigned to either a treatment arm or a control arm (Liu, 2013). The data from MRT can be analyzed in a two-level hierarchical linear model, where the indicator variable for treatment assignment is included in the first level. If a study contains multiple treatments, then multiple indicators will be used. Three types of tests are considered in the function: (1) The "main" type tests treatment main effect; (2) The "site" type tests the variance of cluster/site means; and (3) The "variance" type tests variance of treatment effects. Details leading to power calculation can be found in Raudenbush (1997) and Liu (2013). This function is used to calculate the effect size with an input data set.

Usage

wp.effect.MRT2arm(file)

Arguments

file

The input data set. The first column of the data is the ID variable, the second column represents cluster, the third column is the outcome variable, and the fourth column is the condition variable (0 for control, 1 for condition).

Value

A list including effect size f.

References


Examples

# To calculate the effect size based on empirical data
wp.effect.MRT2arm (MRT2)
# Effect size for MRT2arm
#
# f
# -0.2986755
#
# NOTE: f is the effect size.
# URL: http://psychstat.org/mrt2arm
Description

This function is for effect size calculation for Multisite randomized trials (MRT) with 3 arms based on empirical data. MRTs are a type of multilevel design for the situation when the entire cluster is randomly assigned to either a treatment arm or a control arm (Liu, 2013). The data from MRT can be analyzed in a two-level hierarchical linear model, where the indicator variable for treatment assignment is included in first level. If a study contains multiple treatments, then multiple indicators will be used. This function is for designs with 3 arms (i.e., two treatments and a control). Three types of tests are considered in the function: (1) The "main" type tests treatment main effect; (2) The "treatment" type tests the difference between the two treatments; and (3) The "omnibus" type tests whether the three arms are all equivalent. Details leading to power calculation can be found in Raudenbush (1997) and Liu (2013). This function is used to calculate the effect size with a input data set.

Usage

wp.effect.MRT3arm(file)

Arguments

- **file**: The input data set. The first column of the data is the ID variable, the second column represents cluster, the third column is the outcome variable, and the fourth column is the condition variable (0 for control, 1 for treatment1, 2 for treatment2).

Value

A list including effect size f.

References


Examples

```r
# To calculate the effect size and ICC based on empirical data
# wp.effect.MRT3arm(MRT3)
# Effect size for MRT3arm
#
# f1  f2
# -0.6214215 -0.355098
```
# # NOTE: f1 for treatment main effect; # f2 for comparing the two treatments. # URL: http://psychstat.org/mrt3arm

## Description

Power analysis for two-way, three-way and k-way ANOVA

## Usage

```r
wp.kanova(n = NULL, ndf = NULL, f = NULL, ng = NULL, alpha = 0.05, power = NULL)
```

## Arguments

- `n`: Sample size
- `ndf`: Numerator degrees of freedom
- `f`: Effect size
- `ng`: Number of groups
- `alpha`: Significance level
- `power`: Statistical power

## References


## Examples

```r
### Chapter 6. two-way and three-way ANOVA ###
## Main effect of two-way ANOVA
wp.kanova(n=120, ndf=2, f=0.2, alph=0.05, ng=6)

## Interaction effect of two-way ANOVA
wp.kanova(n=120, ndf=2, f=0.4, alph=0.05, ng=6)

## Interaction effect of three-way ANOVA
wp.kanova(n=360, ndf=4, f=0.3, alph=0.05, ng=18)
```
Statistical Power Curve for Univariate Latent Change Score Models based on Monte Carlo Simulation

Description

A longitudinal design often involves data collection on multiple variables from multiple participants at multiple times. Growth curve models (GCM) are structural equation models for longitudinal data analysis (McArdle & Epstein, 1987; McArdle & Nesselroade, 2014). Latent change score models (LCSM) combine difference equations with growth curves to investigate change in longitudinal studies. LCSM provide an efficient way to model nonlinear trajectory (e.g., McArdle, 2000; McArdle & Hamagami, 2001; Hamagami et al., 2010). This function is used to conduct power analysis for univariate LCSMs based on a Monte Carlo method (a method also used by Muthén & Muthén, 2002; Thoemmes et al., 2010; Zhang & Wang, 2009; Zhang, 2014). For each Monte Carlo replication, the Maximum likelihood ratio test is used for the model, while the Wald test is used for the parameter test. The method can obtain the power for testing each individual parameter of the models such as the change rate and coupling parameters.

Usage

`wp.lcsm(N = 100, T = 5, R = 1000, betay = 0, my0 = 0, mys = 0, varey = 1, vary0 = 1, varys = 1, vary0ys = 0, alpha = 0.05, ...)`

Arguments

- `N` Sample size. It is 100 by default.
- `T` Number of measurement occasions. It is 5 by default.
- `R` Number of replications for the Monte Carlo simulation. It is 1000 by default.
- `betay` Parameter in the model: The compound rate of change. Its default value is 0.
- `my0` Parameter in the model: Mean of the initial latent score. Its default value is 0.
- `mys` Parameter in the model: Mean of the linear constant effect. Its default value is 0.
- `varey` Parameter in the model: Variance of the measurement error/uniqueness score. Its default value is 1.
- `vary0` Parameter in the model: Variance of the initial latent score. Its default value is 1.
- `varys` Parameter in the model: Variance of the linear constant effect. Its default value is 0.
- `vary0ys` Parameter in the model: Covariance of the initial latent score and the linear constant effect. Its default value is 0.
- `alpha` Significance level chosen for the test. It equals 0.05 by default.
- `...` Extra arguments. It is not required.
Value

An object of the power analysis. The output of the R function includes 4 main pieces of information for each parameter in the model. The first is the Monte Carlo estimate (mc.est). It is calculated as the mean of the R sets of parameter estimates from the simulated data. Note that the Monte Carlo estimates should be close to the population parameter values used in the model. The second is the Monte Carlo standard deviation (mc.sd), which is calculated as the standard deviation of the R sets of parameter estimates. The third is the Monte Carlo standard error (mc.se), which is obtained as the average of the R sets of standard error estimates of the parameter estimates. Lastly, mc.power is the statistical power for each parameter.

References


Examples

```r
## Not run:
# Power analysis for a univariate LCSM
# Power for each parameter given sample size, number of measurement occasions, # true effect (true values of parameters), and significance level:
wp.lcsm(N = 100, T = 5, R = 1000, betay = 0.1, my0 = 20, mys = 1.5,
    varey = 9, vary0 = 2.5, varys = .05, vary0ys = 0, alpha = 0.05)
# pop.par mc.est mc.sd mc.se mc.power N T
# betay  0.10 0.103 0.043 0.044 0.664 100 5
# my0  20.00 19.999 0.324 0.319 1.000 100 5
# mys  1.50 1.418 1.106 1.120 0.274 100 5
# varey  9.00 8.961 0.724 0.732 1.000 100 5
# vary0  2.50 2.463 1.151 1.139 0.583 100 5
# vary0ys  0.00 -0.004 0.408 0.403 0.048 100 5
# varys  0.05 0.053 0.173 0.175 0.050 100 5
#
# #To calculate the Type I error rate and power for parameters
wp.lcsm(N = 100, T = 5, R = 1000, betay = 0, my0 = 0, mys = 0,
    varey = 1, vary0 = 1, varys = 1, vary0ys = 0, alpha = 0.05)
# pop.par mc.est mc.sd mc.se mc.power N T
# betay  0 0.001 0.056 0.056 0.046 100 5
# my0  0 0.001 0.129 0.126 0.056 100 5
# mys  0 0.002 0.105 0.105 0.044 100 5
# varey  1 0.994 0.083 0.081 1.000 100 5
# vary0  1 0.990 0.236 0.230 1.000 100 5
# vary0ys 0 -0.005 0.136 0.136 0.044 100 5
# varys  1 1.006 0.227 0.227 1.000 100 5
#
# # To generate a power curve for different sample sizes for a univariate LCSM
res <- wp.lcsm(N = seq(100, 200, 10), T = 5, R = 1000, betay = 0.1,
    my0 = 20, mys = 1.5, varey = 9, vary0 = 2.5,
    varys = .05, vary0ys = 0, alpha = 0.05)
```
#plot(res, parameter='betay')
#plot(res, parameter='mys')

# To generate a power curve for different numbers of occasions for a univariate LCSM
res <- wp.lcsm(N = 100, T = 4:10, R = 1000, betay = 0.1, my0 = 20, mys = 1.5,
              vary = 9, vary0 = 2.5, varys = .05, vary0ys = 0, alpha = 0.05)
#plot(res, parameter='betay')
#plot(res, parameter='mys')

## End(Not run)

---

**wp.logistic**

**Statistical Power Analysis for Logistic Regression**

**Description**

This function is for Logistic regression models. Logistic regression is a type of generalized linear models where the outcome variable follows Bernoulli distribution. Here, Maximum likelihood methods is used to estimate the model parameters. The estimated regression coefficient is assumed to follow a normal distribution. A Wald test is use to test the mean difference between the estimated parameter and the null parameter (tipically the null hypothesis assumes it equals 0). The procedure introduced by Demidenko (2007) is adopted here for computing the statistical power.

**Usage**

```r
wp.logistic(n = NULL, p0 = NULL, p1 = NULL, alpha = 0.05,
            power = NULL, alternative = c("two.sided", "less", "greater"),
            family = c("Bernoulli", "exponential", "lognormal", "normal", "Poisson",
                        "uniform"), parameter = NULL)
```

**Arguments**

- **n**: Sample size.
- **p0**: \(\text{Prob}(Y=1|X=0)\): the probability of observing 1 for the outcome variable \(Y\) when the predictor \(X\) equals 0.
- **p1**: \(\text{Prob}(Y=1|X=1)\): the probability of observing 1 for the outcome variable \(Y\) when the predictor \(X\) equals 1.
- **alpha**: significance level chosed for the test. It equals 0.05 by default.
- **power**: Statistical power.
- **alternative**: Direction of the alternative hypothesis ("two.sided" or "less" or "greater"). The default is "two.sided".
- **family**: Distribution of the predictor ("Bernoulli", "exponential", "lognormal", "normal", "Poisson", "uniform"). The default is "Bernoulli".
- **parameter**: Corresponding parameter for the predictor’s distribution. The default is 0.5 for "Bernoulli", 1 for "exponential", (0,1) for "lognormal" or "normal", 1 for "Poisson", and (0,1) for "uniform".
Value

An object of the power analysis.

