

# Package ‘PowerTOST’

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**Title** Power and Sample Size for (Bio)Equivalence Studies

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**Description** Contains functions to calculate power and sample size for various study designs used in bioequivalence studies. Use `known.designs()` to see the designs supported. Power and sample size can be obtained based on different methods, amongst them prominently the TOST procedure (two one-sided t-tests). See README and NEWS for further information.

**Imports** mvtnorm, stats, utils, graphics, grDevices, cubature (>= 1.3-6), TeachingDemos

**Suggests** crossdes, knitr, rmarkdown, devtools, tuftex, emmeans

**ByteCompile** yes

**LazyData** true

**VignetteBuilder** knitr

**URL** <https://github.com/Detlew/PowerTOST>

**BugReports** <https://github.com/Detlew/PowerTOST/issues>

**License** GPL (>= 2)

**NeedsCompilation** no

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**R topics documented:**

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bib.CL	<i>Design matrices of period balanced incomplete block designs</i>
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---

## Description

This function returns the ‘design’ matrix of incomplete block designs described by Chow & Liu. The design matrices were recoded 1=R, 2=T1, 3=T2, . . .

## Usage

```
bib.CL(trt, p)
```

## Arguments

trt	Number of treatments (3 to 5).
p	Number of periods (2 to trt-1).

## Value

Matrix containing the sequences in rows and periods in columns.  
The entry (i, j) of the matrix corresponds to the treatment or dose (index) a subject within *i*-th sequence gets in the *j*-th period.

## Author(s)

D. Labes

## References

Chow SC, Liu JP. *Design and Analysis of Bioavailability and Bioequivalence Studies*. Boca Raton: CRC Press; 3<sup>rd</sup> edition 2009. Chapter 2.6.

**Examples**

```
# 4 treatments/doses, 3 periods
bib.CL(4, 3)
# gives 4 sequences
# to see this in Chow & Liu's coding
tmt <- c("R", "T1", "T2", "T3")
matrix(tmt[bib.CL(4, 3)], ncol=3)
```

---

CI.BE

---

*1-2\*alpha confidence interval given point estimate, CV, and n*


---

**Description**

Utility function to calculate the  $1 - 2\alpha$  CI given point estimate, CV, and n for the various designs covered in this package.

**Usage**

```
CI.BE(alpha = 0.05, pe, CV, n, design = "2x2", robust = FALSE)
```

**Arguments**

alpha	Type I error probability, significance level. Defaults to 0.05.
pe	Point estimate (GMR).
CV	Coefficient of variation as ratio (not percent).
n	Total number of subjects if a scalar is given. Number of subjects in (sequence) groups if given as vector.
design	Character string describing the study's design. See <code>known.designs()</code> for designs covered in this package.
robust	Defaults to FALSE. Setting to TRUE will use the degrees of freedom according to the 'robust' evaluation (aka Senn's basic estimator). These degrees of freedom are calculated as <code>n-seq</code> . See <code>known.designs()\$df2</code> for designs covered in this package.

**Value**

Returns the  $1 - 2\alpha$  confidence interval.  
Returns a vector with named elements `lower`, `upper` if arguments `pe` and `CV` are scalars, else a matrix with columns `lower`, `upper` is returned.

**Note**

The function assumes an evaluation using log-transformed data.  
 The function assumes equal variances in case of design="parallel" and the higher order crossover designs.  
 The implemented formula covers balanced and unbalanced designs.

Whether the function vectorizes properly is not thoroughly tested.

**Author(s)**

D. Labes

**Examples**

```
# 90% confidence interval for the 2x2 crossover
# n(total) = 24
CI.BE(pe = 0.95, CV = 0.3, n = 24)
# should give
#   lower   upper
# 0.8213465 1.0988055
# same total number but unequal sequences
CI.BE(pe = 0.95, CV = 0.3, n = c(13, 11))
#   lower   upper
# 0.8209294 1.0993637
```

---

 CI.RatioF

---

*1-2\*alpha Fieller CI given point estimate, CV (, CVb) and n*


---

**Description**

Utility function to calculate the  $1 - 2\alpha$  Fieller confidence interval given the point estimate, CV (, CVb), and n for the parallel group and  $2 \times 2$  crossover.

**Usage**

```
CI.RatioF(alpha = 0.025, pe, CV, CVb, n, design = c("2x2", "parallel"))
```

**Arguments**

alpha	Type I error probability, aka significance level. Defaults here to 0.025 because this function is intended for studies with clinical endpoints.
pe	Point estimate of T/R ratio.
CV	Coefficient of variation as ratio (not percent). In case of design="parallel" this is the CV of the total variability, in case of design="2x2" the intra-subject CV.
CVb	CV of the between-subject variability. Only necessary for design="2x2".

n	Total number of subjects if a scalar is given. Number of subjects in (sequence) groups if given as vector.
design	A character string describing the study design. design="parallel" or design="2x2" allowed for a parallel two-group design or a classical TRIRT crossover design.

**Details**

The CV(within) and CVb(etween) in case of design="2x2" are obtained via an appropriate ANOVA from the error term and from the difference  $(MS(\text{subject within sequence}) - MS(\text{error})) / 2$ .

**Value**

Returns the  $1 - 2\alpha$  confidence interval.

**Note**

The function assumes an evaluation using un-transformed data.  
The function assumes equal variances in case of design="parallel".  
The formula implemented covers balanced and unbalanced designs.

Note that when the mean of the denominator of the ratio is close to zero, confidence intervals might be degenerated and are returned as NA. In such a case a warning is issued.

Whether the function vectorizes properly is not thoroughly tested.

This function is intended for studies with clinical endpoints. In such studies the 95% confidence intervals are usually used for equivalence testing. Therefore, alpha defaults here to 0.025 (see EMA 2000).

**Author(s)**

D. Labes

**References**

Locke CS. *An exact confidence interval from untransformed data for the ratio of two formulation means*. J Pharmacokin Biopharm. 1984;12(6):649–55. doi: [10.1007/BF01059558](https://doi.org/10.1007/BF01059558)

Hauschke D, Steinijans VW, Pigeot I. *Bioequivalence Studies in Drug Development*. Chichester: John Wiley; 2007. Chapter 10. doi: [10.1002/9780470094778.fmatter](https://doi.org/10.1002/9780470094778.fmatter)

European Medicines Agency, Committee for Proprietary Medicinal Products. *Points to consider on switching between superiority and non-inferiority*. London, 27 July 2000. [CPMP/EWP/482/99](https://www.ema.europa.eu/en/medicines/human/CTX/points-to-consider-on-switching-between-superiority-and-non-inferiority)

**See Also**

[CI.BE](#), [power.RatioF](#)

**Examples**

```
# 95% Fieller CI for the 2x2 crossover
CI.RatioF(pe = 0.95, CV = 0.3, CVb = 0.6, n = 32)
```

---

ct5.1+ct5.2+ct5.3+ct5.4.1

*Sample Size Tables for the Classical 2x2 Crossover Design*

---

**Description**

These data.frames give sample size tables calculated with `sampleN.TOST()` for the 2x2 design.

**Details**

The data.frames can be accessed by their names.

data.frame	Description
ct5.1	Multiplicative model, $\theta_1=0.8$ , $\theta_2=1.25$ ( $1/\theta_1$ ), exact
ct5.2	Multiplicative model, $\theta_1=0.75$ , $\theta_2=1.3333$ ( $1/\theta_1$ ), exact
ct5.3	Multiplicative model, $\theta_1=0.9$ , $\theta_2=1.1111$ ( $1/\theta_1$ ), exact
ct5.4.1	Additive model, $\theta_1=-0.2$ , $\theta_2=+0.2$ (BE limits 0.80 – 1.20), exact

**Note**

Scripts for creation of these data.frames can be found in the `/test` sub-directory of the package. Comparing the results of these scripts to the corresponding data.frames can be used for validation purposes.

**Author(s)**

PowerTOST

**Source**

data.frame	Origin	Details
ct5.1	Hauschke <i>et al.</i>	Table 5.1 (p 113–114)
ct5.2	Hauschke <i>et al.</i>	Table 5.2 (p 115–116)
ct5.3	Hauschke <i>et al.</i>	Table 5.3 (p 118)
ct5.4.1	Chow & Liu	Table 5.4.1 (p 158)

## References

Hauschke D, Steinijs VW, Pigeot I. *Bioequivalence Studies in Drug Development*. Chichester: John Wiley; 2007.

Chow SC, Liu JP. *Design and Analysis of Bioavailability and Bioequivalence Studies*. Boca Raton: CRC Press; 3<sup>rd</sup> edition 2009.

## Examples

ct5.1  
ct5.2  
ct5.3  
ct5.4.1

---

ct9.6.2+ct9.6.6

*Sample Size Tables for the 2x2x3 Replicate Crossover Design*

---

## Description

These data.frames give sample size tables calculated with `sampleN.TOST()` for the 2x2x3 replicate crossover design (2-treatment 2-sequence 3-period design).

## Details

The data.frames can be accessed by their names.

data.frame	Description
ct9.6.2	Additive model, $\theta_1 = -0.2$ , $\theta_2 = +0.2$ (BE limits 0.80 – 1.20) approximate power via shifted non-central $t$ -distribution
ct9.6.6	Multiplicative model, $\theta_1 = 0.8$ , $\theta_2 = 1.25$ ( $1/\theta_1$ ) approximate power via shifted non-central $t$ -distribution

Attention! CV is `se` (standard error) of residuals.

## Note

Scripts for creation of these data.frames can be found in the `/test` sub-directory of the package. Comparing the results of these scripts to the corresponding data.frames can be used for validation purposes.

## Author(s)

PowerTOST

## Source

data.frame	Origin	Details
------------	--------	---------



ct9.6.2	Chow & Liu	Table 9.6.2 (p 292)
ct9.6.6	Chow & Liu	Table 9.6.6 (p 293)

## References

Chow SC, Liu JP. *Design and Analysis of Bioavailability and Bioequivalence Studies*. Boca Raton: CRC Press; 3<sup>rd</sup> edition 2009.

## Examples

ct9.6.2  
ct9.6.6

---

ct9.6.4+ct9.6.8

*Sample Size Tables for the 2x4x4 Replicate Crossover Design*

---

## Description

These data.frames give sample size tables calculated with `sampleN.TOST()` for the 2x4x4 replicate crossover design (2-treatment 4-sequence 4-period design).

## Details

The data.frames can be accessed by their names.

data.frame	Description
ct9.6.4	Additive model, $\theta_1 = -0.2$ , $\theta_2 = +0.2$ (BE limits 0.80 – 1.20) approximate power via shifted non-central $t$ -distribution
ct9.6.8	Multiplicative model, $\theta_1 = 0.8$ , $\theta_2 = 1.25$ ( $1/\theta_1$ ) approximate power via shifted non-central $t$ -distribution

Attention! CV is `se` (standard error) of residuals.

## Note

Scripts for creation of these data.frames can be found in the `/test` sub-directory of the package. Comparing the results of these scripts to the corresponding data.frames can be used for validation purposes.

## Author(s)

PowerTOST

**Source**

data.frame	Origin	Details
ct9.6.4	Chow & Liu	Table 9.6.4 (p 294)
ct9.6.8	Chow & Liu	Table 9.6.8 (p 298)

## References

Chow SC, Liu JP. *Design and Analysis of Bioavailability and Bioequivalence Studies*. Boca Raton: CRC Press; 3<sup>rd</sup> edition 2009.

## Examples

ct9.6.4  
ct9.6.8

---

ctSJ.VIII.10+ctSJ.VIII.20+ctCW.III

*Sample Size Tables for the Parallel Group Design*

---

## Description

These data.frames give sample size tables calculated with `sampleN.TOST()` for the parallel group design (2 groups).

## Details

The data.frames can be accessed by their names.

data.frame	Description
ctSJ.VIII.10	Multiplicative model, $\theta_1=0.9$ , $\theta_2=1.1111$ ( $1/\theta_1$ ), target power=90% approximate power via non-central $t$ -distribution
ctSJ.VIII.20	Multiplicative model, $\theta_1=0.8$ , $\theta_2=1.25$ ( $1/\theta_1$ ), target power=90% approximate power via non-central $t$ -distribution
ctCW.III	Additive model, $\theta_1=-0.2$ , $\theta_2=+0.2$ (BE limits 0.80 – 1.20), exact

Attention! Julious gives sample size per group.

## Note

Scripts for creation of these data.frames can be found in the `/test` sub-directory of the package. Comparing the results of these scripts to the corresponding data.frames can be used for validation purposes.

**Author(s)**

PowerTOST

**Source**

data.frame	Origin	Details
ctSJ.VIII.10	Julious	Table VIII (p. 1972), column 'Level of bioequivalence 10%'
ctSJ.VIII.20	Julious	Table VIII (p. 1972), column 'Level of bioequivalence 20%'
ctCW.III	Chow & Wang	Table III (p. 164)

Seems the last reference is not very reliable (compare to the table in the paper).

**References**

Julious SA. *Tutorial in Biostatistics. Sample sizes for clinical trials with Normal data.* Stat Med. 2004;23(12):1921–86. doi: [10.1002/sim.1783](https://doi.org/10.1002/sim.1783)

Chow SC, Wang H. *On Sample Size Calculation in Bioequivalence Trials.* J Pharmacokinet Pharmacodyn. 2001;28(2):155–69. doi: [10.1023/A:1011503032353](https://doi.org/10.1023/A:1011503032353)

**Examples**

```
ctSJ.VIII.10
ctSJ.VIII.20
ctCW.III
```

---

CV2se+se2CV+CV2mse+mse2CV

*Helper functions*

---

**Description**

Calculates the standard error or the mean squared error from a given CV and vice versa for log-normal data.

**Usage**

```
CV2se(CV)
se2CV(se)
CV2mse(CV)
mse2CV(mse)
```

**Arguments**

CV	coefficient of variatio as ratio (not percent)
se	standard error
mse	mean squared error (aka residual variance)

**Value**

Returns  
 $se = \sqrt{\log(CV^2+1)}$   
 $CV = \sqrt{\exp(se^2)-1}$   
 $mse = \log(CV^2+1)$   
 $CV = \sqrt{\exp(mse)-1}$

**Note**

These functions were originally intended for internal use only but may be useful for others.

**Author(s)**

D. Labes

**Examples**

```
# these functions are one liners:
CV2se <- function(CV) return(sqrt(log(1.0 + CV^2)))
se2CV <- function(se) return(sqrt(exp(se^2)-1))

CV2se(0.3)
# should give:
# [1] 0.2935604

se2CV(0.2935604)
# [1] 0.3
```

---

CVCL

*Confidence limits of a CV for log-normal data*

---

**Description**

The function calculates the  $1 - \alpha$  confidence limits (either 1-sided or 2-sided) via the  $\chi^2$  distribution of the error variance the CV is based on.

**Usage**

```
CVCL(CV, df, side = c("upper", "lower", "2-sided"), alpha = 0.05)
```

**Arguments**

CV	Coefficient of variation as ratio (not percent)
df	degrees of freedom of the CV (error variance)
side	Side(s) to calculate the confidence limits for, defaults to upper
alpha	Type I error probability, aka significance level

**Value**

Numeric vector of the confidence limits named as lower CL and upper CL.  
 In case of the one-sided upper confidence limit the lower CL is = 0.  
 In case of the one-sided lower confidence limit the upper CL is = Inf.

**Author(s)**

D. Labes

**Examples**

```
# upper one-sided 95% CL of a CV=0.3
# from a study with df=22 (f.i. a 2x2 crossover with n=24)
# default side="upper" since not explicitly given
CVCL(0.3, df = 22)
# should give:
# lower CL upper CL
# 0.0000000 0.4075525
```

---

 CVfromCI

---

*CV from a given Confidence interval*


---

**Description**

Calculates the CV (coefficient of variation) from a known confidence interval of a BE study.  
 Useful if no CV but the 90% CI was given in literature.

**Usage**

```
CVfromCI(pe, lower, upper, n, design = "2x2", alpha = 0.05, robust = FALSE)
CI2CV(pe, lower, upper, n, design = "2x2", alpha = 0.05, robust = FALSE)
```

**Arguments**

pe	Point estimate of the T/R ratio. The pe may be missing. In that case it will be calculated as geometric mean of lower and upper.
lower	Lower confidence limit of the BE ratio.
upper	Upper confidence limit of the BE ratio.
n	Total number of subjects under study if given as scalar. Number of subjects in (sequence) groups if given as vector.
design	Character string describing the study design. See known.designs() for designs covered in this package.
alpha	Error probability. Set it to (1-confidence)/2 (i.e. to 0.05 for the usual 90% confidence intervals).

robust            With robust=FALSE (the default) usual degrees of freedom of the designs are used.  
 With robust=TRUE the degrees of freedom for the so-called robust evaluation (df2 in known.designs()) will be used. This may be helpful if the CI was evaluated via a mixed model or via intra-subject contrasts (aka Senn's basic estimator).

### Details

See Helmut Schütz' [presentation](#) for the algebra underlying this function.

### Value

Numeric value of the CV as ratio.

### Note

The calculations are based on the assumption of evaluation via log-transformed values.  
 The calculations are further based on a common variance of Test and Reference treatments in replicate crossover studies or parallel group study, respectively.

In case of argument n given as n(total) and is not divisible by the number of (sequence) groups the total sample size is partitioned to the (sequence) groups to have small imbalance only. A message is given in such cases.

The estimated CV is conservative (*i.e.*, higher than actually observed) in case of unbalancedness.

CI2CV() is simply an alias to CVfromCI().

### Author(s)

Original by D. Labes with suggestions by H. Schütz.  
 Reworked and adapted to unbalanced studies by B. Lang.

### References

Yuan J, Tong T, Tang M-L. *Sample Size Calculation for Bioequivalence Studies Assessing Drug Effect and Food Effect at the Same Time With a 3-Treatment Williams Design*. Regul Sci. 2013;47(2):242–7. doi: [10.1177/2168479012474273](https://doi.org/10.1177/2168479012474273)

### Examples

```
# Given a 90% confidence interval (without point estimate)
# from a classical 2x2 crossover with 22 subjects
CVfromCI(lower=0.91, upper=1.15, n=22, design="2x2")
# will give [1] 0.2279405, i.e a CV ~ 23%
#
# unbalanced 2x2 crossover study, but not reported as such
CI2CV(lower=0.89, upper=1.15, n=24)
# will give a CV ~ 26.3%
# unbalancedness accounted for
CI2CV(lower=0.89, upper=1.15, n=c(16,8))
```

# should give CV ~ 24.7%

---

CVp2CV

*Decompose CV(T) and CV(R) from 'pooled' CV of T/R*

---

### Description

Helper function to calculate CV(T) and CV(R) from a pooled CV(T/R) assuming a ratio of the intra-subject variances.

### Usage

```
CVp2CV(CV, ratio = 1.5)
```

### Arguments

CV	'pooled' CV of T and R (as ratio, not percent).
ratio	Ratio of the intra-subject variances $s^2(T)/s^2(R)$ . May be a vector.

### Details

In case of knowing only the CV(T/R) f.i. from an ordinary cross-over you can calculate the components CV(T) and CV(R) assuming a ratio of the intra-subject variances.

The formula the function is based on:

$$\log(1.0 + CV^2) = (sWT^2 + sWR^2) / 2$$

Insert  $sWT^2 = ratio * sWR^2$  and solve for  $sWR^2$ .

### Value

Returns a numeric vector of the CV values for Test and Reference if only one ratio is given.

Returns a matrix with named columns CVwT and CVwR if ratio is given as vector.

### Author(s)

D. Labes

### Examples

```
CVp2CV(0.4, ratio=2)
# gives
# [1] 0.4677952 0.3225018
```



CVpooled

*Pooled CV from several studies***Description**

This function pools CVs of several studies.

**Usage**

```
CVpooled(CVdata, alpha = 0.2, logscale = TRUE, robust = FALSE)
## S3 method for class 'CVp'
print(x, digits = 4, verbose = FALSE, ...)
```

**Arguments**

CVdata	A data.frame that must contain the columns CV, n and design where CV are the error CVs from the studies, n the number of subjects and design is a character string describing the study design. See <code>known.designs()</code> for designs covered in this package. If the design column is missing the classical 2×2 crossover is assumed for each study. A message is displayed under that circumstances.
alpha	A data.frame that contains the columns CV and giving the degrees of freedom df directly is also accepted as CVdata. Error probability for calculating an upper confidence limit of the pooled CV. Recommended 0.2–0.25 for use in subsequent sample size estimation. See f.i one of H. Schütz' <a href="#">presentations</a> .
logscale	Should the calculations be done for log-transformed data? Defaults to TRUE.
robust	Defaults to FALSE. Set to TRUE will use the degrees of freedom according to the 'robust' evaluation (aka Senn' basic estimator). These dfs are calculated as n-seq. They are also often more appropriate if the CV comes from a 'true' mixed effects model evaluation (FDA model for average bioequivalence). See <code>known.designs()\$df2</code> for the designs covered in this package.
x	An object of class "CVp".
digits	Number of significant digits for the CV and the CL.
verbose	Defaults to FALSE. Prints only the pooled CV and df. If set to TRUE the upper confidence limit is also printed.
...	More args to print(). None used.

**Details**

The pooled CV is obtained from the weighted average of the error variances obtained from the CVs of the single studies, weights are the degrees of freedom df.  
If only n is given in the input CVdata, the dfs are calculated via the formulas given in `known.designs()`.

If both `n` and `df` are given the `df` column precedes.

If `logscale=TRUE` the error variances are obtained via function `CV2se()`. Otherwise the pooled CV is obtained via pooling the  $CV^2$ .

### Value

A list of class "CVp" with components

CV	value of the pooled CV
df	pooled degrees of freedom
CVupper	upper confidence interval of the pooled CV
alpha	input value

The class "CVp" has a S3 methods `print.CVp`.

### Warning

Pooling of CVs from parallel group and crossover designs does not make any sense. Also the function *does not* throw an error if you do so.

### Note

The calculations for `logscale=FALSE` are not described in the references. They are implemented by analogy to the case via log-transformed data.

The calculations are based on a common variance of Test and Reference formulations in replicate crossover studies or a parallel group study, respectively.

### Author(s)

D. Labes

### References

H. Schütz' [presentations](#) about sample size challenges.

Patterson S, Jones B. *Bioequivalence and Statistics in Clinical Pharmacology*. Boca Raton: Chapman & Hall / CRC Press; 2<sup>nd</sup> edition 2017. Chapter 5.7 "Determining Trial Size".

### See Also

[known.designs,CVfromCI](#)

### Examples

```
# some data:
# the values for AUC, study 1 and study 2 are Example 3 of H. Schuetz' presentation
CVs <- ("
  PKmetric | CV   | n |design| source
  AUC      | 0.20 | 24 | 2x2  | study 1
  Cmax     | 0.25 | 24 | 2x2  | study 1
```

```

    AUC | 0.30 | 12 | 2x2 | study 2
    Cmax | 0.31 | 12 | 2x2 | study 2
    AUC | 0.25 | 12 | 2x2x4 | study 3 (full replicate)
  ")
txtcon <- textConnection(CVs)
CVdata <- read.table(txtcon, header = TRUE, sep = "|",
                    strip.white = TRUE, as.is = TRUE)
close(txtcon)

# evaluation of the AUC CVs
CVsAUC <- subset(CVdata, PKmetric == "AUC")
CVpooled(CVsAUC, alpha = 0.2, logscale = TRUE)
# df of the 'robust' evaluation
CVpooled(CVsAUC, alpha = 0.2, logscale = TRUE, robust = TRUE)
# print also the upper CL, data example 3
CVsAUC3 <- subset(CVsAUC, design != "2x2x4")
print(CVpooled(CVsAUC3, alpha = 0.2, robust = TRUE), digits = 3, verbose = TRUE)
# will give the output:
# Pooled CV = 0.235 with 32 degrees of freedom (robust dfs)
# Upper 80% confidence limit of CV = 0.266
#
# Combining CVs from studies evaluated by ANOVA (robust=FALSE) and
# by a mixed effects model (robust=TRUE). dfs have to be provided!
CVs <- ("
  CV | n | design | source | model | df
  0.212 | 24 | 2x2 | study 1 | fixed | 22
  0.157 | 27 | 3x3 | study 2 | fixed | 50
  0.148 | 27 | 3x3 | study 3 | mixed | 24
")
txtcon <- textConnection(CVs)
CVdata <- read.table(txtcon, header = TRUE, sep = "|",
                    strip.white = TRUE, as.is = TRUE)
close(txtcon)
print(CVpooled(CVdata, alpha = 0.2), digits = 3, verbose = TRUE)
# will give the output:
# Pooled CV = 0.169 with 96 degrees of freedom
# Upper 80% confidence limit of CV = 0.181

```

---

CVwRfromU

*CVwR from the upper expanded limit (ABEL)*


---

## Description

Calculates the intra-subject CV (coefficient of variation) of the reference from the upper expanded limit of a BE study (replicate design for ABEL). Useful if no  $CV_{wR}$  but the expanded limits were given.

## Usage

```

CVwRfromU(U, regulator = "EMA")
U2CVwR(U, regulator = "EMA")

```

**Arguments**

U	Upper expanded limit. Must be within {1.2500, 1.4319} if regulator="EMA" and within {1.2500, 1.5000} if regulator="HC".
regulator	Regulatory body's settings for expanding the BE acceptance limits, given as a string from the choices "EMA" or "HC". Defaults to regulator="EMA".

**Details**

Only the upper expanded limit is supported since it offers one more significant digit than the lower expanded limit.

**Value**

Numeric value of the CVwR as ratio, where  $CVwR = \sqrt{\exp((\log(U)/r\_const)^2) - 1}$ .

**Note**

U2CVwR() is simply an alias to CVwRfromU().

**Author(s)**

H. Schütz

**Examples**

```
# Given the upper expanded limit and using the defaults
CVwRfromU(U = 1.38)
# should give [1] 0.44355, i.e., a CVwR ~ 44%
# Upper limit from a study according the Health Canada's rules
CVwRfromU(U = 1.48, regulator = "HC")
# should give [1] 0.55214
```

---

exppower.noninf

*Expected power of the non-inferiority test*

---

**Description**

Calculates the so-called expected, *i.e.*, unconditional, power for a variety of study designs used in bioequivalence studies.

**Usage**

```
exppower.noninf(alpha = 0.025, logscale = TRUE, theta0, margin, CV, n,
  design = "2x2", robust = FALSE,
  prior.type = c("CV", "theta0", "both"), prior.parm = list(),
  method = c("exact", "approx"))
```

**Arguments**

alpha	Significance level (one-sided). Defaults here to 0.025.
logscale	Should the data be used on log-transformed or on original scale? TRUE (default) or FALSE.
theta0	Assumed 'true' (or 'observed' in case of <code>prior.type != "CV"</code> ) ratio or difference. In case of <code>logscale=TRUE</code> it must be given as ratio T/R. If <code>logscale=FALSE</code> , the difference in means. In this case, the difference may be expressed in two ways: relative to the same (underlying) reference mean, i.e. as $(T-R)/R = T/R - 1$ ; or as difference in means T-R. Note that in the former case the units of margin and CV need also be given relative to the reference mean (specified as ratio). Defaults to 0.95 if <code>logscale=TRUE</code> or to -0.05 if <code>logscale=FALSE</code>
margin	Non-inferiority margin. In case of <code>logscale=TRUE</code> it is given as ratio. If <code>logscale=FALSE</code> , the limit may be expressed in two ways: difference of means relative to the same (underlying) reference mean or in units of the difference of means. Note that in the former case the units of CV and <code>theta0</code> need also be given relative to the reference mean (specified as ratio). Defaults to 0.8 if <code>logscale=TRUE</code> or to -0.2 if <code>logscale=FALSE</code> .
CV	In case of <code>logscale=TRUE</code> the (geometric) coefficient of variation given as ratio. If <code>logscale=FALSE</code> the argument refers to (residual) standard deviation of the response. In this case, standard deviation may be expressed two ways: relative to a reference mean (specified as ratio $\sigma/\mu_R$ ), i.e. again as a coefficient of variation; or untransformed, i.e. as standard deviation of the response. Note that in the former case the units of <code>theta0</code> , <code>theta1</code> and <code>theta2</code> need also be given relative to the reference mean (specified as ratio).  In case of cross-over studies this is the within-subject CV, in case of a parallel-group design the CV of the total variability.
n	Number of subjects under study. Is total number if given as scalar, else number of subjects in the (sequence) groups. In the latter case the length of n has to be equal to the number of (sequence) groups.
design	Character string describing the study design. See <code>known.designs()</code> for designs covered in this package.
robust	Defaults to FALSE. Set to TRUE will use the degrees of freedom according to the 'robust' evaluation (aka Senn's basic estimator). These degrees of freedom are calculated as $n - \text{seq}$ . See <code>known.designs()\$df2</code> for designs covered in this package.
prior.type	Specifies which parameter uncertainty should be accounted for. In case of <code>prior.type = "CV"</code> (the default), only the uncertainty with respect to the CV will be considered (i.e. the given treatment effect is assumed to be fix). In case of <code>prior.type = "theta0"</code> only uncertainty with respect to the treatment ratio/difference will be accounted for (i.e. the given CV is assumed to be fix).

	In case of <code>prior.type = "both"</code> the power value will be unconditional with respect to both the CV and $\theta_0$ .
<code>prior.parm</code>	<p>A list of parameters expressing the prior information about the variability and/or treatment effect. Possible components are <code>df</code>, <code>SEM</code>, <code>m</code> and <code>design</code>.</p> <p>For <code>prior.type = "CV"</code> the degrees of freedom from the prior trial are required. This information can be provided by specifying the single component <code>df</code> or the combination consisting of <code>m</code> and <code>design</code>.</p> <p>For <code>prior.type = "theta0"</code> the standard error of the treatment difference from the prior trial is required. This information can be provided by specifying the single component <code>SEM</code> or the combination consisting of <code>m</code> and <code>design</code>.</p> <p>For <code>prior.type = "both"</code> the degrees of freedom and the standard error of the treatment difference are required. This information can be provided by specifying the combination consisting of <code>df</code> and <code>SEM</code> or via the combination <code>m</code> and <code>design</code>.</p> <p>See 'Details' for a technical description on each component.</p>
<code>method</code>	<p>Defaults to <code>method="exact"</code>. In that case the expected power will be calculated as expected value of the power with respect to the (prior) distribution of the respective parameter(s).</p> <p>Set to <code>method="approx"</code> the expected power according to the approximate formulas given in the book from Julious or in the Julious/Owen paper will be calculated (using non-central <math>t</math>); this only affects <code>prior.type = "CV"</code>.</p>

## Details

This function calculates the so-called expected power taking into account that usually the parameters (CV and/or  $\theta_0$ ) are not known but *estimated* from a prior study with some uncertainty. The expected power is an unconditional power and can therefore be seen as probability for success. See references for further details.

The `prior.parm` argument is a list that can supply any of the following components:

`df` Error degrees of freedom from the prior trial ( $>4$ , maybe non-integer). `df = Inf` is allowed and for `method = "exact"` the result will then coincide with `power.noninf(...)`.

Note: This corresponds to the `df` of both the CV and the difference of means.

`SEM` Standard error of the difference of means from the prior trial; must always be on additive scale (*i.e.*, usually log-scale).

`m` Number of subjects from prior trial. Specification is analogous to the main argument `n`.

`design` Study design of prior trial. Specification is analogous to the main argument `design`.

For `prior.parm`, the combination consisting of `df` and `SEM` requires a somewhat advanced knowledge of the prior trial (provided in the raw output from for example the software SAS, or may be obtained via `emmeans` of package `emmeans`). However, it has the advantage that if there were missing data the exact degrees of freedom and standard error of the difference can be used, the former possibly being non-integer valued (*e.g.* if the Kenward-Roger method was used).

