

# Package ‘replicateBE’

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**Title** Average Bioequivalence with Expanding Limits (ABEL)

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**Depends** R (>= 3.5.0)

**Imports** readxl (>= 1.0.0), PowerTOST (>= 1.3.3), lmerTest, nlme,  
pbkrtest, graphics, grDevices

**Suggests** knitr, rmarkdown, testthat, devtools

**Description** Performs comparative bioavailability calculations for Average Bioequivalence with Expanding Limits (ABEL). Implemented are 'Method A' and 'Method B' and the detection of outliers.  
If the design allows, assessment of the empiric Type I Error and iteratively adjusting alpha to control the consumer risk.  
Average Bioequivalence - optionally with a tighter (narrow therapeutic index drugs) or wider acceptance range (Gulf Cooperation Council: Cmax) - is implemented as well.

**License** GPL (>=3)

**LazyData** true

**VignetteBuilder** knitr

**URL** <https://github.com/Helmut01/replicateBE>

**BugReports** <https://github.com/Helmut01/replicateBE/issues>

**NeedsCompilation** no

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ABE	<i>Comparative BA-calculation for Average Bioequivalence</i>
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## Description

This function performs the required calculations for the BE decision via conventional (unscaled) Average Bioequivalence based on ANOVA as recommended in the EMA's guideline.

## Usage

```
ABE(alpha = 0.05, path.in = "~/", path.out = "~/",
     file, set = "", ext, na = ".", sep = ",", dec = ".",
     logtrans = TRUE, print = TRUE, details = FALSE,
     verbose = FALSE, ask = FALSE, data = NULL, theta1, theta2)
```

## Arguments

alpha	Type I Error (TIE) probability (nominal level of the test). Conventionally set to 0.05, resulting in a $100(1 - 2\alpha)$ confidence interval.
path.in	Path to the data file for import. If missing or not existing the user's home folder "~/ " will be used.
path.out	Path to save the result file if print=TRUE. The user must have write-permission to the directory. If missing or not existing the user's home folder "~/ " will be used.
file	Name of the dataset for import ( <i>without</i> extension). Must be a string ( <i>i.e.</i> , enclosed in single or double quotation marks). The name is case-sensitive.
set	Name of the sheet of an Excel-file (mandatory). Must be a string ( <i>i.e.</i> , enclosed in single or double quotation marks). The name is case-sensitive.
ext	File-extension ("csv" or "xls(x)") enclosed in single or double quotation marks.

na	Character string denoting missing values. Acceptable are "NA" (not available), "ND" (not determined), "." (SAS), "Missing" (Phoenix WinNonlin), and "" (EXCEL; empty cell). Missings will be converted to NA in the imported data. Defaults to ".".
sep	Variable separator in the CSV-file. Acceptable are "," (comma = ASCII 44), ";" (semicolon = ASCII 59), and "\t" (tabulator = ASCII 9). Defaults to ",".
dec	Decimal separator in the CSV-file. Acceptable are "." (period = ASCII 46) or "," (comma = ASCII 44). Defaults to ".".
logtrans	If TRUE (default) the raw data (provided in column PK) will be internally log-transformed and used in the calculations. If FALSE the already log-transformed data (provided in the column logPK) will be used in the calculations.
print	If TRUE (default), the function prints its results to a file. If FALSE, returns a data.frame of results.
details	Defaults to FALSE. If TRUE, the function sends its results in 7-digits precision to a data.frame.
verbose	Defaults to FALSE. If TRUE the ANOVA-table is send to the console.
ask	Defaults to FALSE. If TRUE the user will be asked whether an already existing result file should be overwritten.
data	Specification of one of the internal reference datasets (rds01 – rds28). If given, path.in, file, set, and ext are ignored. For its use see the examples. If not given, defaults to NULL ( <i>i.e.</i> , import data from a file).
theta1	Lower limit of the acceptance range. Defaults to 0.80. If missing will be set to 1/theta2.
theta2	Upper limit of the acceptance range. Defaults to 1.25. If missing will be set to 1/theta1.

## Details

The model for the treatment comparison is

```
lm(log(PK) ~ sequence + subject%in%sequence + period + treatment, data = data)
```

where all effects are fixed.

