Package ‘mpe’

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Title Multiple Primary Endpoints

Description Functions for calculating sample size and power for clinical trials with multiple (co-)primary endpoints.

License LGPL-3

LazyData TRUE

Depends R (>= 3.1.0), mvtnorm

Imports stats

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

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R topics documented:

atleast.one.endpoint *At least one Endpoint with Known Covariance*

Description

The function calculates either sample size or power for continuous multiple primary endpoints for at least one endpoint with known covariance.

Usage

```
atleast.one.endpoint(K, n = NULL, delta = NULL, Sigma, SD, rho, sig.level = 0.05/K,
                            power = NULL, tol = .Machine$double.eps^0.25)
```

Arguments

`K`	number of endpoints
`n`	optional: sample size
`delta`	expected effect size
`Sigma`	A covariance of known matrix
`SD`	known standard deviations (length `K`)
`rho`	known correlations (length `0.5*K*(K-1)`)
`sig.level`	Significance level (Type I error probability)
`power`	optional: Power of test (1 minus Type II error probability)
`tol`	The desired accuracy

Details

The function can be used to either compute sample size or power for continuous multiple primary endpoints with known covariance where a significant difference for at least one endpoint is expected. The implementation is based on the formulas given in the references below.

The null hypothesis reads

$$\mu_{Tk} - \mu_{Ck} \leq 0$$

for all

$$k \in \{1, \ldots, K\}$$

where Tk is treatment k, Ck is control k and K is the number of co-primary endpoints.

One has to specify either `n` or `power`, the other parameter is determined. Moreover, either covariance matrix `Sigma` or standard deviations `SD` and correlations `rho` must be given.

Value

Object of class `power.mpe.test`, a list of arguments (including the computed one) augmented with method and note elements.

References

Sugimoto, T. and Sozu, T. and Hamasaki, T. (2012). A convenient formula for sample size calculations in clinical trials with multiple co-primary continuous endpoints. *Pharmaceut. Statist.*, **11**: 118-128. doi:10.1002/pst.505

Sozu, T. and Sugimoto, T. and Hamasaki, T. and Evans, S.R. (2015). *Sample Size Determination in Clinical Trials with Multiple Endpoints*. Springer Briefs in Statistics, ISBN 978-3-319-22005-5.

Examples

```
## compute power
atleast.one.endpoint(K = 2, delta = c(0.2,0.2), Sigma = diag(c(1,1)), power = 0.8)

## compute sample size
atleast.one.endpoint(K = 2, delta = c(0.2,0.2), Sigma = diag(c(2,2)), power = 0.9)

## known covariance matrix
Sigma <- matrix(c(1.440, 0.840, 1.296, 0.840,
                  0.840, 1.960, 0.168, 1.568,
                  1.296, 0.168, 1.440, 0.420,
                  0.840, 1.568, 0.420, 1.960), ncol = 4)
## compute power
atleast.one.endpoint(K = 4, n = 60, delta = c(0.5, 0.75, 0.5, 0.75), Sigma = Sigma)
## equivalent: known SDs and correlation rho
atleast.one.endpoint(K = 4, n = 60, delta = c(0.5, 0.75, 0.5, 0.75),
                SD = c(1.2, 1.4, 1.2, 1.4), rho = c(0.5, 0.9, 0.5, 0.1, 0.8, 0.25))
```

`mpe.t.test` *Intersection-Union t-Test for Testing Multiple Co-Primary Endpoints*

Description

The function computes the intersection-union t-test which forms the basis for the sample size and power calculations in function `power.unknown.var`.

Usage

```
mpe.t.test(X, Y, conf.level = 0.975)
```

Arguments

`X`	matrix with observations of group 1 in rows
`Y`	matrix with obersvations of group 2 in rows
`conf.level`	confidence level of the interval.

Details

The function computes the intersection-union t-test which forms the basis for the sample size and power calculations for continuous multiple co-primary endpoints with unknown covariance as computed by function `power.unknown.var`. The implementation is based on the formulas given in the references below.