Details on argument `prior.type`:

`CV` The expectation is calculated with respect to the Inverse-gamma distribution.

theta0 The expectation is calculated with respect to the conditional distribution  $\theta_0 \mid \sigma^2 = s^2$  of the posteriori distribution of  $(\theta_0, \sigma^2)$  from the prior trial.

both The expectation is calculated with respect to the posteriori distribution of  $(\theta_0, \sigma^2)$  from the prior trial. Numerical calculation of the two-dimensional integral is performed via cubature: :hcubature.

#### Notes on the underlying hypotheses

If the supplied margin is  $< 0$  (logscale=FALSE) or  $< 1$  (logscale=TRUE), then it is assumed higher response values are better. The hypotheses are

H0:  $\theta_0 \leq \text{margin}$  vs. H1:  $\theta_0 > \text{margin}$

where  $\theta_0 = \text{mean}(\text{test}) - \text{mean}(\text{reference})$  if logscale=FALSE

or

H0:  $\log(\theta_0) \leq \log(\text{margin})$  vs. H1:  $\log(\theta_0) > \log(\text{margin})$

where  $\theta_0 = \text{mean}(\text{test}) / \text{mean}(\text{reference})$  if logscale=TRUE.

If the supplied margin is  $> 0$  (logscale=FALSE) or  $> 1$  (logscale=TRUE), then it is assumed lower response values are better. The hypotheses are

H0:  $\theta_0 \geq \text{margin}$  vs. H1:  $\theta_0 < \text{margin}$

where  $\theta_0 = \text{mean}(\text{test}) - \text{mean}(\text{reference})$  if logscale=FALSE

or

H0:  $\log(\theta_0) \geq \log(\text{margin})$  vs. H1:  $\log(\theta_0) < \log(\text{margin})$

where  $\theta_0 = \text{mean}(\text{test}) / \text{mean}(\text{reference})$  if logscale=TRUE.

This latter case may also be considered as ‘non-superiority’.

#### Value

Value of expected power according to the input.

#### Author(s)

B. Lang, D. Labes

#### References

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### See Also

[expsampleN.noninf](#), [power.noninf](#)

### Examples

```
# Expected power for non-inferiority test for a 2x2 crossover
# with 40 subjects. CV 30% known from a pilot 2x2 study with
# 12 subjects
# using all the defaults for other parameters (theta0 carved in stone)
# should give: [1] 0.6761068
exppower.noninf(CV = 0.3, n = 40, prior.parm = list(df = 12-2))
# or equivalently
exppower.noninf(CV = 0.3, n = 40, prior.parm = list(m = 12, design = "2x2"))

# May be also calculated via exppower.TOST() after setting upper acceptance limit
# to Inf and alpha=0.025
exppower.TOST(CV = 0.3, n = 40, prior.parm = list(df = 10), theta2 = Inf, alpha=0.025)

# In contrast: Julious approximation
exppower.noninf(CV = 0.3, n = 40, prior.parm = list(df = 10), method = "approx")
# should give: [1] 0.6751358

# Compare this to the usual (conditional) power (CV known, "carved in stone")
power.noninf(CV = 0.3, n = 40)
# should give: [1] 0.7228685
# same as if setting df = Inf in function exppower.noninf()
exppower.noninf(CV = 0.3, n = 40, prior.parm = list(df = Inf))

# Expected power for a 2x2 crossover with 40 subjects
# CV 30% and theta0 = 0.95 known from a pilot 2x2 study with 12 subjects
# using uncertainty with respect to both CV and theta0
exppower.noninf(CV = 0.3, theta0 = 0.95, n = 40,
                prior.parm = list(m = 12, design = "2x2"), prior.type = "both")
# should give a decrease of expected power to 0.5982852
```

---

exppower.TOST

*Expected power of the TOST procedure*

---

### Description

Calculates the so-called expected, *i.e.*, unconditional, power for a variety of study designs used in bioequivalence studies.



**Usage**

```
exppower.TOST(alpha = 0.05, logscale = TRUE, theta0, theta1, theta2,
              CV, n, design = "2x2", robust = FALSE,
              prior.type = c("CV", "theta0", "both"), prior.parm = list(),
              method = c("exact", "approx"))
```

**Arguments**

alpha	Significance level (one-sided). Commonly set to 0.05.
logscale	Should the data be used on log-transformed or on original scale? TRUE (default) or FALSE.
theta0	Assumed 'true' (or 'observed' in case of <code>prior.type != "CV"</code> ) ratio or difference. In case of <code>logscale=TRUE</code> it must be given as ratio T/R. If <code>logscale=FALSE</code> , the difference in means. In this case, the difference may be expressed in two ways: relative to the same (underlying) reference mean, i.e. as $(T-R)/R = T/R - 1$ ; or as difference in means T-R. Note that in the former case the units of CV, theta1 and theta2 need also be given relative to the reference mean (specified as ratio). Defaults to 0.95 if <code>logscale=TRUE</code> or to 0.05 if <code>logscale=FALSE</code>
theta1	Lower (bio-)equivalence limit. In case of <code>logscale=TRUE</code> it is given as ratio. If <code>logscale=FALSE</code> , the limit may be expressed in two ways: difference of means relative to the same (underlying) reference mean or in units of the difference of means. Note that in the former case the units of CV, theta0 and theta2 need also be given relative to the reference mean (specified as ratio). Defaults to 0.8 if <code>logscale=TRUE</code> or to -0.2 if <code>logscale=FALSE</code> .
theta2	Upper (bio-)equivalence limit. In case of <code>logscale=TRUE</code> it is given as ratio. If <code>logscale=FALSE</code> , the limit may be expressed in two ways: difference of means relative to the same (underlying) reference mean or in units of the difference of means. Note that in the former case the units of CV, theta0 and theta1 need also be given relative to the reference mean (specified as ratio). If not given, theta2 will be calculated as $1/\theta_1$ if <code>logscale=TRUE</code> or as $-\theta_1$ if <code>logscale=FALSE</code> .
CV	In case of <code>logscale=TRUE</code> the (geometric) coefficient of variation given as ratio. If <code>logscale=FALSE</code> the argument refers to (residual) standard deviation of the response. In this case, standard deviation may be expressed two ways: relative to a reference mean (specified as ratio $\sigma/\mu_R$ ), i.e. again as a coefficient of variation; or untransformed, i.e. as standard deviation of the response. Note that in the former case the units of theta0, theta1 and theta2 need also be given relative to the reference mean (specified as ratio).  In case of cross-over studies this is the within-subject CV, in case of a parallel-group design the CV of the total variability.
n	Number of subjects under study. Is total number if given as scalar, else number of subjects in the (sequence)

	groups. In the latter case the length of <code>n</code> has to be equal to the number of (sequence) groups.
<code>design</code>	Character string describing the study design. See <a href="#">known.designs</a> for designs covered in this package.
<code>robust</code>	Defaults to FALSE. Set to TRUE will use the degrees of freedom according to the 'robust' evaluation (aka Senn's basic estimator). These df are calculated as <code>n-seq</code> . See <code>known.designs()\$df2</code> for designs covered in this package.
<code>prior.type</code>	Specifies which parameter uncertainty should be accounted for. In case of <code>prior.type = "CV"</code> (the default), only the uncertainty with respect to the CV will be considered (i.e. the given treatment effect is assumed to be fix). In case of <code>prior.type = "theta0"</code> only uncertainty with respect to the treatment ratio/difference will be accounted for (i.e. the given CV is assumed to be fix). In case of <code>prior.type = "both"</code> the power value will be unconditional with respect to both the CV and <code>theta0</code> .
<code>prior.parm</code>	A list of parameters expressing the prior information about the variability and/or treatment effect. Possible components are <code>df</code> , <code>SEM</code> , <code>m</code> and <code>design</code> . For <code>prior.type = "CV"</code> the degrees of freedom from the prior trial are required. This information can be provided by specifying the single component <code>df</code> or the combination consisting of <code>m</code> and <code>design</code> . For <code>prior.type = "theta0"</code> the standard error of the treatment difference from the prior trial is required. This information can be provided by specifying the single component <code>SEM</code> or the combination consisting of <code>m</code> and <code>design</code> . For <code>prior.type = "both"</code> the degrees of freedom and the standard error of the treatment difference are required. This information can be provided by specifying the combination consisting of <code>df</code> and <code>SEM</code> or via the combination <code>m</code> and <code>design</code> . See 'Details' for a technical description on each component.
<code>method</code>	Defaults to <code>method="exact"</code> . In that case the expected power will be calculated as expected value of the power with respect to the (prior) distribution of the respective parameter(s). Set to <code>method="approx"</code> the expected power according to the approximate formulas given in the book from Julious or in the Julious/Owen paper will be calculated (using non-central $t$ ); this only affects <code>prior.type = "CV"</code> .

## Details

This function calculates the so-called expected power taking into account that usually the parameters (CV and/or `theta0`) are not known but estimated from a prior study with some uncertainty. The expected power is an unconditional power and can therefore be seen as probability for success. See references for further details.

The `prior.parm` argument is a list that can supply any of the following components:

`df` Error degrees of freedom from the prior trial ( $>4$ , maybe non-integer). `df = Inf` is allowed and for `method = "exact"` the result will then coincide with `power.TOST(...)`.

Note: This corresponds to the `df` of both the CV and the difference of means.

`SEM` Standard error of the difference of means from the prior trial; must always be on additive scale (i.e., usually log-scale).

m Number of subjects from prior trial. Specification is analogous to the main argument n.

design Study design of prior trial. Specification is analogous to the main argument design.

For prior.parm, the combination consisting of df and SEM requires a somewhat advanced knowledge of the prior trial (provided in the raw output from for example the software SAS, or may be obtained via `emmeans` of package `emmeans`. However, it has the advantage that if there were missing data the exact degrees of freedom and standard error of the difference can be used, the former possibly being non-integer valued (*e.g.*, if the Kenward-Roger method was used).

Details on argument prior.type:

CV The expectation is calculated with respect to the Inverse-gamma distribution.

theta0 The expectation is calculated with respect to the conditional distribution  $\theta_0 \mid \sigma^2 = s^2$  of the posteriori distribution of  $(\theta_0, \sigma^2)$  from the prior trial.

both The expectation is calculated with respect to the posteriori distribution of  $(\theta_0, \sigma^2)$  from the prior trial. Numerical calculation of the two-dimensional integral is performed via `hcubature`.

### Value

Value of expected power according to the input.

### Author(s)

B. Lang (thanks to G. Nehmiz for the helpful discussions), D. Labes

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### See Also

[expsampleN.TOST](#), [power.TOST](#)

## Examples

```
# Expected power for a 2x2 crossover with 40 subjects
# CV 30% known from a pilot 2x2 study with 12 subjects
# using all the defaults for other parameters (theta0 carved in stone)
exppower.TOST(CV = 0.3, n = 40, prior.parm = list(df = 12-2))
# should give: [1] 0.7365519
# or equivalently
exppower.TOST(CV = 0.3, n = 40, prior.parm = list(m = 12, design = "2x2"))

# In contrast: Julious approximation
exppower.TOST(CV = 0.3, n = 40, prior.parm = list(df = 10), method = "approx")
# should give: [1] 0.7359771

# Compare this to the usual (conditional) power (CV known, "carved in stone")
power.TOST(CV = 0.3, n = 40)
# should give: [1] 0.8158453
# same as if setting df = Inf in function exppower.TOST()
exppower.TOST(CV = 0.3, n = 40, prior.parm = list(df = Inf))

# Expected power for a 2x2 crossover with 40 subjects
# CV 30% and theta0 = 0.95 known from a pilot 2x2 study with 12 subjects
# using uncertainty with respect to both CV and theta0
exppower.TOST(CV = 0.3, theta0 = 0.95, n = 40,
              prior.parm = list(m = 12, design = "2x2"), prior.type = "both")
# should give [1] 0.5114685
```

---

expsampleN.noninf

*Sample size based on expected power for the non-inferiority test*

---

## Description

Estimates the sample size based on the expected power for a variety of designs used in bioequivalence studies. See [known.designs](#) for the study designs covered.

## Usage

```
expsampleN.noninf(alpha = 0.025, targetpower = 0.8, logscale = TRUE,
                  theta0, margin, CV, design = "2x2", robust = FALSE,
                  prior.type = c("CV", "theta0", "both"), prior.parm = list(),
                  method = c("exact", "approx"), print = TRUE, details)
```

## Arguments

alpha	Significance level (one-sided). Defaults here to 0.025.
targetpower	Power to achieve at least. Must be >0 and <1. Typical values are 0.8 or 0.9.
logscale	Should the data used on log-transformed or on original scale? TRUE or FALSE. Defaults to TRUE.

theta0	<p>Assumed ‘true’ (or ‘observed’ in case of <code>prior.type != "CV"</code>) ratio or difference.</p> <p>In case of <code>logscale=TRUE</code> it must be given as ratio <math>T/R</math>.</p> <p>If <code>logscale=FALSE</code>, the difference in means. In this case, the difference may be expressed in two ways: relative to the same (underlying) reference mean, i.e. as <math>(T-R)/R = T/R - 1</math>; or as difference in means <math>T-R</math>. Note that in the former case the units of margin and CV need also be given relative to the reference mean (specified as ratio).</p> <p>Defaults to 0.95 if <code>logscale=TRUE</code> or to -0.05 if <code>logscale=FALSE</code></p>
margin	<p>Non-inferiority margin.</p> <p>In case of <code>logscale=TRUE</code> it is given as ratio.</p> <p>If <code>logscale=FALSE</code>, the limit may be expressed in two ways: difference of means relative to the same (underlying) reference mean or in units of the difference of means. Note that in the former case the units of CV and theta0 need also be given relative to the reference mean (specified as ratio).</p> <p>Defaults to 0.8 if <code>logscale=TRUE</code> or to -0.2 if <code>logscale=FALSE</code>.</p>
CV	<p>In case of <code>logscale=TRUE</code> the (geometric) coefficient of variation given as ratio.</p> <p>If <code>logscale=FALSE</code> the argument refers to (residual) standard deviation of the response. In this case, standard deviation may be expressed two ways: relative to a reference mean (specified as ratio <math>\sigma/\mu_R</math>), i.e. again as a coefficient of variation; or untransformed, i.e. as standard deviation of the response. Note that in the former case the units of theta0, theta1 and theta2 need also be given relative to the reference mean (specified as ratio).</p> <p>If <code>prior.type="CV"</code> may be given as vector: The CVs are then pooled (as a weighted mean with their degrees of freedoms as weights).</p> <p>In case of cross-over studies this is the within-subject CV, in case of a parallel-group design the CV of the total variability.</p>
design	<p>Character string describing the study design.</p> <p>See <code>known.designs()</code> for designs covered in this package.</p>
robust	<p>Defaults to FALSE. With that value the usual degrees of freedom will be used.</p> <p>Setting to TRUE will use the degrees of freedom according to the ‘robust’ evaluation (aka Senn’s basic estimator). These df are calculated as <math>n - seq</math>.</p> <p>See <code>known.designs()</code> for designs covered in this package.</p>
prior.type	<p>Specifies which parameter uncertainty should be accounted for. In case of <code>prior.type="CV"</code> (the default), only the uncertainty with respect to the CV will be considered (i.e., the given treatment effect is assumed to be fix). In case of <code>prior.type="theta0"</code> only uncertainty with respect to the treatment ratio/difference will be accounted for (i.e., the given CV is assumed to be fix). In case of <code>prior.type="both"</code> the power value will be unconditional with respect to both the CV and theta0.</p>
prior.parm	<p>A list of parameters expressing the prior information about the variability and/or treatment effect. Possible components are <code>df</code>, <code>SEM</code>, <code>m</code>, <code>design</code>.</p> <p>For <code>prior.type="CV"</code> the degrees of freedom from the prior trial are required. This information can be provided by specifying the single component <code>df</code> or the combination consisting of <code>m</code> and <code>design</code>.</p>

	<p>For <code>prior.type = "theta0"</code> the standard error of the treatment difference from the prior trial is required. This information can be provided by specifying the single component SEM or the combination consisting of <code>m</code> and <code>design</code>.</p> <p>For <code>prior.type = "both"</code> the degrees of freedom and the standard error of the treatment difference are required. This information can be provided by specifying the combination consisting of <code>df</code> and SEM or via the combination <code>m</code> and <code>design</code>.</p> <p>See section 'Details' for a technical description of each component.</p>
method	<p>Defaults to <code>method="exact"</code>. In that case the expected power will be calculated as expected value of the power with respect to the (prior) distribution of the respective parameter(s).</p> <p>Set to <code>method="approx"</code> the expected power according to the approximate formulas given by Julious or Julious &amp; Owen will be calculated (using the non-central <math>t</math>); this only affects <code>prior.type = "CV"</code>.</p>
print	<p>If TRUE (default) the function prints its results.</p> <p>If FALSE only a data.frame with the results will be returned.</p>
details	<p>If TRUE the design characteristics and the steps during sample size calculations will be shown.</p> <p>If not specified, the default value is FALSE for <code>prior.type != "both"</code> and TRUE otherwise.</p>

### Details

The sample size is estimated based on iterative evaluation of expected power. The starting value of the sample size search is taken from a large sample approximation if `prior.type="CV"`. Else an empirical start value is obtained. Note that in case of `prior.type="both"` the calculation may still take several seconds.

Note also that the expected power is always bounded above by the so-called probability of technical success (PTS) which may be a value less than 1. Therefore, it may be possible that it is either not possible to calculate the required sample size at all or that the sample size gets very large if the given `targetpower` is less but close to the PTS.

#### Notes on the underlying hypotheses

If the supplied margin is  $< 0$  (`logscale=FALSE`) or  $< 1$  (`logscale=TRUE`), then it is assumed *higher* response values are better. The hypotheses are

H0:  $\theta_0 \leq \text{margin}$

H1:  $\theta_0 > \text{margin}$

where  $\theta_0 = \text{mean}(\text{test}) - \text{mean}(\text{reference})$  if `logscale=FALSE`

or

H0:  $\log(\theta_0) \leq \log(\text{margin})$

H1:  $\log(\theta_0) > \log(\text{margin})$

where  $\theta_0 = \text{mean}(\text{test}) / \text{mean}(\text{reference})$  if `logscale=TRUE`.

If the supplied margin is  $> 0$  (`logscale=FALSE`) or  $> 1$  (`logscale=TRUE`), then it is assumed *lower* response values are better. The hypotheses are

H0:  $\theta_0 \geq \text{margin}$

H1:  $\theta_0 < \text{margin}$

where  $\theta_0 = \text{mean}(\text{test}) - \text{mean}(\text{reference})$  if `logscale=FALSE`  
 or  
 $H_0: \log(\theta_0) \geq \log(\text{margin})$   
 $H_1: \log(\theta_0) < \log(\text{margin})$   
 where  $\theta_0 = \text{mean}(\text{test}) / \text{mean}(\text{reference})$  if `logscale=TRUE`.  
 This latter case may also be considered as ‘non-superiority’.

### Value

A data.frame with the input values and the result of the sample size estimation.  
 The Sample size column contains the *total* sample size in case of all designs implemented.

### Author(s)

B. Lang, D. Labes

### References

- Grieve AP. *Confidence Intervals and Sample Sizes*. Biometrics. 1991;47:1597–603. doi: [10.2307/2532411](https://doi.org/10.2307/2532411)
- O’Hagan, Stevens, JW, Campell MJ. *Assurance in Clinical Trial Design*. Pharm Stat. 2005;4:187–201. doi: [10.1002/pst.175](https://doi.org/10.1002/pst.175)
- Julious SA, Owen RJ. *Sample size calculations for clinical studies allowing for uncertainty in variance*. Pharm Stat. 2006;5:29–37. doi: [10.1002/pst.197](https://doi.org/10.1002/pst.197)
- Julious SA. *Sample sizes for Clinical Trials*. Boca Raton: CRC Press; 2010.
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- Senn S. *Cross-over Trials in Clinical Research*. Chichester: John Wiley & Sons; 2<sup>nd</sup> edition 2002.
- Zierhut ML, Bycott P, Gibbs MA, Smith BP, Vicini P. *Ignorance is not bliss: Statistical power is not probability of trial success*. Clin Pharmacol Ther. 2015;99:356–9. doi: [10.1002/cpt.257](https://doi.org/10.1002/cpt.257)

### See Also

[expower.noninf](#), [known.designs](#), [sampleN.noninf](#)

### Examples

```
# Classical 2x2 cross-over, target power = 80%,
# assumed true ratio = 95%, margin = 0.8,
# intra-subject CV=30% estimated from prior 2x2 trial
# with m = 12 subjects
expsampleN.noninf(theta0 = 0.95, margin = 0.8, CV = 0.3, design = "2x2",
                  prior.parm = list(m = 12, design = "2x2"))
# gives n = 58 with achieved expected power 0.809148
```

```

# Compare this to the usual sample size with CV assumed
# as 'carved in stone'
sampleN.noninf(theta0 = 0.95, margin = 0.8, CV = 0.3)

# Perform 'non-superiority' (lower is better) with assumed
# true ratio = 105% and margin 125%
expsampleN.noninf(theta0 = 1.05, margin = 1.25, CV = 0.3, design = "2x2",
                  prior.parm = list(m = 12, design = "2x2"))
# should give n = 56 with achieved expected power 0.806862

# More than one CV with corresponding degrees of freedom
# other settings as above in first example
CVs <- c(0.25, 0.3)
dfs <- c(22, 10)
expsampleN.noninf(theta0 = 0.95, margin = 0.8, CV = CVs,
                  prior.parm = list(df = dfs))
# should give a pooled CV=0.2664927 with 32 df and a sample
# size n=42 with achieved expected power 0.814073 exact
# achieved expected power 0.816163 approximate acc. to Julious

# Uncertainty is accounted for CV and theta0

expsampleN.noninf(CV = 0.3, prior.type = "both",
                  prior.parm = list(m = 12, design = "2x2"))
# gives a dramatic increase in sample size (n = 194)
# due to small pilot trial

```

---

expsampleN.TOST

*Sample size based on expected power*


---

## Description

Estimates the sample size based on the expected power for a variety of study designs used in bioequivalence studies. See [known.designs](#) for the study designs covered.

## Usage

```

expsampleN.TOST(alpha = 0.05, targetpower = 0.8, logscale=TRUE, theta0,
                theta1, theta2, CV, design = "2x2", robust = FALSE,
                prior.type = c("CV", "theta0", "both"), prior.parm = list(),
                method = c("exact", "approx"), print = TRUE, details)

```

## Arguments

alpha	Significance level (one-sided). Commonly set to 0.05.
targetpower	Power to achieve at least. Must be >0 and <1. Typical values are 0.8 or 0.9.
logscale	Should the data used on log-transformed or on original scale? TRUE (default) or FALSE.



theta0	<p>Assumed ‘true’ (or ‘observed’ in case of <code>prior.type != "CV"</code>) bioequivalence ratio or difference.</p> <p>In case of <code>logscale=TRUE</code> it must be given as ratio <math>T/R</math>.</p> <p>If <code>logscale=FALSE</code>, the difference in means. In this case, the difference may be expressed in two ways: relative to the same (underlying) reference mean, i.e. as <math>(T-R)/R = T/R - 1</math>; or as difference in means <math>T-R</math>. Note that in the former case the units of <code>CV</code>, <code>theta1</code> and <code>theta2</code> need also be given relative to the reference mean (specified as ratio).</p> <p>Defaults to 0.95 if <code>logscale=TRUE</code> or to 0.05 if <code>logscale=FALSE</code></p>
theta1	<p>Lower (bio-)equivalence limit.</p> <p>In case of <code>logscale=TRUE</code> it is given as ratio.</p> <p>If <code>logscale=FALSE</code>, the limit may be expressed in two ways: difference of means relative to the same (underlying) reference mean or in units of the difference of means. Note that in the former case the units of <code>CV</code>, <code>theta0</code> and <code>theta2</code> need also be given relative to the reference mean (specified as ratio).</p> <p>Defaults to 0.8 if <code>logscale=TRUE</code> or to -0.2 if <code>logscale=FALSE</code>.</p>
theta2	<p>Upper (bio-)equivalence limit.</p> <p>In case of <code>logscale=TRUE</code> it is given as ratio. If <code>logscale=FALSE</code>, the limit may be expressed in two ways: difference of means relative to the same (underlying) reference mean or in units of the difference of means. Note that in the former case the units of <code>CV</code>, <code>theta0</code> and <code>theta1</code> need also be given relative to the reference mean (specified as ratio).</p> <p>If not given, <code>theta2</code> will be calculated as <math>1/\theta1</math> if <code>logscale=TRUE</code> or as <math>-\theta1</math> if <code>logscale=FALSE</code>.</p>
CV	<p>In case of <code>logscale=TRUE</code> the (geometric) coefficient of variation given as ratio. If <code>logscale=FALSE</code> the argument refers to (residual) standard deviation of the response. In this case, standard deviation may be expressed two ways: relative to a reference mean (specified as ratio <math>\sigma/\mu_R</math>), i.e. again as a coefficient of variation; or untransformed, i.e. as standard deviation of the response. Note that in the former case the units of <code>theta0</code>, <code>theta1</code> and <code>theta2</code> need also be given relative to the reference mean (specified as ratio).</p> <p>If <code>prior.type="CV"</code> may be given as vector: The CVs are then pooled (as a weighted mean with their degrees of freedoms as weights).</p> <p>In case of cross-over studies this is the within-subject CV, in case of a parallel-group design the CV of the total variability.</p>
design	<p>Character string describing the study design.</p> <p>See <a href="#">known.designs</a> for designs covered in this package.</p>
robust	<p>Defaults to <code>FALSE</code>. With that value the usual degrees of freedom will be used. Set to <code>TRUE</code> will use the degrees of freedom according to the ‘robust’ evaluation (aka Senn’s basic estimator). These <code>df</code> are calculated as <math>n - \text{seq}</math>.</p> <p>See <code>known.designs()\$df2</code> for designs covered in this package.</p>
prior.type	<p>Specifies which parameter uncertainty should be accounted for. In case of <code>prior.type = "CV"</code> (the default), only the uncertainty with respect to the CV will be considered (<i>i.e.</i>, the given treatment effect is assumed to be fix). In case</p>

	of <code>prior.type = "theta0"</code> only uncertainty with respect to the treatment ratio/difference will be accounted for ( <i>i.e.</i> , the given CV is assumed to be fix). In case of <code>prior.type = "both"</code> the power value will be unconditional with respect to both the CV and <code>theta0</code> .
<code>prior.parm</code>	A list of parameters expressing the prior information about the variability and/or treatment effect. Possible components are <code>df</code> , <code>SEM</code> , <code>m</code> , <code>design</code> . For <code>prior.type = "CV"</code> the degrees of freedom from the prior trial are required. This information can be provided by specifying the single component <code>df</code> or the combination consisting of <code>m</code> and <code>design</code> . For <code>prior.type = "theta0"</code> the standard error of the treatment difference from the prior trial is required. This information can be provided by specifying the single component <code>SEM</code> or the combination consisting of <code>m</code> and <code>design</code> . For <code>prior.type = "both"</code> the degrees of freedom and the standard error of the treatment difference are required. This information can be provided by specifying the combination consisting of <code>df</code> and <code>SEM</code> or via the combination <code>m</code> and <code>design</code> . See 'Details' for a technical description on each component.
<code>method</code>	Defaults to <code>method="exact"</code> . In that case the expected power will be calculated as expected value of the power with respect to the (prior) distribution of the respective parameter(s). Set to <code>method="approx"</code> the expected power according to the approximate formulas given in the book from Julious or in the Julious/Owen paper will be calculated (using non-central $t$ ); this only affects <code>prior.type = "CV"</code> .
<code>print</code>	If TRUE (default) the function prints its results. If FALSE only a data.frame with the results will be returned.
<code>details</code>	If TRUE the design characteristics and the steps during sample size calculations will be shown. If not specified, the default value is FALSE for <code>prior.type != "both"</code> and TRUE otherwise.

### Details

The sample size is calculated based on iterative evaluation of expected power. The starting value of the sample size search is taken from a large sample approximation if `prior.type = "CV"`. Otherwise, an empirical start value is obtained. Note that in case of `prior.type = "both"` the calculation may still take several seconds.

Note also that the expected power is always bounded above by the so-called probability of technical success (PTS) which may be a value less than 1. Therefore, it may be possible that it is either not possible to calculate the required sample size at all or that the sample size gets very large if the given `targetpower` is less but close to the PTS.

The estimated sample size gives always the *total* number of subjects (not subject/sequence in crossovers or subjects/group in parallel designs – like in some other software packages).

### Value

A data.frame with the input values and the result of the sample size estimation.

The Sample size column contains the total sample size in case of all designs implemented.

**Author(s)**

B. Lang, D. Labes

**References**

- Grieve AP. *Confidence Intervals and Sample Sizes*. Biometrics. 1991;47:1597–603. doi: [10.2307/2532411](https://doi.org/10.2307/2532411)
- O'Hagan, Stevens, JW, Campell MJ. *Assurance in Clinical Trial Design*. Pharm Stat. 2005;4:187–201. doi: [10.1002/pst.175](https://doi.org/10.1002/pst.175)
- Julious SA, Owen RJ. *Sample size calculations for clinical studies allowing for uncertainty in variance*. Pharm Stat. 2006;5:29–37. doi: [10.1002/pst.197](https://doi.org/10.1002/pst.197)
- Julious SA. *Sample sizes for Clinical Trials*. Boca Raton: CRC Press / Chapman & Hall; 2010.
- Bertsche A, Nehmitz G, Beyersmann J, Grieve AP. *The predictive distribution of the residual variability in the linear-fixed effects model for clinical cross-over trials*. Biom J. 2016;58(4):797–809. doi: [10.1002/bimj.201500245](https://doi.org/10.1002/bimj.201500245)
- Box GEP, Tiao GC. *Bayesian Inference in Statistical Analysis*. Boston: Addison-Wesley; 1992.
- Held L, Sabanes Bove D. *Applied Statistical Inference. Likelihood and Bayes*. Berlin, Heidelberg: Springer; 2014. doi: [10.1007/9783642378874](https://doi.org/10.1007/9783642378874)
- Senn S. *Cross-over Trials in Clinical Research*. Chichester: John Wiley & Sons; 2<sup>nd</sup> edition 2002.
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**See Also**

[exppower.TOST](#), [known.designs](#), [sampleN.TOST](#)

**Examples**

```
# Classical 2x2 cross-over, target power = 80%,
# BE limits 80 ... 125%, assumed true BE ratio = 95%,
# intra-subject CV=30% estimated from prior 2x2 trial
# with m = 30 subjects
expsampleN.TOST(CV=0.3, prior.parm = list(m = 30, design = "2x2"))
# -> gives n = 42 with achieved expected power 0.806262
# Compare this to the usual sample size with CV assumed known ('carved in stone')
sampleN.TOST(CV=0.3)
# -> gives n = 40 subjects
# Compare this to the case where uncertainty is accounted for CV and theta0
# Not run due to timing policy of CRAN - may run several seconds

expsampleN.TOST(CV=0.3, prior.parm = list(m = 30, design = "2x2"),
                prior.type = "both")
# -> gives n = 72 subjects

# More than one CV with corresponding degrees of freedom
# other settings as above in first example
CVs <- c(0.25, 0.3)
dfs <- c(22, 10)
```

```

expsampleN.TOST(CV=CVs, prior.parm = list(df = dfs))
# -> gives a pooled CV=0.2664927 with df=32
# and a sample size n=34 with achieved expected power 0.812653 exact
# achieved expected power 0.815019 approximate acc. Julious

```

---

known.designs

*Show the 'known' designs*

---

### Description

Returns the known study designs for which power and sample size can be calculated within this package.

### Usage

```
known.designs()
```

### Details

This function is for informal purposes and used internally for obtaining characteristics of the designs used in calculation formulas.