Tested designs

- 4-period 2-sequence full replicates  
TRTR | RTRT  
TRRT | RTTR  
TTRR | RRTT
- 2-period 4-sequence replicate  
TR | RT | TT | RR (Balaam's design)
- 4-period 4-sequence full replicates  
TRTR | RTRT | TRRT | RTTR  
TRRT | RTTR | TTRR | RRTT
- 3-period 2-sequence full replicates  
TRT | RTR  
TRR | RTT

- 3-period (partial) replicates  
TRR | RTR | RRT  
TRR | RTR (extra-reference design)

#### Data structure

- Columns must have the headers subject, period, sequence, treatment, PK, and/or logPK. Any order of columns is acceptable. Uppercase and mixed case headers will be internally converted to lowercase headers.
  - subject must be integer numbers or (any combination of) alphanumerics [A-Z, a-z, -, \_, #, 0-9]
  - period must be integer numbers.
  - sequence must be contained in the tested designs (numbers or *e.g.*, ABAB are not acceptable).
  - The Test treatment must be coded T and the Reference R.

#### Value

Prints results to a file if argument `print = TRUE` (default).

If argument `print = FALSE`, returns a `data.frame` with the elements:

Design	<i>e.g.</i> , TRTR RTRT
Method	ABE
n	total number of subjects
nTT	number of subjects with two treatments of T (full replicates only)
nRR	number of subjects with two treatments of R
Sub/seq	number of subjects per sequence
Miss/seq	if the design is unbalanced, number of missings per sequence
Miss/per	if the design is incomplete, number of missings per period
alpha	nominal level of the test
DF	degrees of freedom of the treatment comparison
CVwT(%)	intra-subject coefficient of variation of the test treatment (full replicates only)
CVwR(%)	intra-subject coefficient of variation of the reference treatment
BE.lo(%)	lower bioequivalence limit ( <i>e.g.</i> , 80)
BE.hi(%)	upper bioequivalence limit ( <i>e.g.</i> , 125)
CI.lo(%)	lower confidence limit of the treatment comparison
CI.hi(%)	upper confidence limit of the treatment comparison
PE(%)	point estimate of the treatment comparison (aka GMR)
BE	assessment whether the $100(1 - 2\alpha)$ CI lies entirely within the acceptance range (pass/fail)

#### Warning

Files may contain a commentary header. If reading from a CSV-file, *each* line of the commentary header *must* start with "# " (hash space = ASCII 35 ASCII 32). If reading from an Excel-file all lines preceding the column headers are treated as a comment.

## Clarification

The ‘graphical’ presentation in the result file gives the confidence limits with filled black squares and the point estimate as a white rhombus. If a confidence limit exceeds the drawing range, it is shown as a triangle. The BE limits and 100% are given with single vertical lines. The ‘resolution’ is approximately 0.5% and therefore, not all symbols might be shown. The CI and PE take precedence over the limits.

## Note

The EMA’s model assumes equal [*sic!*] intra-subject variances of test and reference (like in 2×2×2 trials) – even if proven false in one of the full replicate designs (were *both*  $CV_{wT}$  and  $CV_{wR}$  can be estimated). Hence, amongst biostatisticians it is called the “crippled model” because the replicative nature of the study is ignored.

Conventional unscaled ABE has to be employed for  $C_{max}$  (if widening of the acceptance range is clinically not justifiable),  $AUC_{0-t}$ ,  $AUC_{0-72}$  (immediate release products) and  $C_{max,ss}$ ,  $C_{\tau,ss}$ , *partial*  $AUC$  (if widening of the acceptance range is clinically not justifiable), and  $AUC_{0-t}$ ,  $AUC_{0-\infty}$ ,  $AUC_{0-\tau}$  (modified release products).