The null hypothesis reads

$$\mu_{Tk} - \mu_{Ck} \leq 0$$

for at least one

$$k \in \{1, \ldots, K\}$$

where Tk is treatment k, Ck is control k and K is the number of co-primary endpointss (i.e. number of columns of `X` and `Y`).

Value

Object of class `"mpe.test"`.

References

Sugimoto, T. and Sozu, T. and Hamasaki, T. (2012). A convenient formula for sample size calculations in clinical trials with multiple co-primary continuous endpoints. *Pharmaceut. Statist.*, **11**: 118-128. doi:10.1002/pst.505

Sozu, T. and Sugimoto, T. and Hamasaki, T. and Evans, S.R. (2015). *Sample Size Determination in Clinical Trials with Multiple Endpoints*. Springer Briefs in Statistics, ISBN 978-3-319-22005-5.

See Also

`power.unknown.var`

Examples

```
delta <- c(0.25, 0.5)
Sigma <- matrix(c(1, 0.75, 0.75, 1), ncol = 2)
n <- 50
X <- rmvnorm(n=n, mean = delta, sigma = Sigma)
Y <- rmvnorm(n=n, mean = rep(0, length(delta)), sigma = Sigma)
mpe.t.test(X = X, Y = Y)
```

`mpe.z.test` *Intersection-Union z-Test for Testing Multiple Co-Primary Endpoints*

Description

The function computes the intersection-union z-test which forms the basis for the sample size and power calculations in function `power.known.var`.

Usage

```
mpe.z.test(X, Y, Sigma, conf.level = 0.975)
```

Arguments

`X`	matrix with observations of group 1 in rows
`Y`	matrix with obersvations of group 2 in rows
`Sigma`	known covariance matrix.
`conf.level`	confidence level of the interval.

Details

The function computes the intersection-union z-test which forms the basis for the sample size and power calculations for continuous multiple co-primary endpoints with known covariance as computed by function `power.known.var`. The implementation is based on the formulas given in the references below.

The null hypothesis reads

$$\mu_{Tk} - \mu_{Ck} \leq 0$$

for at least one

$$k \in \{1, \ldots, K\}$$

where Tk is treatment k, Ck is control k and K is the number of co-primary endpoints (i.e. number of columns of `X` and `Y`).

Value

Object of class `"mpe.test"`.

References

Sugimoto, T. and Sozu, T. and Hamasaki, T. (2012). A convenient formula for sample size calculations in clinical trials with multiple co-primary continuous endpoints. *Pharmaceut. Statist.*, **11**: 118-128. doi:10.1002/pst.505

Sozu, T. and Sugimoto, T. and Hamasaki, T. and Evans, S.R. (2015). *Sample Size Determination in Clinical Trials with Multiple Endpoints*. Springer Briefs in Statistics, ISBN 978-3-319-22005-5.

See Also

`power.known.var`, `mpe.t.test`

Examples

```
delta <- c(0.25, 0.5)
Sigma <- matrix(c(1, 0.75, 0.75, 1), ncol = 2)
n <- 50
X <- rmvnorm(n=n, mean = delta, sigma = Sigma)
Y <- rmvnorm(n=n, mean = rep(0, length(delta)), sigma = Sigma)
mpe.z.test(X = X, Y = Y, Sigma = Sigma)
```

power.known.var *Multiple Co-Primary Endpoints with Known Covariance*

Description

The function calculates either sample size or power for continuous multiple co-primary endpoints with known covariance.

Usage

```
power.known.var(K, n = NULL, delta = NULL, Sigma, SD, rho,
  sig.level = 0.05, power = NULL, tol = .Machine$double.eps^0.25)
```

Arguments

`K`	number of co-primary endpoints
`n`	optional: sample size
`delta`	expected effect size (length `K`)
`Sigma`	known covariance matrix (dimension `K` x `K`)
`SD`	known standard deviations (length `K`)
`rho`	known correlations (length `0.5*K*(K-1)`)
`sig.level`	significance level (Type I error probability)
`power`	optional: power of test (1 minus Type II error probability)
`tol`	the desired accuracy for `uniroot`.