### Value

Returns a data.frame with

no	number of the design
design	character string for identifying the design
df	degrees of freedom of the design
df2	'robust' degrees of freedom of the design
steps	step width in the iterative sample size estimation
bk	so-called design constant in terms of total n
bkni	design constant in terms of number of subjects in (sequence) groups

The design character string has to be used in the functions calls for power and sample size.

### Note

The design string for higher order crossover designs is named as:  
 treatments x sequences x periods in case of replicate designs and  
 treatments x periods in case of crossover designs for more then 2 treatments with number of  
 sequences equal number of treatments.

The df for the replicate crossover designs are those without carry-over in the model.  
 Chen *et al.* used models with carry-over, *i.e.*, one df lower than here.

The design constant  $b_k$  in case of design  $2 \times 2 \times 4$  is here  $b_k=1$ .  
Chen *et al.* used  $b_k=1.1$  due to carry-over in the model.

$n$  is the **total** number of subjects for all designs implemented.  
 $df_2$  = degrees of freedom for the so-called ‘robust’ analysis (aka Senn’s basic estimator).  
These degrees of freedom are often also more appropriate in case of evaluation via a ‘true’ mixed model (*e.g.* the FDA’ for replicate designs).

The design  $2 \times 2 \times 2r$  is the 2-treatment-2-sequence-2-period design with 2 repeated targets determined in each period (sequences TTIR or RRIT) described by Liu. Implemented are the characteristics of this design for the evaluation via assuming no S×F interaction and equal variabilities of Test and Reference.

### Author(s)

D. Labes

### References

Chen KW, Chow SC, Liu G. *A Note on Sample Size Determination for Bioequivalence Studies with Higher-order Crossover Designs*. J Pharmacokin Biopharm. 1997;25(6):753–65.

Senn S. *Cross-over Trials in Clinical Research*. Chichester: John Wiley & Sons; 2<sup>nd</sup> edition 2002.

U.S. Department of Health and Human Services, Food and Drug Administration, Center for Drug Evaluation and Research (CDER). *Guidance for Industry. Statistical Approaches to Establishing Bioequivalence*. January 2001. [download](#)

Liu J-p. *Use of the Repeated Crossover design in Assessing Bioequivalence*. Stat Med. 1995;14(9-10):1067–78.

### Examples

```
known.designs()
```

---

OwensQ

*Owen’s Q-function*

---

### Description

Calculates Owen’s Q function.

### Usage

```
OwensQ(nu, t, delta, a=0, b)
```

**Arguments**

nu	degree of Owen's Q
t	parameter t
delta	parameter delta
a	lower integration limit, only a=0 implemented
b	upper integration limit

**Details**

Uses the relationship to non-central  $t$ -distribution (see Chou)

$\text{OwensQ} = pt(t, df=nu, ncp=delta) - \text{Integral}_b_{\text{Inf}}(Q_{\text{integrand}})$

The definite integral is numerically evaluated using [integrate](#) after a variables transformation resulting in the integration range from 0 to 1 instead of the semi-infinite original range. This may result in higher precision and better numerical stability.

The arguments to the function must be scalars. No vectors allowed.

**Value**

Numeric value of Owen's Q-function at given input arguments.

**Note**

This function is intended for internal use in the power calculations.  
But may be useful for others.

**Author(s)**

D. Labes

**References**

Owen DB. *A special case of a bivariate non-central t-distribution*. Biometrika. 1965;52(3/4):437–46. doi: [10.2307/2333696](#)

Chou YM. *A bivariate noncentral T-distribution with applications*. Commun Stat Theory Methods. 1992;21(12):3427–62. doi: [10.1080/03610929208830988](#)

**See Also**

[OwensQOwen](#)

**Examples**

```
# This function is mainly intended for internal use.
OwensQ(10, 2.5, 5, 0, 2)
#should give [1] 9.388137e-06
OwensQ(10, -2.5, -5, 0, 2)
#should give [1] 0.05264363
```

OwensQOwen

*Owen's Q-function via repeated integration by parts***Description**

This is an implementation of the algorithm given by Owen via repeated integration by parts.

**Usage**

```
OwensQOwen(nu, t, delta, a=0, b)
```

**Arguments**

nu	degree of Owen's Q
t	parameter t
delta	parameter delta
a	lower integration limit. Only a=0 implemented, other values give an error.
b	upper integration limit

**Value**

Numeric value of Owen's Q function.

**Note**

The argument a=0 could be dropped but is retained for sake of completeness.

**Note**

This function is mainly for comparative / validation purposes.  
The function requires [OwensT](#) function.

**Author(s)**

D. Labes

**References**

Owen DB. *A special case of a bivariate non-central t-distribution*. *Biometrika*. 1965;52(3/4):437–46. doi: [10.2307/2333696](https://doi.org/10.2307/2333696)

**See Also**

[OwensQ](#), [OwensT](#)

**Examples**

```
# comparison of the results of both implementations
# both should give [1] 0.0731726
OwensQ(2, 2.92, 4.2135, 0, 2.0407)
OwensQOwen(2, 2.92, 4.2135, 0, 2.0407)
```

---

OwensT

*Owen's T-function*

---

**Description**

Calculates the definite integral from 0 to a of  $\exp(-0.5 \cdot h^2 \cdot (1+x^2)) / (1+x^2) / (2 \cdot \pi)$ .

**Usage**

```
OwensT(h, a)
```

**Arguments**

h	parameter h
a	upper limit of integration

**Details**

The function is an R port of FORTRAN code given in the references and MATLAB code given by John Burkardt under the GNU LGPL license.

The arguments of `OwensT()` have to be scalars because the implementation doesn't vectorize.

**Value**

Numerical value of the definite integral.

**Note**

This function is only needed as auxiliary in [OwensQOwen](#). But may be useful for others.

**Author(s)**

MATLAB code by J. Burkardt, R port by D. Labes



## References

- Goedhart PW, Jansen MJW. *Remark AS R89: A Remark on Algorithm AS 76: An Integral Useful in Calculating Central  $t$  and Bivariate Normal Probabilities.* J Royal Stat Soc C. 1992;41(2):496–7. doi: [10.2307/2347586](https://doi.org/10.2307/2347586)
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- Burkardt J. ASA076. *Owen's  $T$  Function.* Last revised 25 November 2018. [https://people.sc.fsu.edu/~jburkardt/m\\_src/asa076/asa076.html](https://people.sc.fsu.edu/~jburkardt/m_src/asa076/asa076.html)
- Owen DB. *Tables for Computing Bivariate Normal Probabilities.* Ann Math Stat. 1956;27(4):1075–90. doi: [10.1214/aoms/1177728074](https://doi.org/10.1214/aoms/1177728074)

## See Also

[OwensQOwen](#), [OwensQ](#)

## Examples

```
OwensT(2.5, 0.75)
# should give [1] 0.002986697
# value from Owen's tables is 0.002987
OwensT(2.5, -0.75)
# should give [1] -0.002986697
```

## Description

An analysis tool for exploration/visualization of the impact of expected values (CV, theta0, reduced sample size due to drop-outs) on power of BE decision via ABE if these values deviate from the ones assumed in planning the sample size of the study.

**Usage**

```
pa.ABE(CV, theta0 = 0.95, targetpower = 0.8, minpower = 0.7, design = "2x2", ...)
## S3 method for class 'pwrA'
print(x, digits = 4, plotit = TRUE, ...)
## S3 method for class 'pwrA'
plot(x, pct = TRUE, ratiolabel = "theta0", cols = c("blue", "red"), ...)
```

**Arguments**

CV	Coefficient of variation as ratio (not percent). In case of cross-over studies this is the within-subject CV.
theta0	'True' or assumed T/R ratio. Often named GMR. Must be given as ratio.
targetpower	Power to achieve at least in sample size estimation. Must be >0 and <1. Typical values are 0.8 or 0.9. Defaults to 0.8. Note that targetpower < 0.5 doesn't make much sense.
minpower	Minimum acceptable power to have if deviating from assumptions for sample size plan. Has to be lower than targetpower. Defaults to 0.7. minpower < 0.5 doesn't make much sense.
design	Character string describing the study design. See known.designs() for designs covered in this package.
...	More arguments to pass to power.TOST(). F.i. alpha, theta1, theta2 or robust if other values then the defaults for these arguments are needed. See man page of power.TOST().  More arguments passed to the S3 methods. Here currently ignored. Additional arguments of the S3 methods:
x	Object of class 'pwrA'.
digits	Digits for rounding power in printing. The '...' argument is currently ignored in print().
plotit	If set to TRUE, the default, the print method calls plot(x) if R is running interactively.
pct	If set to TRUE (the default) scales CV, theta0, and power in percent in plot(). Else they will be given as ratios, the usual standard in PowerTOST.
ratiolabel	Label of the T/R-ratio. Can be set to any string, e.g. to "GMR". Defaults to "theta0", the usual standard in PowerTOST.
cols	Colors for the plots. cols[1] gives the color for plotting points with power > targetpower. From targetpower toward minpower the color changes gradually to cols[2].

## Details

Power calculations are done via `power.TOST()` and calculations of CV and `theta0` which gave a `power=minpower` are derived via R base `uniroot`. While one of the parameters (CV, `theta0`, N) is varied, the respective two others are kept constant. The tool shows the relative impact of single parameters on power.

The tool takes a minimum of 12 subjects as required in most BE guidances into account.

It should be kept in mind that this is **not** a substitute for the “Sensitivity Analysis” recommended in ICH-E9. In a real study a combination of all effects occurs simultaneously. It is up to *you* to decide on reasonable combinations and analyze their respective power.

## Value

Returns a list with class "pwrA" with the components

<code>p1an</code>	A data.frame with the result of the sample size estimation. See output of <code>sampleN.TOST()</code> .
<code>paCV</code>	A data.frame with value pairs CV, pwr for impact of deviations from CV.
<code>paGMR</code>	A data.frame with value pairs <code>theta0</code> , pwr for impact of deviations from <code>theta0</code> (GMR).
<code>paN</code>	A data.frame with value pairs N, pwr for impact of deviations from planned N (dropouts).
<code>method</code>	Method of BE decision. Here <code>fix = "ABE"</code> .
<code>minpower</code>	Minimum acceptable power.

The class 'pwrA' has the S3 methods `print()` and `plot()`. See [pa.scABE](#) for usage.

## Note

The code of deviations from planned sample size tries to keep the degree of imbalance as low as possible between (sequence) groups. This results in a lesser decrease of power than more extreme dropout-patterns.

## Author(s)

Idea and original code by H. Schütz with modifications by D. Labes to use PowerTOST infrastructure.

## References

Schütz H. *Deviating from assumptions*. August 08, 2014. [BEBA Forum](#)

## See Also

[power.TOST](#), [known.designs](#), [pa.scABE](#), [pa.NTIDFDA](#)

## Examples

```
# using the defaults
# design="2x2", targetpower=0.8, minpower=0.7, theta0/GMR=0.95
# BE margins from defaults of sampleN.TOST() 0.8 ... 1.25
# print & plot implicitly
pa.ABE(CV = 0.2)
# print & plot

res <- pa.ABE(CV = 0.2)
print(res, plotit = FALSE)           # print only
plot(res, pct = FALSE, ratiolabel = "GMR") # changed from defaults
```

---

pa.NTIDFDA

*Power analysis for scaled ABE for NTIDs according to FDA*

---

## Description

An analysis tool for exploration/visualization of the impact of expected values (CV, theta0, reduced sample size due to drop-outs) on power of BE decision via scABE for narrow therapeutic drugs (NTIDs) if these values deviate from the ones assumed in planning the sample size of the study. The only implemented design is the full replicate design "2x2x4" according to the FDA Warfarin guidance.

## Usage

```
pa.NTIDFDA(CV, theta0 = 0.975, targetpower = 0.8, minpower = 0.7, ...)
```

## Arguments

CV	Coefficient of variation of the intra-subject variabilities of Test and Reference as ratio (not percent). Here only the case $CV_{wT}=CV_{wR}$ is implemented, <i>i.e.</i> , CV has to be a scalar.
theta0	'True' or assumed T/R ratio. Often named GMR. Must be given as ratio. Defaults here to 0.975.
targetpower	Power to achieve at least in sample size estimation. Must be >0 and <1. Typical values are 0.8 or 0.9. Defaults to 0.8. Note that targetpower < 0.5 doesn't make much sense.
minpower	Minimum acceptable power to have if deviating from assumptions for sample size plan. Has to be lower than targetpower. Defaults to 0.7. minpower < 0.5 doesn't make much sense.
...	More arguments to pass to power.NTIDFDA(). F.i., alpha, theta1, theta2 or nsims if other values than the defaults for these arguments are needed. See man page of power.NTIDFDA().

## Details

Power calculations are done via `power.NTIDFDA()` and calculations of CV and `theta0` which result in `minpower` are derived via `uniroot()`.

While one of the parameters (CV, `theta0`, n) is varied, the respective two others are kept constant. The tool shows the relative impact of single parameters on power.

The tool takes a minimum of 12 subjects into account as demanded in most BE guidances. However, it should be kept in mind that the FDA requires at least 24 subjects to be enrolled in studies intended for reference-scaling.

It should be kept in mind that this is **not** a substitute for the “Sensitivity Analysis” recommended in ICH-E9. In a real study a combination of all effects occurs simultaneously. It is up to *you* to decide on reasonable combinations and analyze their respective power.

## Value

Returns a list with class 'pwrA' with the components

<code>plan</code>	A data.frame with the result of the sample size estimation. See output of <code>sampleN.NTIDFDA()</code> .
<code>paCV</code>	A data.frame with value pairs CV, pwr for impact of deviations from CV.
<code>paGMR</code>	A data.frame with value pairs <code>theta0</code> , pwr for impact of deviations from <code>theta0</code> (GMR).
<code>paN</code>	A data.frame with value pairs N, pwr for impact of deviations from planned N (dropouts).
<code>method</code>	Method of BE decision. Here <code>fix = "NTID FDA"</code> .
<code>regulator</code>	Here <code>fix = "FDA"</code> .
<code>minpower</code>	Minimum acceptable power from the call of the function.

The class 'pwrA' has the S3 methods `print()` and `plot()`. See [pa.ABE](#) for usage.

## Warning

Be extremely carefull if your sample size plan has extremely small CV near or below 0.05 (5%). Adapt in that case your expected true ratio (`theta0`) to values nearer to 1 to not run into errors and/or long execution times.

## Note

The code for impact of deviations from planned sample size tries to keep the degree of imbalance as low as possible between (sequence) groups. This results in a lesser decrease of power than more extreme dropout-patterns.

## Author(s)

D. Labes according to code by H. Schütz for `pa.ABE()` and `pa.scABE()`.

## References

- Food and Drug Administration, Office of Generic Drugs (OGD). *Draft Guidance on Warfarin Sodium*. Recommended Dec 2012. [download](#)
- Yu LX, Jiang W, Zhang X, Lionberger R, Makhlof F, Schuirmann DJ, Muldowney L, Chen ML, Davit B, Conner D, Woodcock J. *Novel bioequivalence approach for narrow therapeutic index drugs*. Clin Pharmacol Ther. 2015;97(3):286–91. doi: [10.1002/cpt.28](#)
- Jiang W, Makhlof F, Schuirmann DJ, Zhang X, Zheng N, Conner D, Yu LX, Lionberger R. *A Bioequivalence Approach for Generic Narrow Therapeutic Index Drugs: Evaluation of the Reference-Scaled Approach and Variability Comparison Criterion*. AAPS J. 2015;17(4):891–901. doi: [10.1208/s1224801597535](#)
- Endrényi L, Tóthfalusi L. *Determination of Bioequivalence for Drugs with Narrow Therapeutic Index: Reduction of the Regulatory Burden*. J Pharm Pharm Sci. 2013;16(5):676–82. [open access](#)

## See Also

[power.NTIDFDA](#), [print.pwrA](#), [plot.pwrA](#), [pa.ABE](#), [pa.scABE](#)

## Examples

```
# using the defaults:
# targetpower=0.8, minpower=0.7, theta0/GMR=0.975
# BE margins from defaults of sampleN.NTIDFDA() 0.9002 ... 1.1108
# 1E5 sims in power.NTIDFDA()
# not run due to timing policy of CRAN for examples
# may run some ten seconds or more

plot(pa.NTIDFDA(CV=0.1))
```

---

pa.scABE

*Power analysis for scaled average bioequivalence (scABE)*

---

## Description

An analysis tool for exploration/visualization of the impact of expected values (CV, theta0, reduced sample size due to drop-outs) on power of BE decision via scABE (for highly variable drugs) if these values deviate from the ones assumed in planning the sample size of the study.

## Usage

```
pa.scABE(CV, theta0 = 0.9, targetpower = 0.8, minpower = 0.7,
         design = c("2x3x3", "2x2x4", "2x2x3"),
         regulator = c("EMA", "HC", "FDA", "GCC"), ...)
```

**Arguments**

CV	Coefficient of variation of the intra-subject variability as ratio (not percent). Here only the case $CV_wT=CV_wR$ is implemented, <i>i.e.</i> , CV has to be a scalar.
theta0	‘True’ or assumed T/R ratio. Often named GMR. Must be given as ratio. Defaults to 0.9 here since HVD have a greater scatter in point estimates of T/R.
targetpower	Power to achieve at least in sample size estimation. Must be >0 and <1. Typical values are 0.8 or 0.9. Defaults to 0.8. Note that targetpower < 0.5 doesn’t make much sense.
minpower	Minimum acceptable power to have if deviating from assumptions for sample size plan. Has to lower than targetpower. Defaults to 0.7. minpower < 0.5 doesn’t make much sense.
design	Character string describing the study design. Defaults to 2x3x3, the partial replicate design (TRRIRTRIRRT).
regulator	Character string describing the scaled ABE method recommended by the regulatory bodies "EMA", "HC", "FDA" or "GCC". Defaults to "EMA", method of scaled (expanded) bioequivalence limits.
...	More arguments to pass to power.scABEL() or power.RSABE(). F.i., alpha, theta1, theta2 or nsims if other values than the defaults for these arguments are needed. See man pages of power.scABEL() or power.RSABE().

**Details**

Power calculations are done via power.scABEL() or power.RSABE() and calculations of CV and theta0 which result in minpower derived via R base [uniroot](#).

While one of the parameters (CV, GMR, N) is varied, the respective two others are kept constant. The tool shows the relative impact of single parameters on power.

The tool takes a minimum of 12 subjects as required in most BE guidances into account. However, the sample size will be increased from the estimated one if one of the following conditions is applicable:

- The FDA requires at least 24 subjects *enrolled* in studies intended for reference-scaling.
- The EMA requires at least 12 *eligible* subjects in the sequence RTR of the TRTIRTR-design (hence the minimum sample size is 24).

You should be aware that this is **not** a substitute for the “Sensitivity Analysis” recommended in ICH-E9. In a real study a combination of all effects occurs simultaneously. It is up to *you* to decide on reasonable combinations and analyze their respective power.

**Value**

Returns a list with class 'pwrA' with the components

plan	A data.frame with the result of the sample size estimation. See output of sampleN.scABEL() or sampleN.RSABE().
------	---

paCV	A data.frame with value pairs CV, pwr for impact of deviations from CV.
paGMR	A data.frame with value pairs theta0, pwr for impact of deviations from theta0 (GMR).
paN	A data.frame with value pairs N, pwr for impact of deviations from planned N (dropouts).
method	Method of BE decision. Here fix = "scABE".
regulator	"EMA", "HC", or "FDA".
minpower	Minimum acceptable power from the call of the function.

The class 'pwrA' has the S3 methods `print()` and `plot()`. See [pa.ABE](#) for usage.

### Note

The code for impact of deviations from planned sample size tries to keep the degree of imbalance as low as possible between (sequence) groups. This results in a lesser decrease of power than more extreme dropout-patterns.

### Author(s)

Idea and original code by H. Schütz with modifications by D. Labes to use PowerTOST infrastructure.

### References

Schütz H. *Deviating from assumptions*. August 08, 2014. [BEBA Forum](#)

### See Also

[power.scABEL](#), [power.RSABE](#), [known.designs](#), [print.pwrA](#), [plot.pwrA](#), [pa.ABE](#), [pa.NTIDFDA](#)

### Examples

```
# Implicitly using the defaults:
# design = "2x3x3", targetpower = 0.8, minpower = 0.7,
# theta0 = 0.9, GMR = 0.90, regulator = "EMA"
# widened BE margins from defaults of sampleN.scABEL() 0.7462 ... 1.3402
# 1E5 sims in power.scABEL()
# not run due to timing policy of CRAN, may run some ten seconds

# Implicit print & plot
pa.scABE(CV = 0.4)
```



power.2TOST

*Power for two simultaneous TOST procedures***Description**

Calculates the exact power of two simultaneous TOST procedures (where the two parameters of the two TOSTs are correlated with some correlation) for various study designs used in BE studies

**Usage**

```
power.2TOST(alpha = c(0.05, 0.05), logscale = TRUE, theta0, theta1, theta2,
             CV, n, rho, design = "2x2", robust = FALSE, nsims, setseed = TRUE,
             details = FALSE)
```

**Arguments**

alpha	Vector; contains one-sided significance level for each of the two TOSTs. For one TOST, by convention mostly set to 0.05.
logscale	Should the data used on log-transformed (TRUE, default) or on original scale (FALSE)?
theta1	Vector; contains lower bioequivalence limit for each of the two TOSTs. In case of logscale=TRUE it is given as ratio, otherwise as diff. to 1. Defaults to c(0.8, 0.8) if logscale=TRUE or to c(-0.2, -0.2) if logscale=FALSE.
theta2	Vector; contains upper bioequivalence limit for each of the two TOSTS. If not given theta2 will be calculated as 1/theta1 if logscale=TRUE or as -theta1 if logscale=FALSE.
theta0	Vector; contains 'true' assumed bioequivalence ratio for each of the two TOSTs. In case of logscale=TRUE each element must be given as ratio, otherwise as difference to 1. See examples. Defaults to c(0.95, 0.95) if logscale=TRUE or to c(0.05, 0.05) if logscale=FALSE.
CV	Vector of coefficient of variations (given as as ratio, e.g., 0.2 for 20%). In case of cross-over studies this is the within-subject CV, in case of a parallel-group design the CV of the total variability. In case of logscale=FALSE CV is assumed to be the respective standard deviation.
n	Number of subjects under study. Is total number if given as scalar, else number of subjects in the (sequence) groups. In the latter case the length of n vector has to be equal to the number of (sequence) groups.
rho	Correlation between the two PK metrics (e.g., AUC and Cmax) under consideration. This is defined as correlation between the estimator of the treatment difference of PK metric one and the estimator of the treatment difference of PK metric two. Has to be within {-1, +1}.
design	Character string describing the study design. See known.designs() for designs covered in this package.

robust	Defaults to FALSE. With that value the usual degrees of freedom will be used. Setting to TRUE will use the degrees of freedom according to the 'robust' evaluation (aka Senn's basic estimator). These degrees of freedom are calculated as $n - \text{seq}$ . See <code>known.designs()</code> \$df2 for designs covered in this package. Has only effect for higher-order crossover designs.
nsims	Number of studies to simulate. Defaults to 1E5.
setseed	Logical; if TRUE, the default, a seed of 1234567 is set.
details	Logical; if TRUE, run time will be printed. Defaults to FALSE.

### Details

Calculations are based on simulations and follow the distributional properties as described in Phillips. This is in contrast to the calculations via the 4-dimensional non-central  $t$ -distribution as described in Hua *et al.* which was implemented in versions up to 1.4-6.

The formulas cover balanced and unbalanced studies w.r.t (sequence) groups.

In case of parallel group design and higher order crossover designs (replicate crossover or crossover with more than two treatments) the calculations are based on the assumption of equal variances for Test and Reference products under consideration.

The formulas for the paired means 'design' do not take an additional correlation parameter into account. They are solely based on the paired  $t$ -test (TOST of differences = zero).

### Value

Value of power.

### Note

If  $n$  is given as scalar (total sample size) and this number is not divisible by the number of (sequence) groups of the design an unbalanced design with small imbalance is assumed. A corresponding message is thrown showing the assumed numbers of subjects in (sequence) groups.

The function does not vectorize properly if design is a vector. Moreover, the  $\tau_0$  and CV must be of length two, thus further vectorizing is not possible.

Other vector input is not tested yet.

### Author(s)

B. Lang, D. Labes

### References

Phillips KF. *Power for Testing Multiple Instances of the Two One-Sided Tests Procedure*. Int J Biostat. 2009;5(1):Article 15.

Hua SY, Xu S, D'Agostino RB Sr. *Multiplicity adjustments in testing for bioequivalence.* Stat Med. 2015;34(2):215–31. doi: [10.1002/sim.6247](https://doi.org/10.1002/sim.6247)

Lang B, Fleischer F. *Letter to the Editor: Comments on 'Multiplicity adjustments in testing for bioequivalence.'* Stat Med. 2016;35(14):2479–80. doi: [10.1002/sim.6488](https://doi.org/10.1002/sim.6488)

### See Also

[sampleN.2TOST](#), [known.designs](#)

### Examples

```
# Power for the 2x2x2 cross-over design with 24 subjects, intra-subject
# standard deviation of 0.3 (CV = 30.7%) and assumed ratios of 1.05 for both
# parameters, and correlation 0.75 between parameters (using all the other
# default values)
power.2TOST(theta0 = rep(1.05, 2), CV = rep(se2CV(0.3), 2),
            n = 24, rho = 0.75)
# should give: 0.38906

# Setting as before but use rho 1 and high number of simulations
# to reproduce result of power.TOST()
p1 <- power.2TOST(theta0 = rep(1.05, 2), CV = rep(se2CV(0.3), 2),
                 n = 24, rho = 1, nsims=1E7)
p2 <- power.TOST(theta0 = 1.05, CV = se2CV(0.3), n = 24)
all.equal(p1, p2, tolerance = 1e-04)
```

---

power.dp

*Power of dose-proportionality studies evaluated via Power model*

---

### Description

Calculates the power of dose-proportionality studies using the power model for crossover (Latin square) or parallel group designs via a confidence interval equivalence criterion.

### Usage

```
power.dp(alpha = 0.05, CV, doses, n, beta0, theta1 = 0.8, theta2 = 1/theta1,
         design = c("crossover", "parallel", "IBD"), dm = NULL, CVb)
```

### Arguments

alpha	Type 1 error. Commonly set to 0.05.
CV	Coefficient of variation for intra-subject variability if design="crossover" or CV of total variability in case of design="parallel".
doses	Vector of dose levels. At least two doses have to be given.

n	Number of subjects. Is total number if given as scalar, else number of subjects in the (sequence) groups. In the latter case the length of n vector has to be the same as length of vector doses. n has to be >2.
beta0	'True' slope of power model. If missing defaults to $1 + \log(0.95) / \log(rd)$ where rd is the ratio of highest to lowest dose.
theta1	Lower acceptance limit for the ratio of dose normalized means (Rdmn). Transformes into slope acceptance range as described under item beta0.
theta2	Upper acceptance limit for the ratio of dose normalized means (Rdmn).
design	Crossover design (default), parallel group design or incomplete block design (IBD). Crossover design means Latin square design with number of doses as dimension.
dm	'Design matrix' of the incomplete block design (IBD) if design="IBD". This matrix contains the sequences in rows and periods in columns. The entry (i, j) of the design matrix corresponds to the dose (index) a subject with i-th sequence gets in the j-th period. Can be obtained f.i. via functions of package crossdes or via function bib.CL().
CVb	Coefficient of variation of the between-subject variability. Only necessary if design="IBD". Will be set to 2*CV if missing. This is only a crude rule of thumb. Better obtain an estimate of CVb from a previous crossover study.  Set CVb=0 if an all-effects-fixed model shall be used. This model gives higher power than the random subject effects model.

### Details

The power calculations are based on TOST for testing equivalence of the slope of the power model with alternativ hypothesis slope = 1.

Power is calculated via non-central t-approximation only.

The calculations are based on mixed effects model (random intercept aka random subject effect).

For design="cossover" or design="parallel" the results coincide with all-effects-fixed model.

### Value

Value of power according to the input arguments.

### Warning

This function is 'experimental' only since it is not thoroughly tested yet. Especially for design="IBD" reliable test cases are missing.

### Author(s)

D. Labes

## References

Patterson S, Jones B. *Bioequivalence and Statistics in Clinical Pharmacology*. Boca Raton: Chapman & Hall/CRC: 2006. p. 239.

(contains presumably a bug)

Sethuraman VS, Leonov S, Squassante L, Mitchell TR, Hale MD. *Sample size calculation for the Power Model for dose proportionality studies*. Pharm Stat. 2007;6(1):35–41. doi: [10.1002/pst.241](https://doi.org/10.1002/pst.241)

Hummel J, McKendrick S, Brindley C, French R. *Exploratory assessment of dose proportionality: review of current approaches and proposal for a practical criterion*. Pharm. Stat. 2009;8(1):38–49. doi: [10.1002/pst.326](https://doi.org/10.1002/pst.326)

## See Also

[sampleN.dp](#), [bib.CL](#)

## Examples

```
# using all the defaults, i.e. latin square crossover design, alpha=0.05,
# beta0=1+log(0.95)/log(rd), theta1=0.8, theta2=1.25
power.dp(CV = 0.2, doses = c(1,2,8), n = 15)
#
# period balanced IBD with 3 doses, 2 periods and 3 sequences,
ibd <- matrix(c(1, 2, 3, 2, 3, 1), nrow = 3, ncol = 2)
power.dp(CV = 0.2, doses = c(1,2,8), n = 12, design = "IBD", dm = ibd)
# considerably lower than 3x3 Latin square
```

---

power.HVNTID	<i>(Empirical) Power for BE decision via FDA method for highly variable NTIDs</i>
--------------	---

---

## Description

This function performs the power calculation of the BE decision via the FDA's method for highly variable narrow therapeutic index drugs (NTIDs) as described in respective guidances based on simulations. The study design could be the full replicate design 2x2x4 with 4-periods (TRTR|RTRT) or the 2x2x3 replicate design with 3-periods and sequences TRT|RTR.

## Usage

```
power.HVNTID(alpha = 0.05, theta1, theta2, theta0, CV, n, design = c("2x2x4", "2x2x3"),
             nsims = 1e+05, details = FALSE, setseed = TRUE)
```

## Arguments

alpha	Type I error probability, significance level. Commonly set to 0.05.
theta1	Conventional lower ABE limit to be applied in the FDA procedure. Defaults to 0.8 if not given explicitly.

theta2	Conventional upper ABE limit to be applied in the FDA procedure. Defaults to 1.25 if not given explicitly.
theta0	'True' or assumed T/R ratio. Defaults to 0.95 if not given explicitly.
CV	Intra-subject coefficient(s) of variation as ratio (not percent). <ul style="list-style-type: none"> <li>• If given as a scalar (<code>length(CV)==1</code>) the <i>same</i> CV of Test and Reference is assumed (homoscedasticity, <code>CVwT==CVwR</code>).</li> <li>• If given as a vector (<code>length(CV)==2</code>), <i>i.e.</i>, assuming heteroscedasticity, the CV of the Test <b>must</b> be given in <code>CV[1]</code> and the one of the Reference in the <code>CV[2]</code>.</li> </ul>
n	Number of subjects under study. May be given as vector. In that case it is assumed that n contains the number of subjects per sequence groups. Attention! In case of the "2x2x3" (TRT RTR) design the order of sample sizes is important if given as vector. <code>n[1]</code> is for sequence group 'TRT' and <code>n[2]</code> is for sequence group 'RTR'. If n is given as single number (total sample size) and this number is not divisible by the number of sequences of the design an unbalanced design is assumed. A corresponding message is thrown showing the numbers of subjects in the sequence groups.
design	Design of the study to be planned. "2x2x4" is the full replicate design with 2 sequences and 4 periods (TRTR RTRT). "2x2x3" is the 3-period full replicate design with sequences TRT RTR. Defaults to <code>design="2x2x4"</code> .
nsims	Number of simulations to be performed to obtain the empirical power. Defaults to 100,000 = 1e+5.
details	If set to TRUE the computational time is shown as well as the components for the BE decision. <code>p(BE-ABE)</code> is the simulated probability for the conventional ABE test. <code>p(BE-ratio)</code> is the probability that the upper 90% confidence limit of the ratio of <code>sWT/sWR</code> is < 2.5.
setseed	Simulations are dependent on the starting point of the (pseudo) random number generator. To avoid differences in power for different runs a <code>set.seed(123456)</code> is issued if <code>setseed=TRUE</code> , the default.

