

Package ‘anomo’

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Type Package

Title Analysis of Moderation, Statistical Power, and Optimal Design
for Studies Detecting Difference and Equivalence

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Description Analysis of moderation (ANOMO) method conceptualizes
the difference and equivalence tests as a moderation problem to
test the difference and equivalence of
two estimates (e.g., two means or two effects).

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Contents

mcci	2
od.l.eq	4
plot.power.eq	5
power.l.eq	6
re	9
Index	10

Description

Compute Monte Carlo confidence intervals (MCCIs) for the difference and equivalence tests.

Usage

```
mcci(
  d = NULL,
  se = NULL,
  mediation = FALSE,
  n.mcci = 10000,
  sig.level = 0.05,
  sig.adjusted = TRUE,
  two.tailed = TRUE,
  seed = 123,
  eq.bd = NULL,
  xlim = NULL,
  xlab = NULL,
  ylab = NULL,
  dashed.lines = TRUE,
  verbose = TRUE
)
```

Arguments

d	The estimated effect(s), it has a length of one, two, and four. (1) When the length is one, it is an estimated main or moderation effect, the MCCI compute the CI for this estimate; (2) When the length is two, they represent two estimated effects. These two estimated effects are main or moderation effects when mediation is FALSE, the MCCI compute the CI for the difference of the two estimates; These two estimated effects are the treatment-mediator and mediator-outcome path estimates for a mediation effect when mediation is TRUE; the MCCI compute the CI for the mediation effects. (3) When the length is four, they represent the mediation effects in two studies in the following order: the treatment-mediator and mediator-outcome path estimates in studies (groups) 1 and 2.
se	The corresponding standard error(s) for parameter d.
mediation	Logical; d and se represent parameters for a mediation effect if TRUE; d and se represent parameters for a main or moderation effect if FALSE; default value is FALSE.
n.mcci	The number of draws for the MCCI method. Default is 10,000.
sig.level	The significance level. Default is .05.

sig.adjusted	Logical; use Bonferroni correction (i.e., dividing the original significance level by the number of tests) if TRUE, otherwise not; default value is TRUE.
two.tailed	Logical of two tailed test for difference test. Default is TRUE.
seed	Random seed for replication, default is 123.
eq.bd	The limit of the equivalence bounds for an equivalence test. Default is the MCCI for the equivalence test. It can be specified in the arguments as eq.bd = a positive number or eq.bd = c(lower bound #, upper bound #).
xlim	The limits set for the x-axis in the plot. Default is the MCCI for the difference test. It can be specified in the arguments as xlim = c(lower #, higher #).
xlab	The label for the x-axis in the plot. Default is "Differences in Effects".
ylab	The label for the y-axis in the plot. Default is NULL.
dashed.lines	Logical of whether dashed lines of equivalence bounds and zero should be added in the plot. Default is TRUE.
verbose	Logical; print the process if TRUE, otherwise not; default value is TRUE.

Value

The results of moderation analysis and equivalence tests using the MCCI method. It will also provide a plot for the MCCIs.

Examples

```
library(anomo)
# 1. Compute MCCIs for main or moderation effects-----
# 1.1. Compute MCCIs for one main or moderation effect from one study
myci <- mcci(d = .1, se = .02); myci$out
# 1.2 Compute MCCIs for differences in two main (or moderation) effects
myci <- mcci(d = c(0.1, 0.15), se = c(.02, 0.01)); myci$out
# 1.3 Compute MCCIs for differences across five main (or moderation) effects
myci <- mcci(d = c(0.10, 0.15, 0.20, 0.25, 0.30),
             se = c(0.01, 0.01, 0.02, 0.02, 0.03))
myci$out

# 2. Compute MCCIs for mediation effects
# 2.1. Compute MCCIs for an estimated mediation effect
myci <- mcci(d = c(.1, 0.15), se = c(.02, 0.01), mediation = TRUE)
myci$out
# 2.1. Compute MCCIs for differences in two mediation effects
myci <- mcci(d = c(0.30, 0.50, 0.33, 0.55),
             se = c(0.02, 0.01, 0.02, 0.03), mediation = TRUE)
myci$out

# 3. Explicitly specify other parameters
myci <- mcci(d = .05, se = .02, eq.bd = 0.1) # equivalence bounds
myci <- mcci(d = .05, se = .02, xlim = c(-0.15, 0.15)) # Range of x-axis
```

od.1.eq

*Optimal sample allocation calculation for equivalence test of two-group means***Description**

The optimal design of single-level experiments detecting equivalence of two-group means is to choose the optimal sample allocation that minimizes the variance of a treatment effect under a fixed budget, which is approximately the optimal sample allocation that maximizes statistical power under a fixed budget. The optimal design parameter is the proportion of individuals to be assigned to treatment (p).