References


Examples

#To calculate the statistical power given sample size and effect size:
wp.logistic(n = 200, p0 = 0.15, p1 = 0.1, alpha = 0.05,
            power = NULL, family = "normal", parameter = c(0,1))
# Power for logistic regression
#
#   p0   p1   beta0   beta1   n   alpha power
# 0.15 0.1 -1.734601 -0.4626235 200 0.05 0.6299315
#
# URL: http://psychstat.org/logistic

#To generate a power curve given a sequence of sample sizes:
res <- wp.logistic(n = seq(100,500,50), p0 = 0.15, p1 = 0.1, alpha = 0.05,
                   power = NULL, family = "normal", parameter = c(0,1))
res
# Power for logistic regression
#
#   p0   p1   beta0   beta1   n   alpha power
# 0.15 0.1 -1.734601 -0.4626235 100 0.05 0.3672683
# 0.15 0.1 -1.734601 -0.4626235 150 0.05 0.5098635
# 0.15 0.1 -1.734601 -0.4626235 200 0.05 0.6299315
# 0.15 0.1 -1.734601 -0.4626235 250 0.05 0.7264597
# 0.15 0.1 -1.734601 -0.4626235 300 0.05 0.8014116
# 0.15 0.1 -1.734601 -0.4626235 350 0.05 0.8580388
# 0.15 0.1 -1.734601 -0.4626235 400 0.05 0.8998785
# 0.15 0.1 -1.734601 -0.4626235 450 0.05 0.9302222
# 0.15 0.1 -1.734601 -0.4626235 500 0.05 0.9518824
#
# URL: http://psychstat.org/logistic

#To plot the power curve:
plot(res)

#To calculate the required sample size given power and effect size:
wp.logistic(n = NULL, p0 = 0.15, p1 = 0.1, alpha = 0.05,
            power = 0.8, family = "normal", parameter = c(0,1))
# Power for logistic regression
#
#   p0   p1   beta0   beta1   n   alpha power

wp.mc.chisq.diff

# 0.15 0.1 -1.734601 -0.4626235 298.9207 0.05 0.8
# URL: http://psychstat.org/logistic

### Description
This function is for SEM power analysis based on the chi-square difference test.

### Usage
```r
wp.mc.chisq.diff(full.model.pop, full.model, reduced.model, N=100, R=1000, alpha=0.05)
```

### Arguments
- `full.model.pop` Full model (under the alternative hypothesis) with population parameters.
- `full.model` Full model (under the alternative hypothesis) lavaan specification.
- `reduced.model` Reduced model (under the null hypothesis) lavaan specification.
- `N` Sample size.
- `R` Number of Monte Carlo replications.
- `alpha` Significance level chosen for the test. It equals 0.05 by default.

### Value
An object of the power analysis.

- `power` Statistical power.
- `df` Degrees of freedom.
- `chi.diff` Chi-square differences between the reduced model and the full model.

### References
Examples

```r
set.seed(20220722)
full.model.pop <-
  y1 ~ 0.4*x
  y2 ~ 0.5*x + 0.2*y1
  y3 ~ 0.4*x
  y4 ~ 0.4*y1 + 0.4*y2 + 0.4*y3
  y1 ~~ 0.84*y1
  y2 ~~ 0.61*y2
  y3 ~~ 0.84*y3
  y4 ~~ 0.27*y4

full.model <-
  y1 ~ x
  y2 ~ x + y1
  y3 ~ x
  y4 ~ y1 + y2 + y3

reduced.model <-
  y1 ~ x
  y2 ~ x
  y3 ~ x
  y4 ~ y1 + y3

wp.mc.chisq.diff(full.model.pop, full.model, reduced.model)
```

Description

Structural equation modeling (SEM) is a multivariate technique used to analyze relationships among observed and latent variables. It can be viewed as a combination of factor analysis and multivariate regression analysis. A mediation model can be viewed as a SEM model. Functions `wp.sem.chisq` and `wp.sem.rmsea` provide analytical solutions of power analysis for SEM. Function `wp.mediation` provides analytical solutions of power analysis for a simple mediation model. This function provides a solution based on Monte Carlo simulation (see Zhang, 2014). If the model is a mediation, Sobel test is used for the mediation / indirect effects. The solution is extended from the general framework for power analysis for complex mediation models using Monte Carlo simulation in Mplus (Muthén & Muthén, 2011) proposed by Thoemmes et al. (2010). We extended the framework in two ways. First, the method allows the specification of nonnormal data in the Monte Carlo simulation and can
thereby reflect more closely practical data collection. Second, the function \texttt{wp.mc.sem.basic} of a free, open-source R package, WebPower, is developed to ease power analysis for mediation models using the proposed method.

**Usage**

\begin{verbatim}
wp.mc.sem.basic(model, indirect = NULL, nobs = 100, nrep = 1000, alpha = 0.95, skewness = NULL, kurtosis = NULL, ovnames = NULL, se = "default", estimator = "default", parallel = "no", ncore = Sys.getenv("NUMBER_OF_PROCESSORS"), cl = NULL, ...)
\end{verbatim}

**Arguments**

- **model**: Model specified using lavaan syntax. More about model specification can be found in Rosseel (2012).
- **indirect**: Indirect effect defined using lavaan syntax.
- **nobs**: Sample size.
- **nrep**: Number of replications for the Monte Carlo simulation.
- **alpha**: Significance level chosen for the test. It equals 0.05 by default.
- **skewness**: A sequence of skewnesses of the observed variables.
- **kurtosis**: A sequence of kurtosises of the observed variables.
- **ovnames**: Names of the observed variables in the model.
- **se**: The method for calculating the standard errors. Its default method "default" is regular standard errors. More about methods specification standard errors calculation can be found in Rosseel (2012).
- **estimator**: Estimator. It is Maximum likelihood estimator by default. More about estimator specification can be found in Rosseel (2012).
- **parallel**: Parallel computing ("no" or "parallel" or "snow"). It is "no" by default, which means it will not use parallel computing. The option "parallel" is to use multiple cores in a computer for parallel computing. It is used with the number of cores (ncore). The option "snow" is to use clusters for parallel computing. It is used with the number of clusters (cl).
- **ncore**: Number of processors used for parallel computing. By default, ncore = Sys.getenv('NUMBER_OF_PROCESSORS')
- **cl**: Number of clusters. It is NULL by default. When it is NULL, the program will detect the number of clusters automatically.
- **...**: Extra arguments. It is not required.

**Value**

An object of the power analysis. The power for all parameters in the model as well as the indirect effects if specified.
References


Examples

set.seed(20220722)

#To calculate power for mediation based on Monte Carlo simulation when Sobel test is used:
#To specify the model
demo = "
y ~ cp*x + start(0)*x + b*m + start(0.39)* m
m ~ a*x + start(0.39)*x
x ~~ start(1)*x
m ~~ start(1)*m
y ~~ start(1)*y"

#To specify the indirect effects
mediation = "
ab := a*b
abc:= a*b + cp"

#To calculate power for mediation using regular standard errors
## change nrep to at least 1,000 in real data analysis
sobel.regular = wp.mc.sem.basic(model=demo, indirect=mediation, nobs=100, nrep=10,
                              skewness=c(0, 0, 1.3), kurtosis=c(0,0,10), ovnames=c("x","m","y"))

#To calculate power for mediation using robust standard errors
sobel.robust = wp.mc.sem.basic(model=demo, indirect=mediation, nobs=100, nrep=10,
                               skewness=c(0, 0, 1.3), kurtosis=c(0,0,10), ovnames=c("x","m","y"), se="robust")

#To print the power for mediation based on Sobel test using regular standard errors:
summary(sobel.regular)
#  Basic information:
#  #  Estimation method        ML
#  #  Standard error           standard
#  #  Number of requested replications  1000


Number of successful replications 1000

Regressions:

<table>
<thead>
<tr>
<th></th>
<th></th>
<th>True Estimate</th>
<th>MSE</th>
<th>SD</th>
<th>Power</th>
<th>Coverage</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>y ~</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>x  (cp)</td>
<td>0.000</td>
<td>0.003</td>
<td>0.106</td>
<td>0.107</td>
<td>0.045</td>
</tr>
<tr>
<td></td>
<td>m  (b)</td>
<td>0.390</td>
<td>0.387</td>
<td>0.099</td>
<td>0.113</td>
<td>0.965</td>
</tr>
<tr>
<td></td>
<td>m ~</td>
<td></td>
<td></td>
<td></td>
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<td></td>
</tr>
<tr>
<td></td>
<td>x  (a)</td>
<td>0.390</td>
<td>0.389</td>
<td>0.100</td>
<td>0.101</td>
<td>0.976</td>
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Variances:

<table>
<thead>
<tr>
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<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
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<td>y</td>
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Intercepts:

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<tr>
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<th></th>
<th></th>
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</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>m</td>
<td>0.000</td>
<td>0.000</td>
<td>0.100</td>
<td>0.104</td>
<td>0.058</td>
</tr>
<tr>
<td></td>
<td>x</td>
<td>0.000</td>
<td>0.000</td>
<td>0.100</td>
<td>0.105</td>
<td>0.054</td>
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</table>

Indirect/Mediation effects:

<table>
<thead>
<tr>
<th></th>
<th></th>
<th>ab</th>
<th></th>
<th></th>
<th></th>
<th></th>
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</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>0.152</td>
<td>0.150</td>
<td>0.056</td>
<td>0.060</td>
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</tr>
<tr>
<td></td>
<td>abc</td>
<td>0.152</td>
<td>0.153</td>
<td>0.106</td>
<td>0.109</td>
<td>0.305</td>
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</tbody>
</table>

To print the power analysis results for mediation based on Sobel test using robust standard errors:

summary(sobel.robust)

Basic information:

<table>
<thead>
<tr>
<th></th>
<th></th>
<th>Estimation method</th>
<th>ML</th>
</tr>
</thead>
<tbody>
<tr>
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<td></td>
<td>Standard error</td>
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<td></td>
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<td>1000</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Number of successful replications</td>
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</tr>
</tbody>
</table>

Regressions:

<table>
<thead>
<tr>
<th></th>
<th></th>
<th>True Estimate</th>
<th>MSE</th>
<th>SD</th>
<th>Power</th>
<th>Coverage</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>y ~</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>x  (cp)</td>
<td>0.000</td>
<td>-0.003</td>
<td>0.106</td>
<td>0.113</td>
<td>0.055</td>
</tr>
<tr>
<td></td>
<td>m  (b)</td>
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<td>0.398</td>
<td>0.111</td>
<td>0.119</td>
<td>0.972</td>
</tr>
<tr>
<td></td>
<td>m ~</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>x  (a)</td>
<td>0.390</td>
<td>0.389</td>
<td>0.099</td>
<td>0.101</td>
<td>0.974</td>
</tr>
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</table>