## Details

For deciding BE the study must pass the conventional ABE test (90% CI within the acceptance range) and additionally the test that the ratio of `sWT/sWR` is < 2.5.

The simulations are done via the distributional properties of the statistical quantities necessary for deciding BE based on this method.

Details can be found in a document `Implementation_scaledABE_sims` located in the `/doc` sub-directory of the package.

**Value**

Returns the value of the (empirical) power if argument `details=FALSE`.

Returns a named vector if argument `details=TRUE`.

`p(BE)` is the power, `p(BE-ABE)` is the power of the ABE test alone and `p(BE-sratio)` is the power of the criterion 'ratio of `sWT/sWR` is  $\leq 2.5$ ' alone.

**Note**

The FD's guidances recommend only the full replicate design "2x2x4" (TRTRIRTRT). The results for the design "2x2x3" (TRTIRTR) are to be considered as experimental since at present not thoroughly tested.

**Author(s)**

D. Labes

**References**

Food and Drug Administration, Office of Generic Drugs (OGD). *Draft Guidance on Dabigatran Etexilate Mesylate*. Recommended Jun 2012; Revised Sep 2015, Jul 2017. [download](#)

Food and Drug Administration, Office of Generic Drugs (OGD). *Draft Guidance on Rivaroxaban*. Recommended Sep 2015. [download](#)

**See Also**

[sampleN.HVNTID](#) and [power.NTIDFDA](#), [sampleN.NTIDFDA](#) for NTIDs with low variability

**Examples**

```
# using the defaults:
# GMR=0.95, theta1=0.8, theta2=1.25, full replicate design 2x2x4, 100,000 simulations
# and a CV of 0.3 (=30%) for both Reference and Test, with 24 subjects, balanced
power.HVNTID(CV = 0.3, n = 24)
# should give a power of 0.86354
```

---

power.noninf

*Power of the one-sided non-inferiority t-test*

---

**Description**

Function calculates of the power of the one-sided non-inferiority *t*-test for normal or log-normal distributed data.

**Usage**

```
power.noninf(alpha = 0.025, logscale = TRUE, margin, theta0, CV, n,
             design = "2x2", robust = FALSE)
```

**Arguments**

alpha	Significance level (one-sided). Defaults here to 0.025.
logscale	Should the data used on log-transformed or on original scale? TRUE (default) or FALSE.
theta0	‘True’ or assumed T/R ratio or difference. In case of logscale=TRUE it must be given as ratio T/R. If logscale=FALSE, the difference in means. In this case, the difference may be expressed in two ways: relative to the same (underlying) reference mean, i.e. as $(T-R)/R = T/R - 1$ ; or as difference in means T-R. Note that in the former case the units of margin and CV need also be given relative to the reference mean (specified as ratio). Defaults to 0.95 if logscale=TRUE or to -0.05 if logscale=FALSE
margin	Non-inferiority margin. In case of logscale=TRUE it is given as ratio. If logscale=FALSE, the limit may be expressed in two ways: difference of means relative to the same (underlying) reference mean or in units of the difference of means. Note that in the former case the units of CV and theta0 need also be given relative to the reference mean (specified as ratio). Defaults to 0.8 if logscale=TRUE or to -0.2 if logscale=FALSE.
CV	In case of logscale=TRUE the (geometric) coefficient of variation given as ratio. If logscale=FALSE the argument refers to (residual) standard deviation of the response. In this case, standard deviation may be expressed two ways: relative to a reference mean (specified as ratio $\sigma/\mu_R$ ), i.e. again as a coefficient of variation; or untransformed, i.e. as standard deviation of the response. Note that in the former case the units of theta0, theta1 and theta2 need also be given relative to the reference mean (specified as ratio).  In case of cross-over studies this is the within-subject CV, in case of a parallel-group design the CV of the total variability.
n	Number of subjects under study. Is total number if given as scalar, else number of subjects in the (sequence) groups. In the latter case the length of the n vector has to be equal to the number of (sequence) groups.
design	Character string describing the study design. See <a href="#">known.designs</a> for designs covered in this package.
robust	Defaults to FALSE. With that value the usual degrees of freedom will be used. Set to TRUE will use the degrees of freedom according to the ‘robust’ evaluation (aka Senn’s basic estimator). These degrees of freedom are calculated as $n - \text{seq}$ . See <code>known.designs()\$df2</code> for designs covered in this package. Has only effect for higher-order crossover designs.

**Details**

The power is calculated exact via non-central  $t$ -distribution.



**Notes on the underlying hypotheses**

If the supplied margin is  $< 0$  (logscale=FALSE) or  $< 1$  (logscale=TRUE), then it is assumed higher response values are better. The hypotheses are

H0:  $\theta_0 \leq \text{margin}$  vs. H1:  $\theta_0 > \text{margin}$

where  $\theta_0 = \text{mean}(\text{test}) - \text{mean}(\text{reference})$  if logscale=FALSE

or

H0:  $\log(\theta_0) \leq \log(\text{margin})$  vs. H1:  $\log(\theta_0) > \log(\text{margin})$

where  $\theta_0 = \text{mean}(\text{test}) / \text{mean}(\text{reference})$  if logscale=TRUE.

If the supplied margin is  $> 0$  (logscale=FALSE) or  $> 1$  (logscale=TRUE), then it is assumed lower response values are better. The hypotheses are

H0:  $\theta_0 \geq \text{margin}$  vs. H1:  $\theta_0 < \text{margin}$

where  $\theta_0 = \text{mean}(\text{test}) - \text{mean}(\text{reference})$  if logscale=FALSE

or

H0:  $\log(\theta_0) \geq \log(\text{margin})$  vs. H1:  $\log(\theta_0) < \log(\text{margin})$

where  $\theta_0 = \text{mean}(\text{test}) / \text{mean}(\text{reference})$  if logscale=TRUE.

This latter case may also be considered as ‘non-superiority’.

**Value**

Value of power according to the input arguments.

**Warning**

The function does not vectorize if design is a vector.

The function vectorize properly if CV or theta0 are vectors.

Other vector input is not tested yet.

**Note**

This function does not rely on TOST but may be useful in planning BE studies if the question is not equivalence but ‘non-superiority’.

Hint: Evaluation of Fluctuation in the [EMEA’s Note for Guidance](#) between a modified release formulation and an immediate release product.

**Author(s)**

D. Labes

**References**

Julious SA. *Sample sizes for clinical trials with Normal data*. Stat Med. 2004;23(12):1921–86. doi: [10.1002/sim.1783](https://doi.org/10.1002/sim.1783)

**See Also**

[known.designs](#), [sampleN.noninf](#)

**Examples**

```
# using all the defaults: margin=0.8, theta0=0.95, alpha=0.025
# log-transformed, design="2x2"
# should give: 0.4916748
power.noninf(CV=0.3, n=24)
```

---

power.NTIDFDA

*(Empirical) Power for BE decision via FDA method for NTIDs*


---

**Description**

This function performs the power calculation of the BE decision via the FDA's method for narrow therapeutic index drugs (NTIDs) by simulations. The study design could be the full replicate design 2x2x4 with 4-periods (TRTR|RTRT) or the 2x2x3 replicate design with sequences TRT|RTR.

**Usage**

```
power.NTIDFDA(alpha = 0.05, theta1, theta2, theta0, CV, n, design=c("2x2x4", "2x2x3"),
              nsims = 1e+05, details = FALSE, setseed = TRUE)
```

**Arguments**

alpha	Type I error probability, significance level. Conventionally mostly set to 0.05.
theta1	Conventional lower ABE limit to be applied in the FDA procedure. Defaults to 0.8 if not given explicitly.
theta2	Conventional upper ABE limit to be applied in the FDA procedure. Defaults to 1.25 if not given explicitly.
theta0	'True' or assumed T/R ratio. Attention! Defaults here to 0.975 if not given explicitly. The value was chosen closer to 1 because the potency (contents) settings for NTIDs are tightened by the FDA.
CV	Intra-subject coefficient(s) of variation as ratio (not percent). <ul style="list-style-type: none"> <li>• If given as a scalar (<code>length(CV)==1</code>) the <i>same</i> CV of Test and Reference is assumed (homoscedasticity, <code>CVwT==CVwR</code>).</li> <li>• If given as a vector (<code>length(CV)==2</code>), <i>i.e.</i>, assuming heteroscedasticity, the CV of the Test <b>must</b> be given in <code>CV[1]</code> and the one of the Reference in the <code>CV[2]</code>.</li> </ul>
n	Number of subjects under study. May be given as vector. In that case it is assumed that n contains the number of subjects per sequence groups. Attention! In case of the "2x2x3" (TRT RTR) design the order of sample sizes important if given as vector. <code>n[1]</code> is for sequence group 'TRT' and <code>n[2]</code> is for sequence group 'RTR'.

	If n is given as single number (total sample size) and this number is not divisible by the number of sequences of the design an unbalanced design is assumed. A corresponding message is thrown showing the numbers of subjects in the sequence groups.
design	Design of the study to be planned. "2x2x4" is the full replicate design with 2 sequences and 4 periods (TRTRIRTRT). "2x2x3" is the full replicate design with 2 sequences and 3 periods (TRTIRTR). Defaults to design="2x2x4".
nsims	Number of simulations to be performed to obtain the empirical power. Defaults to 100,000 = 1e+5.
details	If set to TRUE the computational time is shown as well as the components for the BE decision. p(BE-ABE) is the simulated probability for the conventional ABE test. p(BE-sABEc) is the probability that the 95% CI of the ABE criterion is <0. p(BE-sratio) is the probability that the ratio of sWT/sWR is <= 2.5.
setseed	Simulations are dependent on the starting point of the (pseudo) random number generator. To avoid differences in power for different runs a set . seed(123456) is issued if setseed=TRUE, the default.

### Details

The linearized scaled ABE criterion is calculated according to the SAS code given in the FDA Warfarin guidance. For deciding BE the study must pass that criterion, the conventional ABE test and additionally the test that the ratio of sWT/sWR is <= 2.5.

The simulations are done via the distributional properties of the statistical quantities necessary for deciding BE based on these methods.

Details can be found in a document Implementation\_scaledABE\_sims located in the /doc sub-directory of the package.

### Value

Returns the value of the (empirical) power if argument details=FALSE.

Returns a named vector if argument details=TRUE.

p(BE) is the power, p(BE-sABEc) is the power of the BE test via scaled ABE criterion alone, p(BE-ABE) is the power of the conventional ABE test alone and p(BE-sratio) is the power of the criterion 'ratio of sWT/sWR is <= 2.5' alone.

### Note

The FDA's method is described for the ABE limits 0.8 ... 1.25 only. Setting theta1, theta2 to other values may not be reasonable and is not tested.

The results for the design "2x2x3" are to be considered as experimental since at present not thoroughly tested.

**Author(s)**

D. Labes

**References**

Food and Drug Administration, Office of Generic Drugs (OGD). *Draft Guidance on Warfarin Sodium*. Recommended Dec 2012. [download](#)

Yu LX, Jiang W, Zhang X, Lionberger R, Makhlof F, Schuirmann DJ, Muldowney L, Chen ML, Davit B, Conner D, Woodcock J. *Novel bioequivalence approach for narrow therapeutic index drugs*. Clin Pharmacol Ther. 2015;97(3):286–91. doi: [10.1002/cpt.28](#)

Jiang W, Makhlof F, Schuirmann DJ, Zhang X, Zheng N, Conner D, Yu LX, Lionberger R. *A Bioequivalence Approach for Generic Narrow Therapeutic Index Drugs: Evaluation of the Reference-Scaled Approach and Variability Comparison Criterion*. AAPS J. 2015;17(4):891–901. doi: [10.1208/s1224801597535](#)

Endrényi L, Tóthfalusi L. *Determination of Bioequivalence for Drugs with Narrow Therapeutic Index: Reduction of the Regulatory Burden*. J Pharm Pharm Sci. 2013;16(5):676–82. [open access](#)

**See Also**

[sampleN.NTIDFDA](#)

and [power.HVNTID](#), [sampleN.HVNTID](#) for NTIDs with high variability

**Examples**

```
# using the all defaults:
# GMR=0.975, theta1=0.8, theta2=1.25, 100,000 simulations
# and a CV of 0.1 (= 10%) with 12 subjects, balanced
power.NTIDFDA(CV = 0.1, n = 12)
# should give a power of 0.62553
```

---

power.RatioF

*Power for equivalence of the ratio of two means with normality on original scale*

---

**Description**

Calculates the power of the test of equivalence of the ratio of two means with normality on original scale.

This test is based on Fieller's confidence ('fiducial') interval and Sasabuchi's test (a TOST procedure as well).

**Usage**

```
power.RatioF(alpha = 0.025, theta1 = 0.8, theta2, theta0 = 0.95,
             CV, CVb, n, design = "2x2", setseed=TRUE)
```

**Arguments**

alpha	Type I error probability, aka significance level. Defaults here to 0.025 because this function is intended for studies with clinical endpoints.
theta1	Lower bioequivalence limit. Typically 0.8 (default).
theta2	Upper bioequivalence limit. Typically 1.25. Is set to 1/theta1 if missing.
theta0	'True' or assumed T/R ratio. Typically set to 0.95 for planning.
CV	Coefficient of variation as ratio. In case of design="parallel" this is the CV of the total variability, in case of design="2x2" the intra-subject CV (CVw in the reference).
CVb	CV of the between-subject variability. Only necessary for design="2x2".
n	Number of subjects to be planned. n is for both designs implemented the <b>total</b> number of subjects.
design	A character string describing the study design. design="parallel" or design="2x2" allowed for a two-parallel group design or a classical TRIRT crossover design.
setseed	If set to TRUE the dependence of the power from the state of the random number generator is avoided. With setseed = FALSE you may see the dependence from the state of the random number generator.

**Details**

The power is calculated exact using the bivariate non-central  $t$ -distribution via function `pmvt` of the package `mvtnorm`.

Due to the calculation method of the used package `mvtnorm` – randomized Quasi-Monte-Carlo – these probabilities are dependent from the state of the random number generator within the precision of the power. See argument `setseed`.

**Value**

Value of power according to the input.

**Note**

This function is intended for studies with clinical endpoints where the 95% confidence intervals are usually used for equivalence testing.

Therefore, alpha defaults here to 0.025 (see EMEA 2000).

The formulas given in the references rely on the assumption of equal variances in the two treatment groups for the parallel group design or on assuming equal within-subject and between-subject variabilities for the 2x2 crossover design.

**Author(s)**

D. Labes

## References

Fieller EC. *Some Problems in Interval Estimation*. J Royal Stat Soc B. 1954;16(2):175–85. doi: [10.1111/j.25176161.1954.tb00159.x](https://doi.org/10.1111/j.25176161.1954.tb00159.x)

Sasabuchi S. *A test of a multivariate normal mean with composite hypotheses determined by linear inequalities*. Biometrika. 1980;67(2):429–39. doi: [10.1093/biomet/67.2.429](https://doi.org/10.1093/biomet/67.2.429)

Hauschke D, Kieser M, Diletti E, Burke M. *Sample size determination for proving equivalence based on the ratio of two means for normally distributed data*. Stat Med. 1999;18(1):93–105.

Hauschke D, Steinijans V, Pigeot I. *Bioequivalence Studies in Drug Development*. Chichester: Wiley; 2007. Chapter 10.

European Agency for the Evaluation of Medicinal Products, CPMP. *Points to Consider on Switching between Superiority and Non-Inferiority*. London, 27 July 2000. [CPMP/EWP/482/99](https://www.ema.europa.eu/en/documents/regulatory-procedure-guideline/cpmp-ewp-482-99_en.pdf)

## See Also

[sampleN.RatioF](#)

## Examples

```
# power for alpha=0.025, ratio=0.95, theta1=0.8, theta2=1/theta1=1.25
# within-subject CV=0.2, between-subject CV=0.4
# 2x2 crossover study, n=24
# using all the defaults:
power.RatioF(CV = 0.2, CVb = 0.4, n = 24)
# gives [1] 0.7315357
```

---

power.RSABE

(Empirical) Power for BE decision via linearized scaled ABE criterion

---

## Description

This function performs the power calculation of the BE decision via linearized scaled ABE criterion by simulations as recommended by the FDA.

## Usage

```
power.RSABE(alpha = 0.05, theta1, theta2, theta0, CV, n,
            design = c("2x3x3", "2x2x4", "2x2x3"), regulator,
            nsims = 1e+05, details = FALSE, setseed=TRUE)
```

## Arguments

alpha	Type I error probability, significance level. Conventionally mostly set to 0.05.
theta1	Conventional lower ABE limit to be applied in the mixed procedure if CV <sub>SWR</sub> <= CV <sub>switch</sub> . Also lower limit for the point estimate constraint. Defaults to 0.8 if not given explicitly.

theta2	Conventional upper ABE limit to be applied in the mixed procedure if CV <sub>SWR</sub> ≤ CV <sub>switch</sub> . Also upper limit for the point estimate constraint. Defaults to 1.25 if not given explicitly.
theta0	‘True’ or assumed T/R ratio. Defaults to 0.90 according to the two Lászlós if not given explicitly.
CV	Intra-subject coefficient(s) of variation as ratio (not percent). <ul style="list-style-type: none"> <li>• If given as a scalar (length(CV)==1) the <i>same</i> CV of Test and Reference is assumed (homoscedasticity, CV<sub>wT</sub>==CV<sub>wR</sub>).</li> <li>• If given as a vector (length(CV)==2), <i>i.e.</i>, assuming heteroscedasticity, the CV of the Test <b>must</b> be given in CV[1] and the one of the Reference in the CV[2].</li> </ul>
n	Number of subjects under study. May be given as vector. In that case it is assumed that n contains the number of subjects in the sequence groups.  If n is given as single number (total sample size) and this number is not divisible by the number of sequences of the design an unbalanced design is assumed. A corresponding message is thrown showing the numbers of subjects in sequence groups used. Attention! In case of the "2x2x3" (TRT RTR) design the order of sample sizes / sequence is important if given as a vector. n[1] is for sequence group 'TRT' and n[2] is for sequence group 'RTR'.
design	Design of the study. "2x3x3" is the partial replicate design. "2x2x4" is a full replicate design with 2 sequences and 4 periods. "2x2x3" is a full replicate design with 2 sequences and 3 periods. Defaults to "2x3x3". Details are given the section about Designs.
regulator	Regulatory settings for RSABE. May be given as character from the choices "EMA" or "FDA" or as an object of class 'regSet' (see <a href="#">reg_const</a> ). Defaults to regulator="FDA" if missing. This argument may be given also in lower case if given as character.  Also the linearized scaled ABE criterion is usually calculated with the FDA constant r_const=log(1.25)/0.25 you can override this behavior to use the EMA setting r_const=0.76 to avoid the discontinuity at CV=30% and be more stringent.
nsims	Number of simulations to be performed to obtain the empirical power. Defaults to 100,000 = 1e+5. If simulations are aimed for empirical alpha nsims=1e+06 is recommended.
details	If set to TRUE the computational time is shown as well as the components for the BE decision. p(BE-sABEc) is the probability that the 95% CI of the ABE criterion is <0. p(BE-PE) is the probability that the point estimate is within theta1 ... theta2. p(BE-ABE) is the simulated probability for the conventional ABE test given for comparison purposes.

`setseed` Simulations are dependent on the starting point of the (pseudo) random number generator. To avoid differences in power for different runs a `set.seed()` is issued if `setseed=TRUE`, the default.

### Details

The linearized scaled ABE criterion is calculated according to the SAS code given in the FDA's progesterone guidance.

The simulations are done via the distributional properties of the statistical quantities necessary for deciding BE based on scaled ABE criterion.

Details can be found in a document `Implementation_scaledABE_simsVx.yy.pdf` located in the `/doc` sub-directory of the package.

If a `CVcap` is defined for the regulator, the BE decision is based on the inclusion of the CI in the capped widened acceptance limits in case of `CVwR > CVcap`. This resembles method 'Howe-EMA' in Muñoz *et al.* and is the standard behavior now if `regulator="EMA"` is chosen.

### Value

Returns the value of the (empirical) power if argument `details=FALSE`.

Returns a named vector if argument `details=TRUE`.

`p(BE)` is the power, `p(BE-sABEc)` is the power of the scaled ABE criterion alone and `p(BE-pe)` is the power of the criterion 'point estimat within acceptance range' alone.

`p(BE-ABE)` is the power of the conventional ABE test given for comparative purposes.

### Designs

Although some designs are more 'popular' than others, power calculations are valid for *all* of the following designs:

"2x2x4"	TRTR   RTRT TRRT   RTTR TTRR   RRTT
"2x2x3"	TRT   RTR TRR   RTT
"2x3x3"	TRR   RTR   RRT

### Warning

In case of the design "2x2x3" heteroscedasticity (*i.e.*,  $CVwT \neq CVwR$ ) may lead to poor agreement of the power values compared to those calculated via the 'classical' way of subject data simulations if the design is unbalanced in respect to the number of subjects in the sequence groups. Therefore, the function issues a warning for that cases.

### Author(s)

D. Labes



## References

Food and Drug Administration, Office of Generic Drugs (OGD). *Draft Guidance on Progesterone*. Recommended Apr 2010. Revised Feb 2011. [download](#)

Tóthfalusi, L, Endrényi, L. *Sample Sizes for Designing Bioequivalence Studies for Highly Variable Drugs*. J Pharm Pharmaceut Sci. 2011;15(1):73–84. [open access](#)

Tóthfalusi L, Endrényi L, García Arieta A. *Evaluation of Bioequivalence for Highly Variable Drugs with Scaled Average Bioequivalence*. Clin Pharmacokin. 2009;48(11):725–43. doi: [10.2165/1131804000000000000000](#)

Muñoz J, Alcaide D, Ocaña J. *Consumer's risk in the EMA and FDA regulatory approaches for bioequivalence in highly variable drugs*. Stat Med. 2015;35(12):1933–43. doi: [10.1002/sim.6834](#)

## See Also

[sampleN.RSABE](#), [power.scABEL](#)

## Examples

```
# using all the defaults:
# design="2x3x3" = partial replicate
# ABE limits, PE constraint 0.8-1.25
# true ratio = 0.90, 1E+5 simulations
power.RSABE(CV = 0.4, n = 36)
# should give
# [1] 0.83634
#
# to explore the simulation error due to the state of the
# random number generator
power.RSABE(CV = 0.4, n = 36, setseed = FALSE)
# will give something like
# [1] 0.83725
#
# explore pure RSABE (without mixed method, without pe constraint)
rs      <- reg_const("FDA")
rs$CVswitch <- 0
rs$pe_constr <- FALSE
power.RSABE(CV = 0.4, n = 36, regulator = rs)
# should give
# [1] 0.84644
```

---

power.RSABE2L.sdsims (Empirical) Power of BE Decision via Reference Scaled ABE

---

## Description

This function performs the power calculation of the BE decision via the reference scaled ABE based on **subject data** simulations. Implemented are the methods ABEL, Hyslop and ‘exact’ as described in the references.

The estimation method of the key statistics needed to perform the RSABE decision is the usual ANOVA.

**Usage**

```
power.RSABE2L.sdsims(alpha = 0.05, theta1, theta2, theta0, CV, n,
  design = c("2x3x3", "2x2x4", "2x2x3"), design_dta = NULL,
  SABE_test = "exact", regulator, nsims = 1e+05,
  details = FALSE, setseed = TRUE, progress)
```

**Arguments**

alpha	Type I error probability, significance level. Conventionally mostly set to 0.05.
theta1	Conventional lower ABE (Average Bioequivalence) limit to be applied in the mixed procedure if CVsWR <= CVswitch. Also lower limit for the point estimate constraint. Defaults to 0.8 if not given explicitly.
theta2	Conventional upper ABE limit to be applied in the mixed procedure if CVsWR <= CVswitch. Also upper limit for the point estimate constraint. Defaults to 1.25 if not given explicitly.
theta0	'True' or assumed T/R ratio. Defaults to 0.90 according to the two Lászlós if not given explicitly.
CV	Intra-subject coefficient(s) of variation as ratio (not percent). <ul style="list-style-type: none"> <li>• If given as a scalar (length(CV)==1) the <i>same</i> CV of Test and Reference is assumed (homoscedasticity, CVwT==CVwR).</li> <li>• If given as a vector (length(CV)==2), <i>i.e.</i>, assuming heteroscedasticity, the CV of the Test <b>must</b> be given in CV[1] and the one of the Reference in the CV[2].</li> </ul>
n	Number of subjects under study. May be given as vector. In that case it is assumed that n contains the number of subjects in the sequence groups. If n is given as single number (total sample size) and this number is not divisible by the number of sequences of the design an unbalanced design is assumed. A corresponding message is thrown (showing the numbers of subjects in sequence groups). Attention! In case of the "2x2x3" (TRT RTR) design the order of sample sizes per sequence is important if given as vector. n[1] is for sequence group 'TRT' and n[2] is for sequence group 'RTR'.
design	Design of the study. "2x3x3" is the partial replicate design. "2x2x4" is a full replicate design with 2 sequences and 4 periods. "2x2x3" is a full replicate design with 2 sequences and 3 periods. Defaults to design="2x3x3". Details are given the section about Designs.
design_dta	Alternatively to using the arguments design and n the design may be defined via a data.frame with columns subject, sequence, period and tmt. This feature is experimental in the sense that the data.frame is not checked for complying with the assumed structure. If you use the argument design_dta you don't need to specify the arguments design and n.

	The default <code>design_dta=NULL</code> means that <code>design</code> and <code>n</code> are used for the internal construction of the <code>design.data.frame</code> .
<code>SABE_test</code>	This argument specifies the test method to be used for the reference scaled ABE decision. Default is the "exact" 'ncTOST' method of the two Laszlós. Other choices are "ABEL", "hyslop" and "fda". See Details.
<code>regulator</code>	Regulatory settings for the widening of the BE acceptance limits. May be given as character "EMA" or as an object of class 'regSet' (see <a href="#">reg_const</a> ). Defaults to <code>regulator="EMA"</code> if missing. This argument may be given also in lower case if given as character.
<code>nsims</code>	If given as object of class 'regSet' the component <code>est_method</code> can not be "ISC". Number of simulations to be performed to obtain the empirical power. Defaults to $100,000 = 1e+05$ . If simulations are aimed for empirical alpha <code>nsims=1e+06</code> is recommended.
<code>details</code>	If set to TRUE the computational time is shown as well as the components for the BE decision. <code>p(BE-RSABE)</code> is the probability of a positive outcome of the SABE test. <code>p(BE-PE)</code> is the probability that the point estimate is within <code>theta1 ... theta2</code> . <code>p(BE-ABE)</code> is the simulated probability for the conventional ABE test.
<code>setseed</code>	Simulations are dependent on the starting point of the (pseudo) random number generator. To avoid differences in power for different runs a <code>set.seed()</code> is issued if <code>setseed=TRUE</code> , the default.
<code>progress</code>	Should a progressbar be shown? Defaults to TRUE if missing and <code>nsims &gt; 5e5</code> .

## Details

The methods rely on the analysis of log-transformed data, *i.e.*, assumes a log-normal distribution on the original scale.

The `data.frame` with columns `subject`, `sequence`, `period` and `tmt` necessary for evaluation of simulated subject data is constructed internally from the arguments `design` and `n` or may be given user defined via the argument `design_dta`. The last option is usefull if missing data have to be considered or if designs have to be evaluated which are not in the list of argument `design`.

The estimation method for obtaining the statistics necessary to perform the reference scaled ABE decision is the usual ANOVA with effects treatment, period, sequence and subject within sequence for the evaluation of all data and period, sequence and subject within sequence for the evaluation of the Reference formulation data only.

The SABE tests implemented are:

"exact"	'exact' based method of the two Laszlós (see references, called there 'ncTOST')
"ABEL"	Average bioequivalence with expanding limits
"hyslop"	BE decision via the linearized RSABE criterion and its upper 95% CI
"fda"	Hyslop with an additional bias correction term as implemented in the SAS code of the FDA's Guidance on Progesterone.

**Value**

Returns the value of the (empirical) power if argument `details=FALSE`.

Returns a named vector if argument `details=TRUE`.

`p(BE)` is the power, `p(BE-RSABE)` is the power of using the reference scaled ABE alone, and `p(BE-pe)` is the power of the criterion ‘point estimate within acceptance range’ alone. `p(BE-ABE)` is the power of the conventional ABE test given for comparative purposes.

**Designs**

Although some designs are more ‘popular’ than others, power calculations are valid for *all* of the following designs:

"2x2x4"	TRTR   RTRT TRRT   RTTR TTRR   RRTT
"2x2x3"	TRT   RTR TRR   RTT
"2x3x3"	TRR   RTR   RRT

**Note**

The function is relatively slow. The run-time for 1 Mio. simulations is between ~ 1 up to 6 minutes for `n=12` or `n=120` and 1 Mio. sim’s (see the call under examples) on a machine with an Intel core i7 processor.

Thus be patient and go for a cup of coffee if you use this function with higher sample sizes and aim for estimating the type 1 error!

**Author(s)**

D. Labes

**References**

Food and Drug Administration, Office of Generic Drugs (OGD). *Draft Guidance on Progesterone*. Recommended Apr 2010. Revised Feb 2011. [download](#)

Tóthfalusi L, Endrényi L. *An Exact Procedure for the Evaluation of Reference-Scaled Average Bioequivalence*. AAPS J. 2016;18(2):476–89. doi: [10.1208/s1224801698736](https://doi.org/10.1208/s1224801698736).

Tóthfalusi L, Endrényi L. *Algorithms for evaluating reference scaled average bioequivalence: power, bias, and consumer risk*. Stat Med. 2017;36(27):4378–4390. doi: [10.1002/sim.7440](https://doi.org/10.1002/sim.7440)

**See Also**

[power.RSABE](#), [reg\\_const](#)

**Examples**

```
# Not run due to timing policy of CRAN
```

```

# pure EMA settings without mixed procedure, cap on widening and PE constraint
# as in the reference from 2017
reg          <- reg_const("EMA")
reg$CVswitch <- 0
reg$CVcap    <- Inf
reg$pe_constr <- FALSE
reg$name     <- "EMA pure"
power.RSABE2L.sds(CV = 0.4, n = 12, theta0 = exp(0.05),
                  design = "2x2x4", regulator = reg, nsims = 50000)

# should give:
# [1] 0.46504 (compared to 47.1% in the 2017 reference)

```

---

power.scABEL	<i>(Empirical) Power of BE decision via scaled (widened) BE acceptance limits</i>
--------------	---

---

## Description

This function performs the power calculation of the BE decision via scaled (widened) BE acceptance limits by simulations.