Usage

```
od.1.eq(
  p = NULL,
  r12 = NULL,
  c1 = NULL,
  c1t = NULL,
  m = NULL,
  plots = TRUE,
  plim = NULL,
  varlim = NULL,
  plab = NULL,
  varlab = NULL,
  vartitle = NULL,
  verbose = TRUE
)
```

Arguments

<code>p</code>	The proportion of individuals to be assigned to treatment.
<code>r12</code>	The proportion of outcome variance explained by covariates.
<code>c1</code>	The cost of sampling one unit in the control condition.
<code>c1t</code>	The cost of sampling one unit in the treated condition.
<code>m</code>	Total budget, default value is the total costs of sampling 600 individuals across treatment conditions.
<code>plots</code>	Logical, provide variance plots if TRUE, otherwise not; default value is TRUE.
<code>plim</code>	The plot range for p , default value is $c(0, 1)$.
<code>varlim</code>	The plot range for variance, default value is $c(0, 0.05)$.
<code>plab</code>	The plot label for p , default value is "Proportion of Units in Treatment: p ".
<code>varlab</code>	The plot label for variance, default value is "Variance".
<code>vartitle</code>	The title of variance plot, default value is NULL.
<code>verbose</code>	Logical; print the value of p if TRUE, otherwise not; default value is TRUE.

Value

Unconstrained or constrained optimal sample allocation (p). The function also returns function name, design type, and parameters used in the calculation.

Examples

```
# Unconstrained optimal design #-----
myod <- od.1.eq(r12 = 0.5, c1 = 1, c1t = 50)
myod$out # output
```

plot.power.eq	<i>Plot statistical power curves under a fixed budget across optimal design parameters for equivalence testing</i>
---------------	--

Description

This function plots statistical power curves (for equivalence testing) under a fixed budget across optimal design parameters.

Usage

```
## S3 method for class 'power.eq'
plot(
  expr = NULL,
  nlim = c(2, 300),
  plim = c(0.01, 0.99),
  Jlim = c(3, 300),
  powerlim = c(0, 1),
  plot.title = NULL,
  m = NULL,
  d = NULL,
  q = 1,
  power = 0.8,
  eq.dis = NULL,
  by = c("n", "p", "J"),
  legend = TRUE,
  nlab = "Level-One Sample Size (n)",
  plab = "Proportion (p)",
  Jlab = "Level-Two Sample Size (J)",
  powerlab = "Statistical Power"
)
```

Arguments

expr Returned objects from an od function (e.g., od.1.eq).

nlim	The limits of the level-1 sample size (n) for calculating and plotting power curves.
plim	The limits of the proportion to the treated (p) for calculating and plotting power curves.
Jlim	The limits of the level-2 sample size (J) for calculating and plotting power curves.
powerlim	The power limits for plotting power curves.
plot.title	The title of the plot (e.g., plot.title = "Power Curves"). The default is NULL.
m	Total budget, default value is the total costs of sampling 600 individuals across treatment conditions.
d	The estimated difference in two-group means.
q	The number of predictors in the combined linear regression model. Default is 1.
power	Statistical power.
eq.dis	A positive number to specify the distance from equivalence bounds to d. The equivalence bounds are $c(-\text{abs}(d)-\text{eq.dis}, \text{abs}(d)+\text{eq.dis})$.
by	Dimensions to plot power curves by the optimal design parameters. The default value is by all optimal design parameters for a type of design. For example, default values are by = "p" for single-level designs, by = c("n", "p") for two-level designs, and by = c("n", "p", "J") for three-level designs.
legend	Logical; present plot legend if TRUE. The default is TRUE.
nlab	Label for the x-axis when the plot is by the optimal design parameter "n".
plab	Label for the x-axis when the plot is by the optimal design parameter "p".
Jlab	Label for the x-axis when the plot is by the optimal design parameter "J".
powerlab	The label for the statistical power.

Examples

```
# Optimal sample allocation identification
od <- od.l.eq(r12 = 0.5, c1 = 1, c1t = 10)
# plot the power curve
plot.power.eq(expr = od, d = 0.1, eq.dis = 0.1)
```

Description

Statistical power analysis for equivalence test of two-group means.