Intercepts:

<table>
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<tr>
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<th>y</th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>m</td>
<td>0.000</td>
<td>0.000</td>
<td>0.100</td>
<td>0.104</td>
<td>0.058</td>
</tr>
<tr>
<td></td>
<td>x</td>
<td>0.000</td>
<td>-0.004</td>
<td>0.100</td>
<td>0.104</td>
<td>0.066</td>
</tr>
</tbody>
</table>

Variances:

<table>
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<tr>
<th></th>
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<th>x</th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>m</td>
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<tr>
<td></td>
<td>y</td>
<td>1.000</td>
<td>0.976</td>
<td>0.135</td>
<td>0.135</td>
<td>1.000</td>
</tr>
</tbody>
</table>

Indirect/Mediation effects:

<table>
<thead>
<tr>
<th></th>
<th></th>
<th>ab</th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
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<td>0.060</td>
<td>0.064</td>
<td>0.870</td>
</tr>
<tr>
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<td>abc</td>
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<td>0.153</td>
<td>0.108</td>
<td>0.117</td>
<td>0.303</td>
</tr>
</tbody>
</table>
Description

Structural equation modeling (SEM) is a multivariate technique used to analyze relationships among observed and latent variables. It can be viewed as a combination of factor analysis and multivariate regression analysis. A mediation model can be viewed as a SEM model. Functions `wp.sem.chisq` and `wp.sem.rmsea` provide analytical solutions of power analysis for SEM. Function `wp.mediation` provides analytical solutions of power analysis for a simple mediation model. This function provides a solution based on Monte Carlo simulation (see Zhang, 2014) and a bootstrap method for testing the indirect/mediation effects. The solution is extended from the general framework for power analysis for complex mediation models using Monte Carlo simulation in Mplus (Muthén & Muthén, 2011) proposed by Thoemmes et al. (2010). We extended the framework in three ways. First, we propose a general method to conduct power analysis for mediation models based on the bootstrap method. The method is still based on Monte Carlo simulation but uses the bootstrap method to test mediation effects. Second, the method allows the specification of nonnormal data in the Monte Carlo simulation and can thereby reflect more closely practical data collection. Third, the function `wp.mc.sem.boot` of a free, open-source R package, WebPower, is developed to ease power analysis for mediation models using the proposed method.

Usage

```r
wp.mc.sem.boot(model, indirect = NULL, nobs = 100, nrep = 1000, nboot = 1000, alpha = 0.95, skewness = NULL, kurtosis = NULL, ovnames = NULL, se = "default", estimator = "default", parallel = "no", ncore = Sys.getenv("NUMBER_OF_PROCESSORS"), cl = NULL, ...)
```

Arguments

- `model` Model specified using lavaan syntax. More about model specification can be found in Rosseel (2012).
- `indirect` Indirect effect defined using lavaan syntax.
- `nobs` Sample size. It is 100 by default.
- `nrep` Number of replications for the Monte Carlo simulation. It is 1000 by default.
- `nboot` Number of replications for the bootstrap to test the specified parameter (e.g., mediation). It is 1000 by default.
- `alpha` Significance level chosen for the test. It equals 0.05 by default.
- `skewness` A sequence of skewnesses of the observed variables. It is not required.
- `kurtosis` A sequence of kurtosises of the observed variables. It is not required.
- `ovnames` Names of the observed variables in the model. It is not required.
se

The method for calculating the standard errors. Its default method "default" is regular standard errors. More about methods specification standard errors calculation can be found in Rosseel (2012).

estimator

Estimator. It is Maximum likelihood estimator by default. More about estimator specification can be found in Rosseel (2012).

parallel

Parallel computing ("no" or "parallel" or "snow"). It is "no" by default, which means it will not use parallel computing. The option "parallel" is to use multiple cores in a computer for parallel computing. It is used with the number of cores (ncore). The option "snow" is to use clusters for parallel computing. It is used with the number of clusters (cl).

ncore

Number of processors used for parallel computing. By default, ncore = Sys.getenv('NUMBER_OF_PROCESSORS').

c1

Number of clusters. It is NULL by default. When it is NULL, the program will detect the number of clusters automatically.

... Extra arguments. It is not required.

Value

An object of the power analysis. The power for all parameters in the model as well as the indirect effects if specified.

References


Examples

```r
set.seed(20220722)

#To specify the model
demo = "
y ~ cp*x + start(0)*x + b*m + start(0.39)* m
m ~ a*x + start(0.39)*x
x ~ start(1)*x
m ~ start(1)*m
y ~ start(1)*y
#

#To specify the indirect effects
mediation = "
ab := a*b
abc:= a*b + cp
```
# Power for mediation based on MC method when bootstrap method is used to test the effects:
# change nrep and nboot to at least 1,000 in real analysis

mediation.boot = wp.mc.sem.boot(model=demo, indirect=mediation, nobs=100,
                                 nrep=10, nboot=10,
                                 skewness=c(0, 0, 1.3), kurtosis=c(0,0,10), ovnames=c("x","m","y"))

# To print the power analysis results
summary(mediation.boot)

# Example: Power for Simple Mediation Analysis
ex1model <- "
  math ~ c*ME + start(0)*ME + b*HE + start(0.39)*HE
  HE ~ a*ME + start(0.39)*ME
"

indirect <- "ab:=a*b"

# change nrep and nboot to at least 1,000 in real analysis
boot.normal <- wp.mc.sem.boot(ex1model, indirect, 50, nrep=10, nboot=10)
summary(boot.normal)

boot.non.normal <- wp.mc.sem.boot(ex1model, indirect, 100, nrep=10, nboot=10,
                                   skewness=c(-0.3, -0.7, 1.3),
                                   kurtosis=c(1.5, 0, 5), ovnames=c("Var ME","Var HE","Var math"))
summary(boot.non.normal)

# Example: Multiple Group Mediation Analysis (Moderated Mediation)
ex3model <- "
  y ~ start(c(0.283, 0.283))*x + c(c1,c2)*x + start(c(0.36, 0.14))*m + c(b1,b2)*m
  m ~ start(c(0.721, 0.721))*x + c(a1,a2)*x
  m =~ start(c(0.8, 0.8))*m1 + start(c(0.8, 0.8))*m2 + start(c(0.8, 0.8))*m3
  x ~~ start(c(0.25, 0.25))*x
  y ~~ start(c(0.81, 0.95))*y
  m ~~ start(c(0.87, 0.87))*m
  m1 ~~ start(c(0.36, 0.36))*m1
  m2 ~~ start(c(0.36, 0.36))*m2
  m3 ~~ start(c(0.36, 0.36))*m3
"

# med1 and med2 are the mediation effect for group1 and group2, respectively.
indirect = "
  med1 := a1*b1
  med2 := a2*b2
  diffmed := a1*b1 - a2*b2"

# change nrep and nboot to at least 1,000 in real analysis
bootstrap <- wp.mc.sem.boot(ex3model, indirect, nobs=c(400,200),
                             nrep=10, nboot=10)
summary(bootstrap)
Example: A Longitudinal Mediation Model

```r
ex4model <- "
x2 ~ start(.9)*x1 + x*x1
x3 ~ start(.9)*x2 + x*x2
m2 ~ start(.3)*x1 + a*x1 + start(.3)*m1 + m*m1
m3 ~ start(.3)*x2 + a*x2 + start(.3)*m2 + m*m2
y2 ~ start(.3)*m1 + b*m1 + start(.7)*y1 + y*y1
y3 ~ start(.3)*m2 + b*m2 + start(.7)*y2 + y*y2 + start(0)*x1 + c*x1
x1 -- start(.37)*m1
x1 -- start(.27)*y1
y1 -- start(.2278)*m1
x2 -- start(.19)*x2
x3 -- start(.19)*x3
m2 -- start(.7534)*m2
m3 -- start(.7534)*m3
y2 -- start(.3243)*y2
y3 -- start(.3243)*y3
"

indirect <- "ab := a*b"
```

Change nrep and nboot to at least 1,000 in real analysis.

```r
set.seed(10)
bootstrap <- wp.mc.sem.boot(ex4model, indirect, nobs=500, nrep=10, nboot=10)
summary(bootstrap)
```

---

**wp.mc.sem.power.curve**  
Statistical Power Curve for Structural Equation Modeling / Mediation based on Monte Carlo Simulation

**Description**

A power curve is useful to graphically display how power changes with sample size (e.g., Zhang & Wang). This function is to generate a power curve for SEM based on Monte Carlo simulation, either using Sobel test or bootstrap method to test the indirect / mediation effects if applicable.

**Usage**

```r
wp.mc.sem.power.curve(model, indirect = NULL, nobs = 100, type = "basic",
nrep = 1000, nboot = 1000, alpha = 0.95, skewness = NULL,
kurtosis = NULL, oynames = NULL, se = "default",
estimator = "default", parallel = "no",
ncore = Sys.getenv("NUMBER_OF_PROCESSORS"), cl = NULL, ...)
```

**Arguments**

- `model`  
  Model specified using lavaan syntax. More about model specification can be found in Rosseel (2012).
indirect                Indirect effect defined using lavaan syntax.
nobs                   Sample size. It is 100 by default.
type                   The method used to test the indirect effects ('basic' or 'boot'). By default type='basic'. The type 'basic' is to use Sobel test (see also wp.mc.sem.basic), while 'boot' is to use bootstrap method (see also wp.mc.sem.boot).
nrep                   Number of replications for the Monte Carlo simulation. It is 1000 by default.
nboot                  Number of replications for the bootstrap to test the specified parameter (e.g., mediation). It is 1000 by default.
alpha                  Significance level chosen for the test. It equals 0.05 by default.
skewness               A sequence of skewnesses of the observed variables. It is not required.
kurtosis               A sequence of kurtosises of the observed variables. It is not required.
vnames                 Names of the observed variables in the model. It is not required.
se                      The method for calculating the standard errors. Its default method "default" is regular standard errors. More about methods specification standard errors calculation can be found in Rosseel (2012).
estimator              Estimator. It is Maximum likelihood estimator by default. More about estimator specification can be found in Rosseel (2012).
parallel               Parallel computing ("no" or "parallel" or "snow"). It is "no" by default, which means it will not use parallel computing. The option "parallel" is to use multiple cores in a computer for parallel computing. It is used with the number of cores (ncore). The option "snow" is to use clusters for parallel computing. It is used with the number of clusters (cl).
ncore                  Number of processors used for parallel computing. By default, ncore = Sys.getenv('NUMBER_OF_PROCESSORS').
cl                      Number of clusters. It is NULL by default. When it is NULL, the program will detect the number of clusters automatically.
...                     Extra arguments. It is not required.