Details

The function can be used to either compute sample size or power for continuous multiple co-primary endpoints with known covariance where a multivariate normal distribution is assumed. The implementation is based on the formulas given in the references below.

The null hypothesis reads

$$\mu_{Tk} - \mu_{Ck} \le 0$$

for at least one

$$k \in \{1, \dots, K\}$$

where Tk is treatment k, Ck is control k and K is the number of co-primary endpoints.

One has to specify either `n` or `power`, the other parameter is determined. Moreover, either covariance matrix `Sigma` or standard deviations `SD` and correlations `rho` must be given.

Value

Object of class `power.mpe.test`, a list of arguments (including the computed one) augemented with method and note elements.

References

Sugimoto, T. and Sozu, T. and Hamasaki, T. (2012). A convenient formula for sample size calculations in clinical trials with multiple co-primary continuous endpoints. *Pharmaceut. Statist.*, **11**: 118-128. doi:10.1002/pst.505

Sozu, T. and Sugimoto, T. and Hamasaki, T. and Evans, S.R. (2015). *Sample Size Determination in Clinical Trials with Multiple Endpoints*. Springer Briefs in Statistics, ISBN 978-3-319-22005-5.

See Also

power.unknown.var, mpe.z.test

Examples

```
## compute power
power.known.var(K = 2, n = 20, delta = c(1,1), Sigma = diag(c(1,1)))

## compute sample size
power.known.var(K = 2, delta = c(1,1), Sigma = diag(c(2,2)), power = 0.9,
                sig.level = 0.025)

## known covariance matrix
Sigma <- matrix(c(1.440, 0.840, 1.296, 0.840,
                  0.840, 1.960, 0.168, 1.568,
                  1.296, 0.168, 1.440, 0.420,
                  0.840, 1.568, 0.420, 1.960), ncol = 4)
## compute power
power.known.var(K = 4, n = 60, delta = c(0.5, 0.75, 0.5, 0.75), Sigma = Sigma)
## equivalent: known SDs and correlation rho
power.known.var(K = 4, n = 60,delta = c(0.5, 0.75, 0.5, 0.75),
                SD = c(1.2, 1.4, 1.2, 1.4), rho = c(0.5, 0.9, 0.5, 0.1, 0.8, 0.25))
```

`power.unknown.var` *Multiple Co-Primary Endpoints with Unknown Covariance*

Description

The function calculates either sample size or power for continuous multiple co-primary endpoints with unknown covariance.

Usage

```
power.unknown.var(K, n = NULL, delta = NULL, Sigma, SD, rho, sig.level = 0.05,
                  power = NULL, M = 10000, min.n = NULL, max.n = NULL,
                  tol = .Machine$double.eps^0.25, use.uniroot = TRUE)
```

Arguments

K	number of co-primary endpoints
n	optional: sample size
delta	expected effect size (length K)
Sigma	unknown covariance matrix (dimension K x K)
SD	unknown standard deviations (length K)
rho	unknown correlations (length 0.5*K*(K-1))
sig.level	significance level (Type I error probability)
power	optional: power of test (1 minus Type II error probability)
M	Number of replications for the required simulations.
min.n	Starting point of search interval for sample size
max.n	End point of search interval for sample size, must be larger than min.n
tol	the desired accuracy for uniroot
use.uniroot	Finds one root of one equation

Details

The function can be used to either compute sample size or power for continuous multiple co-primary endpoints with unknown covariance. The implementation is based on the formulas given in the references below.

The null hypothesis reads

$$\mu_{Tk} - \mu_{Ck} \leq 0$$

for at least one

$$k \in \{1, \ldots, K\}$$

where Tk is treatment k, Ck is control k and K is the number of co-primary endpoints.