Usage

```
power.1.eq(
  cost.model = FALSE,
  expr = NULL,
  constraint = NULL,
  d = NULL,
  eq.dis = NULL,
  m = NULL,
  c1 = NULL,
  c1t = NULL,
  n = NULL,
  p = NULL,
  q = 1,
  sig.level = 0.05,
  r12 = NULL,
  power = NULL,
  powerlim = NULL,
  nlim = NULL,
  mlim = NULL,
  eq.dislim = NULL,
  verbose = TRUE
)
```

Arguments

cost.model	Logical; power analyses accommodating costs and budget (e.g., required budget for desired power, power, minimum detectable eq.dis under a fixed budget) if TRUE. Otherwise, conventional power analysis is performed (e.g., required sample size, power, or minimum detectable eq.dis calculation); default value is FALSE, and it will be changed to TRUE if expr is not NULL.
expr	Returned object from function od.1.eq ; default value is NULL; if expr is specified, parameter values of r12, c1, c1t, and p used or solved in function od.1.eq will be passed to the current function; only the value of p that specified or solved in function od.1.eq can be overwritten if constraint is specified.
constraint	Specify the constrained value of p in list format to overwrite that from expr; default value is NULL.
d	The estimated difference in two-group means.
eq.dis	A positive number to specify the distance from equivalence bounds to d. The equivalence bounds are $c(-\text{abs}(d) - \text{eq.dis}, \text{abs}(d) + \text{eq.dis})$.
m	Total budget.
c1	The cost of sampling one unit in the control condition.
c1t	The cost of sampling one unit in the treated condition.
n	The total sample size across groups.
p	The proportion of individuals in the intervention group or group 1.
q	The number of predictors in the combined linear regression model. Default is 1.

sig.level	The significance level. Default is .05.
r12	The proportion of variance explained by covariates if any.
power	Statistical power.
powerlim	The range for solving the root of power (power) numerically, default value is c(1e-10, 1 - 1e-10).
nlim	The range for searching the root of sample size (n) numerically, default value is c(10, 10e10).
mlim	The range for searching the root of budget (m) numerically, default value is the costs sampling nlim units across treatment conditions or c(4 * ncost, 10e10 * ncost) with ncost = ((1 - p) * c1 + p * c1t).
eq.dislim	The range for solving the root of equivalence difference with the effect size (d) numerically, default value is c(0, 10).
verbose	Logical; print the process if TRUE, otherwise not; default value is TRUE.

Value

Required budget (and/or required sample size), statistical power, or minimum detectable eq.dis depending on the specification of parameters. The function also returns the function name, design type, and parameters used in the calculation.

Examples

```
library(anomo)
# 1. Conventional Power Analyses from Difference Perspectives
# Calculate the required sample size to achieve certain level of power
mysample <- power.1.eq(d = .1, eq.dis = 0.1, p = .5,
                      r12 = .5, q = 1, power = .8)
mysample$out

# Calculate power provided by a sample size allocation
mypower <- power.1.eq(d = 1, eq.dis = .1, n = 1238, p = .5,
                     r12 = .5, q = 1)
mypower$out

# Calculate the minimum detectable distance a given sample size allocation
# can achieve
myeq.dis <- power.1.eq(d = .1, n = 1238, p = .5,
                     r12 = .5, q = 1, power = .8)
myeq.dis$out

# 2. Power Analyses Using Optimal Sample Allocation
myod <- od.1.eq(r12 = 0.5, c1 = 1, c1t = 10)
budget <- power.1.eq(expr = myod, d = .1, eq.dis = 0.1,
                    q = 1, power = .8)
budget.balanced <- power.1.eq(expr = myod, d = .1, eq.dis = 0.1,
                             q = 1, power = .8,
                             constraint = list(p = .50))
(budget.balanced$out$m-budget$out$m)/budget$out$m *100
# 27% more budget required from the balanced design with p = 0.50.
```

re	<i>Relative efficiency (RE) calculation</i>
----	---

Description

Calculate the relative efficiency (RE) between two designs using the re function from the R package odr.

Usage

```
re(od, subod, rounded = TRUE, verbose = TRUE)
```

Arguments

od	Returned object of first design (e.g., unconstrained optimal design) from function od.1.eq .
subod	Returned object of second design (e.g., constrained optimal design) from function od.1.eq .
rounded	Logical; round the values of p to two decimal places if TRUE. No rounding if FALSE; default is TRUE.
verbose	Logical; print the value of relative efficiency if TRUE, otherwise not; default is TRUE.

Value

Relative efficiency value.

Examples

```
# Unconstrained optimal design #-----
myod1 <- od.1.eq(r12 = 0.5, c1 = 1, c1t = 20)
# Constrained optimal design with p = .50
myod2 <- od.1.eq(r12 = 0.5, c1 = 1, c1t = 20, p = .50)
# Relative efficiency (RE)
myre <- re(od = myod1, subod = myod2)
myre$re # RE = 0.71
```

Index

mcci, [2](#)

od.1.eq, [4](#), [7](#), [9](#)

plot.power.eq, [5](#)

power.1.eq, [6](#)

re, [9](#)