Value

An object of the power analysis. The power for all parameters in the model as well as the indirect effects if specified.

References


Examples

```r
set.seed(20220722)

# To specify the model
ex2model =
  "ept ~ start(0.4)*hvltt + b*hvltt + start(0)*age + start(0)*edu + start(2)*R
  hvltt ~ start(-0.35)*age + a*age + c*edu + start(0.5)*edu
  R ~ start(-0.06)*age + start(0.2)*edu
  R =~ 1*ws + start(0.8)*ls + start(0.5)*lt
  age ~~ start(30)*age
  edu ~~ start(8)*edu
  age ~~ start(-2.8)*edu
  hvltt ~~ start(23)*hvltt
  R ~~ start(14)*R
  ws ~~ start(3)*ws
  ls ~~ start(3)*ls
  lt ~~ start(3)*lt
  ept ~~ start(3)*ept"

# To specify the indirect effects
indirect = "ind1 := a*b + c*b"

nobs <- seq(100, 2000, by = 200)

# To calculate power curve:
# change nrep and nboot to at least 1,000 in real analysis
power.curve = wp.mc.sem.power.curve(model=ex2model, indirect=indirect,
  nobs=nobs, type="Var_boot",
  nrep=10, nboot=10)
```

---

**wp.mc.t**

*Power analysis for t-test based on Monte Carlo simulation*

### Description

Power analysis for t-test based on Monte Carlo simulation

### Usage

```r
wp.mc.t(n = NULL, R0 = 1e+05, R1 = 1000, mu0 = 0, mu1 = 0,
  sd = 1, skewness = 0, kurtosis = 3, alpha = 0.05,
  type = c("two.sample", "one.sample", "paired"),
  alternative = c("two.sided", "less", "greater"))
```

### Arguments

- **n**
  - Sample size

- **R0**
  - Number of replications under the null
wp.mediation

R1  Number of replications
mu0  Population mean under the null
mu1  Population mean under the alternative
sd  Standard deviation
skewness  Skewness
kurtosis  kurtosis
alpha  Significance level
type  Type of anlaysis
alternative  alternative hypothesis

References


Examples

```r
set.seed(20220722)

########## Chapter 16. Monte Carlo t-test ###########
wp.mc.t(n=20 , mu0=0, mu1=0.5, sd=1, skewness=0,
kurtosis=3, type = c("one.sample"), alternative = c("two.sided"))

wp.mc.t(n=40 , mu0=0, mu1=0.3, sd=1, skewness=1,
kurtosis=6, type = c("paired"), alternative = c("greater"))

wp.mc.t(n=c(15, 15), mu1=c(0.2, 0.5), sd=c(0.2, 0.5),
skewness=c(1, 2), kurtosis=c(4, 6), type = c("two.sample"), alternative = c("less"))
```

Description

This function is for mediation models. Mediation models can be used to investigate the underlying mechanisms related to why an input variable x influences an output variable y (e.g., Hayes, 2013; MacKinnon, 2008). The mediation effect is calculated as $a \times b$, where $a$ is the path coefficient from the predictor x to the mediator m, and $b$ is the path coefficient from the mediator m to the outcome variable y. Sobel test statistic (Sobel, 1982) is used to test whether the mediation effect is significantly different from zero.

Usage

```r
wp.mediation(n = NULL, power = NULL, a = 0.5, b = 0.5, varx = 1,
vary = 1, varm = 1, alpha = 0.05, interval = NULL)
```
Arguments

- **n**: Sample size.
- **power**: Statistical power.
- **a**: Coefficient from x to m. The default value is 0.5.
- **b**: Coefficient from m to y. The default value is 0.5.
- **varx**: Variance of x. The default value is 1.
- **vary**: Variance of y. The default value is 1.
- **varm**: Variance of m. The default value is 1.
- **alpha**: Significance level chosen for the test. It equals 0.05 by default.
- **interval**: A vector containing the end-points of the interval to be searched for the root.

Value

An object of the power analysis.

References


Examples

```r
# To calculate the statistical power given sample size and effect size:
wp.mediation(n = 100, power = NULL, a = 0.5, b = 0.5,
             varx = 1, vary = 1, varm = 1, alpha = 0.05)
# Power for simple mediation
#
# n  power  a  b  varx  varm  vary  alpha
# 100 0.9337271 0.5 0.5 1 1 1 0.05
# URL: http://psychstat.org/mediation

# To generate a power curve given a sequence of sample sizes:
res <- wp.mediation(n = seq(50,100,5), power = NULL, a = 0.5, b = 0.5,
                    varx = 1, vary = 1, varm = 1, alpha = 0.05)
res
# Power for simple mediation
#
# n  power  a  b  varx  varm  vary  alpha
# 50 0.6877704 0.5 0.5 1 1 1 0.05
# 55 0.7287681 0.5 0.5 1 1 1 0.05
# 60 0.7652593 0.5 0.5 1 1 1 0.05
```
wp.mmrm

### Description

The two functions are adapted from the R package longpower by Michael C. Donohue. More will be added later.

### Usage

```r
wp.mmrm(N = NULL, Ra = NULL, ra = NULL, sigmaa = NULL,
        Rb = NULL, rb = NULL, sigmab = NULL, lambda = 1,
        delta = NULL, alpha = 0.05, power = NULL,
        alternative = c("two.sided", "one.sided"))

wp.mmrm.ar1(N = NULL, rho = NULL, ra = NULL, sigma = NULL,
             var1 = NULL, var2 = NULL, var3 = NULL,
             lambda = 1, delta = NULL, alpha = 0.05, power = NULL,
             alternative = c("two.sided", "one.sided"))
```

# To plot the power curve:
plot(res)

# To calculate the required sample size given power and effect size:
wp.mediation(n = NULL, power = 0.9, a = 0.5, b = 0.5,
              varx = 1, vary = 1, varm = 1, alpha = 0.05)

# Power for simple mediation
#
#  n  power  a  b  varx  varm  vary  alpha
#  87.56182  0.9  0.5  0.5  1  1  1  0.05

# URL: http://psychstat.org/mediation

# To calculate the minimum detectable effect size of one coefficient given power and sample size:
wp.mediation(n = 100, power = 0.9, a = NULL, b = 0.5,
              varx = 1, vary = 1, varm = 1, alpha = 0.05)

# Power for simple mediation
#
#  n  power  a  b  varx  varm  vary  alpha
#  100 0.9 0.7335197 0.5  1  1  1  0.05

# URL: http://psychstat.org/mediation
```
rb = NULL, sigmab = NULL, lambda = 1, times = 1:length(ra),
delta = NULL, alpha = 0.05, power = NULL,
alternative = c("two.sided", "one.sided"))

### Arguments

| N     | N     |
| Ra    | Ra    |
| ra    | ra    |
| sigmaa| sigmaa|
| Rb    | Rb    |
| rb    | rb    |
| sigmab| sigmab|
| lambda| lambda|
| delta | delta |
| alpha | Significance level |
| power | Statistical power |
| alternative | alternative hypothesis |
| rho   | rho   |
| times | times |

### References


---

### Description

power analysis of model 14 in Introduction to Mediation, Moderation, and Conditional Process Analysis

### Usage

```r
wp.modmed.m14(c
    a1 = 0.2,
    cp = 0.2,
    b1 = 0.5,
    dl = 0.5,
    b2 = 0.2,
    sigx2 = 1,
```
sigw2 = 1,
sige12 = 1,
sige22 = 1,
sigx_w = 0.5,
n = 100,
nrep = 100,
alpha = 0.05,
b = 1000,
wb = n,
w_value = 0,
method = "value",
ncore = 1,
pop.cov = NULL,
mu = NULL,
varnames = c("y", "x", "w", "m", "mw")
)

Arguments

a1  regression coefficient of mediator (m) on predictor (x)
cp  regression coefficient of outcome (y) on predictor (x)
b1  regression coefficient of outcome (y) on mediator (m)
d1  regression coefficient of outcome (y) on moderator (w)
b2  regression coefficient of outcome (y) on the product (mw)
sigx2 variance of predictor (x)
sigw2 variance of moderator (w)
sige12 variance of error in the first regression equation
sige22 variance of error in the second regression equation
sigx_w covariance between predictor (x) and moderator (w)
n  sample size
nrep number of replications
alpha type 1 error rate
b  number of bootstrap iterations
nb  bootstrap sample size, default to n
w_value moderator level
method "value" for using the indirect effect value in power calculation, or "joint" for using joint significance in power calculation
ncore number of cores to use, default is 1, when ncore > 1, parallel is used
pop.cov covariance matrix, default to NULL if using the regression coefficient approach
mu  mean vector, default to NULL if using the regression coefficient approach
varnames name of variables for the covariance matrix
**Value**

power of indirect effect, direct effect, and moderation

**Examples**

```r
test = wp.modmed.m14(a1 = 0.2, cp = 0.2, b1 = 0.5, d1 = 0.5, b2 = 0.2, sigx2 = 1, 
    sigw2 = 1, sige12 = 1, sige22 = 1, sigx_w = 0.5, n = 50, 
    nrep = 100, alpha = 0.05, b = 1000, ncore = 1)
print(test)
```

---

**Description**

power analysis of model 15 in Introduction to Mediation, Moderation, and Conditional Process Analysis

**Usage**

```r
wp.modmed.m15(
  a1 = 0.6,
  cp = 0.2,
  b1 = 0.3,
  b2 = 0.5,
  d1 = 0.2,
  d2 = 0.1,
  sigx2 = 1,
  sigw2 = 1,
  sige12 = 1,
  sige22 = 1,
  sigx_w = 0.4,
  n = 100,
  nrep = 100,
  alpha = 0.05,
  b = 1000,
  nb = n,
  w_value = 0,
  method = "value",
  ncore = 1,
  pop.cov = NULL,
  mu = NULL,
  varnames = c("y", "x", "w", "m", "xw", "mw")
)
```
Arguments

- **a1**: regression coefficient of mediator (m) on predictor (x)
- **cp**: regression coefficient of outcome (y) on predictor (x)
- **b1**: regression coefficient of outcome (y) on mediator (m)
- **b2**: regression coefficient of outcome (y) on the product (mw)
- **d1**: regression coefficient of outcome (y) on moderator (w)
- **d2**: regression coefficient of outcome (y) on the product (xw)
- **sigx2**: variance of predictor (x)
- **sigw2**: variance of moderator (w)
- **sige12**: variance of error in the first regression equation
- **sige22**: variance of error in the second regression equation
- **sigx_w**: covariance between predictor (x) and moderator (w)
- **n**: sample size
- **nrep**: number of replications
- **alpha**: type 1 error rate
- **b**: number of bootstrap iterations
- **nb**: bootstrap sample size, default to n
- **w_value**: moderator level
- **method**: "value" for using the indirect effect value in power calculation, or "joint" for using joint significance in power calculation
- **ncore**: number of cores to use, default is 1, when ncore > 1, parallel is used
- **pop.cov**: covariance matrix, default to NULL if using the regression coefficient approach
- **mu**: mean vector, default to NULL if using the regression coefficient approach
- **varnames**: name of variables for the covariance matrix

Value

power of indirect effect, direct effect, and moderation

Examples