## Usage

```

power.scABEL(alpha = 0.05, theta1, theta2, theta0, CV, n,
             design = c("2x3x3", "2x2x4", "2x2x3"), regulator,
             nsims, details = FALSE, setseed = TRUE)

```

## Arguments

alpha	Type I error probability, significance level. Conventionally mostly set to 0.05.
theta1	Conventional lower ABE limit to be applied in the mixed procedure if CVsWR <= CVswitch. Also lower limit for the point estimate constraint. Defaults to 0.8 if not given explicitly.
theta2	Conventional upper ABE limit to be applied in the mixed procedure if CVsWR <= CVswitch. Also upper limit for the point estimate constraint. Defaults to 1.25 if not given explicitly.
theta0	'True' or assumed T/R ratio. Defaults to 0.90 according to the two Lászlós if not given explicitly.
CV	Intra-subject coefficient(s) of variation as ratio (not percent). <ul style="list-style-type: none"> <li>If given as a scalar (length(CV)==1) the <i>same</i> CV of Test and Reference is assumed (homoscedasticity, CVwT==CVwR).</li> <li>If given as a vector (length(CV)==2), <i>i.e.</i>, assuming heteroscedasticity, the CV of the Test <b>must</b> be given in CV[1] and the one of the Reference in the CV[2].</li> </ul>

n	<p>Number of subjects under study.</p> <p>May be given as vector. In that case it is assumed that n contains the number of subjects in the sequence groups.</p> <p>If n is given as single number (total sample size) and this number is not divisible by the number of sequences of the design an unbalanced design is assumed. A corresponding message is thrown showing the numbers of subjects in sequence groups.</p> <p>Attention! In case of the "2x2x3" (TRT RTR) design the order of sample sizes is important if given as vector. n[1] is for sequence group 'TRT' and n[2] is for sequence group 'RTR'.</p>
design	<p>Design of the study.</p> <p>"2x3x3" is the partial replicate design.</p> <p>"2x2x4" is a full replicate design with 2 sequences and 4 periods.</p> <p>"2x2x3" is a full replicate design with 2 sequences and 3 periods.</p> <p>Defaults to "2x3x3". Details are given the section about Designs.</p>
regulator	<p>Regulatory settings for the widening of the BE acceptance limits.</p> <p>May be given as character from the choices "EMA", "HC", "FDA", "GCC" or as an object of class 'regSet' (see <a href="#">reg_const</a>).</p> <p>Defaults to regulator="EMA" if missing.</p> <p>This argument may be given also in lower case if given as character.</p>
nsims	<p>Number of simulations to be performed to obtain the empirical power. Defaults to 100,000 = 1e+05.</p> <p>If not given and theta0 equals one of the expanded limits (<i>i.e.</i>, simulating empirical alpha), defaults to 1e+06.</p>
details	<p>If set to TRUE the computational time is shown as well as the components for the BE decision.</p> <p>p(BE-wABEL) is the probability that the CI is within (widened) limits.</p> <p>p(BE-PE) is the probability that the point estimate is within theta1 ... theta2.</p> <p>p(BE-ABE) is the simulated probability for the conventional ABE test.</p>
setseed	<p>Simulations are dependent on the starting point of the (pseudo) random number generator. To avoid differences in power for different runs a <code>set.seed()</code> is issued if <code>setseed=TRUE</code>, the default.</p>

## Details

The methods rely on the analysis of log-transformed data, *i.e.*, assume a log-normal distribution on the original scale.

The widened BE acceptance limits will be calculated by the formula

$$[L, U] = \exp(-/+ r\_const * sWR)$$

with `r_const` the regulatory constant and `sWR` the standard deviation of the within subjects variability of the Reference. `r_const = 0.76` ( $-\log(1.25)/0.29356$ ) is used in case of `regulator="EMA"` or `regulator="HC"` and in case of `regulator="FDA"` `r_const = 0.89257...` ( $\log(1.25)/0.25$ ). If the `CVwR` of the Reference is  $< CVswitch=0.3$  the conventional ABE limits apply (mixed procedure).

In case of `regulator="EMA"` a cap is placed on the widened limits if `CVwR>0.5`, *i.e.*, the widened

limits are held at value calculated for CVwR=0.5. In case of regulator="HC" the capping is done such that the acceptance limits are 0.6666 ... 1.5 at maximum.

The case of regulator="GCC" is treated as special case of ABEL with CVswitch = CVcap = 0.3. The  $r\_const = \log(1.25)/CV2se(0.3)$  assures that for CV>0.3 the widened BE limits of 0.7 ... 1.3333 are used.

The simulations are done via the distributional properties of the statistical quantities necessary for deciding BE based on widened ABEL.

For more details see the document Implementation\_scaledABE\_simsVx.yy.pdf in the /doc sub-directory of the package.

Function `power.scABEL()` implements the simulation via distributional characteristics of the 'key' statistics obtained from the EMA recommended evaluation via ANOVA if regulator="EMA" or if the regulator component `est_method` is set to "ANOVA" if regulator is an object of class 'regSet'. Otherwise the simulations are based on the distributional characteristics of the 'key' statistics obtained from evaluation via intra-subject contrasts (ISC), as recommended by the FDA.

### Value

Returns the value of the (empirical) power if argument `details=FALSE`.

Returns a named vector if argument `details=TRUE`.

`p(BE)` is the power, `p(BE-ABEL)` is the power of the widened ABEL criterion alone and `p(BE-pe)` is the power of the criterion 'point estimate within acceptance range' alone. `p(BE-ABE)` is the power of the conventional ABE test given for comparative purposes.

### Designs

Although some designs are more 'popular' than others, power calculations are valid for *all* of the following designs:

```
"2x2x4"  TRTR | RTRT
          TRRT | RTTR
          TTRR | RRTT
"2x2x3"  TRT | RTR
          TRR | RTT
"2x3x3"  TRR | RTR | RRT
```

### Warning

Cross-validation of the simulations as implemented here and via the 'classical' subject data simulation have shown somewhat unsatisfactory results for the 2x3x3 design if the variabilities for Test and Reference are different and/or sequences extremely unbalanced.

The function `power.scABEL()` therefore gives a warning if calculations with different CVwT and CVwR are requested for the 2x3x3 partial replicate design. For "EMA" subject simulations are provided in [power.scABEL.sdsims](#). For more details see the above mentioned document [Implementation\\_scaledABE\\_simsVy.xx.pdf](#).

**Note**

In case of regulator="FDA" the (empirical) power is only approximate since the BE decision method is not exactly what is expected by the FDA. But the "Two Laszlós" state that the scABEL method should be 'operational equivalent' to the FDA method.

To get the power for the FDA favored method via linearized scaled ABE criterion use function [power.RSABE](#).

In case of regulator="HC" (based on ISC), power is also only approximative since Health Canada recommends an evaluation via mixed model approach. This could only implemented via subject data simulations which are very time consuming. But ISC may be a good substitute.

**Author(s)**

D. Labes

**References**

Tóthfalusi L, Endrényi L. *Sample Sizes for Designing Bioequivalence Studies for Highly Variable Drugs*. J Pharm Pharmaceut Sci. 2011;15(1):73–84. [open source](#)

**See Also**

[sampleN.scABEL](#), [power.RSABE](#), [reg\\_const](#)

**Examples**

```
# using all the defaults:
# design="2x3x3", EMA regulatory settings
# PE constraint 0.8-1.25, cap on widening if CV>0.5
# true ratio=0.90, 1E+6 simulations
power.scABEL(CV = 0.4, n = 29)
# should give:
# Unbalanced design. n(i)=10/10/9 assumed.
# [1] 0.66113
#
# with details=TRUE to view the computational time and components
power.scABEL(CV = 0.5, n = 54, theta0 = 1.15, details = TRUE)
# should give (times may differ depending on your machine):
# 1e+05sims. Time elapsed (sec): 0.07
#
#      p(BE) p(BE-wABEL)    p(BE-pe)  p(BE-ABE)
# 0.81727  0.82078      0.85385    0.27542
#
# exploring 'pure ABEL' with the EMA regulatory constant
# (without mixed method, without capping, without pe constraint)
rs      <- reg_const("EMA")
rs$CVswitch <- 0
rs$CVcap   <- Inf
rs$pe_constr <- FALSE
power.scABEL(CV = 0.5, n = 54, theta0 = 1.15, regulator = rs)
# should give
```



```
# [1] 0.8519
```

---

```
power.scABEL.sds      (Empirical) Power of BE decision via scaled (widened) BE acceptance
                      limits
```

---

## Description

This function performs the power calculation of the BE decision via scaled (widened) BE acceptance limits based on **subject data** simulations.  
This function has an alias `power.scABEL.sds()`.

## Usage

```
power.scABEL.sdsims(alpha = 0.05, theta1, theta2, theta0, CV, n,
                    design = c("2x3x3", "2x2x4", "2x2x3"), design_dta=NULL,
                    regulator, nsims = 1e+05, details = FALSE, setseed = TRUE,
                    progress)
```

## Arguments

alpha	Type I error probability, significance level. Conventionally mostly set to 0.05.
theta1	Conventional lower ABE limit to be applied in the mixed procedure if CV <sub>SWR</sub> ≤ CV <sub>switch</sub> . Also lower limit for the point estimate constraint. Defaults to 0.8 if not given explicitly.
theta2	Conventional upper ABE limit to be applied in the mixed procedure if CV <sub>SWR</sub> ≤ CV <sub>switch</sub> . Also upper limit for the point estimate constraint. Defaults to 1.25 if not given explicitly.
theta0	'True' or assumed T/R ratio. Defaults to 0.90 according to the two Lászlós if not given explicitly.
CV	Intra-subject coefficient(s) of variation as ratio (not percent). <ul style="list-style-type: none"> <li>• If given as a scalar (<code>length(CV)==1</code>) the <i>same</i> CV of Test and Reference is assumed (homoscedasticity, CV<sub>wT</sub>==CV<sub>wR</sub>).</li> <li>• If given as a vector (<code>length(CV)==2</code>), <i>i.e.</i>, assuming heteroscedasticity, the CV of the Test <b>must</b> be given in CV[1] and the one of the Reference in the CV[2].</li> </ul>
n	Number of subjects under study. May be given as vector. In that case it is assumed that n contains the number of subjects in the sequence groups. If n is given as single number (total sample size) and this number is not divisible by the number of sequences of the design an unbalanced design is assumed. A corresponding message is thrown showing the numbers of subjects in sequence groups. Attention! In case of the "2x2x3" (TRT RTR) design the order of sample sizes is important if given as vector. n[1] is for sequence group 'TRT' and n[2] is for sequence group 'RTR'.

design	<p>Design of the study to be planned.  "2x3x3" is the partial replicate design (TRRIRTRIRRT).  "2x2x4" is the full replicate design with 2 sequences and 4 periods.  "2x2x3" is the 3-period design with sequences TRTIRTR.  Defaults to design="2x3x3".</p>
design_dta	<p>Alternatively to using the arguments design and n the design may be defined via a data.frame with columns subject, sequence, period and tmt. This feature is experimental in the sense that the data.frame is not checked for complying with the assumed structure.  If you use the argument design_dta you don't need to specify the arguments design and n.  The default design_dta = NULL means that design and n are used for the internal construction of the design data.frame.</p>
regulator	<p>Regulatory settings for the widening of the BE acceptance limits.  May be given as "EMA" or as an object of class 'regSet' (see <a href="#">reg_const</a>).  Defaults to regulator="EMA" if missing.  This argument may be given also in lower case if given as character.</p> <p>If given as object of class 'regSet' the component est_method must not be "ISC".</p>
nsims	<p>Number of simulations to be performed to obtain the empirical power. Defaults to 100,000 = 1e+05.  If simulations are aimed for empirical alpha nsims=1e+06 is recommended.</p>
details	<p>If set to TRUE the computational time is shown as well as the components for the BE decision.  p(BE-wABEL) is the probability that the CI is within (widened) limits.  p(BE-PE) is the probability that the point estimate is within theta1 ... theta2.  p(BE-ABE) is the simulated probability for the conventional ABE test.</p>
setseed	<p>Simulations are dependent on the starting point of the (pseudo) random number generator. To avoid differences in power for different runs a set.seed() is issued if setseed=TRUE, the default.</p>
progress	<p>Should a progressbar be shown? Defaults to TRUE if missing and nsims &gt;5E5.</p>

## Details

The methods rely on the analysis of log-transformed data, *i.e.*, assume a log-normal distribution on the original scale.

The widened BE acceptance limits will be calculated by the formula

$$[L, U] = \exp(\pm r\_const * sWR)$$

with r\_const the regulatory constant and sWR the standard deviation of the within subjects variability of the Reference. r\_const = 0.76 ( $-\log(1.25)/0.29356$ ) is used in case of regulator="EMA". If the CVwR of the Reference is < CVswitch=0.3 the conventional ABE limits apply (mixed procedure).

In case of regulator="EMA" a cap is placed on the widened limits if CVwr>0.5, *i.e.*, the widened limits are held at value calculated for CVwR=0.5.

The simulations are done by simulating subject data (all effects fixed except the residuals) and evaluating these data via ANOVA of all data to get the point estimate of T vs. R along with its 90% CI and an ANOVA of the data under R(eference) only to get an estimate of  $s^2_{wR}$ .

The data.frame with columns subject, sequence, period and tmt necessary for evaluation of simulated subject data is constructed internally from the arguments design and n or may be given user defined via the argument design\_dta. The last option is usefull if missing data have to be considered or if designs have to be evaluated which are not in the list of argument design.

This feature is experimental in the sense that the data.frame is not checked for complying with the assumed structure.

### Value

Returns the value of the (empirical) power if argument details=FALSE.

Returns a named vector if argument details=TRUE.

p(BE) is the power, p(BE-wABEL) is the power of the widened ABEL criterion alone and p(BE-pe) is the power of the criterion 'point estimat within acceptance range' alone. p(BE-ABE) is the power of the conventional ABE test given for comparative purposes.

### Note

The function is mainly intended for crosscheck of power.scABEL() results.

But may be mandatory for cases where power.scABEL() results are inaccurate (low sample sizes and/or heteroscedasticity).

It is relatively slow. The run-time of this function doing 1 Mio sims is between ~ 7-8 sec for n=12 and ~ 3-4 min for n=120 on a machine with an Intel core i7 processor.

Thus be patient and go for a cup of coffee if you use this function with high sample sizes!

### Author(s)

D. Labes, B. Lang

### References

Tóthfalusi L, Endrényi L. *Sample Sizes for Designing Bioequivalence Studies for Highly Variable Drugs*. J Pharm Pharmaceut Sci. 2011;15(1):73–84. [open source](#)

### See Also

[power.scABEL](#), [reg\\_const](#)

### Examples

```
# using all the defaults:
# design="2x3x3", EMA regulatory settings
# PE constraint 0.8-1.25, cap on widening if CV>0.5
# true ratio=0.90, 1E+5 simulations
power.scABEL.sdsims(CV = 0.4, n = 36)
# should give:
# [1] 0.74321
```

power.TOST

*Power of the classical TOST procedure***Description**

Calculates the exact or approximate power of the two-one-sided t-tests (TOST) procedure for various study designs used in BE studies.

**Usage**

```
power.TOST(alpha = 0.05, logscale = TRUE, theta1, theta2, theta0, CV, n,
           design = "2x2", method="exact", robust=FALSE)
```

**Arguments**

alpha	Significance level (one-sided). Commonly set to 0.05.
logscale	Should the data used on log-transformed or on original scale? TRUE (default) or FALSE.
theta0	‘True’ or assumed T/R ratio or difference. In case of logscale=TRUE it must be given as ratio T/R. If logscale=FALSE, the difference in means. In this case, the difference may be expressed in two ways: relative to the same (underlying) reference mean, i.e. as $(T-R)/R = T/R - 1$ ; or as difference in means T-R. Note that in the former case the units of CV, theta1 and theta2 need also be given relative to the reference mean (specified as ratio). Defaults to 0.95 if logscale=TRUE or to 0.05 if logscale=FALSE
theta1	Lower (bio-)equivalence limit. In case of logscale=TRUE it is given as ratio. If logscale=FALSE, the limit may be expressed in two ways: difference of means relative to the same (underlying) reference mean or in units of the difference of means. Note that in the former case the units of CV, theta0 and theta2 need also be given relative to the reference mean (specified as ratio). Defaults to 0.8 if logscale=TRUE or to -0.2 if logscale=FALSE.
theta2	Upper (bio-)equivalence limit. In case of logscale=TRUE it is given as ratio. If logscale=FALSE, the limit may be expressed in two ways: difference of means relative to the same (underlying) reference mean or in units of the difference of means. Note that in the former case the units of CV, theta0 and theta1 need also be given relative to the reference mean (specified as ratio). If not given, theta2 will be calculated as $1/\theta_1$ if logscale=TRUE or as $-\theta_1$ if logscale=FALSE.
CV	In case of logscale=TRUE the (geometric) coefficient of variation given as ratio. If logscale=FALSE the argument refers to (residual) standard deviation of the response. In this case, standard deviation may be expressed two ways: relative to a reference mean (specified as ratio $\sigma/\mu_R$ ), i.e. again as a coefficient of

variation; or untransformed, i.e. as standard deviation of the response. Note that in the former case the units of  $\theta_0$ ,  $\theta_1$  and  $\theta_2$  need also be given relative to the reference mean (specified as ratio).

In case of cross-over studies this is the within-subject CV, in case of a parallel-group design the CV of the total variability.

n	Number of subjects under study. Is total number if given as scalar, else number of subjects in the (sequence) groups. In the latter case the length of n vector has to be equal to the number of (sequence) groups.
design	Character string describing the study design. See <code>known.designs()</code> for designs covered in this package.
method	Method for calculation of the power. Defaults to "exact" in which case the calculation is done based on formulas with Owen's Q. The calculation via Owen's Q can also be chosen with <code>method="owenq"</code> . Another exact method via direct integration of the bivariate non-central $t$ -distribution may be chosen with <code>method="mvt"</code> . This may have somewhat lower precision compared to Owen's Q and longer run-time. Approximate calculations can be chosen via <code>method="noncentral"</code> or <code>method="nct"</code> for the approximation using the non-central $t$ -distribution. With <code>method="central"</code> or <code>method="shifted"</code> the relative crude approximation via 'shifted' central $t$ -distribution is chosen. The strings for method may be abbreviated.
robust	Defaults to FALSE. With that value the usual degrees of freedom will be used. Set to TRUE will use the degrees of freedom according to the 'robust' evaluation (aka Senn's basic estimator). These degrees of freedom are calculated as <code>n-seq</code> . See <code>known.designs()\$df2</code> for designs covered in this package. Has only effect for higher-order crossover designs.

## Details

The exact calculations of power are based on Owen's Q-function or by direct integration of the bivariate non-central  $t$ -distribution via function `pmvt` of package `mvtnorm`. Approximate power is implemented via the non-central  $t$ -distribution or the 'shifted' central  $t$ -distribution.

The formulas cover balanced and unbalanced studies w.r.t (sequence) groups.

In case of parallel group design and higher order crossover designs (replicate crossover or crossover with more than two treatments) the calculations are based on the assumption of equal variances for Test and Reference products under consideration.

The formulas for the paired means 'design' do not take a correlation parameter into account. They are solely based on the paired  $t$ -test (TOST of differences = zero).

**Value**

Value of power according to the input arguments.

**Note**

Of course it is highly recommended to use the default method="exact" :-).  
There is no reason beside testing and for comparative purposes to use an approximation if the exact method is available.

If n is given as scalar (total sample size) and this number is not divisible by the number of (sequence) groups of the design an unbalanced design with small imbalance is assumed. A corresponding message is thrown showing the assumed numbers of subjects in (sequence) groups.  
The function does not vectorize properly if design is a vector.  
The function vectorizes properly if CV or theta0 are vectors.  
Other vector input is not tested yet.

The former function power2.TOST() designed to handle unbalanced studies is defunct since power.TOST() handles balanced as well as unbalanced designs.

**Author(s)**

D. Labes, direct integration of bivariate non-central *t*-distribution by B. Lang

**References**

- Phillips KF. *Power of the Two One-Sided Tests Procedure in Bioequivalence*. J Pharmacokin Bio-pharm. 1990;18(2):137–44. doi: [10.1007/BF01063556](https://doi.org/10.1007/BF01063556)
- Diletti D, Hauschke D, Steinijs VW. *Sample Size Determination for Bioequivalence Assessment by Means of Confidence Intervals*. Int J Clin Pharmacol Ther Toxicol. 1991;29(1):1–8.

**See Also**

[sampleN.TOST](#), [known.designs](#)

**Examples**

```
# power for the 2x2 cross-over design with 24 subjects and CV 25%
# using all the other default values
power.TOST(CV = 0.25, n = 24)
# should give: [1] 0.7391155
# nct approximation very good for this configuration
power.TOST(CV = 0.25, n = 24, method = "nct")
# gives also: [1] 0.7391155
# shifted-central-t approximation
power.TOST(CV = 0.25, n = 24, method = "shifted")
# gives:      [1] 0.7328894

# power for the 2x2 cross-over study with 24 subjects, CV 25%
# and 2 drop-outs in the same sequence group (unbalanced study)
power.TOST(CV=0.25, n=c(10,12))
```

```
# should give: [1] 0.6912935
# not the same compared to the balanced setting
power.TOST(CV=0.25, n=22)
# should give: [1] 0.6953401
```

---

power.TOST.sds	<i>Power calculation of the BE decision with models incorporating groups</i>
----------------	--

---

## Description

The power is obtained via subject data simulations.  
Three models are implemented:

- `gmodel==1` is full FDA model for testing group-by-treatment interaction followed by `gmodel==2` or `gmodel==3` with data of the biggest group depending on the test of the treatment by group interaction
- `gmodel==2` is full FDA model but without group-by-treatment interaction
- `gmodel==3` is model with pooled groups, i.e. without any group term

## Usage

```
power.TOST.sds(alpha = 0.05, theta1, theta2, theta0, CV, n,
               design = c("2x2", "2x2x2", "2x3x3", "2x2x4", "2x2x3"),
               design_dta = NULL, grps = 2, ngrp = NULL, gmodel = 2,
               nsims = 1e+05, details = FALSE, setseed = TRUE, progress)
```

## Arguments

alpha	Type I error probability, significance level. Conventionally mostly set to 0.05.
theta1	Lower BE limit. Defaults to 0.8 if not given explicitly.
theta2	Upper BE limit. Defaults to 1.25 if not given explicitly.
theta0	'True' or assumed T/R ratio. Defaults to 0.95 if not given explicitly.
CV	Intra-subject coefficient(s) of variation as ratio (not percent). <ul style="list-style-type: none"> <li>• If given as a scalar (<code>length(CV)==1</code>) the <i>same</i> CV of Test and Reference is assumed (homoscedasticity, <code>CVwT==CVwR</code>).</li> <li>• If given as a vector (<code>length(CV)==2</code>), <i>i.e.</i>, assuming heteroscedasticity, the CV of the Test <b>must</b> be given in <code>CV[1]</code> and the one of the Reference in the <code>CV[2]</code>.</li> </ul>
n	Number of subjects under study. May be given as vector. In that case it is assumed that n contains the number of subjects in the sequence groups. If n is given as single number (total sample size) and this number is not divisible by the number of sequences of the design an unbalanced design is assumed. A

corresponding message is thrown showing the numbers of subjects in sequence groups.

Attention! In case of the "2x2x3" (TRT|RTR) design the order of sample sizes is important if given as vector. `n[1]` is for sequence group 'TRT' and `n[2]` is for sequence group 'RTR'.

<code>design</code>	<p>Design of the study to be planned.</p> <p>"2x2" or "2x2x2" is the conventional cross-over design.</p> <p>"2x3x3" is the partial replicate design (TRR RTR RRT).</p> <p>"2x2x4" is the full replicate design with 2 sequences and 4 periods.</p> <p>"2x2x3" is the 3-period design with sequences TRT RTR.</p> <p>Defaults to <code>design="2x2"</code>.</p>
<code>design_dta</code>	<p>Alternatively to using the arguments <code>design</code> and <code>n</code> the design may be defined via a data.frame with columns <code>subject</code>, <code>sequence</code>, <code>period</code> and <code>tmt</code>. This feature is experimental in the sense that the data.frame is not checked for complying with the assumed structure.</p> <p>If you use the argument <code>design_dta</code> you don't need to specify the arguments <code>design</code> and <code>n</code>.</p> <p>The default <code>design_dta = NULL</code> means that <code>design</code> and <code>n</code> are used for the internal construction of the design data.frame.</p>
<code>grps</code>	Number of (logistical) groups. Defaults to 2.
<code>ngrp</code>	Vector of number of subjects in groups.
<code>gmodel</code>	<p>Number describing the model incorporating group effects</p> <ul style="list-style-type: none"> <li>• <code>gmodel=1</code> is full FDA model for testing group-by-treatment interaction followed by <code>gmodel=2</code> or <code>gmodel=3</code> with data of the biggest group depending on the test of the treatment by group interaction</li> <li>• <code>gmodel=2</code> is full FDA model but without group-by-treatment interaction</li> <li>• <code>gmodel=3</code> is model with pooled groups, i.e. without any group term</li> </ul> <p>Defaults to <code>gmodel=2</code>.</p>
<code>nsims</code>	<p>Number of simulations to be performed to obtain the empirical power. Defaults to 100,000 = 1e+05.</p> <p>If simulations are aimed for empirical alpha <code>nsims=1e+06</code> is recommended.</p>
<code>details</code>	If set to TRUE the computational time is shown.
<code>setseed</code>	<p>Simulations are dependent on the starting point of the (pseudo) random number generator. To avoid differences in power for different runs a <code>set.seed(123456)</code> is issued if <code>setseed=TRUE</code>, the default.</p>
<code>progress</code>	Should a progressbar be shown? Defaults to TRUE if missing and <code>nsims &gt; 5E5</code> .

## Details

The power is calculated via subject data `sims`.

The evaluation of BE is done via  $1-2*\alpha$  confidence interval using classical ANOVA for the models with group effects.

The data.frame with columns `subject`, `sequence`, `period` and `tmt` necessary for evaluation of simulated subject data is constructed internally from the arguments `design` and `n` or may be given user



defined via the argument `design_dta`. The last option is useful if missing data have to be considered or if designs have to be evaluated which are not in the list of argument `design`. This feature is experimental in the sense that the `data.frame` is not checked for complying with the assumed structure.

### Value

Returns the value of the (empirical) power

### Note

The run time of the function may be relatively long.  
Take a cup of coffee and be patient.

### Author(s)

D. Labes

### References

Schütz H.  
*Multi-Group Studies in Bioequivalence. To pool or not to pool?*  
Presentation at BioBriges 2018, Prague. <https://bebac.at/lectures/Prague2018.pdf>

### Examples

```
# power for gmodel=2, 2x2 crossover, grps=3 with even number of subjects
power.TOST.sds(CV=0.2, n=18, grps=3)
# gives [1] 0.78404
# without considering groups
power.TOST.sds(CV=0.2, n=18, gmodel=3)
# gives [1] 0.7887
```

---

power.TOST.sim

*Power of the TOST procedure obtained via simulations*

---

### Description

Power is calculated by simulations of studies (PE via its normal distribution, MSE via its associated  $\chi^2$  distribution) and application of the two one-sided *t*-tests. Power is obtained via ratio of studies found BE to the number of simulated studies.

### Usage

```
power.TOST.sim(alpha = 0.05, logscale = TRUE, theta1, theta2, theta0, CV, n,
               design = "2x2", robust = FALSE, setseed = TRUE, nsims = 1e+05)
```

**Arguments**

alpha	Significance level (one-sided). Commonly set to 0.05.
logscale	Should the data used on log-transformed or on original scale? TRUE (default) or FALSE.
theta0	<p>‘True’ or assumed T/R ratio or difference.</p> <p>In case of logscale=TRUE it must be given as ratio T/R.</p> <p>If logscale=FALSE, the difference in means. In this case, the difference may be expressed in two ways: relative to the same (underlying) reference mean, i.e. as <math>(T-R)/R = T/R - 1</math>; or as difference in means T-R. Note that in the former case the units of CV, theta1 and theta2 need also be given relative to the reference mean (specified as ratio).</p> <p>Defaults to 0.95 if logscale=TRUE or to 0.05 if logscale=FALSE</p>
theta1	<p>Lower (bio-)equivalence limit.</p> <p>In case of logscale=TRUE it is given as ratio.</p> <p>If logscale=FALSE, the limit may be expressed in two ways: difference of means relative to the same (underlying) reference mean or in units of the difference of means. Note that in the former case the units of CV, theta0 and theta2 need also be given relative to the reference mean (specified as ratio).</p> <p>Defaults to 0.8 if logscale=TRUE or to -0.2 if logscale=FALSE.</p>
theta2	<p>Upper (bio-)equivalence limit.</p> <p>In case of logscale=TRUE it is given as ratio. If logscale=FALSE, the limit may be expressed in two ways: difference of means relative to the same (underlying) reference mean or in units of the difference of means. Note that in the former case the units of CV, theta0 and theta1 need also be given relative to the reference mean (specified as ratio).</p> <p>If not given, theta2 will be calculated as <math>1/\theta_1</math> if logscale=TRUE or as <math>-\theta_1</math> if logscale=FALSE.</p>
CV	<p>In case of logscale=TRUE the (geometric) coefficient of variation given as ratio. If logscale=FALSE the argument refers to (residual) standard deviation of the response. In this case, standard deviation may be expressed two ways: relative to a reference mean (specified as ratio <math>\sigma/\mu_R</math>), i.e. again as a coefficient of variation; or untransformed, i.e. as standard deviation of the response. Note that in the former case the units of theta0, theta1 and theta2 need also be given relative to the reference mean (specified as ratio).</p> <p>In case of cross-over studies this is the within-subject CV, in case of a parallel-group design the CV of the total variability.</p>
n	<p>Number of subjects under study.</p> <p>Is total number if given as scalar, else number of subjects in the (sequence) groups. In the latter case the length of n vector has to be equal to the number of (sequence) groups.</p>
design	<p>Character string describing the study design.</p> <p>See known.designs() for designs covered in this package.</p>
robust	<p>Defaults to FALSE. With that value the usual degrees of freedom will be used. Set to TRUE will use the degrees of freedom according to the ‘robust’ evaluation</p>

	(aka Senn's basic estimator). These degrees of freedom are calculated as $n - \text{seq}$ . See <code>known.designs()\$df2</code> for designs covered in this package. Has only effect for higher-order crossover designs.
setseed	Simulations are dependent on the starting point of the (pseudo) random number generator. To avoid differences in power for different runs a <code>set.seed(1234567)</code> is issued if <code>setseed=TRUE</code> , the default. Set this argument to <code>FALSE</code> to view the variation in power between different runs.
nsims	Number of studies to simulate. Defaults to 100,000 = 1E5.

**Value**

Value of power according to the input arguments.

**Note**

This function was intended for internal check of the analytical power calculation methods. Use of the analytical power calculation methods (`power.TOST()`) for real problems is recommended. For sufficient precision `nsims > 1E5` (default) may be necessary. Be patient if using `nsims=1E6`. May take some seconds.

**Author(s)**

D. Labes

**See Also**

[power.TOST](#),

**Examples**

```
# using the default design 2x2, BE range 0.8 ... 1.25, logscale, theta=0.95
power.TOST.sim(alpha = 0.05, CV = 0.3, n = 12)
# should give 0.15054, with nsims=1E6 it will be 0.148533
# exact analytical is
power.TOST(alpha = 0.05, CV = 0.3, n = 12)
# should give 0.1484695

# very unusual alpha setting
power.TOST.sim(alpha = 0.9, CV = 0.3, n = 12)
# should give the same (within certain precision) as
power.TOST(alpha = 0.95, CV = 0.3, n = 12)
# or also within certain precision equal to
power.TOST(alpha = 0.95, CV = 0.3, n = 12, method = "mvt")
# SAS Proc Power gives here the incorrect value 0.60525
```

---

pvalue.TOST                      *p-value(s) of the TOST procedure*

---

### Description

Calculates the *p*-value(s) of the TOST procedure via students *t*-distribution given pe, CV and n.