One has to specify either n or power, the other parameter is determined. An approach to calculate sample size n, is to first call power.known.var and use the result as min.n. The input for max.n must be larger then min.n. Moreover, either covariance matrix Sigma or standard deviations SD and correlations rho must be given.

The sample size is calculated by simulating Wishart distributed random matrices, hence the results include a certain random variation.

Value

Object of class power.mpe.test, a list of arguments (including the computed one) augmented with method and note elements.

References

Sugimoto, T. and Sozu, T. and Hamasaki, T. (2012). A convenient formula for sample size calculations in clinical trials with multiple co-primary continuous endpoints. *Pharmaceut. Statist.*, **11**: 118-128. doi:10.1002/pst.505

Sozu, T. and Sugimoto, T. and Hamasaki, T. and Evans, S.R. (2015). *Sample Size Determination in Clinical Trials with Multiple Endpoints*. Springer Briefs in Statistics, ISBN 978-3-319-22005-5.

See Also

power.known.var, mpe.t.test

Examples

```
## compute power
## Not run:
power.unknown.var(K = 2, n = 20, delta = c(1,1), Sigma = diag(c(1,1)))

## To compute sample size, first assume covariance as known
power.known.var(K = 2, delta = c(1,1), Sigma = diag(c(2,2)), power = 0.9,
                  sig.level = 0.025)

## The value of n, which is 51, is used as min.n and max.n must be larger
## then min.n so we try 60.
power.unknown.var(K = 2, delta = c(1,1), Sigma = diag(c(2,2)), power = 0.9,
                  sig.level = 0.025, min.n = 51, max.n = 60)

## More complex example with unknown covariance matrix assumed to be
Sigma <- matrix(c(1.440, 0.840, 1.296, 0.840,
                  0.840, 1.960, 0.168, 1.568,
                  1.296, 0.168, 1.440, 0.420,
                  0.840, 1.568, 0.420, 1.960), ncol = 4)
## compute power
power.unknown.var(K = 4, n = 90, delta = c(0.5, 0.75, 0.5, 0.75), Sigma = Sigma)
## equivalent: unknown SDs and correlation rho
power.unknown.var(K = 4, n = 90, delta = c(0.5, 0.75, 0.5, 0.75),
                  SD = c(1.2, 1.4, 1.2, 1.4),
                  rho = c(0.5, 0.9, 0.5, 0.1, 0.8, 0.25))

## End(Not run)
```

---

print.power.mpe.test *Print Methods for Hypothesis Tests, Sample size and Power Calculations*

Description

Printing objects of class "mpe.tst" and "power.mpe.test" by simple print methods.

Usage

```
  ## S3 method for class 'mpe.test'
print(x, digits = getOption("digits"), prefix = "\t", ...)
  ## S3 method for class 'power.mpe.test'
print(x, digits = getOption("digits"), ...)
```

Arguments

`x`	object of class "`mpe.test`" or "`power.mpe.test`".
`digits`	number of significant digits to be used.
`prefix`	string, passed to `strwrap` for displaying the `method` component of the `mpe.test` object.
`...`	further arguments to be passed to or from methods.

Details

The `print` methods are based on the respective methods `print.htest` and `print.power.htest` of package **stats**.

A `power.mpe.test` object is just a named list of numbers and character strings, supplemented with `method` and `note` elements. The `method` is displayed as a title, the `note` as a footnote, and the remaining elements are given in an aligned 'name = value' format.

Value

the argument `x`, invisibly, as for all `print` methods.

See Also

`print.power.htest` `power.known.var`, `power.unknown.var`, `mpe.z.test`, `mpe.t.test`.

Examples

```
(pkv <- power.known.var(K = 2, delta = c(1,1), Sigma = diag(c(2,2)), power = 0.9,
                        sig.level = 0.025))
  print(pkv, digits =  4) # using less digits than default
  print(pkv, digits = 12) # using more  "       "
```

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