```r
test = wp.modmed.m15(a1 = 0.6, cp = 0.2, b1 = 0.3, b2 = 0.2, d1 = 0.2, d2 = 0.1,
                      sigx2 = 1, sigw2 = 1, sige12 = 1, sige22 = 1, sigx_w = 0.4,
                      n = 50, nrep = 100, alpha = 0.05, b = 1000, ncore = 1)
print(test)
```
Description

power analysis of model 58 in Introduction to Mediation, Moderation, and Conditional Process Analysis

Usage

wp.modmed.m58(
  c1 = 0.5,
  a1 = 0.75,
  c2 = 0.1,
  d1 = 0.4,
  b1 = 0.6,
  b2 = 0.1,
  cp = 0.5,
  sigx2 = 1,
  sigw2 = 1,
  sige12 = 1,
  sige22 = 1,
  sigx_w = 0.4,
  n = 100,
  nrep = 100,
  alpha = 0.05,
  b = 1000,
  nb = n,
  w_value = 0,
  method = "value",
  ncore = 1,
  pop.cov = NULL,
  mu = NULL,
  varnames = c("x", "w", "m", "xw", "mw", "y")
)

Arguments

c1    regression coefficient of outcome (m) on moderator (w)

a1    regression coefficient of mediator (m) on predictor (x)

c2    regression coefficient of outcome (m) on the product (xw)

d1    regression coefficient of outcome (y) on moderator (w)

b1    regression coefficient of outcome (y) on mediator (m)

b2    regression coefficient of outcome (y) on the product (mw)

cp    regression coefficient of outcome (y) on predictor (x)
wp.modmed.m7

sigx2 variance of predictor (x)
sigw2 variance of moderator (w)
sige12 variance of error in the first regression equation
sige22 variance of error in the second regression equation
sigt_w covariance between predictor (x) and moderator (w)
n sample size
nrep number of replications
alpha type 1 error rate
b number of bootstrap iterations
nb bootstrap sample size, default to n
w_value moderator level
method "value" for using the indirect effect value in power calculation, or "joint" for using joint significance in power calculation
ncore number of cores to use, default is 1, when ncore > 1, parallel is used
pop.cov covariance matrix, default to NULL if using the regression coefficient approach
mu mean vector, default to NULL if using the regression coefficient approach
varnames name of variables for the covariance matrix

Value
power of indirect effect, direct effect, and moderation

Examples

```r
test = wp.modmed.m58(c1 = 0.2, a1 = 0.2, c2 = 0.1, b2 = 0.1,
                  b1 = 0.2, cp = 0.2, d1 = 0.2,
                  sigx2 = 1, sigw2 = 1, sige12 = 1, sige22 = 1, sigt_w = 0.5,
                  n = 50, nrep = 100, alpha = 0.05, b = 1000, ncore = 1)
print(test)
```

wp.modmed.m7 model7

Description

power analysis of model 7 in Introduction to Mediation, Moderation, and Conditional Process Analysis
Usage

```r
wp.modmed.m7(
    a1 = 0.39,
    cp = 0.2,
    b1 = 0.3,
    c1 = 0.39,
    c2 = 0.2,
    sigx2 = 1,
    sigw2 = 1,
    sige12 = 1,
    sige22 = 1,
    sigx_w = 0.5,
    n = 100,
    nrep = 100,
    alpha = 0.05,
    b = 1000,
    nb = n,
    w_value = 0,
    method = "value",
    ncore = 1,
    pop.cov = NULL,
    mu = NULL,
    varnames = c("y", "x", "w", "m", "xw")
)
```

Arguments

- `a1`: regression coefficient of mediator (m) on predictor (x)
- `cp`: regression coefficient of outcome (y) on predictor (x)
- `b1`: regression coefficient of outcome (y) on mediator (m)
- `c1`: regression coefficient of mediator (m) on moderator (w)
- `c2`: regression coefficient of mediator (m) on the product (xw)
- `sigx2`: variance of predictor (x)
- `sigw2`: variance of moderator (w)
- `sige12`: variance of error in the first regression equation
- `sige22`: variance of error in the second regression equation
- `sigx_w`: covariance between predictor (x) and moderator (w)
- `n`: sample size
- `nrep`: number of replications
- `alpha`: type 1 error rate
- `b`: number of bootstrap iterations
- `nb`: bootstrap sample size, default to n
- `w_value`: moderator level
method  "value" for using the indirect effect value in power calculation, or "joint" for using joint significance in power calculation
ncore  number of cores to use, default is 1, when ncore > 1, parallel is used
pop.cov  covariance matrix, default to NULL if using the regression coefficient approach
mu  mean vector, default to NULL if using the regression coefficient approach
varnames  name of variables for the covariance matrix

Value

power of indirect effect, direct effect, and moderation

Examples

# usage of wp.modmed.m7
test = wp.modmed.m7(a1 = 0.39, cp = 0.2, b1 = 0.3, c1 = 0.39,
c2 = 0.2, sigx2 = 1, sigw2 = 1, sige12 = 1,
sige22 = 1, sigx_w = 0.5, n = 50, nrep = 100,
alpha = 0.05, b = 1000, ncore = 1)
print(test)
alpha = 0.05,
b = 1000,
 nb = n,
w_value = 0,
method = "value",
ncore = 1,
pop.cov = NULL,
mu = NULL,
varnames = c("y", "x", "w", "m", "xw")
)

Arguments

a1 regression coefficient of mediator (m) on predictor (x)
cp regression coefficient of outcome (y) on predictor (m)
b1 regression coefficient of outcome (y) on mediator (x)
c1 regression coefficient of mediator (m) on moderator (w)
d1 regression coefficient of mediator (y) on moderator (w)
c2 regression coefficient of mediator (m) on the product (xw)
d2 regression coefficient of mediator (y) on the product (xw)
sigx2 variance of predictor (x)
sigw2 variance of moderator (w)
sige12 variance of error in the first regression equation
sige22 variance of error in the second regression equation
sigx_w covariance between predictor (x) and moderator (w)
n sample size
nrep number of replications
alpha type 1 error rate
b number of bootstrap iterations
nb bootstrap sample size, default to n
w_value moderator level
method "value" for using the indirect effect value in power calculation, or "joint" for using joint significance in power calculation
ncore number of cores to use, default is 1, when ncore > 1, parallel is used
pop.cov covariance matrix, default to NULL if using the regression coefficient approach
mu mean vector, default to NULL if using the regression coefficient approach
varnames name of variables for the covariance matrix

Value

type 1 error rate, direct effect, and moderation
Examples

```r
# usage of wp.modmed.m8
test = wp.modmed.m8(a1 = 0.2, cp = 0.2, b1 = 0.2,
                   c1 = 0.2, d1 = 0.2, c2 = 0.2, d2 = 0.2,
                   sigx2 = 1, sigw2 = 1, sige12 = 1, sige22 = 1, sigx_w = 0.5,
                   n = 50, nrep = 100, alpha = 0.05, b = 1000, ncore = 1)
print(test)
```

**wp.mrt2arm**

*Statistical Power Analysis for Multisite Randomized Trials with 2 Arms*

**Description**

Multisite randomized trials (MRT) are a type of multilevel design for the situation when the entire cluster is randomly assigned to either a treatment arm or a control arm (Liu, 2013). The data from MRT can be analyzed in a two-level hierarchical linear model, where the indicator variable for treatment assignment is included in first level. If a study contains multiple treatments, then multiple indicators will be used. This function is for designs with 2 arms (i.e., a treatment and a control). Three types of tests are considered in the function: (1) The "main" type tests treatment main effect; (2) The "site" type tests the variance of cluster/site means; and (3) The "variance" type tests variance of treatment effects. Details leading to power calculation can be found in Raudenbush (1997) and Liu (2013).

**Usage**