### Usage

```
pvalue.TOST(pe, CV, n, logscale = TRUE, theta1, theta2, design = "2x2",
            robust = FALSE, both = FALSE)
pvalues.TOST(pe, CV, n, logscale = TRUE, theta1, theta2, design = "2x2",
            robust = FALSE, both = TRUE)
```

### Arguments

pe	Observed point estimate of the T/R ratio or difference. In case of logscale=TRUE it must be given as ratio T/R. If logscale=FALSE, the observed difference in means. In this case, the difference may be expressed in two ways: relative to the same (underlying) reference mean, i.e. as $(T-R)/R = T/R - 1$ ; or as difference in means T-R. Note that in the former case the units of CV, theta1 and theta2 need also be given relative to the reference mean (specified as ratio).
CV	In case of logscale=TRUE the observed (geometric) coefficient of variation given as ratio. If logscale=FALSE the argument refers to the observed (residual) standard deviation of the response. In this case, standard deviation may be expressed two ways: relative to a reference mean (specified as ratio sigma/muR), i.e. again as a coefficient of variation; or untransformed, i.e. as standard deviation of the response. Note that in the former case the units of pe, theta1 and theta2 need also be given relative to the reference mean (specified as ratio).
n	In case of cross-over studies this is the within-subject CV, in case of a parallel-group design the CV of the total variability. Total number of subjects if given as scalar. Number of subjects in (sequence) groups if given as vector.
logscale	Should the data be used after log-transformation or on original scale? TRUE or FALSE. Defaults to TRUE.
theta1	Lower (bio-)equivalence limit. In case of logscale=TRUE it is given as ratio. If logscale=FALSE, the limit may be expressed in two ways: difference of means relative to the same (underlying) reference mean or in units of the difference of means. Note that in the former case the units of CV, pe and theta2 need also be given relative to the reference mean (specified as ratio). Defaults to 0.8 if logscale=TRUE or to -0.2 if logscale=FALSE.

theta2	Upper (bio-)equivalence limit. In case of logscale=TRUE it is given as ratio. If logscale=FALSE, the limit may be expressed in two ways: difference of means relative to the same (underlying) reference mean or in units of the difference of means. Note that in the former case the units of CV, theta0 and theta1 need also be given relative to the reference mean (specified as ratio). If not given, theta2 will be calculated as 1/theta1 if logscale=TRUE or as -theta1 if logscale=FALSE.
design	Character string describing the study design. See known.designs() for designs covered in this package.
robust	If set to TRUE triggers the use of degrees of freedom according to the ‘robust’ evaluation (aka Senn’s basic estimator). These degrees of freedom are calculated as n-seq. See known.designs()\$df2. Has only effect for higher-order crossover designs. Defaults to FALSE. With that value the usual degrees of freedom will be used.
both	Indicates if both $p$ -values ( $t$ -tests of $p_e \geq \theta_1$ and $p_e \leq \theta_2$ ) shall be given back or only the maximum. Defaults to FALSE for the function pvalue.TOST() and to TRUE for the function pvalues.TOST().

### Value

Returns the  $p$ -value(s).  
Returns a vector with named elements p.left, p.right if arguments pe and CV are scalars, else a matrix with columns p.left, p.right.  
p.left gives the  $p$ -value of testing  
HA1:  $\theta \geq \theta_1$   
and p.right the  $p$ -value of testing  
HA2:  $\theta \leq \theta_2$   
against their respective Nulls.

### Note

The formulas implemented cover balanced and unbalanced designs.

In case of argument n given as n(total) and is not divisible by the number of (sequence) groups the total sample size is partitioned to the (sequence) groups to have small imbalance only. A message is given in such cases.

SAS procedure TTEST with the TOST option names p.left = Upper, p.right= Lower according to the tail of the  $t$ -distribution to be used for obtaining the  $p$ -values.

### Author(s)

B. Lang, man page by D. Labes

## References

Schuurmann DJ. *A comparison of the two one-sided tests procedure and the power approach for assessing the equivalence of average bioavailability*. J Pharmacokin Biopharm. 1987;15:657–80. doi: [10.1007/BF01068419](https://doi.org/10.1007/BF01068419)

Hauschke D, Steinijans V, Pigeot I. *Bioequivalence Studies in Drug Development*. Chichester: Wiley; 2007.

## See Also

[CI.BE](#)

## Examples

```
# Defaults: 2x2 crossover, log-transformation
# BE acceptance limits 0.8 ... 1.25, usual dfs
# interested in both p-values
pvalues.TOST(pe = 0.95, CV = 0.3, n = 12)
# gives the vector (named elements)
#   p.left   p.right
# 0.09105601 0.02250985
# i.e. 'left' hypothesis H01: theta<=theta1 can't be rejected
# 'right' hypothesis H02: theta>=theta2 can be rejected

# max. p-value only as 'overall' pvalue, preferred by Benjamin
pvalue.TOST(pe = 0.912, CV = 0.333, n = 24)
# should give 0.08777621, i.e., inequivalence can't be rejected
# this is operationally identical to
CI.BE(pe = 0.912, CV = .333, n = 24)
# lower limit = 0.7766 outside 0.8 ... 1.25, i.e., inequivalence can't be rejected
```

---

reg_const	<i>Constructor of an object with class 'regSet' containing the regulatory settings for ABEL</i>
-----------	---

---

## Description

This function may be used to define regulatory settings not implemented yet in PowerTOST.

## Usage

```
reg_const(regulator, r_const, CVswitch, CVcap, pe_constr)
```

## Arguments

regulator	Name of the regulatory body as a string. Implemented settings are for "EMA", "FDA", "HC", and "GCC". The former (inofficial) settings for "ANVISA" are covered by the EMA settings. In case of regulator="USER" the other arguments must be given. Otherwise, they may be missing.
-----------	---

r_const	Regulatory constant.
CVswitch	CV to switch to the widened acceptance limits.
CVcap	CV for capping the widening of the acceptance limits.
pe_constr	Logical. Shall pe constraint be applied? Defaults to TRUE.

**Value**

Returns an object of class 'regSet', a list with components

name	Name of the settings
CVswitch	see arguments
r_const	Regulatory constant
CVcap	see arguments
pe_constr	see arguments
est_method	"ANOVA" or "ISC"

Class 'regSet' has a S3 print method.

The component est\_method is automatically set to "ANOVA", except for regulator="FDA" or regulator="HC" where "ISC" is used.

**Note**

The former unofficial regulatory settings for regulator="ANVISA" are covered by regulator="EMA" (see the [BEBA Forum, May 2016](#)).

The settings for CVcap of Health Canada (regulator="HC") were chosen in such a way that the limits of the acceptance range are capped nearly exact to 1/1.5 up to 1.5. Literally it is given rounded to 3 significant digits ([Health Canada, April 18, 2016](#)).

**Author(s)**

D. Labes

**Examples**

```
# to retrieve the EMA settings
reg_const("EMA")
# to define the old ANVISA settings
reg      <- reg_const("USER", r_const = 0.76, CVswitch = 0.4, CVcap = 0.5)
reg$name <- "Old ANVISA"
# Use reg as argument in the scaled ABEL power / sample size functions for
```

sampleN.2TOST

*Sample size based on power of two TOSTs***Description**

Estimates the necessary sample size to have at least a given power when two parameters are tested simultaneously.

**Usage**

```
sampleN.2TOST(alpha = c(0.05, 0.05), targetpower = 0.8, logscale = TRUE,
              theta0, theta1, theta2, CV, rho, design = "2x2", setseed = TRUE,
              robust = FALSE, print = TRUE, details = FALSE, imax = 100,
              nsims = 1e+05)
```

**Arguments**

alpha	Vector; contains one-sided significance level for each of the two TOSTs. For one TOST, by convention mostly set to 0.05.
targetpower	Power to achieve at least. Must be >0 and <1. Typical values are 0.8 or 0.9.
logscale	Should the data used on log-transformed or on original scale? TRUE (default) or FALSE.
theta0	Vector; contains 'true' assumed T/R ratio for each of the two TOSTs. In case of logscale=TRUE each element must be given as ratio, otherwise as difference to 1. See examples. Defaults to c(0.95, 0.95) if logscale=TRUE or to c(0.05, 0.05) if logscale=FALSE.
theta1	Vector; contains lower bioequivalence limit for each of the two TOSTs. In case of logscale=TRUE it is given as ratio, otherwise as diff. to 1. Defaults to c(0.8, 0.8) if logscale=TRUE or to c(-0.2, -0.2) if logscale=FALSE.
theta2	Vector; contains upper bioequivalence limit for each of the two TOSTs. If not given theta2 will be calculated as 1/theta1 if logscale=TRUE or as -theta1 if logscale=FALSE.
CV	Vector of coefficient of variations (given as as ratio, e.g., 0.2 for 20%). In case of cross-over studies this is the within-subject CV, in case of a parallel-group design the CV of the total variability. In case of logscale=FALSE CV is assumed to be the respective standard deviation.
rho	Correlation between the two PK metrics (e.g., AUC and Cmax) under consideration. This is defined as correlation between the estimator of the treatment difference of PK metric one and the estimator of the treatment difference of PK metric two. Has to be within {-1, +1}.
design	Character string describing the study design. See known.designs() for designs covered in this package.



setseed	Logical; if TRUE, the default, a seed of 1234567 is set.
robust	Defaults to FALSE. With that value the usual degrees of freedom will be used. Set to TRUE will use the degrees of freedom according to the ‘robust’ evaluation (aka Senn’s basic estimator). These degrees of freedom are calculated as $n - seq$ . See <code>known.designs()\$df2</code> for designs covered in this package. Has only effect for higher-order crossover designs.
print	If TRUE (default) the function prints its results. If FALSE only the result list will be returned.
details	If TRUE the design characteristics and the steps during sample size calculations will be shown. Defaults to FALSE.
imax	Maximum number of steps in sample size search. Defaults to 100.
nsims	Number of studies to simulate. Defaults to 100,000 = 1E5.

### Details

The sample size is estimated via iterative evaluation of power of the two TOSTs. Start value for the sample size search is taken from a large sample approximation (one TOST) according to Zhang, modified.  
The sample size is bound to 4 as minimum.

The estimated sample size gives always the *total* number of subjects (not subject/sequence in crossovers or subjects/group in parallel designs – like in some other software packages).

### Value

A list with the input and results will be returned.  
The element name "Sample size" contains the total sample size.

### Warning

The function does not vectorize properly.  
If you need sample sizes with varying CVs, use `f.i.` for-loops or the `apply-family`.

### Note

If both the  $\theta$  are near the acceptance limits then the starting value may not be a good approximation resulting in a lot of iteration steps; `imax` may need to be increased to obtain the required sample size.

### Author(s)

B. Lang, D. Labes

## References

- Phillips KF. *Power for Testing Multiple Instances of the Two One-Sided Tests Procedure*. Int J Biostat. 2009;5(1):Article 15.
- Hua SY, Xu S, D'Agostino RB Sr. *Multiplicity adjustments in testing for bioequivalence*. Stat Med. 2015;34(2):215–31. doi: [10.1002/sim.6247](https://doi.org/10.1002/sim.6247)
- Lang B, Fleischer F. *Letter to the Editor: Comments on 'Multiplicity adjustments in testing for bioequivalence'*. Stat Med. 2016;35(14):2479–80. doi: [10.1002/sim.6488](https://doi.org/10.1002/sim.6488)
- Zhang P. *A Simple Formula for Sample Size Calculation in Equivalence Studies*. J Biopharm Stat. 2003;13(3):529–538. doi: [10.1081/BIP120022772](https://doi.org/10.1081/BIP120022772)

## See Also

[power.2TOST,known.designs](#)

## Examples

```
# Sample size for 2x2x2 cross-over design, intra-subject CV = 30% and assumed
# ratios of 0.95 for both parameters, and correlation 0.9 between parameters
# (using all the other default values)
# Should give n=44 with power=0.80684
sampleN.2TOST(theta0 = rep(0.95, 2), CV = rep(0.3, 2), rho = 0.9)

# Sample size for a parallel group design,
# evaluation on the original (untransformed) scale
# BE limits 80 ... 120% = -20% ... +20% of reference,
# assumed true BE ratio 0.95% = -5% to reference mean for both parameters,
# total CV=20% for both parameters, and correlation 0.9 between parameters
# should give n=54 with power=0.8149
sampleN.2TOST(logscale=FALSE, theta0 = rep(-0.05, 2), CV = c(0.2, 0.2),
              rho = 0.9, design = "parallel")
```

---

sampleN.dp

*Sample size estimation of dose-proportionality studies evaluated via the power model*

---

## Description

Performs a sample size estimation for dose-proportionality studies using the power model for crossover (Latin square), parallel group designs or incomplete block designs via a confidence interval equivalence criterion.

## Usage

```
sampleN.dp(alpha = 0.05, CV, doses, targetpower = 0.8, beta0, theta1 = 0.8,
           theta2 = 1/theta1, design = c("crossover", "parallel", "IBD"),
           dm=NULL, CVb, print = TRUE, details = FALSE, imax = 100)
```

**Arguments**

alpha	Type 1 error. Usually set to 0.05.
CV	Coefficient of variation. Is intra-subject CV for design="crossover" and CV of total variability in case of design="parallel"
doses	Vector of dose values under study. At least two doses have to be given.
targetpower	Power to achieve at least. Must be >0 and <1. Typical values are 0.8 or 0.9.
beta0	'True' or assumed slope of the power model. If missing defaults to $1+\log(0.95)/\log(\text{rd})$ where rd is the ratio of the highest to the lowest dose. Has to be within slope acceptance range according to $1+\log(\text{theta1})/\log(\text{rd})$ and $1+\log(\text{theta2})/\log(\text{rd})$ . Otherwise, the function issues an error.
theta1	Lower acceptance limit for the ratio of dose normalized means (Rdmn). Transformes into slope acceptance range as described under item beta0.
theta2	Upper acceptance limit for the ratio of dose normalized means (Rdmn).
design	Crossover design (default), parallel group design or incomplete block design (IBD). Crossover design means Latin square design with number of doses as dimension.
dm	'Design matrix' of the incomplete block design (IBD) if design="IBD". This matrix contains the sequences in rows and periods in columns. The entry (i, j) of the design matrix corresponds to the dose (index) a subject with i-th sequence gets in the j-th period. Can be obtained f.i. via functions of package crossdes. See examples. Function <a href="#">bib.CL</a> returns some IBDs described by Chow & Liu.
CVb	Coefficient of variation of the between-subject variability. Only necessary if design="IBD". Will be set to 2*CV if missing. This is only a crude rule of thumb. Better obtain an estimate of CVb from a previous crossover study.  Set CVb=0 if all-effects-fixed model shall be used. This model gives lower sample sizes than the mixed model with random subject effects (random intercept).
print	If TRUE (default) the function prints its results. If set to FALSE only the data.frame with the results will be returned.
details	If details=TRUE the steps during sample size search will be shown. Defaults to FALSE.
imax	Maximum number of steps in sample size search. Defaults to 100. Adaption only in rare cases needed, if any.

**Details**

The sample size is estimated via iterative evaluation of `power.dp()`.  
Start value for the sample size search is taken from a large sample approximation.  
The sample size is bound to number of dose or sequence groups as minimum.  
Balanced designs are used although this is not absolutely necessary.

The estimated sample size gives always the *total* number of subjects (not subject/sequence in crossovers or subjects/group in parallel designs – like in some other software packages).

**Value**

A data.frame with the input and results will be returned.  
The Sample size column contains the total sample size.

**Warning**

This function is ‘experimental’ only, since it is not thoroughly tested yet. Especially for design="IBD" reliable test cases are missing.

**Author(s)**

D. Labes

**References**

Chow SC, Liu JP. *Design and Analysis of Bioavailability and Bioequivalence Studies*. Boca Raton: CRC Press; 3<sup>rd</sup> edition 2009.

Patterson S, Jones B. *Bioequivalence and Statistics in Clinical Pharmacology*. Boca Raton: Chapman & Hall/CRC: 2006. p. 239.  
(contains presumably a bug)

Sethuraman VS, Leonov S, Squassante L, Mitchell TR, Hale MD. *Sample size calculation for the Power Model for dose proportionality studies*. Pharm Stat. 2007;6(1):35–41. doi: [10.1002/pst.241](https://doi.org/10.1002/pst.241)

Hummel J, McKendrick S, Brindley C, French R. *Exploratory assessment of dose proportionality: review of current approaches and proposal for a practical criterion*. Pharm. Stat. 2009;8(1):38–49. doi: [10.1002/pst.326](https://doi.org/10.1002/pst.326)

**See Also**

[power.dp](#), [bib.CL](#)

**Examples**

```
# using all the defaults, i.e. crossover design, alpha=0.05
# theta1=0.8, theta2=1.25 but true slope slightly off 1
sampleN.dp(CV = 0.2, doses = c(1, 2, 8), beta0 = 1.02)
# should give n=18, power=0.854528

# incomplete block design with 5 doses, 3 periods
# from library(crossdes)
doses <- c(5, 25, 50, 100, 200)
CVb <- mse2CV(0.8)
levels <- length(doses)
per <- 3
block <- levels*(levels-1)/(per-1)
# IBD based on balanced repeated measurements design
# gives n=30 and 10 sequences
ibd <- crossdes::balmin.RMD(levels, block, per)
sampleN.dp(CV = 0.2, doses = doses, beta0 = 1, design = "IBD", dm = ibd,
           CVb = CVb, targetpower=0.9)
```

---

sampleN.HVNTID	<i>Sample size estimation for BE decision via FDA method for highly variable (HV) narrow therapeutic index drugs (NTIDs)</i>
----------------	--

---

## Description

This function performs the sample size estimation for the BE decision via the FDA's method for highly variable NTIDs as described in respective guidances based on simulations.

The study designs may be the full replicate design 2x2x4 with 4 periods (TRTR|RTTR) and the 3-period replicate design 2x2x3 with sequences RTR|TRT.

## Usage

```
sampleN.HVNTID(alpha = 0.05, targetpower = 0.8, theta0, theta1, theta2, CV,
  design = c("2x2x4", "2x2x3"), nsims = 1e+05, nstart, imax = 100,
  print = TRUE, details = TRUE, setseed = TRUE)
```

## Arguments

alpha	Type I error probability. Per convention mostly set to 0.05.
targetpower	Power to achieve at least. Must be >0 and <1. Typical values are 0.8 or 0.9.
theta0	'True' or assumed T/R ratio. Defaults to 0.95 if not given explicitly.
theta1	Conventional lower ABE limit to be applied in the FDA procedure. Defaults to 0.8 if not given explicitly.
theta2	Conventional upper ABE limit to be applied in the FDA procedure. Defaults to 1.25 if not given explicitly.
CV	Intra-subject coefficient(s) of variation as ratio (not percent). <ul style="list-style-type: none"> <li>• If given as a scalar (length(CV)==1) the <i>same</i> CV of Test and Reference is assumed (homoscedasticity, CVwT==CVwR).</li> <li>• If given as a vector (length(CV)==2), <i>i.e.</i>, assuming heteroscedasticity, the CV of the Test <b>must</b> be given in CV[1] and the one of the Reference in the CV[2].</li> </ul>
design	Design of the study to be planned. "2x2x4" is the full replicate with 2 sequences and 4 periods (TRTR RTTR). "2x2x3" is the full replicate with 2 sequences and 3 periods (TRT RTTR). Defaults to design="2x2x4".
nsims	Number of simulations to be performed to obtain the empirical power. Defaults to 100,000 = 1e+5.
nstart	Set this to a start value for the sample size if a previous run failed. May be missing.
imax	Maximum number of steps in sample size search. Defaults to 100.

print	If TRUE (default) the function prints its results. If FALSE only the resulting dataframe will be returned.
details	If set to TRUE, the default, the steps during sample size search are shown. Moreover the details of the method settings are printed.
setseed	Simulations are dependent on the starting point of the (pseudo) random number generator. To avoid differences in power values for different runs a set . seed(123456) is issued if setseed=TRUE, the default.

### Details

For deciding BE the study must pass the conventional ABE test and additionally the test that the ratio of sWT/sWR is  $\leq 2.5$ .

The simulations are done via the distributional properties of the statistical quantities necessary for deciding BE based on these method.

Details can be found in a document Implementation\_scaledABE\_sims located in the /doc sub-directory of the package.

The estimated sample size gives always the *total* number of subjects (not subject/sequence – like in some other software packages).

### Value

Returns a data.frame with the input and sample size results.

The Sample size column contains the total sample size.

The nlast column contains the last n value. May be useful for re-starting.

### Warning

For some input constellations the sample size search may be very time consuming and will eventually also fail since the start values chosen may not really reasonable for them.

In case of a failed sample size search you may restart with setting the argument nstart.

### Note

The design recommended by the FDA is the full replicate design "2x2x4".

The sample size estimation is done only for balanced studies since the break down of the total subject number in case of unbalanced sequence groups is not unique. Moreover the formulas used are only valid for balanced designs.

The FDA method is described for the ABE limits 0.8 ... 1.25 only. Setting theta1, theta2 to other values may not be reasonable and is not tested.

The minimum sample size is 6, even if the power is higher than the intended targetpower.

### Author(s)

D. Labes

## References

Food and Drug Administration, Office of Generic Drugs (OGD). *Draft Guidance on Dabigatran Etexilate Mesylate*. Recommended Jun 2012; Revised Sep 2015, Jul 2017. [download](#)

Food and Drug Administration, Office of Generic Drugs (OGD). *Draft Guidance on Rivaroxaban*. Recommended Sep 2015. [download](#)

## See Also

[power.HVNTID](#)  
and [power.NTIDFDA](#), [sampleN.NTIDFDA](#) for NTIDs with low variability

## Examples

```
# using all defaults but CV
sampleN.HVNTID(CV = 0.3)
# should give
# n=22 with an (empirical) power of 0.829700

# Test formulation with lower variability but same pooled CV
CVs <- CVp2CV(0.3, ratio = 0.25)
sampleN.HVNTID(CV = CVs)
# should give (no distinct difference to example above)
# n=22 with an (empirical) power of 0.837520
```

---

sampleN.noninf

*Sample size for the non-inferiority t-test*

---

## Description

Function for estimating the sample size needed to have a pre-specified power for the one-sided non-inferiority *t*-test for normal or log-normal distributed data.

## Usage

```
sampleN.noninf(alpha = 0.025, targetpower = 0.8, logscale = TRUE,
               margin, theta0, CV, design = "2x2", robust = FALSE,
               details = FALSE, print = TRUE, imax=100)
```

## Arguments

alpha	Significance level (one-sided). Defaults here to 0.025.
targetpower	Power to achieve at least. Must be >0 and <1. Typical values are 0.8 or 0.9.
logscale	Should the data used on log-transformed or on original scale? TRUE (default) or FALSE.

theta0	<p>‘True’ or assumed T/R ratio or difference.          In case of logscale=TRUE it must be given as ratio T/R.          If logscale=FALSE, the difference in means. In this case, the difference may be expressed in two ways: relative to the same (underlying) reference mean, i.e. as <math>(T-R)/R = T/R - 1</math>; or as difference in means T-R. Note that in the former case the units of margin and CV need also be given relative to the reference mean (specified as ratio).          Defaults to 0.95 if logscale=TRUE or to -0.05 if logscale=FALSE</p>
margin	<p>Non-inferiority margin.          In case of logscale=TRUE it is given as ratio.          If logscale=FALSE, the limit may be expressed in two ways: difference of means relative to the same (underlying) reference mean or in units of the difference of means. Note that in the former case the units of CV and theta0 need also be given relative to the reference mean (specified as ratio).          Defaults to 0.8 if logscale=TRUE or to -0.2 if logscale=FALSE.</p>
CV	<p>In case of logscale=TRUE the (geometric) coefficient of variation given as ratio.          If logscale=FALSE the argument refers to (residual) standard deviation of the response. In this case, standard deviation may be expressed two ways: relative to a reference mean (specified as ratio <math>\sigma/\mu_R</math>), i.e. again as a coefficient of variation; or untransformed, i.e. as standard deviation of the response. Note that in the former case the units of theta0, theta1 and theta2 need also be given relative to the reference mean (specified as ratio).</p>
design	<p>In case of cross-over studies this is the within-subject CV, in case of a parallel-group design the CV of the total variability.          Character string describing the study design.          See <a href="#">known.designs</a> for designs covered in this package.</p>
robust	<p>Defaults to FALSE. With that value the usual degrees of freedom will be used. Set to TRUE will use the degrees of freedom according to the ‘robust’ evaluation (aka Senn’s basic estimator). These df are calculated as <math>n - seq</math>.          See <code>known.designs()\$df2</code> for designs covered in this package.          Has only effect for higher-order crossover designs.</p>
details	<p>If TRUE the design characteristics and the steps during sample size calculations will be shown.          Defaults to FALSE.</p>
print	<p>If TRUE (default) the function prints its results.          If FALSE only the data.frame with the results will be returned.</p>
imax	<p>Maximum number of steps in sample size search.          Defaults to 100. Adaption only in rare cases needed.</p>

## Details

The sample size is calculated via iterative evaluation of `power.noninf()`.  
 Start value for the sample size search is taken from a large sample approximation.  
 The sample size is bound to 4 as minimum.

The estimated sample size gives always the *total* number of subjects (not subject/sequence in



crossovers or subjects/group in parallel designs – like in some other software packages).

#### Notes on the underlying hypotheses

If the supplied margin is  $< 0$  (logscale=FALSE) or  $< 1$  (logscale=TRUE), then it is assumed higher response values are better. The hypotheses are

H0:  $\theta_0 \leq \text{margin}$  vs. H1:  $\theta_0 > \text{margin}$ ,  
 where  $\theta_0 = \text{mean}(\text{test}) - \text{mean}(\text{reference})$  if logscale=FALSE  
 or

H0:  $\log(\theta_0) \leq \log(\text{margin})$  vs. H1:  $\log(\theta_0) > \log(\text{margin})$ ,  
 where  $\theta_0 = \text{mean}(\text{test}) / \text{mean}(\text{reference})$  if logscale=TRUE.

If the supplied margin is  $> 0$  (logscale=FALSE) or  $> 1$  (logscale=TRUE), then it is assumed lower response values are better. The hypotheses are

H0:  $\theta_0 \geq \text{margin}$  vs. H1:  $\theta_0 < \text{margin}$   
 where  $\theta_0 = \text{mean}(\text{test}) - \text{mean}(\text{reference})$  if logscale=FALSE  
 or

H0:  $\log(\theta_0) \geq \log(\text{margin})$  vs. H1:  $\log(\theta_0) < \log(\text{margin})$   
 where  $\theta_0 = \text{mean}(\text{test}) / \text{mean}(\text{reference})$  if logscale=TRUE.

This latter case may also be considered as ‘non-superiority’.

#### Value

A data.frame with the input settings and results will be returned.

Explore it with `str(sampleN.noninf(...))`

#### Warning

The function does not vectorize properly.

If you need sample sizes with varying CVs, use f.i. for-loops or the apply-family.

#### Author(s)

D. Labes

#### References

Julious SA. *Sample sizes for clinical trials with Normal data*. Stat Med. 2004;23(12):1921–86.  
 doi: [10.1002/sim.1783](https://doi.org/10.1002/sim.1783)

#### See Also

[known.designs](#), [power.noninf](#)

#### Examples

```
# using all the defaults: margin=0.8, theta0=0.95, alpha=0.025
# log-transformed, design="2x2"
sampleN.noninf(CV = 0.3)
# should give n=48
#
```

```
# 'non-superiority' case, log-transformed data
# with assumed 'true' ratio somewhat above 1
sampleN.noninf(CV = 0.3, targetpower = 0.9,
               margin = 1.25, theta0 = 1.05)
# should give n=62
```

---

sampleN.NTIDFDA	<i>Sample size estimation for BE decision via the FDA's method for narrow therapeutic index drugs (NTIDs)</i>
-----------------	---

---

## Description

This function performs the sample size estimation for the BE decision for the FDA's method for NTIDs based on simulations. The study design is the full replicate design 2x2x4 (TRTR|IRTRT) or the 3-period replicate design with sequences TRT|IRTR.

## Usage

```
sampleN.NTIDFDA(alpha = 0.05, targetpower = 0.8, theta0, theta1, theta2, CV,
                design = c("2x2x4", "2x2x3"), nsims = 1e+05, nstart, imax = 100,
                print = TRUE, details = TRUE, setseed = TRUE)
```

## Arguments

alpha	Type I error probability. Per convention mostly set to 0.05.
targetpower	Power to achieve at least. Must be >0 and <1. Typical values are 0.8 or 0.9.
theta0	'True' or assumed T/R ratio. Attention! Defaults here to 0.975 if not given explicitly. The value was chosen closer to 1 because the potency (contents) settings for NTIDs are tightened by the FDA.
theta1	Conventional lower ABE limit to be applied in the FDA procedure. Defaults to 0.8 if not given explicitly.
theta2	Conventional upper ABE limit to be applied in the FDA procedure. Defaults to 1.25 if not given explicitly.
CV	Intra-subject coefficient(s) of variation as ratio (not percent). <ul style="list-style-type: none"> <li>• If given as a scalar (<code>length(CV)==1</code>) the <i>same</i> CV of Test and Reference is assumed (homoscedasticity, <code>CVwT==CVwR</code>).</li> <li>• If given as a vector (<code>length(CV)==2</code>), <i>i.e.</i>, assuming heteroscedasticity, the CV of the Test <b>must</b> be given in <code>CV[1]</code> and the one of the Reference in the <code>CV[2]</code>.</li> </ul>
design	Design of the study to be planned. "2x2x4" is the full replicate with 2 sequences and 4 periods (TRTR IRTRT). "2x2x3" is the full replicate with 2 sequences and 3 periods (TRT IRTR). Defaults to <code>design="2x2x4"</code> .

nsims	Number of simulations to be performed to obtain the empirical power. Defaults to 100,000 = 1e+5.
nstart	Set this to a start value for the sample size if a previous run failed. May be missing.
imax	Maximum number of steps in sample size search. Defaults to 100.
print	If TRUE (default) the function prints its results. If FALSE only the resulting dataframe will be returned.
details	If set to TRUE, the default, the steps during sample size search are shown. Moreover the details of the method settings are printed.
setseed	Simulations are dependent on the starting point of the (pseudo) random number generator. To avoid differences in power values for different runs a set . seed(123456) is issued if setseed=TRUE, the default.

### Details

The linearized scaled ABE criterion is calculated according to the SAS code given in the FDA Warfarine guidance. For deciding BE the study must pass that criterion, the conventional ABE test and additionally the test that the ratio of  $sWT/sWR \leq 2.5$ .

The simulations are done via the distributional properties of the statistical quantities necessary for deciding BE based on these method.

Details can be found in a document Implementation\_scaledABE\_sims located in the /doc sub-directory of the package.

The estimated sample size gives always the *total* number of subjects (not subject/sequence – like in some other software packages).

### Value

Returns a data.frame with the input settings and sample size results.

The Sample size column contains the total sample size.

The nlast column contains the last n value. May be useful for re-starting.

### Warning

For some input constellations the sample size search may be very time consuming and will eventually also fail since the start values chosen may not really be reasonable for them. This applies especially for theta0 values near to the implied scaled (tightened/widened) ABE limits according to  $\exp(\pm 1.053605 * swR)$ .

In case of a failed sample size search you may restart with setting the argument nstart.

In case of theta0 values outside the implied scaled (tightened/widened) ABE limits no sample size estimation is possible and the function throws an error (f.i. CV=0.04, theta0=0.95).

### Note

The design recommended by the FDA is the full replicate design "2x2x4".

The sample size estimation is done only for balanced studies since the break down of the total subject number in case of unbalanced sequence groups is not unique. Moreover the formulas used are

only valid for balanced designs.

The FDA method is described for the ABE limits 0.8 ... 1.25 only. Setting  $\theta_1$ ,  $\theta_2$  to other values may not be reasonable and is not tested.

The results for the design "2x2x3" are to be considered as experimental since at present not thoroughly tested.

The minimum sample size is 6, even if the power is higher than the intended targetpower.