```r
wp.mrt2arm(n = NULL, f = NULL, J = NULL, tau00 = NULL, tau11 = NULL,
           sg2 = NULL, power = NULL, alpha = 0.05, alternative = c("two.sided",
           "one.sided"), type = c("main", "site", "variance"), interval = NULL)
```

**Arguments**

- `n` Sample size. It is the number of individuals within each cluster.
- `f` Effect size. It specifies the main effect of treatment, the mean difference between the treatment clusters/sites and the control clusters/sites. Effect size must be positive.
- `J` Number of clusters / sites. It tells how many clusters are considered in the study design. At least two clusters are required.
- `tau00` Variance of cluster/site means. It is one of the residual variances in the second level. Its value must be positive.
- `tau11` Variance of treatment effects across sites. It is one of the residual variances in the second level. Its value must be positive.
- `sg2` Level-one error Variance. The residual variance in the first level.
- `power` Statistical power.
alpha  significance level chosen for the test. It equals 0.05 by default.
alternative Type of the alternative hypothesis ("two.sided" or "one.sided"). The default is "two.sided". The option "one.sided" can be either "less" or "greater".
type  Type of effect ("main" or "site" or "variance") with "main" as default. The type "main" tests treatment main effect, no tau00 needed; Type "site" tests the variance of cluster/site means, no tau11 or f needed; and Type "variance" tests variance of treatment effects, no tau00 or f needed.
interval A vector containing the end-points of the interval to be searched for the root.

Value
An object of the power analysis.

References

Examples
# To calculate the statistical power given sample size and effect size:
# For main effect
wp.mrt2arm(n = 45, f = 0.5, J = 20, tau11 = 0.5,
   sg2 = 1.25, alpha = 0.05, power = NULL)
# Power analysis for Multileve model Multisite randomized trials with 2 arms
#
#   J  n  f   tau11  sg2  power  alpha
# 20 45 0.5 0.5 1.25 0.8583253 0.05
#
# NOTE: n is the number of subjects per cluster
# URL: http://psychstat.org/mrt2arm

# For variance of treatment effect
wp.mrt2arm(n = 45, f = 0.5, J = 20, tau11 = 0.5,
   sg2 = 1.25, alpha = 0.05, power = NULL, type = "variance")
# Power analysis for Multileve model Multisite randomized trials with 2 arms
#
#   J  n  f   tau11  sg2  power  alpha
# 20 45 0.5 0.5 1.25 0.9987823 0.05
#
# NOTE: n is the number of subjects per cluster
# URL: http://psychstat.org/mrt2arm

# For testing site variability
res<- wp.mrt2arm(n = 45, J = 20, tau00 = 0.5,
   sg2 = 1.25, alpha = 0.05, power = NULL, type = "site")
Multisite randomized trials (MRT) are a type of multilevel design for the situation when the entire cluster is randomly assigned to either a treatment arm or a control arm (Liu, 2013). The data from MRT can be analyzed in a two-level hierarchical linear model, where the indicator variable for
treatment assignment is included in first level. If a study contains multiple treatments, then multiple indicators will be used. This function is for designs with 3 arms (i.e., two treatments and a control). Three types of tests are considered in the function: (1) The "main" type tests treatment main effect; (2) The "treatment" type tests the difference between the two treatments; and (3) The "omnibus" type tests whether the three arms are all equivalent. Details leading to power calculation can be found in Raudenbush (1997) and Liu (2013).

Usage

wp.mrt3arm(n = NULL, f1 = NULL, f2 = NULL, J = NULL, tau = NULL, sg2 = NULL, power = NULL, alpha = 0.05, alternative = c("two.sided", "one.sided"), type = c("main", "treatment", "omnibus"), interval = NULL)

Arguments

n
Sample size. It is the number of individuals within each cluster.

f1
Effect size for treatment main effect. Effect size must be positive.

f2
Effect size for the difference between two treatments. Effect size must be positive.

J
Number of clusters/sites. It tells how many clusters are considered in the study design. At least two clusters are required.

tau
Variance of treatment effects across sites/clusters.

sg2
Level-one error Variance. The residual variance in the first level.

power
Statistical power.

alpha
significance level chose for the test. It equals 0.05 by default.

alternative
Type of the alternative hypothesis ("two.sided" or "one.sided"). The default is "two.sided". The option "one.sided" can be either "less" or "greater".

type
Type of effect ("main" or "treatment" or "omnibus") with "main" as default. The type "main" tests the difference between the average treatment arms and the control arm; Type "treatment" tests the difference between the two treatment arms; and Type "omnibus" tests whether the three arms are all equivalent.

interval
A vector containing the end-points of the interval to be searched for the root.

Value

An object of the power analysis.

References


Examples

# To calculate the statistical power given sample size and effect size:
# For main effect
wp.mrt3arm(n = 30, f1 = 0.43, J = 20, tau = 0.4,
          sg2 = 2.25, alpha = 0.05, power = NULL)
#  Multisite randomized trials with 3 arms
#  J  n  f1  tau  sg2  power  alpha
#  20 30 0.43 0.4 2.25 0.8066964 0.05
#  NOTE: n is the number of subjects per cluster
#  URL: http://psychstat.org/mrt3arm

# For testing difference between effects
wp.mrt3arm(n = 30, f2 = 0.2, J = 20, tau = 0.4, sg2 = 2.25,
           alpha = 0.05, power = NULL, type="treatment")
#  Multisite randomized trials with 3 arms
#  J  n  f2  tau  sg2  power  alpha
#  20 30 0.2 0.4 2.25 0.2070712 0.05
#  NOTE: n is the number of subjects per cluster
#  URL: http://psychstat.org/mrt3arm

# For testing site variability
wp.mrt3arm(n = 30, f1=0.43, f2 = 0.2, J = 20, tau = 0.4, sg2 = 2.25,
           alpha = 0.05, power = NULL, type="omnibus")
#  Multisite randomized trials with 3 arms
#  J  n  f1  f2  tau  sg2  power  alpha
#  20 30 0.43 0.2 0.4 2.25 0.7950757 0.05
#  NOTE: n is the number of subjects per cluster
#  URL: http://psychstat.org/mrt3arm

# To generate a power curve given a sequence of numbers of sites/clusters:
res <- wp.mrt3arm(n = 30, f2 = 0.2, J = seq(20,120,10), tau = 0.4,
                  sg2 = 2.25, alpha = 0.05, power = NULL, type="treatment")
res
#  Multisite randomized trials with 3 arms
#  J  n  f2  tau  sg2  power  alpha
#  20 30 0.2 0.4 2.25 0.2070712 0.05
#  30 30 0.2 0.4 2.25 0.2953799 0.05
#  40 30 0.2 0.4 2.25 0.3804554 0.05
#  50 30 0.2 0.4 2.25 0.4603091 0.05
#  60 30 0.2 0.4 2.25 0.5337417 0.05
#  70 30 0.2 0.4 2.25 0.6001544 0.05
#  80 30 0.2 0.4 2.25 0.6593902 0.05
#  90 30 0.2 0.4 2.25 0.7116052 0.05
# 100 30 0.2 0.4 2.25 0.7571648 0.05
# 110 30 0.2 0.4 2.25 0.7965644 0.05
# wp.poisson

# 120 30 0.2 0.4 2.25 0.8303690 0.05
# NOTE: n is the number of subjects per cluster
# URL: http://psychstat.org/mrt3arm

#To plot the power curve:
plot(res, "J", "power")

#To calculate the required sample size given power and effect size:
wp.mrt3arm(n = NULL, f1 = 0.43, J = 20, tau = 0.4, sg2 = 2.25, alpha = 0.05, power = 0.8)
# Multisite randomized trials with 3 arms
#
# J  n  f1 tau sg2 power alpha
# 20 28.61907 0.43 0.4 2.25 0.8 0.05
#
# NOTE: n is the number of subjects per cluster
# URL: http://psychstat.org/mrt3arm

---

**wp.poisson**

*Statistical Power Analysis for Poisson Regression*

**Description**

This function is for Poisson regression models. Poisson regression is a type of generalized linear models where the outcomes are usually count data. Here, Maximum likelihood methods is used to estimate the model parameters. The estimated regression coefficient is assumed to follow a normal distribution. A Wald test is used to test the mean difference between the estimated parameter and the null parameter (typically the null hypothesis assumes it equals 0). The procedure introduced by Demidenko (2007) is adopted here for computing the statistical power.

**Usage**

```r
wp.poisson(n = NULL, exp0 = NULL, exp1 = NULL, alpha = 0.05, power = NULL, alternative = c("two.sided", "less", "greater"), family = c("Bernoulli", "exponential", "lognormal", "normal", "Poisson", "uniform"), parameter = NULL, subdivisions=200L, i.method=c("numerical", "MC"), mc.iter=20000)
```

**Arguments**

- **n**  
  Sample size.
- **exp0**  
  The base rate under the null hypothesis. It always takes positive value. See the article by Demidenko (2007) for details.
- **exp1**  
  The relative increase of the event rate. It is used for calculation of the effect size. See the article by Demidenko (2007) for details.
- **alpha**  
  Significance level chosen for the test. It equals 0.05 by default.
wp.poisson

- **power**: Statistical power.
- **alternative**: Direction of the alternative hypothesis ("two.sided" or "less" or "greater"). The default is "two.sided".
- **family**: Distribution of the predictor ("Bernoulli","exponential","lognormal","normal", "Poisson","uniform"). The default is "Bernoulli".
- **parameter**: Corresponding parameter for the predictor’s distribution. The default is 0.5 for "Bernoulli", 1 for "exponential", (0,1) for "lognormal" or "normal", 1 for "Poisson", and (0,1) for "uniform".
- **subdivisions**: Number of divisions for integration
- **i.method**: Integration method
- **mc.iter**: Number of iterations for Monte Carlo integration

**Value**

An object of the power analysis.

**References**


**Examples**

#To calculate the statistical power given sample size and effect size:
wp.poisson(n = 4406, exp0 = 2.798, exp1 = 0.8938, alpha = 0.05, 
    power = NULL, family = "Bernoulli", parameter = 0.53)
# Power for Poisson regression
#
# n   power   alpha exp0  exp1 beta0 beta1 paremeter
# 4406 0.9999789  0.05 2.798 0.8938 1.028905 -0.1122732  0.53
#
# URL: http://psychstat.org/poisson

#To generate a power curve given a sequence of sample sizes:
res <- wp.poisson(n = seq(800, 1500, 100), exp0 = 2.798, exp1 = 0.8938, 
    alpha = 0.05, power = NULL, family = "Bernoulli", parameter = 0.53)
res
# Power for Poisson regression
#
# n   power   alpha exp0  exp1 beta0 beta1 paremeter
# 800  0.7324097 0.05 2.798 0.8938 1.028905 -0.1122732 0.53
# 900  0.7813088 0.05 2.798 0.8938 1.028905 -0.1122732 0.53
# 1000 0.8224254 0.05 2.798 0.8938 1.028905 -0.1122732 0.53
# 1100 0.8566618 0.05 2.798 0.8938 1.028905 -0.1122732 0.53
# 1200 0.8849241 0.05 2.798 0.8938 1.028905 -0.1122732 0.53
# 1300 0.9080755 0.05 2.798 0.8938 1.028905 -0.1122732 0.53
wp.popPar

Extract Population Value Table

Description

This function is used to extract population value table for parameters form an power analysis object for SEM based on Monte Carlo methods (class = 'power').

Usage

wp.popPar(object)

Arguments

object Object of power analysis. It is an object returned by a webpower function for SEM based on Monte Carlo methods with class = 'power'.

Value

Population value table of parameters from the input object of power analysis.
Tests of proportions are a technique used to compare proportions of success or agreement in one or two samples. The one-sample test of proportion tests the null proportion of success, usually 0.5. The two-sample test of proportions tests the null hypothesis that the two samples are drawn from populations with the same proportion of success. A z-test is used to evaluate whether the given difference in proportions is statistically significantly different from the null hypothesis. The power calculation is based on the arcsine transformation of the proportion (see Cohen, 1988, p.548).

Usage

```r
wp.prop(h = NULL, n1 = NULL, n2 = NULL, alpha = 0.05, power = NULL, type = c("1p", "2p", "2p2n"), alternative = c("two.sided", "less", "greater"))
```

Arguments

- **h**: Effect size of the proportion comparison. Cohen (1992) suggested that effect size values of 0.2, 0.5, and 0.8 represent "small", "medium", and "large" effect sizes, respectively.
- **n1**: Sample size of the first group.
- **n2**: Sample size of the second group if applicable.
- **alpha**: Significance level chosen for the test. It equals 0.05 by default.
- **power**: Statistical power.
- **type**: Type of comparison ("1p" or "2p" or "2p2n"). The default is "1p". 1p: one sample; 2p: two sample with equal sample size; 2p2n: two sample with unequal sample size.
- **alternative**: Direction of the alternative hypothesis ("two.sided" or "less" or "greater"). The default is "two.sided".

Value

An object of the power analysis.

References

Examples

#To calculate the power for two groups of proportion with unequal sample size:
wp.prop(h=0.52,n1=35,n2=50,alternative="greater",type="2p2n")
# Power for two-sample proportion (unequal n)
#
# h n1 n2 alpha power
# 0.52 35 50 0.05 0.7625743
#
# NOTE: Sample size for each group
# URL: http://psychstat.org/prop2p2n

#To calculate the power curve with a sequence of sample sizes:
res <- wp.prop(h=0.52,n1=seq(10,100,10),alternative="greater",type="1p")
res
# Power for one-sample proportion test
#
# h n alpha power
# 0.52 10 0.05 0.4998128
# 0.52 20 0.05 0.7519557
# 0.52 30 0.05 0.8855706
# 0.52 40 0.05 0.9499031
# 0.52 50 0.05 0.9789283
# 0.52 60 0.05 0.9914150
# 0.52 70 0.05 0.9965928
# 0.52 80 0.05 0.9986772
# 0.52 90 0.05 0.9994960
# 0.52 100 0.05 0.9998111
#
# URL: http://psychstat.org/prop

#To plot the power curve:
plot(res, type='b')

#To estimate the sample size with a given power:
wp.prop(h=0.52,n1=NULL,power=0.8,alternative="greater",type="1p")
# Power for one-sample proportion test
#
# h n alpha power
# 0.52 22.86449 0.05 0.8
#
# URL: http://psychstat.org/prop

#To estimate the minimum detectable effect size with a given power:
wp.prop(h=NULL,n1=35,power=0.8,alternative="greater",type="1p")
# Power for one-sample proportion test
#
# h n alpha power
# 0.4202907 35 0.05 0.8
#
# URL: http://psychstat.org/prop

#To calculate the power curve with a sequence of effect sizes:
wp.regression

# Power for one-sample proportion test
#
#   h  n   alpha    power
# 0.1 100 0.05 0.2595110
# 0.2 100 0.05 0.6387600
# 0.3 100 0.05 0.9123145
# 0.4 100 0.05 0.9907423
# 0.5 100 0.05 0.9996034
# 0.6 100 0.05 0.9999934
# 0.7 100 0.05 1.0000000
# 0.8 100 0.05 1.0000000
#
# URL: http://psychstat.org/prop

Description

This function is for power analysis for regression models. Regression is a statistical technique for examining the relationship between one or more independent variables (or predictors) and one dependent variable (or the outcome). Regression provides an F-statistic that can be formulated using the ratio between variation in the outcome variable that is explained by the predictors and the unexplained variation (Cohen, 1988). The test statistic can also be expressed in terms of comparison between Full and Reduced models (Maxwell & Delaney, 2003).

Usage

wp.regression(n = NULL, p1 = NULL, p2 = 0, f2 = NULL, alpha = 0.05,
             power = NULL, type=c("regular", "Cohen"))

Arguments

n  Sample size.
p1 Number of predictors in the full model.
p2 Number of predictors in the reduced model, it is 0 by default. See the book by Maxwell and Delaney (2003) for the definition of the reduced model.
f2 Effect size. We use the statistic f2 as the measure of effect size for linear regression proposed by Cohen(1988, p.410). Cohen discussed the effect size in three different cases. The calculation of f2 can be generalized using the idea of a full model and a reduced model by Maxwell and Delaney (2003).
alpha significance level chosen for the test. It equals 0.05 by default.
power Statistical power.
type If set to "Cohen", the formula used in the Cohen’s book will be used (not recommended).
Value

An object of the power analysis

References


Examples

#To calculate the statistical power given sample size and effect size:
wp.regression(n = 100, p1 = 3, f2 = 0.1, alpha = 0.05, power = NULL)
# Power for multiple regression
#
#  n  p1  p2  f2  alpha    power
#  100 3 0 0.1 0.05 0.7420463
#
# URL: http://psychstat.org/regression

#To generate a power curve given a sequence of sample sizes:
res <- wp.regression(n = seq(50,300,50), p1 = 3, f2 = 0.1,
                      alpha = 0.05, power = NULL)
res
# Power for multiple regression
#
#  n  p1  p2  f2  alpha    power
#  50 3 0 0.1 0.05 0.4077879
#  100 3 0 0.1 0.05 0.7420463
#  150 3 0 0.1 0.05 0.9092082
#  200 3 0 0.1 0.05 0.9724593
#  250 3 0 0.1 0.05 0.9925216
#  300 3 0 0.1 0.05 0.9981375
#
# URL: http://psychstat.org/regression

#To plot the power curve:
plot(res)

#To calculate the required sample size given power and effect size:
wp.regression(n = NULL, p1 = 3, f2 = 0.1, alpha = 0.05, power = 0.8)
# Power for multiple regression
#
#  n  p1  p2  f2  alpha    power
#  113.0103 3 0 0.1 0.05 0.8
#
# URL: http://psychstat.org/regression
The statistical power given sample size and effect size when controlling two predictors:

```r
wp.regression(n = 100, p1 = 3, p2 = 2, f2 = 0.1429, alpha = 0.05, power = NULL)
# Power for multiple regression
#
# n p1 p2  f2  alpha  power
# 100   3   2 0.1429 0.05  0.9594695
#
# URL: http://psychstat.org/regression
```

To generate a power curve given a sequence of effect sizes:

```r
res <- wp.regression(n = 50, p1 = 3, f2 = seq(0.05, 0.5, 0.05),
                      alpha = 0.05, power = NULL)
res
# Power for multiple regression
#
# n p1 p2  f2  alpha  power
# 50    3   0 0.05 0.05  0.2164842
# 50    3   0 0.10 0.05  0.4077879
# 50    3   0 0.15 0.05  0.5821296
# 50    3   0 0.20 0.05  0.7210141
# 50    3   0 0.25 0.05  0.8220164
# 50    3   0 0.30 0.05  0.8906954
# 50    3   0 0.35 0.05  0.9350154
# 50    3   0 0.40 0.05  0.9624324
# 50    3   0 0.45 0.05  0.9788077
# 50    3   0 0.50 0.05  0.9883012
#
# URL: http://psychstat.org/regression
```

---

**wp.rmanova**

**Statistical Power Analysis for Repeated Measures ANOVA**

**Description**

Repeated-measures ANOVA can be used to compare the means of a sequence of measurements (e.g., *O’brien & Kaiser, 1985*). In a repeated-measures design, every subject is exposed to all different treatments, or more commonly measured across different time points. Power analysis for (1) the within-effect test about the mean difference among measurements by default. If the subjects are from more than one group, the power analysis is also available for (2) the between-effect test about mean difference among groups and (3) the interaction effect test of the measurements and groups.

**Usage**