### Author(s)

D. Labes

### References

Food and Drug Administration, Office of Generic Drugs (OGD). *Draft Guidance on Warfarin Sodium*. Recommended Dec 2012. [download](#)

Yu LX, Jiang W, Zhang X, Lionberger R, Makhlof F, Schuirmann DJ, Muldowney L, Chen ML, Davit B, Conner D, Woodcock J. *Novel bioequivalence approach for narrow therapeutic index drugs*. Clin Pharmacol Ther. 2015;97(3):286–91. doi: [10.1002/cpt.28](#)

Jiang W, Makhlof F, Schuirmann DJ, Zhang X, Zheng N, Conner D, Yu LX, Lionberger R. *A Bioequivalence Approach for Generic Narrow Therapeutic Index Drugs: Evaluation of the Reference-Scaled Approach and Variability Comparison Criterion*. AAPS J. 2015;17(4):891–901. doi: [10.1208/s1224801597535](#)

Endrényi L, Tóthfalusi L. *Determination of Bioequivalence for Drugs with Narrow Therapeutic Index: Reduction of the Regulatory Burden*. J Pharm Pharm Sci. 2013;16(5):676–82. [open access](#)

### See Also

[power.NTIDFDA](#) and [power.HVNTID](#), [sampleN.HVNTID](#) for NTIDs with high variability

### Examples

```
sampleN.NTIDFDA(CV = 0.04,theta0 = 0.975)
# should give
# n=54 with an (empirical) power of 0.809590
#
# Test formulation with lower variability
sampleN.NTIDFDA(CV = c(0.04,0.06),theta0 = 0.975)
# should give
# n=20 with an (empirical) power of 0.0.814610
#
# alternative 3-period design
sampleN.NTIDFDA(CV = 0.04,theta0 = 0.975, design="2x2x3")
# should give
# n=86 with power = 0.80364
```

---

sampleN.RatioF	<i>Sample size for equivalence of the ratio of two means with normality on original scale</i>
----------------	---

---

### Description

Estimates the necessary sample size to have at least a given power based on Fieller's confidence ('fiducial') interval.

### Usage

```
sampleN.RatioF(alpha = 0.025, targetpower = 0.8, theta1 = 0.8, theta2,
               theta0 = 0.95, CV, CVb, design = "2x2", print = TRUE,
               details = FALSE, imax=100, setseed=TRUE)
```

### Arguments

alpha	Type I error probability. Defaults here to 0.025 because this function is intended for studies with clinical endpoints.
targetpower	Power to achieve at least. Must be >0 and <1. Typical values are 0.8 or 0.9.
theta1	Lower bioequivalence limit. Typically 0.8 (default).
theta2	Upper bioequivalence limit. Typically 1.25. Is set to 1/theta1 if missing.
theta0	'True' or assumed T/R ratio. Typically set to 0.95.
CV	Coefficient of variation as ratio. In case of design="parallel" this is the CV of the total variability, in case of design="2x2" the intra-subject CV (CVw in the reference).
CVb	CV of the between-subject variability. Only necessary for design="2x2".
design	A character string describing the study design. design="parallel" or design="2x2" allowed for a two-parallel group design or a classical TRIRT crossover design.
print	If TRUE (default) the function prints its results. If FALSE only a data.frame with the results will be returned.
details	If TRUE the steps during sample size calculations will be shown. Defaults to FALSE.
imax	Maximum number of steps in sample size search. Defaults to 100. Adaption only in rare cases needed.
setseed	If set to TRUE the dependence of the power from the state of the random number generator is avoided.

### Details

The sample size is based on exact power calculated using the bivariate non-central  $t$ -distribution via function `pmvt` of the package `mvtnorm`.

Due to the calculation method used in package `mvtnorm` these probabilities are dependent from the state of the random number generator within the precision of the power.

The CV(within) and CVb(etween) in case of `design="2x2"` are obtained via an appropriate ANOVA from the error term and from the difference  $(MS(\text{subject within sequence}) - MS(\text{error}))/2$ .

The estimated sample size gives always the *total* number of subjects (not subject/sequence in crossovers or subjects/group in parallel designs – like in some other software packages).

### Value

A data.frame with the input values and results will be returned.

The sample size `n` returned is the total sample size for both designs.

### Note

This function is intended for studies with clinical endpoints.

In such studies the 95% confidence intervals are usually used for equivalence testing.

Therefore, `alpha` defaults here to 0.025 (see EMEA 2000).

### Author(s)

D. Labes

### References

Fieller EC. *Some Problems in Interval Estimation*. J Royal Stat Soc B. 1954;16(2):175–85. doi: [10.1111/j.25176161.1954.tb00159.x](https://doi.org/10.1111/j.25176161.1954.tb00159.x)

Sasabuchi S. *A test of a multivariate normal mean with composite hypotheses determined by linear inequalities*. Biometrika. 1980;67(2):429–39. doi: [10.1093/biomet/67.2.429](https://doi.org/10.1093/biomet/67.2.429)

Hauschke D, Kieser M, Diletti E, Burke M. *Sample size determination for proving equivalence based on the ratio of two means for normally distributed data*. Stat Med. 1999;18(1):93–105.

Hauschke D, Steinijans V, Pigeot I. *Bioequivalence Studies in Drug Development*. Chichester: Wiley; 2007. Chapter 10.

European Agency for the Evaluation of Medicinal Products, CPMP. *Points to Consider on Switching between Superiority and Non-Inferiority*. London, 27 July 2000. [CPMP/EWP/482/99](https://www.ema.europa.eu/en/documents/other/cpmp-ewp-482-99_en.pdf)

### See Also

[power.RatioF](#)

**Examples**

```

# sample size for a 2x2 cross-over study
# with CVw=0.2, CVb=0.4
# alpha=0.025 (95% CIs), target power = 80%
# 'true' ratio = 95%, BE acceptance limits 80-125%
# using all the defaults:
sampleN.RatioF(CV = 0.2, CVb = 0.4)
# gives n=28 with an achieved power of 0.807774
# see Hauschke et.al. (2007) Table 10.3a

# sample size for a 2-group parallel study
# with CV=0.4 (total variability)
# alpha=0.025 (95% CIs), target power = 90%
# 'true' ratio = 90%, BE acceptance limits 75-133.33%
sampleN.RatioF(targetpower = 0.9, theta1 = 0.75,
               theta0 = 0.90, CV = 0.4, design = "parallel")
# gives n=236 with an achieved power of 0.900685
# see Hauschke et.al. (2007) Table 10.2

# a rather strange setting of ratio0! have a look at n.
# it would be better this is not the sample size but your account balance ;-).
sampleN.RatioF(theta0 = 0.801, CV = 0.2, CVb = 0.4)

```

---

sampleN.RSABE

*Sample size estimation for BE decision via linearized scaled ABE criterion*


---

**Description**

This function performs the sample size estimation for the BE decision via linearized scaled ABE criterion based on simulations.

**Usage**

```

sampleN.RSABE(alpha = 0.05, targetpower = 0.8, theta0, theta1, theta2, CV,
              design = c("2x3x3", "2x2x4", "2x2x3"), regulator = c("FDA", "EMA"),
              nsims = 1e+05, nstart, imax=100, print = TRUE,
              details = TRUE, setseed=TRUE)

```

**Arguments**

alpha	Type I error probability. Per convention mostly set to 0.05.
targetpower	Power to achieve at least. Must be >0 and <1. Typical values are 0.8 or 0.9.
theta0	'True' or assumed T/R ratio. Defaults to 0.90 according to the two Lászlós if not given explicitly.

theta1	Conventional lower ABE limit to be applied in the mixed procedure if CV <sub>SWR</sub> <= CV <sub>switch</sub> . Also Lower limit for the point estimate constraint. Defaults to 0.8 if not given explicitly.
theta2	Conventional upper ABE limit to be applied in the mixed procedure if CV <sub>SWR</sub> <= CV <sub>switch</sub> . Also upper limit for the point estimate constraint. Defaults to 1.25 if not given explicitly.
CV	Intra-subject coefficient(s) of variation as ratio (not percent). <ul style="list-style-type: none"> <li>• If given as a scalar (length(CV)==1) the <i>same</i> CV of Test and Reference is assumed (homoscedasticity, CV<sub>wT</sub>==CV<sub>wR</sub>).</li> <li>• If given as a vector (length(CV)==2), <i>i.e.</i>, assuming heteroscedasticity, the CV of the Test <b>must</b> be given in CV[1] and the one of the Reference in the CV[2].</li> </ul>
design	Design of the study to be planned. "2x3x3" is the partial replicate design. "2x2x4" is a full replicate design with 2 sequences and 4 periods. "2x2x3" is a full replicate design with 2 sequences and 3 periods. Defaults to design="2x3x3". Details are given the section about Designs.
regulator	Regulatory body settings for the scaled ABE criterion. Defaults to design="FDA". Also the scaled ABE criterion is usually calculated with the FDA constant r_const=log(1.25)/0.25 you can override this behavior to use the EMA setting r_const=0.76 to avoid the discontinuity at CV=30% and be more stringent.
nsims	Number of simulations to be performed to obtain the (empirical) power.
nstart	Set this to a start for the sample size search if a previous run failed. After reworking the start n in version 1.1-05 rarely needed.
imax	Maximum number of steps in sample size search. Defaults to 100.
print	If TRUE (default) the function prints its results. If FALSE only the result data.frame will be returned.
details	If set to TRUE, the default, the steps during sample size search are shown.
setseed	Simulations are dependent on the starting point of the (pseudo) random number generator. To avoid differences in power for different runs a set.seed(123456) is issued if setseed=TRUE, the default.

## Details

The linearized scaled ABE criterion is calculated according to the SAS code given in the FDA progesterone guidance.

The simulations are done via the distributional properties of the statistical quantities necessary for deciding BE based on scaled ABE.

For more details see a document Implementation\_scaledABE\_simsVx.yy.pdf in the /doc sub-directory of the package.

If a CV<sub>cap</sub> is defined for the regulator, the BE decision is based on the inclusion of the CI in



the capped widened acceptance limits in case of  $CV_{wR} > CV_{cap}$ . This resembles method ‘Howe-EMA’ in Muñoz *et al.* and is the standard behavior now if `regulator="EMA"` is chosen.

The estimated sample size gives always the *total* number of subjects (not subject/sequence – like in some other software packages).

### Value

Returns a data.frame with the input and sample size results.

The `Sample size` column contains the total sample size.

The `nlast` column contains the last n value. May be useful for restarting.

### Designs

Although some designs are more ‘popular’ than others, sample size estimations are valid for *all* of the following designs:

"2x2x4"	TRTR   RTRT TRRT   RTTR TTRR   RRTT
"2x2x3"	TRT   RTR TRR   RTT
"2x3x3"	TRR   RTR   RRT

### Warning

The sample size estimation for  $\theta_0 > 1.2$  and  $< 0.85$  may be very time consuming and will eventually also fail since the start values chosen are not really reasonable in that ranges. This is especially true in the range about  $CV = 0.3$  and regulatory constant according to FDA.

If you really need sample sizes in that range be prepared to restart the sample size estimation via the argument `nstart`.

Since the dependence of power from n is very flat in the mentioned region you may also consider to adapt the number of simulations not to tap in the simulation error trap.

### Note

The sample size estimation is done only for balanced designs since the break down of the total subject number in case of unbalanced sequence groups is not unique. Moreover the formulas used are only for balanced designs.

The minimum sample size is  $n=6$ , even if the power is higher than the intended targetpower.

### Author(s)

D. Labes

### References

Food and Drug Administration, Office of Generic Drugs (OGD). *Draft Guidance on Progesterone*. Recommended Apr 2010. Revised Feb 2011. [download](#)

Tóthfalusi, L, Endrényi, L. *Sample Sizes for Designing Bioequivalence Studies for Highly Variable Drugs*. J Pharm Pharmaceut Sci. 2011;15(1):73–84. [open access](#)

Tóthfalusi L, Endrényi L, García Arieta A. *Evaluation of Bioequivalence for Highly Variable Drugs with Scaled Average Bioequivalence*. Clin Pharmacokin. 2009;48(11):725–43. doi: [10.2165/1131804000000000000000](#)

Muñoz J, Alcaide D, Ocaña J. *Consumer's risk in the EMA and FDA regulatory approaches for bioequivalence in highly variable drugs*. Stat Med. 2015;35(12):1933–43. doi: [10.1002/sim.6834](#)

## See Also

[power.RSABE](#), [power.scABEL](#)

## Examples

```
# using all the defaults:
# design=2x3x3 (partial replicate design), theta0=0.90,
# ABE limits, PE constraint 0.8 - 1.25
# targetpower=80%, alpha=0.05, 1E5 simulations
sampleN.RSABE(CV = 0.3)
# should result in a sample size n=45, power=0.80344
```

---

sampleN.RSABE2L.sdsims

*Sample size estimation for BE Decision via Reference Scaled ABE*

---

## Description

These functions performs the sample size estimation of the BE decision via the reference scaled ABE based on **subject data** simulations. Implemented are the methods ABEL, Hyslop and ‘exact’ (see the References in [power.RSABE2L.sdsims](#)).

The estimation method of the key statistics needed to perform the RSABE decision is the usual ANOVA.

This function has an alias `sampleN.RSABE2L.sds()`.

## Usage

```
sampleN.RSABE2L.sdsims(alpha = 0.05, targetpower = 0.8, theta0,
  theta1, theta2, CV,
  design = c("2x3x3", "2x2x4", "2x2x3"),
  SABE_test = "exact", regulator, nsims=1e5,
  nstart, imax = 100, print = TRUE,
  details = TRUE, setseed = TRUE, progress)
```

**Arguments**

alpha	Type I error probability. Per convention mostly set to 0.05.
targetpower	Power to achieve at least. Must be >0 and <1. Typical values are 0.8 or 0.9.
theta0	'True' or assumed T/R ratio. Defaults to 0.90 according to the two Lászlós if not given explicitly.
theta1	Conventional lower ABE limit to be applied in the mixed procedure if CV <sub>SWR</sub> <= CV <sub>switch</sub> . Also Lower limit for the point estimate constraint. Defaults to 0.8 if not given explicitly.
theta2	Conventional upper ABE limit to be applied in the mixed procedure if CV <sub>SWR</sub> <= CV <sub>switch</sub> . Also upper limit for the point estimate constraint. Defaults to 1.25 if not given explicitly.
CV	Intra-subject coefficient(s) of variation as ratio (not percent). <ul style="list-style-type: none"> <li>• If given as a scalar (length(CV)==1) the <i>same</i> CV of Test and Reference is assumed (homoscedasticity, CV<sub>wT</sub>=CV<sub>wR</sub>).</li> <li>• If given as a vector (length(CV)==2), <i>i.e.</i>, assuming heteroscedasticity, the CV of the Test <b>must</b> be given in CV[1] and the one of the Reference in the CV[2].</li> </ul>
design	Design of the study to be planned. "2x3x3" is the partial replicate design. "2x2x4" is a full replicate design with 2 sequences and 4 periods. "2x2x3" is a full replicate design with 2 sequences and 3 periods. Defaults to design="2x3x3". Details are given the section about Designs.
SABE_test	This argument specifies the test method to be used for the reference scaled ABE decision. Default is the "exact" 'ncTOST' method of the two Laszlós. Other choices are "ABEL", "Hyslop" and "FDA". See Details. This argument may be given also in lower case.
regulator	Regulatory settings for the widening of the BE acceptance limits. May be given as character "EMA" or as an object of class 'regSet' (see <a href="#">reg_const</a> ). Defaults to regulator="EMA" if missing. This argument may be given also in lower case if given as character. If given as object of class 'regSet' the component est_method can not be "ISC".
nsims	Number of simulations to be performed to obtain the (empirical) power. The default value 100,000 = 1e+5 is usually sufficient. Consider to rise this value if theta0<=0.85 or >=1.25. But see the warning section.
nstart	Set this to a start for the sample size search if a previous run failed. After reworking the start n in version 1.1-05 rarely needed.
imax	Maximum number of steps in sample size search. Defaults to 100.
print	If TRUE (default) the function prints its results. If FALSE only the result data.frame will be returned.
details	If set to TRUE (default), the steps during sample size search are shown.

setseed	Simulations are dependent on the starting point of the (pseudo) random number generator. To avoid differences in power for different runs a <code>set.seed(123456)</code> is issued if <code>setseed=TRUE</code> , the default.
progress	Should a progressbar be shown? Defaults to <code>TRUE</code> if missing and <code>nsims &gt; 5E5</code> .

### Details

The methods rely on the analysis of log-transformed data, *i.e.*, assume a log-normal distribution on the original scale.

The widened BE acceptance limits will be calculated by the formula

$$[L, U] = \exp(\pm r\_const * sWR)$$

with `r_const` the regulatory constant and `sWR` the standard deviation of the within subjects variability of the Reference. `r_const = 0.76` ( $-\log(1.25)/0.29356$ ) is used in case of `regulator="EMA"`. If the `CVwR` of the Reference is `< CVswitch=0.3` the conventional ABE limits apply (mixed procedure).

In case of `regulator="EMA"` a cap is placed on the widened limits if `CVwr > 0.5`, *i.e.*, the widened limits are held at value calculated for `CVwR=0.5`.

The simulations are done by simulating subject data (all effects fixed except the residuals) and evaluating these data via ANOVA of all data to get the point estimate of T vs. R along with its 90% CI and an ANOVA of the data under R(eference) only to get an estimate of `s2wR`.

The estimated sample size gives always the *total* number of subjects (not subject/sequence – like in some other software packages).

### Value

Returns a `data.frame` with the input settings and sample size results.

The `Sample size` column contains the total sample size.

The `nlast` column contains the last `n` value. May be useful for restarting.

### Designs

Although some designs are more ‘popular’ than others, sample size estimations are valid for *all* of the following designs:

"2x2x4"	TRTR   RTRT TRRT   RTTR TTRR   RRTT
"2x2x3"	TRT   RTR TRR   RTT
"2x3x3"	TRR   RTR   RRT

### Warning

The sample size estimation for very extreme `theta0` (`< 0.83` or `> 1.21`) may be very time consuming and will eventually also fail since the start values chosen are not really reasonable in that ranges.

If you really need sample sizes in that range be prepared to restart the sample size estimation via

the argument `nstart`.

Since the dependence of power from `n` is very flat in the mentioned region you may also consider to adapt the number of simulations not to tap in the simulation error trap.

### Note

We are doing the sample size estimation only for balanced designs since the break down of the total subject number in case of unbalanced sequence groups is not unique. Moreover the formulas used are only for balanced designs.

The minimum sample size is 6, even if the power is higher than the intended targetpower.

Subject simulations are relatively slow. Thus be patient and go for a cup of coffee if you use this function with high sample sizes!

### Author(s)

H. Schütz

### See Also

[power.RSABE2L.sdsims](#), [sampleN.scABEL](#), [reg\\_const](#)

### Examples

```
# using the defaults:
# partial replicate design, targetpower=80%,
# true assumed ratio = 0.90, 1E+5 simulated studies
# ABE limits, PE constraint 0.8 - 1.25
# EMA regulatory settings
# compare results

CV      <- 0.4
method <- c("exact", "abel", "hyslop", "fda")
res     <- data.frame(SABE_test = c("ncTOST", "ABEL",
                                   "Hyslop", "FDA"),
                     n = NA, power = NA)
for (i in 1:nrow(res)) {
  res[i, 2:3] <- sampleN.RSABE2L.sdsims(CV = CV,
                                       SABE_test = method[i],
                                       details = FALSE,
                                       print = FALSE)[8:9]
}
print(res, digits = 4, row.names = FALSE)
# should result in a sample size n=48 with all methods,
# power=0.8197 (ncTOST), 0.8411 (ABEL), 0.8089 (Hyslop), 0.8113 (FDA)
```

---

sampleN.scABEL	<i>Sample size estimation for BE decision via scaled (expanded) BE acceptance limits</i>
----------------	--

---

## Description

This function performs the sample size estimation via power calculations of the BE decision via scaled (expanded) BE acceptance limits, based on simulations.

## Usage

```
sampleN.scABEL(alpha = 0.05, targetpower = 0.8, theta0, theta1, theta2, CV,
  design = c("2x3x3", "2x2x4", "2x2x3"), regulator,
  nsims = 1e+05, nstart, imax = 100, print = TRUE, details = TRUE,
  setseed = TRUE)
```

## Arguments

alpha	Type I error probability. Per convention mostly set to 0.05.
targetpower	Power to achieve at least. Must be >0 and <1. Typical values are 0.8 or 0.9.
theta0	‘True’ or assumed T/R ratio. Defaults to 0.90 according to the two Lászlós if not given explicitly.
theta1	Conventional lower ABE limit to be applied in the mixed procedure if CVsWR <= CVswitch. Also Lower limit for the point estimate constraint. Defaults to 0.8 if not given explicitly.
theta2	Conventional upper ABE limit to be applied in the mixed procedure if CVsWR <= CVswitch. Also upper limit for the point estimate constraint. Defaults to 1.25 if not given explicitly.
CV	Intra-subject coefficient(s) of variation as ratio (not percent). <ul style="list-style-type: none"> <li>• If given as a scalar (length(CV)==1) the <i>same</i> CV of Test and Reference is assumed (homoscedasticity, <math>CV_{WT} = CV_{WR}</math>).</li> <li>• If given as a vector (length(CV)==2), <i>i.e.</i>, assuming heteroscedasticity, the <i>CV</i> of the Test <b>must</b> be given in CV[1] and the one of the Reference in the CV[2].</li> </ul>
design	Design of the study to be planned. "2x3x3" is the partial replicate design. "2x2x4" is a full replicate design with 2 sequences and 4 periods. "2x2x3" is a full replicate design with 2 sequences and 3 periods. Defaults to design="2x3x3". Details are given the section about Designs.
regulator	Regulatory settings for the widening of the BE acceptance limits. May be given as character from the choices "EMA", "HC", "GCC", "FDA" or as an object of class 'regSet' (see <a href="#">reg_const</a> ).

Defaults to regulator="EMA" if missing.  
 This argument may be given also in lower case if given as character.

nsims	Number of simulations to be performed to obtain the (empirical) power. The default value 100,000 = 1e+5 is usually sufficient. Consider to rise this value if $\theta \leq 0.85$ or $\geq 1.20$ . But see the warning section.
nstart	Set this to a start for the sample size search if a previous run failed. After reworking the start n in version 1.1-05 rarely needed.
imax	Maximum number of steps in sample size search. Defaults to 100.
print	If TRUE (default) the function prints its results. If FALSE only the result data.frame will be returned.
details	If set to TRUE (default), the steps during sample size search are shown.
setseed	Simulations are dependent on the starting point of the (pseudo) random number generator. To avoid differences in power for different runs a set.seed(123456) is issued if setseed=TRUE, the default.

## Details

The simulations are done via the distributional properties of the statistical quantities necessary for deciding BE based on ABEL ('Average Bioequivalence with Expanded Limits'). For more details see a description in the /doc sub-directory of the package.

Function sampleN.scABEL() is based on power calculations via simulations using the distributional characteristics of the 'key' statistics obtained from the EMA recommended evaluation via ANOVA if regulator="EMA" or if the regulator component est\_method is set to "ANOVA" if regulator is an object of class 'regSet'.

Otherwise, the simulations are based on the distributional characteristics of the 'key' statistics obtained from evaluation via intra-subject contrasts (ISC), as recommended by the FDA.

The estimated sample size gives always the *total* number of subjects (not subject/sequence – like in some other software packages).

Function sampleN.scABEL2() is solely based on power calculations via simulation using the distributional characteristics of the 'key' statistics obtained from evaluation via intra-subject contrasts (ISC). This function is deprecated.

## Value

Returns a data.frame with the input settings and sample size results.  
 The Sample size column contains the total sample size.  
 The nlast column contains the last n value. May be useful for restarting.

## Designs

Although some designs are more 'popular' than others, sample size estimations are valid for *all* of the following designs:

```

"2x2x4"  TRTR | RTRT
          TRRT | RTTR
          TTRR | RRTT
"2x2x3"  TRT | RTR
          TRR | RTT
"2x3x3"  TRR | RTR | RRT

```

### Warning

The sample size estimation for extreme  $\theta_0$  ( $<0.83$  or  $>1.21$ ) may be very time consuming and will eventually also fail since the start values chosen are not really reasonable in that ranges. This is especially true in the range around  $CV = 0.3$  and regulatory constant according to FDA.

If you really need sample sizes in that range be prepared to restart the sample size estimation via the argument `nstart`.

Since the dependence of power from  $n$  is very flat in the mentioned region you may also consider to adapt the number of simulations not to get caught in the simulation error trap.

If results of `power.scABEL` are expected to be inaccurate (partial replicate design with unbalanced sequences and/or heteroscedasticity in the case of  $CV_{WT} > CV_{WR}$ , subject data via `sampleN.scABEL.sdsims` should be simulated instead. Very time consuming (easily 100times slower)! Subject data simulations are only supported for `regulator="EMA"` and `regulator="GCC"`.

### Note

We are doing the sample size estimation only for balanced designs since the break down of the total subject number in case of unbalanced sequence groups is not unique. Moreover the formulas used are only for balanced designs.

In case of `regulator="FDA"` the sample size is only approximate since the BE decision method is not exactly what is expected by the FDA. But the two Lászlós state that the `scABEL` method should be 'operationally' equivalent to the FDA method. Thus the sample size should be comparable.

Consider in case of `regulator="FDA"` to use the function `sampleN.RSABE()` instead.

In case of `regulator="HC"` the underlying power is only approximative since the Health Canada recommends evaluation by a mixed model approach. But this could only implemented via subject data simulations which are very time consuming.

The minimum sample size is 6, even if the power is higher than the intended targetpower.

### Author(s)

D. Labes

### References

Tóthfalusi L, Endrényi L. *Sample Sizes for Designing Bioequivalence Studies for Highly Variable Drugs*. J Pharm Pharmaceut Sci. 2011;15(1):73–84. [open access](#)



**See Also**

[power.scABEL](#), [sampleN.scABEL.sdsims](#), [sampleN.RSABE](#), [reg\\_const](#)

**Examples**

```
# using all the defaults:
# partial replicate design, targetpower=80%,
# true assumed ratio = 0.90, 1E+5 simulated studies
# ABE limits, PE constraint 0.8 - 1.25
# EMA regulatory settings
sampleN.scABEL(CV = 0.3)
# should result in a sample size n=54, power=0.8159

# Now with former (inofficial) ANVISA settings, CVswitch=40%
# (since 2016 ANVISA uses the same settings as EMA)
reg    <- reg_const("USER", r_const = 0.76, CVswitch = 0.4, CVcap = 0.5)
reg$name <- "Old ANVISA"
sampleN.scABEL(CV = 0.3, regulator = reg)
# should result in a sample size n=60, power=0.8101

# For the full replicate design, target power = 90%
# true assumed ratio = 0.9, FDA regulatory settings
# sims based on evaluation via ISC
sampleN.scABEL(CV = 0.4, targetpower = 0.9, design = "2x2x4",
               regulator = "FDA")
# should result in a sample size n=32, power=0.9125

# Fixed wider limits (0.7500 - 1.3333) for the GCC
sampleN.scABEL(CV = 0.4, targetpower = 0.9, design = "2x2x4",
               regulator = "GCC")
# should result in a sample size n=40, power=0.9039
```

---

sampleN.scABEL.ad      *Sample size estimation for ABEL and iteratively adjusted alpha*

---

**Description**

This function performs a sample size estimation for the BE decision via Average Bioequivalence with Expanding Limits (ABEL) based on simulations. Simultaneously alpha is iteratively adjusted in order to maintain the consumer risk at the nominal level.

**Usage**

```
sampleN.scABEL.ad(alpha = 0.05, targetpower = 0.8, theta0, theta1, theta2,
                  CV, design = c("2x3x3", "2x2x4", "2x2x3"), regulator,
                  nstart = NA, nsims = 1e+06, imax = 100, tol, print = TRUE,
                  details = FALSE, alpha.pre = 0.05, setseed = TRUE,
                  sdsims = FALSE, progress)
```

**Arguments**

alpha	Type I error (TIE) probability (nominal level of the test). Per convention commonly set to 0.05.
targetpower	Power to achieve at least. Must be >0 and <1. Typical values are 0.80 to 0.90 ( <i>i.e.</i> , 80% to 90%). Defaults to 0.80 if not given explicitly.
theta0	‘True’ or assumed T/R ratio. Defaults to 0.90 according to the two Lászlós if not given explicitly.
theta1	Conventional lower ABE limit to be applied in the mixed procedure if CVwR==CVswitch. Also lower limit for the point estimate constraint. Defaults to 0.80 if not given explicitly.
theta2	Conventional upper ABE limit to be applied in the mixed procedure if CVwR==CVswitch. Also upper limit for the point estimate constraint. Defaults to 1.25 if not given explicitly.
CV	Intra-subject coefficient(s) of variation as ratio (not percent). <ul style="list-style-type: none"> <li>• If given as a scalar (length(CV)==1) the <i>same CV</i> of Test and Reference is assumed (homoscedasticity: <math>CV_{wT} = CV_{wR}</math>).</li> <li>• If given as a vector (length(CV)==2) – assuming heteroscedasticity – the <i>CV</i> of Test <b>must</b> be given in the <i>first</i> element and the one of Reference in the <i>second</i>.</li> </ul>
design	Design of the study to be planned. “2x3x3” is the partial replicate design. “2x2x4” is a full replicate design with 2 sequences and 4 periods. “2x2x3” is a full replicate design with 2 sequences and 3 periods. Defaults to “2x3x3”. Details are given the section about Designs.
regulator	Regulatory settings for the widening of the BE acceptance limits. Choose from “EMA” (default), “HC”, or “GCC”. This argument may be given also in lower case.
nstart	Best “guess” sample size. If not given (default), simulations start with the sample size estimated for alpha (or alpha.pre, if given), theta0, and targetpower. Can also be set to start the sample size search if a previous run failed. According to regulatory requirements must be >=12 for the EMA and >=24 for ANVISA.
nsims	Number of simulations to be performed to estimate the (empirical) TIE and in each iteration of adjusting alpha. The default value 1,000,000 = 1E+6 should not be lowered.
imax	Maximum number of steps in sample size search. Defaults to 100.
tol	Desired accuracy (convergence tolerance). Defaults to 1E-6.
print	If TRUE (default), the function sends its results to the console.
details	If TRUE (default), the steps during sample size search are shown. Additionally information about the impact on power by adjusting alpha and change of study costs due to the increased sample size is given.
alpha.pre	Pre-specified alpha (optional). Must be <=alpha. ABEL will be performed at level alpha.pre and the TIE assessed at level alpha. Less powerful than adjusting alpha but an alternative in the critical region of

	<p>maximum inflation of the TIE. In certain scenarios Bonferroni's 0.025 is not sufficient to preserve the Type I Error.</p> <p>Not recommended if <math>CV_{WR} \geq 0.45</math> due to poor power characteristics.</p>
setseed	<p>Simulations are dependent on the starting point of the (pseudo) random number generator. To avoid differences in power for different runs <code>set.seed(123456)</code> is issued if <code>setseed=TRUE</code> (default).</p>
sdsims	<p>If FALSE (default) power is estimated by the respective 'key' statistics. Recommended for speed reasons.</p> <p>Set to TRUE if results of <code>power.scABEL</code> are expected to be inaccurate (partial replicate design with unbalanced sequences and/or heteroscedasticity where <math>CV_{WT} &gt; CV_{WR}</math>) and subject data via <code>power.scABEL.sdsims</code> should be simulated instead. Very time consuming (easily 100times slower)! Subject data simulations are only supported for <code>regulator="EMA"</code> and <code>regulator="GCC"</code>.</p>
progress	<p>Set to TRUE if a progress bar should be displayed. Defaults to FALSE.</p> <p>Ignored if <code>sdsims=FALSE</code>.</p>

## Details

The simulations are done via the distributional properties of the statistical quantities necessary for assessing BE based on ABEL. Simulations of the TIE are performed at the upper (expanded) limit  $U$  of the acceptance range. Due to the symmetry around 1 results are valid for the lower (expanded) limit  $L$  as well.

$U$  at the EMA's and Health Canada's CVcap, the GCC's for *any*  $CV_{WR} > 0.30$ :

```
scABEL(CV=0.5, reg="EMA")[[ "upper" ]]
[1] 1.43191
scABEL(CV=0.57382, reg="HC")[[ "upper" ]]
[1] 1.5
scABEL(CV=0.31, reg="GCC")[[ "upper" ]]
[1] 1.333333
```

Simulated studies are evaluated by ANOVA (Method A) as recommended in the EMA's Q&A-document and by intra-subject contrasts if `regulator="HC"`. Health Canada requires a mixed effects model which cannot be implemented in R. However, intra-subjects contrasts are a sufficiently close approximation.

If an inflation of the TIE is expected (*i.e.*,  $>\alpha$ ),  $\alpha$  is iteratively adjusted until at least the target power is reached and the consumer risk is maintained ( $\leq\alpha$ ). For details about the algorithm see the respective section of `scABEL.ad`.

The estimated sample size gives always the *total* number of subjects (not subject/sequence – like in some other software packages).

## Value

Returns a data.frame with the input and results for adjusted  $\alpha$ , type I error, sample size, and achieved power.

The Sample size column contains the total sample size. If no adjustment is necessary, NA will be returned in the `alpha.adj` column and other results are identical to the ones obtained by `sampleN.scABEL`.

## Designs

Although some designs are more ‘popular’ than others, sample size estimations are valid for *all* of the following designs:

"2x2x4"	TRTR   RTRT TRRT   RTTR TTRR   RRTT
"2x2x3"	TRT   RTR TRR   RTT
"2x3x3"	TRR   RTR   RRT

## Warning

The sample size estimation for extreme  $\theta_0$  ( $<0.83$  or  $>1.21$ ) may be time consuming and will eventually also fail since the start values chosen are not really reasonable in that ranges.

If you really need sample sizes in that range be prepared to restart the sample size estimation with `nstart` above the last one before failure.

Since the dependence of power from  $n$  is very flat in the mentioned region you may also consider to adapt the number of simulations not to tap in the simulation error trap.

See also the Warning section of the function `power.scABEL` concerning the power value agreement to those obtained from simulations via subject data.

For the GCC and  $CV_{wR} \leq 0.30$

## Note

We are doing the sample size estimation only for balanced designs since the break down of the total subject number in case of unbalanced sequences is not unique. Moreover the formulas used are only for balanced designs.

## Author(s)

H. Schütz

## References

Tóthfalusi L, Endrényi L. *Sample Sizes for Designing Bioequivalence Studies for Highly Variable Drugs*. J Pharm Pharmaceut Sci. 2011;15(1):73–84. [open access](#)

Wonnemann M, Frömke C, Koch A. *Inflation of the Type I Error: Investigations on Regulatory Recommendations for Bioequivalence of Highly Variable Drugs*. Pharm Res. 2015;32(1):135–43. doi: [10.1007/s110950141450z](#)

Muñoz J, Alcaide D, Ocaña J. *Consumer’s risk in the EMA and FDA regulatory approaches for bioequivalence in highly variable drugs*. Stat Med. 2015;35(12):1933–43. doi: [10.1002/sim.6834](#)

Labes D, Schütz H. *Inflation of Type I Error in the Evaluation of Scaled Average Bioequivalence, and a Method for its Control*. Pharm Res. 2016;33(11):2805–14. doi: [10.1007/s1109501620061](#)

**See Also**

[scABEL.ad](#), [sampleN.scABEL](#), [power.scABEL](#), [scABEL](#)

**Examples**

```
# --- Not run due to timing policy of CRAN for examples
# each may run some ten seconds or more
# using all the defaults:
# TRR|RTR|RRT, target power 80%, assumed ratio 0.90, 1E+6 simulated studies,
# EMA regulatory settings (ABE limits, PE constraint 0.8 - 1.25)

sampleN.scABEL.ad(CV = 0.3)
# should result in n 60, power 0.8022.
# Note: Without adjustment by sampleN.scABEL(): n 54, power 0.8159
# Easier to show the details:

sampleN.scABEL.ad(CV = 0.3, details = TRUE)
#
# TRTR|RTRT, target power 90%, pre-specified alpha 0.025

sampleN.scABEL.ad(CV = 0.3, targetpower = 0.9, design = "2x2x4", alpha.pre = 0.025)
# should result in n 60, power 0.9021; pre-specified alpha justified.
```

---

sampleN.scABEL.sdsims *Sample size estimation for BE decision via scaled (expanded) BE acceptance limits*

---

**Description**

These functions performs the sample size estimation via power calculations of the BE decision via scaled (expanded) BE acceptance limits, based on **subject data** simulations. This function has an alias `sampleN.scABEL.sds()`.

**Usage**

```
sampleN.scABEL.sdsims(alpha = 0.05, targetpower = 0.8, theta0, theta1, theta2, CV,
  design = c("2x3x3", "2x2x4", "2x2x3"), regulator, nsims = 1e5,
  nstart, imax = 100, print = TRUE, details = TRUE,
  setseed = TRUE, progress)
```

**Arguments**

alpha	Type I error probability. Per convention mostly set to 0.05.
targetpower	Power to achieve at least. Must be >0 and <1. Typical values are 0.8 or 0.9.
theta0	'True' or assumed T/R ratio. Defaults to 0.90 according to the two Lászlós if not given explicitly.

theta1	Conventional lower ABE limit to be applied in the mixed procedure if CV <sub>SWR</sub> <= CV <sub>switch</sub> . Also Lower limit for the point estimate constraint. Defaults to 0.8 if not given explicitly.
theta2	Conventional upper ABE limit to be applied in the mixed procedure if CV <sub>SWR</sub> <= CV <sub>switch</sub> . Also upper limit for the point estimate constraint. Defaults to 1.25 if not given explicitly.
CV	Intra-subject coefficient(s) of variation as ratio (not percent). <ul style="list-style-type: none"> <li>• If given as a scalar (length(CV)==1) the <i>same CV</i> of Test and Reference is assumed (homoscedasticity, <math>CV_{wT} = CV_{wR}</math>).</li> <li>• If given as a vector (length(CV)==2), <i>i.e.</i>, assuming heteroscedasticity, the <i>CV</i> of the Test <b>must</b> be given in CV[1] and the one of the Reference in the CV[2].</li> </ul>
design	Design of the study to be planned. "2x3x3" is the partial replicate design. "2x2x4" is a full replicate design with 2 sequences and 4 periods. "2x2x3" is a full replicate design with 2 sequences and 3 periods. Defaults to design="2x3x3". Details are given the section about Designs.
regulator	Regulatory settings for the widening of the BE acceptance limits. May be given as "EMA", "GCC", or as an object of class 'regSet' (see <a href="#">reg_const</a> ). Defaults to regulator="EMA" if missing. This argument may be given also in lower case if given as character. If given as object of class 'regSet' the component est_method must not be "ISC".
nsims	Number of simulations to be performed to obtain the (empirical) power. The default value 100,000 = 1e+5 is usually sufficient. Consider to rise this value if theta0 <=0.85 or >=1.20. But see the warning section.
nstart	Set this to a start for the sample size search if a previous run failed. After reworking the start n in version 1.1-05 rarely needed.
imax	Maximum number of steps in sample size search. Defaults to 100.
print	If TRUE (default) the function prints its results. If FALSE only the result data.frame will be returned.
details	If set to TRUE (default), the steps during sample size search are shown.
setseed	Simulations are dependent on the starting point of the (pseudo) random number generator. To avoid differences in power for different runs a set.seed(123456) is issued if setseed=TRUE, the default.
progress	Should a progressbar be shown? Defaults to TRUE if missing and nsims >5E5.

### Details

The methods rely on the analysis of log-transformed data, *i.e.*, assume a log-normal distribution on the original scale.

The expanded BE acceptance limits will be calculated by the formula  
 $[L, U] = \exp(\pm r\_const * sWR)$

with  $r\_const$  the regulatory constant and  $sWR$  the standard deviation of the within subjects variability of the Reference.  $r\_const = 0.76$  ( $-\log(1.25)/0.29356$ ) is used in case of `regulator="EMA"`. If the  $CV_{WR}$  is  $< CV_{switch}=0.3$  the conventional ABE limits apply (mixed procedure).

In case of `regulator="EMA"` a cap is placed on the widened limits if  $CV_{WR} > 0.50$ , *i.e.*, the widened limits are held at value calculated for  $CV_{WR} = 0.50$ .

In case of `regulator="GCC"` *fixed* wider limits of  $0.7500 - 1.3333$  for  $CV_{WR} > 0.30$  are applied and the conventional limits otherwise.

The simulations are done by simulating subject data (all effects fixed except the residuals) and evaluating these data via ANOVA of all data to get the point estimate of T vs. R along with its 90% CI and an ANOVA of the data under R(eference) only to get an estimate of  $s_{WR}^2$ .

The estimated sample size gives always the *total* number of subjects (not subject/sequence – like in some other software packages).

### Value

Returns a data.frame with the input settings and sample size results.

The Sample size column contains the total sample size.

The `nlast` column contains the last n value. May be useful for restarting.

### Designs

Although some designs are more ‘popular’ than others, sample size estimations are valid for *all* of the following designs:

"2x2x4"	TRTR   RTRT TRRT   RTTR TTRR   RRTT
"2x2x3"	TRT   RTR TRR   RTT
"2x3x3"	TRR   RTR   RRT

### Warning

The sample size estimation for very extreme  $\theta_0$  ( $<0.83$  or  $>1.21$ ) may be very time consuming and will eventually also fail since the start values chosen are not really reasonable in that ranges.

If you really need sample sizes in that range be prepared to restart the sample size estimation via the argument `nstart`.

Since the dependence of power from n is very flat in the mentioned region you may also consider to adapt the number of simulations not to get caught in the simulation error trap.

### Note

We are doing the sample size estimation only for balanced designs since the break down of the total subject number in case of unbalanced sequence groups is not unique. Moreover the formulas used are only for balanced designs.

The minimum sample size is 6, even if the power is higher than the intended targetpower.

Subject simulations are easily more than 100times slower than simulations based on the ‘key’ statistics. We recommend this function only for the partial replicate design (TRRIRTRIRRT) assuming heteroscedasticity in the case of  $CV_{wT} > CV_{wR}$ .

Thus be patient and go for a cup of coffee if you use this function with high sample sizes!

### Author(s)

H. Schütz

### References

Tóthfalusi L, Endrényi L. *Sample Sizes for Designing Bioequivalence Studies for Highly Variable Drugs*. J Pharm Pharmaceut Sci. 2011;15(1):73–84. [open access](#)

### See Also

[power.scABEL.sdsims](#), [sampleN.scABEL](#), [reg\\_const](#)

### Examples

```
# using the defaults:
# partial replicate design, targetpower=80%,
# true assumed ratio = 0.90, 1E+5 simulated studies
# ABE limits, PE constraint 0.8 - 1.25
# EMA regulatory settings
# Heteroscedasticity (CVwT 0.4, CVwR 0.3)
# compare results and run times

CV      <- c(0.4, 0.3)
expl    <- data.frame(method = c("subject simulations", "'key' statistics"),
                      n = NA, power = NA, seconds = NA)

start   <- proc.time()[[3]]
expl[1, 2:3] <- sampleN.scABEL.sdsims(CV = CV, print = FALSE,
                                     details = FALSE)[8:9]

expl[1, 4] <- proc.time()[[3]] - start
start     <- proc.time()[[3]]
expl[2, 2:3] <- sampleN.scABEL(CV = CV, print = FALSE,
                              details = FALSE)[8:9]

expl[2, 4] <- proc.time()[[3]] - start
print(expl, row.names = FALSE)
# should result in a sample size n=69, power=0.80198 for
# the subject simulations and n=66, power=0.80775 for the
# 'key' statistics
```

---

sampleN.TOST

*Sample size based on power of TOST*

---

### Description

Estimates the necessary sample size to have at least a given power.



**Usage**

```
sampleN.TOST(alpha = 0.05, targetpower = 0.8, logscale = TRUE,
             theta0, theta1, theta2, CV, design = "2x2", method="exact",
             robust=FALSE, print = TRUE, details = FALSE, imax=100)
```

**Arguments**

alpha	Significance level (one-sided). Commonly set to 0.05.
targetpower	Power to achieve at least. Must be >0 and <1. Typical values are 0.8 or 0.9.
logscale	Should the data used on log-transformed (TRUE) or on original scale (FALSE)? Defaults to TRUE.
theta0	‘True’ or assumed T/R ratio or difference. In case of logscale=TRUE it must be given as ratio T/R. If logscale=FALSE, the difference in means. In this case, the difference may be expressed in two ways: relative to the same (underlying) reference mean, i.e. as $(T-R)/R = T/R - 1$ ; or as difference in means T-R. Note that in the former case the units of CV, theta1 and theta2 need also be given relative to the reference mean (specified as ratio). Defaults to 0.95 if logscale=TRUE or to 0.05 if logscale=FALSE
theta1	Lower (bio-)equivalence limit. In case of logscale=TRUE it is given as ratio. If logscale=FALSE, the limit may be expressed in two ways: difference of means relative to the same (underlying) reference mean or in units of the difference of means. Note that in the former case the units of CV, theta0 and theta2 need also be given relative to the reference mean (specified as ratio). Defaults to 0.8 if logscale=TRUE or to -0.2 if logscale=FALSE.
theta2	Upper (bio-)equivalence limit. In case of logscale=TRUE it is given as ratio. If logscale=FALSE, the limit may be expressed in two ways: difference of means relative to the same (underlying) reference mean or in units of the difference of means. Note that in the former case the units of CV, theta0 and theta1 need also be given relative to the reference mean (specified as ratio). If not given, theta2 will be calculated as $1/\theta_1$ if logscale=TRUE or as $-\theta_1$ if logscale=FALSE.
CV	In case of logscale=TRUE the (geometric) coefficient of variation given as ratio. If logscale=FALSE the argument refers to (residual) standard deviation of the response. In this case, standard deviation may be expressed two ways: relative to a reference mean (specified as ratio $\sigma/\mu_R$ ), i.e. again as a coefficient of variation; or untransformed, i.e. as standard deviation of the response. Note that in the former case the units of theta0, theta1 and theta2 need also be given relative to the reference mean (specified as ratio).

In case of cross-over studies this is the within-subject CV, in case of a parallel-group design the CV of the total variability.

design	Character string describing the study design. See <code>known.designs()</code> for designs covered in this package.
method	Method for calculation of the power. Defaults to "exact" in which case the calculation is done based on formulas with Owen's Q. The calculation via Owen's Q can also be chosen with <code>method="owenq"</code> . Another exact method via direct use of the bivariate non-central <i>t</i> -distribution may be chosen with <code>method="mvt"</code> . This may have somewhat lower precision compared to Owen's Q and has a much longer run-time. Approximate calculations can be chosen via <code>method="noncentral"</code> or <code>method="nct"</code> for the approximation using the non-central <i>t</i> -distribution. With <code>method="central"</code> or <code>method="shifted"</code> the relatively crude approximation via the 'shifted' central <i>t</i> -distribution is chosen. The strings for method may be abbreviated.
robust	Defaults to FALSE. With that value the usual degrees of freedom will be used. Set to TRUE will use the degrees of freedom according to the 'robust' evaluation (aka Senn's basic estimator). These df are calculated as <code>n-seq</code> . See <code>known.designs()\$df2</code> for designs covered in this package. Has only effect for higher-order crossover designs.
print	If TRUE (default) the function prints its results. If FALSE only the data.frame with the results will be returned.
details	If TRUE the design characteristics and the steps during sample size calculations will be shown. Defaults to FALSE.
imax	Maximum number of steps in sample size search. Defaults to 100. Adaption only in rare cases needed.

### Details

The sample size is estimated via iterative evaluation of power of the TOST procedure. Start value for the sample size search is taken from a large sample approximation according to Zhang, modified.  
The sample size is bound to 4 as minimum.

The estimated sample size gives always the *total* number of subjects (not subject/sequence in crossovers or subjects/group in parallel designs – like in some other software packages).

### Value

A data.frame with the input and results will be returned.  
The Sample size column contains the total sample size.

### Warning

The function does not vectorize properly.  
If you need sample sizes with varying CVs, use f.i. for-loops or the apply-family.

**Note**

Of course it is highly recommended to use the default method="exact". :-)  
 There is no reason besides testing and for comparative purposes to use an approximation if the exact method is available at no extra costs.

**Author(s)**

D. Labes

**References**

Phillips KF. *Power of the Two One-Sided Tests Procedure in Bioequivalence*. J Pharmacokin Bio-pharm. 1990;18:137–44. doi: [10.1007/BF01063556](https://doi.org/10.1007/BF01063556)

Diletti D, Hauschke D, Steinijs VW. *Sample Size Determination for Bioequivalence Assessment by Means of Confidence Intervals*. Int J Clin Pharmacol Ther Toxicol. 1991;29(1):1–8.

Diletti D, Hauschke D, Steinijs VW. *Sample size determination: Extended tables for the multiplicative model and bioequivalence ranges of 0.9 to 1.11 and 0.7 to 1.43*. Int J Clin Pharmacol Ther Toxicol. 1992;30(Suppl 1):S59–62.

Zhang P. *A Simple Formula for Sample Size Calculation in Equivalence Studies*. J Biopharm Stat. 2003;13(3):529–538. doi: [10.1081/BIP120022772](https://doi.org/10.1081/BIP120022772)

**See Also**

[power.TOST](#), [known.designs](#)

**Examples**

```
# Exact calculation for a classical 2x2 cross-over (TR/RT),
# BE limits 80 ... 125%, assumed true BE ratio 0.95, intra-subject CV=30%,
# using all the default values
# should give n=40 power=0.815845
sampleN.TOST(CV = 0.3)

# Exact calculation for a parallel group design
# evaluation on the original (untransformed) scale
# BE limits 80 ... 120% = -20% ... +20% of reference,
# assumed true BE ratio 0.95% = -5% to reference mean,
# total CV=20%
# should give n=48 (total) power=0.815435
sampleN.TOST(logscale = FALSE, theta1 = -0.2, theta0 = -0.05,
              CV = 0.2, design = "parallel")

# A rather strange setting of theta0! Have a look at n.
# It would be better this is not the sample size but the running total
# of my bank account. But the first million is the hardest. ;-)
sampleN.TOST(CV = 0.2, theta0 = 0.8005, theta1 = 0.8)
```

---

 scABEL *Scaled (widened) BE Acceptance Limits*


---

**Description**

The (widened) scaled BE acceptance limits are calculated according to the regulatory settings of EMA, HC, FDA or via user defined regulatory settings.

**Usage**

```
scABEL(CV, regulator)
```

**Arguments**

CV	Coefficient of variation (of the Reference) as ratio.
regulator	Regulatory body settings for the widening of the BE acceptance limits. May be given as character from the choices "EMA", "HC" (Health Canada), "GCC" (Gulf Cooperation Council), "FDA" or as an object of class 'regSet' (see <a href="#">reg_const</a> ). Defaults to regulator="EMA" if missing. The former regulator="ANVISA" is no longer allowed. The ANVISA recommends since 2016 the EMA's regulatory settings. The former regulator="USER" is no longer accepted but can be handled now via function <code>reg_const()</code> to define an object with class 'regSet'.

**Details**

The widened BE acceptance limits are calculated by the formula  
 $[L, U] = \exp(-/+ r\_const * sWR)$   
 with `r_const` the regulatory constant and `sWR` the standard deviation of the within subjects variability of the Reference.

- regulator="EMA" or regulator="HC"  
 $r\_const = 0.76$  ( $\sim \log(1.25)/\sqrt{\log(0.30^2+1)}$ )
- regulator="GCC"  
 $r\_const = 0.97997 \dots$  ( $= \log(1/0.75)/\sqrt{\log(0.30^2+1)}$ )
- regulator="FDA"  
 $r\_const = 0.89257 \dots$  ( $= \log(1.25)/0.25$ )

If the CVwR of the Reference is  $< CVswitch=0.3$  the conventional ABE limits apply (mixed procedure).

In case of regulator="EMA" a cap is placed on the widened limits if  $CVwR > 0.5$ , *i.e.*, the widened limits are held at the value calculated for  $CVwR=0.5$ .

In case of regulator="HC" the capping is done such that the acceptance limits are 0.6666 ... 1.5 at maximum, *i.e.*,  $CVcap=0.57382$ . Literally it is given by Health Canada rounded to three significant digits as 57.4%.

**Value**

Returns a vector of length 2 if one CV is given or a matrix if CV is given as vector with named components lower and upper of the scaled acceptance limits.

**Note**

The scaled acceptance limits (coined '*implied limits*' by Davit *et al.*) are not directly used in the BE evaluation for HVDP(s) recommended by the FDA. They are included here for comparative purposes. Moreover, there are controversies where to locate the '*implied limits*' and whether the so-called '*desired consumer-risk model*' should be used.

**Author(s)**

D. Labes

**References**

Davit BM, Chen ML, Conner DP, Haidar SH, Kim S, Lee CH, Lionberger RA, Makhlof FT, Nwakama PE, Patel DT, Schuirmann DJ, Yu LX. *Implementation of a Reference-Scaled Average Bioequivalence Approach for Highly Variable Generic Drug Products by the US Food and Drug Administration*. AAPS J. 2012;14(4):915–24. doi: [10.1208/s122480129406x](https://doi.org/10.1208/s122480129406x)

Health Canada, Therapeutic Products Directorate. *Guidance Document. Comparative Bioavailability Standards: Formulations Used for Systemic Effects*. 2018/06/08. ISBN: 978-0-660-25514-9

**See Also**

[power.scABEL](#), [sampleN.scABEL](#), [reg\\_const](#)

**Examples**

```
scABEL(CV = 0.3, regulator = "EMA")
# should give the conventional (unscaled) BE limits:
# lower upper
# 0.80 1.25

scABEL(CV = 0.5, regulator = "EMA")
# should give the (maximum) expanded limits:
# lower upper
# 0.6983678 1.4319102

# define old ANVISA settings via reg_const()
rc <- reg_const("USER", r_const = 0.76,
               CVswitch = 0.4, CVcap = 0.5)
rc$name <- "ANVISAold"
scABEL(CV = 0.4, regulator = rc)
# should give the conventional (not expanded) limits:
# lower upper
# 0.80 1.25

scABEL(CV = 0.55, regulator = "HC")
```

```
# should give the widened limits:
#   lower   upper
# 0.6765789 1.4780241

scABEL(CV = 0.55, regulator = "GCC")
# should give the widened limits:
#   lower   upper
# 0.7500000 1.3333333

scABEL(CV = 0.55, regulator = "FDA")
# should give the 'implied' limits:
#   lower   upper
# 0.6320032 1.5822705
```

---

scABEL.ad

*Iteratively adjusted alpha for ABEL*


---

## Description

This function iteratively adjusts alpha for the BE decision via Average Bioequivalence with Expanding Limits (ABEL) based on simulations in order to maintain the consumer risk at the nominal level.

## Usage

```
scABEL.ad(alpha = 0.05, theta0, theta1, theta2, CV,
          design = c("2x3x3", "2x2x4", "2x2x3"), regulator,
          n, alpha.pre = 0.05, imax = 100, tol, print = TRUE,
          details = FALSE, setseed = TRUE, nsims = 1e+06,
          sdsims = FALSE, progress)
```

## Arguments

alpha	Type I Error (TIE) probability (nominal level of the test). Per convention commonly set to 0.05.
theta0	'True' or assumed T/R ratio. Defaults to 0.90 according to the two Lászlós if not given explicitly.
theta1	Conventional lower ABE limit to be applied in the mixed procedure if CVwR==CVswitch. Also lower limit for the point estimate constraint. Defaults to 0.80 if not given explicitly.
theta2	Conventional upper ABE limit to be applied in the mixed procedure if CVwR==CVswitch. Also upper limit for the point estimate constraint. Defaults to 1.25 if not given explicitly.
CV	Intra-subject coefficient(s) of variation as ratio (not percent). <ul style="list-style-type: none"> <li>If given as a scalar (length(CV)==1) the <i>same</i> CV of Test and Reference is assumed (homoscedasticity, CVwT==CVwR).</li> </ul>

- If given as a vector ( $\text{length}(\text{CV})=2$ ), *i.e.*, assuming heteroscedasticity, the CV of the Test **must** be given in CV[1] and the one of the Reference in the CV[2].

design	Design of the study. "2x3x3" is the partial replicate design. "2x2x4" is a full replicate design with 2 sequences and 4 periods. "2x2x3" is a full replicate design with 2 sequences and 3 periods. Defaults to "2x3x3". Details are given the section about Designs.
regulator	Regulatory settings for the expanding of the BE acceptance limits. Choose from "EMA" (default), "HC", "GCC", or "FDA". This argument may also be given in lower case.
n	Total sample size of the study or a vector of sample size / sequences. If n leads to an unbalanced design ( <i>i.e.</i> , is not a multiple of two in the full replicate designs or not a multiple of three in the partial replicate), the code tries to keep subjects / sequence as balanced as possible. In evaluating a particular <i>unbalanced</i> study <b>always</b> give n as a vector. Only if design="2x2x3" (TRT RTR) the <i>order</i> of sample sizes is important. n[1] is for sequence TRT and n[2] for sequence RTR. If n is missing, a sample size is estimated with target power 0.80 and pre-specified alpha if defined. Otherwise, alpha is used.
alpha.pre	Pre-specified alpha (optional). Must be $\leq \alpha$ . ABEL will be performed at level alpha.pre and the TIE assessed at level alpha. Less powerful than adjusting alpha but an alternative in the critical region of maximum inflation of the TIE. In certain scenarios Bonferroni's 0.025 is not sufficient to preserve the Type I Error ( <i>e.g.</i> , the third example). Not recommended if $\text{CVwR} \geq 0.45$ due to poor power characteristics.
imax	Maximum number of steps in sample size search. Defaults to 100.
tol	Desired accuracy (convergence tolerance). Defaults to 1E-6.
print	If TRUE (default), the function sends its results to the console.
details	If TRUE, the <i>relative</i> change of the consumer risk in percent is shown. Additionally information about the impact on power (for specified $\theta_0$ and target power 0.80), runtime, and number of simulations (iterations) are given. Defaults to FALSE.
setseed	Simulations are dependent on the starting point of the (pseudo) random number generator. To avoid differences in power for different runs <code>set.seed(123456)</code> is issued if <code>setseed=TRUE</code> (default).
nsims	Number of simulations to be performed to estimate the (empirical) TIE error and in each iteration of adjusting alpha. The default value 1,000,000 = 1E+6 should not be lowered.
sdsims	If FALSE (default) power is estimated by the respective 'key' statistics. Recommended for speed reasons. Set to TRUE if results of <code>power.scABEL</code> are expected to be inaccurate (partial replicate design with unbalanced sequences and/or heteroscedasticity where $\text{CVwT} > \text{CVwR}$ ) and subject data via <code>power.scABEL.sdsims</code> should be simulated instead. Very time consuming (easily 100times slower)! Subject data simulations are only supported for <code>regulator="EMA"</code> and <code>regulator="GCC"</code> .

progress            Set to TRUE if a progress bar should be displayed. Ignored if sdsims=FALSE.

### Details

The simulations are done via the distributional properties of the statistical quantities necessary for assessing BE based on ABEL. Simulations for the TIE are performed at the upper (expanded) limit  $U$  of the acceptance range. Due to the symmetry around 1 results are valid for the lower (expanded) limit  $L$  as well.

$U$  at the EMA's and Health Canada's CVcap, the GCC's for *any* CVwR > 0.3:

```
scABEL(CV=0.5, reg="EMA")[[ "upper" ]]
[1] 1.43191
scABEL(CV=0.57382, reg="HC")[[ "upper" ]]
[1] 1.5
scABEL(CV=0.5, reg="GCC")[[ "upper" ]]
[1] 1.333333
```

Simulated studies are evaluated by ANOVA (Method A) as recommended in the EMA' Q&A-document and by intra-subject contrasts if regulator="HC". Health Canada requires a mixed-effects model which cannot be implemented in R. However, intra-subjects contrasts are a sufficiently close approximation.

The Type I Error in ABEL depends only on CVwR and – to a minor degree – the sample size. Algorithm:

1. The TIE is assessed based on alpha (or alpha.pre) and compared to the nominal level of the test alpha.
2. If no inflation of the TIE is found, the algorithm stops.
3. Otherwise, alpha is iteratively adjusted (*i.e.*, alpha.adj < alpha) until no more relevant inflation of the TIE is detected (*i.e.*, abs(TIE - alpha) <= tol).

### Value

Sends results to the console if argument print=TRUE (default).

Returns a list with the input, adjusted alpha, and Type I Error (for nominal and adjusted alpha) if argument print=FALSE.

If no adjustment is necessary, NAs will be returned for the respective variables (alpha.adj, TIE.adj, rel.change, pwr.adj, rel.loss).

### Designs

Although some designs are more 'popular' than others, power calculations are valid for *all* of the following designs:

```
"2x2x4"  TRTR | RTRT
          TRRT | RTTR
          TTRR | RRTT
"2x2x3"  TRT | RTR
          TRR | RTT
"2x3x3"  TRR | RTR | RRT
```



### Warning

See the Warning section of the function `power.scABEL` concerning the power value agreement to the one obtained by simulations via subject data.

### Note

Specifying `theta0` is not necessary.

If `theta0` is not given, achievable power for the common target of 0.80 (both for `alpha` and adjusted `alpha`) will be estimated. If `theta0` is specified, its value will be used; again for target power 0.80. If you are interested in other levels of power, use `sampleN.scABEL.ad`.

The EMA's method is currently recommended in other jurisdictions as well (e.g., by the WHO; in ASEAN States, Australia, Brazil, Egypt, the Eurasian Economic Union, New Zealand, the Russian Federation, and the East African Community).

If `CVwR > 30%`, fixed wider limits of 0.7500–1.3333 are recommended by the Gulf Cooperation Council (Bahrain, Kuwait, Oman, Qatar, Saudi Arabia, United Arab Emirates).

### Author(s)

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**See Also**

[sampleN.scABEL.ad](#), [power.scABEL](#), [power.scABEL.sdsims](#), [scABEL](#)

**Examples**

```
# Using all defaults:
# TRR|RTR|RRT, target power 80% for assumed ratio 0.90 (estimated sample size 54),
# EMA regulatory settings (ABE limits and PE constraint 0.80 - 1.25),
# 1E+6 simulated studies.
# Not run: due to timing policy of CRAN for examples

scABEL.ad(CV = 0.3)
# Should result in adjusted alpha 0.03389 (TIE 0.5000, TIE for nominal alpha 0.07189).
#
# As above but subject data simulations.

scABEL.ad(CV = 0.3, sdsims = TRUE)
# Should result in adjusted alpha 0.03336 (TIE 0.5000, TIE for nominal alpha 0.07237).
#
# TRT|RTR, heteroscedasticity, sample size 48 (unbalanced), subject data simulations.

scABEL.ad(CV = c(0.25, 0.3), design = "2x2x3", n = c(23, 25), sdsims = TRUE)
# Should result in adjusted alpha 0.02465 (TIE 0.5000, TIE for nominal alpha 0.09050).
#
# TRTR|RTRT, CV 0.35, sample size 33 (unbalanced).

scABEL.ad(CV = 0.35, design = "2x2x4", n = c(16, 17))
# Should result in adjusted alpha 0.03632 (TIE 0.5000, TIE for nominal alpha 0.06544).
```

---

type1error.2TOST

*Type I error rate for two simultaneous TOST procedures*

---

**Description**

Was designed to calculate the type I error rate of two simultaneous TOST procedures (where the two parameters of the two TOSTs are correlated with some correlation) for various study designs used in BE studies.

Is defunct now since it suffers from insufficient precision to obtain the type 1 error (TIE) via simulations.

Due to the intersection-union principle the TIE is always upper bounded to alpha by theory.

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