```r
wp.rmanova(n = NULL, ng = NULL, nm = NULL, f = NULL, nscor = 1,
          alpha = 0.05, power = NULL, type = 0)
```
Arguments

n        Sample size.
ng       Number of groups.
nm       Number of measurements.
f        Effect size. We use the statistic f as the measure of effect size for repeated-measures ANOVA as in Cohen (1988, p.275).
nskor    Nonsphericity correction coefficient. The nonsphericity correction coefficient is a measure of the degree of sphericity in the population. A coefficient of 1 means sphericity is met, while a coefficient less than 1 means not met. The smaller value of the coefficient means the further departure from sphericity. The lowest value of the coefficient is 1/(nm-1) where nm is the total number of measurements. Two viable approaches for computing the empirical nonsphericity correction coefficient are suggested. One is by Greenhouse and Geisser (1959), the other is by Huynh and Feldt (1976).
alpha    significance level chosen for the test. It equals 0.05 by default.
power    Statistical power.
type     Type of analysis (0 or 1 or 2). The value "0" is for between-effect; "1" is for within-effect; and "2" is for interaction effect.

Value

An object of the power analysis

References


Examples

# To calculate the statistical power for repeated-measures ANOVA:
wp.rmanova(n=30, ng=3, nm=4, f=0.36, nscor=0.7)
# Repeated-measures ANOVA analysis
#
#  n   f   ng  nm  nscor  alpha  power
#   30 0.36 3   4   0.7   0.05  0.2674167
#
# NOTE: Power analysis for between-effect test
# URL: http://psychstat.org/rmanova

# To generate a power curve given a sequence of sample sizes:
res <- wp.rmanova(n=seq(30, 150, 20), ng=3, nm=4, f=0.36, nscor=0.7)
# Repeated-measures ANOVA analysis
#
# n  f  ng  nm  nscor  alpha  power
# 30 0.36 3 4 0.7 0.05 0.2674167
# 50 0.36 3 4 0.7 0.05 0.4386000
# 70 0.36 3 4 0.7 0.05 0.5894599
# 90 0.36 3 4 0.7 0.05 0.7110142
# 110 0.36 3 4 0.7 0.05 0.8029337
# 130 0.36 3 4 0.7 0.05 0.8691834
# 150 0.36 3 4 0.7 0.05 0.9151497
#
# NOTE: Power analysis for between-effect test
# URL: http://psychstat.org/rmanova

# To plot the power curve:
plot(res)

# To calculate the required sample size given power and effect size:
wp.rmanova(n=NULL, ng=3, nm=4, f=0.36, power=0.8, nscor=0.7)
# Repeated-measures ANOVA analysis
#
# n  f  ng  nm  nscor  alpha  power
# 109.2546 0.36 3 4 0.7 0.05 0.8
#
# NOTE: Power analysis for between-effect test
# URL: http://psychstat.org/rmanova

# To calculate the minimum detectable effect size given power and sample size:
wp.rmanova(n=30, ng=3, nm=4, f=NULL, power=0.8, nscor=0.7)
# Repeated-measures ANOVA analysis
#
# n  f  ng  nm  nscor  alpha  power
# 30 0.716768 3 4 0.7 0.05 0.8
#
# NOTE: Power analysis for between-effect test
# URL: http://psychstat.org/rmanova

# To generate a power curve given a sequence of effect sizes:
wp.rmanova(n=30, ng=3, nm=4, f=seq(0.1, 0.5, 0.05), nscor=0.7)
# Repeated-measures ANOVA analysis
#
# n  f  ng  nm  nscor  alpha  power
# 30 0.10 3 4 0.7 0.05 0.0644235
# 30 0.15 3 4 0.7 0.05 0.08327866
# 30 0.20 3 4 0.7 0.05 0.1101678
# 30 0.25 3 4 0.7 0.05 0.14853115
# 30 0.30 3 4 0.7 0.05 0.19640404
# 30 0.35 3 4 0.7 0.05 0.25460008
wp.sem.chisq

Statistical Power Analysis for Structural Equation Modeling based on Chi-Squared Test

Description

Structural equation modeling (SEM) is a multivariate technique used to analyze relationships among observed and latent variables. It can be viewed as a combination of factor analysis and multivariate regression analysis. Two methods are widely used in power analysis for SEM. One is based on the likelihood ratio test proposed by Satorra and Saris (1985). The other is based on RMSEA proposed by MacCallum et al. (1996). This function is for SEM power analysis based on the likelihood ratio test.

Usage

wp.sem.chisq(n = NULL, df = NULL, effect = NULL, power = NULL, alpha = 0.05)

Arguments

n Sample size.
df Degrees of freedom. The degrees of freedom of the chi-squared test.
effect Effect size. It specifies the population misfit of a SEM model, which is the difference between two SEM models: a full model (Mf) and a reduced model (Mr). A convenient way to get the effect size is to fit the reduced model using SEM software such R package ‘lavaan’ (Rossel, 2012). Then the effect size is calculated as the chi-squared statistics dividing by the sample size.
power Statistical power.
alpha significance level choosed for the test. It equals 0.05 by default.

Value

An object of the power analysis.
References


Examples

#To calculate the statistical power given sample size and effect size:
wp.sem.chisq(n = 100, df = 4, effect = 0.054, power = NULL, alpha = 0.05)
# Power for SEM (Satorra & Saris, 1985)

# n df effect power alpha
# 100 4 0.054 0.4221152 0.05

# URL: http://psychstat.org/semchisq

#To generate a power curve given a sequence of sample sizes:
res <- wp.sem.chisq(n = seq(100,600,100), df = 4,
                   effect = 0.054, power = NULL, alpha = 0.05)
res
# Power for SEM (Satorra & Saris, 1985)

# n df effect power alpha
# 100 4 0.054 0.4221152 0.05
# 200 4 0.054 0.7510630 0.05
# 300 4 0.054 0.9145660 0.05
# 400 4 0.054 0.9750481 0.05
# 500 4 0.054 0.9935453 0.05
# 600 4 0.054 0.9984820 0.05

# URL: http://psychstat.org/semchisq

#To plot the power curve:
plot(res)

#To generate a power curve given a sequence of alphas:
res <- wp.sem.chisq(n = 100, df = 4, effect = 0.054, power = NULL,
                   alpha = c(0.001, 0.005, 0.01, 0.025, 0.05))
res
# Power for SEM (Satorra & Saris, 1985)

# n df effect power alpha
# 100 4 0.054 0.06539478 0.001
# 100 4 0.054 0.14952768 0.005
# 100 4 0.054 0.20867087 0.010
# 100 4 0.054 0.31584011 0.025
# 100 4 0.054 0.42211515 0.050

# URL: http://psychstat.org/semchisq
**wp.sem.rmsea**  

Statistical Power Analysis for Structural Equation Modeling based on RMSEA

**Description**

Structural equation modeling (SEM) is a multivariate technique used to analyze relationships among observed and latent variables. It can be viewed as a combination of factor analysis and multivariate regression analysis. Two methods are widely used in power analysis for SEM. One is based on the likelihood ratio test proposed by Satorra and Saris (1985). The other is based on RMSEA proposed by MacCallum et al. (1996). This function is for SEM power analysis based on RMSEA.

**Usage**

```r
wp.sem.rmsea(n = NULL, df = NULL, rmsea0 = NULL, rmsea1 = NULL, power = NULL, alpha = 0.05, type = c("close", "notclose"))
```

**Arguments**

- `n` Sample size.
- `df` Degrees of freedom. The degrees of freedom of the chi-squared test.
- `rmsea0` RMSEA for H0. It usually equals zero.
- `rmsea1` RMSEA for H1.
- `power` Statistical power.
- `alpha` Significance level chosen for the test. It equals 0.05 by default.
- `type` Close fit or non-close fit ("close" or "notclose"). It is "close" by default.
wp.sem.rmsea

Value

An object of the power analysis.

References


Examples

#To calculate the statistical power given sample size and effect size:
wp.sem.rmsea (n = 100, df = 4, rmsea0 = 0,
             rmsea1 = 0.116, power = NULL, alpha = 0.05)
# Power for SEM based on RMSEA
#
#  n   df  rmsea0  rmsea1    power    alpha
# 100   4      0   0.116  0.4208173   0.05
#
# URL: http://psychstat.org/rmsea

#To generate a power curve given a sequence of sample sizes:
res <- wp.sem.rmsea (n = seq(100,600,100), df = 4, rmsea0 = 0,  
                     rmsea1 = 0.116, power = NULL, alpha = 0.05)
res
# Power for SEM based on RMSEA
#
#  n   df  rmsea0  rmsea1    power    alpha
# 100   4      0   0.116  0.4208173   0.05
# 200   4      0   0.116  0.7494932   0.05
# 300   4      0   0.116  0.9135968   0.05
# 400   4      0   0.116  0.9746240   0.05
# 500   4      0   0.116  0.9933963   0.05
# 600   4      0   0.116  0.9984373   0.05
#
# URL: http://psychstat.org/rmsea

#To plot the power curve:
plot(res)

#To calculate the required sample size given power and effect size:
wp.sem.rmsea (n = NULL, df = 4, rmsea0 = 0,  
              rmsea1 = 0.116, power = 0.8, alpha = 0.05)
# Power for SEM based on RMSEA
#
#  n   df  rmsea0  rmsea1    power   alpha
# 222.7465   4      0   0.116  0.8   0.05
#
# URL: http://psychstat.org/rmsea
# To calculate the minimum detectable effect size of rmsea1 given power and sample size:
wp.sem.rmsea(n = 100, df = 4, rmsea0 = 0, rmsea1 = NULL, power = 0.8, alpha = 0.05)

# Power for SEM based on RMSEA

# n df rmsea0 rmsea1 power alpha
# 100 4 0 0.1736082 0.8 0.05

# URL: http://psychstat.org/rmsea

---

**wp.t**

### Statistical Power Analysis for t-Tests

**Description**

A t-test is a statistical hypothesis test in which the test statistic follows a Student’s t distribution if the null hypothesis is true and follows a non-central t distribution if the alternative hypothesis is true. The t test can assess the statistical significance of (1) the difference between population mean and a specific value, (2) the difference between two independent population means, and (3) difference between means of matched pairs.

**Usage**

```r
wp.t(n1 = NULL, n2 = NULL, d = NULL, alpha = 0.05, power = NULL, type = c("two.sample", "one.sample", "paired", "two.sample.2n"), alternative = c("two.sided", "less", "greater"), tol = .Machine$double.eps^0.25)
```

**Arguments**

- `n1`: Sample size of the first group.
- `n2`: Sample size of the second group if applicable.
- `alpha`: Significance level chosen for the test. It equals 0.05 by default.
- `power`: Statistical power.
- `type`: Type of comparison ("one.sample" or "two.sample" or "two.sample.2n" or "two.sample.2n" or "paired"). "two.sample" is two-sample t-test with equal sample sizes, two.sample.2n" is two-sample t-test with unequal sample sizes, "paired" is paired t-test
- `alternative`: Direction of the alternative hypothesis ("two.sided" or "less" or "greater"). The default is "two.sided".
- `tol`: Tolerance in root solver.

**Value**

An object of the power analysis.
References


Examples

#To calculate the power for one sample t-test given sample size and effect size:
wpt(n1=150, d=0.2, type="one.sample")
# One-sample t-test
#
# n  d  alpha  power
# 150 0.2 0.05  0.682153
#
# URL: http://psychstat.org/ttest

#To calculate the power for paired t-test given sample size and effect size:
wpt(n1=40, d=-0.4, type="paired", alternative="less")
# Paired t-test
#
# n  d  alpha  power
# 40 -0.4 0.05 0.799737
#
# NOTE: n is number of *pairs*
# URL: http://psychstat.org/ttest

#To estimate the required sample size given power and effect size for paired t-test:
wpt(d=0.4, power=0.8, type="paired", alternative="greater")
# Paired t-test
#
# n  d  alpha  power
# 40.02908 0.4 0.05 0.8
#
# NOTE: n is number of *pairs*
# URL: http://psychstat.org/ttest

#To estimate the power for balanced two-sample t-test given sample size and effect size:
wpt(n1=70, d=0.3, type="two.sample", alternative="greater")
# Two-sample t-test
#
# n  d  alpha  power
# 70 0.3 0.05 0.5482577
#
# NOTE: n is number in *each* group
# URL: http://psychstat.org/ttest

#To estimate the power for unbalanced two-sample t-test given sample size and effect size:
wpt(n1=30, n2=40, d=0.356, type="two.sample.2n", alternative="two.sided")
# Unbalanced two-sample t-test
#
# n1 n2 d alpha power
# 30 40 0.356 0.05 0.3064767
#
# NOTE: n1 and n2 are number in *each* group
# URL: http://psychstat.org/ttest2n

To estimate the power curve for unbalanced two-sample t-test given a sequence of effect sizes:
res <- wp.t(n1=30, n2=40, d=seq(0.2,0.8,0.05), type="two.sample.2n",
            alternative="two.sided")

res
# Unbalanced two-sample t-test
#
# n1 n2 d alpha power
# 30 40 0.20 0.05 0.1291567
# 30 40 0.25 0.05 0.1751916
# 30 40 0.30 0.05 0.2317880
# 30 40 0.35 0.05 0.2979681
# 30 40 0.40 0.05 0.3719259
# 30 40 0.45 0.05 0.4510800
# 30 40 0.50 0.05 0.5322896
# 30 40 0.55 0.05 0.6121937
# 30 40 0.60 0.05 0.6876059
# 30 40 0.65 0.05 0.7558815
# 30 40 0.70 0.05 0.8151817
# 30 40 0.75 0.05 0.8645929
# 30 40 0.80 0.05 0.9040910
#
# NOTE: n1 and n2 are number in *each* group
# URL: http://psychstat.org/ttest2n

To plot a power curve:
plot(res, xvar='d', yvar='power')
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