**Program offered for Use without any Guarantees and Absolutely No Warranty. No Liability is accepted for any Loss and Risk to Public Health Resulting from Use of this R-Code.**

## Author(s)

Helmut Schütz

## References

European Medicines Agency, Committee for Medicinal Products for Human Use. *Guideline on the Investigation of Bioequivalence*. London, 20 January 2010. [CPMP/EWP/QWP/1401/98 Rev. 1/ Corr \\*\\*](#)

European Medicines Agency, Committee for Medicinal Products for Human Use. *Guideline on the pharmacokinetic and clinical evaluation of modified release dosage forms*. London, 20 November 2014. [EMA/CPMP/EWP/280/96 Corr1](#)

## See Also

[method.A](#) evaluation for ABEL by a fixed effects model (ANOVA)  
[method.B](#) evaluation for ABEL by a linear mixed effects model

## Examples

```
# Importing from a CSV-file, using most of the defaults: variable
# separator comma, decimal separator period, print to file.
# Note: You must adapt the path-variables. The example reads from
# the data provided by the library. Write-permissions must be granted
```

```
# for 'path.out' in order to save the result file. If 'path.out' is
# not specified, results are written to the home folder.
path.in <- paste0(find.package("replicateBE"), "/extdata/")
ABE(path.in = path.in, file = "DS", set = "02", ext = "csv")
# Should result in:
# BE-limits      : 80.00% ... 125.00%
# Confidence interval: 97.32% ... 107.46% pass
# Point estimate  : 102.26%
# Generate the data.frame of results (7-digits precision) and show
# in the console. Use an internal dataset.
x <- ABE(details = TRUE, print = FALSE, data = rds02)
print(x, row.names = FALSE)

# Assuming a NTID and assess BE with narrower limits.
ABE(data = rds02, theta1 = 0.90)
# Should result in:
# BE-limits      : 90.00% ... 111.11%
# Confidence interval: 97.32% ... 107.46% pass
# Point estimate  : 102.26%
```

---

method.A	<i>Comparative BA-calculation for Average Bioequivalence with Expanding Limits by the EMA's 'Method A'</i>
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**Description**

This function performs the required calculations for the mixed (or aggregate) BE decision via Average Bioequivalence with Expanding Limits (ABEL) based on ANOVA ('Method A') as recommended in *Annex I*.

**Usage**

```
method.A(alpha = 0.05, path.in = "~/", path.out = "~/",
         file, set = "", ext, na = ".", sep = ",", dec = ".",
         logtrans = TRUE, ola = FALSE, print = TRUE, details = FALSE,
         adjust = FALSE, verbose = FALSE, ask = FALSE,
         plot.bxp = FALSE, fence = 2, data = NULL)
```

**Arguments**

alpha	Type I Error (TIE) probability (nominal level of the test). Conventionally set to 0.05, resulting in a $100(1 - 2\alpha)$ confidence interval.
path.in	Path to the data file for import. If missing or not existing the user's home folder "~/ " will be used.
path.out	Path to save the result file if print = TRUE. The user must have write-permission to the directory. If missing or not existing the user's home folder "~/ " will be used.

file	Name of the dataset for import ( <i>without</i> extension). Must be a string ( <i>i.e.</i> , enclosed in single or double quotation marks).
set	Name of the sheet of an Excel-file (mandatory). Must be a string ( <i>i.e.</i> , enclosed in single or double quotation marks).
ext	File-extension enclosed in single or double quotation marks. Acceptable are "csv" for comma delimited variables (CSV) or "xls", "xlsx" for Excel-files. The file-extension is not case-sensitive.
na	Character string denoting missing values. Acceptable are "NA" (not available), "ND" (not determined), "." (SAS), "Missing" (Phoenix WinNonlin), and "" (EXCEL; empty cell). Missings will be converted to NA in the imported data. Defaults to ".".
sep	Variable separator in the CSV-file. Acceptable are "," (comma = ASCII 44), ";" (semicolon = ASCII 59), and "\t" (tabulator = ASCII 9). Defaults to ",".
dec	Decimal separator in the CSV-file. Acceptable are "." (period = ASCII 46) or ",", (comma = ASCII 44). Defaults to ".".
logtrans	If TRUE (default) the raw data (provided in column PK) will be internally log-transformed and used in the calculations. If FALSE the already log-transformed data (provided in the column logPK) will be used in the calculations.
ola	Defaults to FALSE. If TRUE an outlier analysis based on the studentized and standardized (aka internally studentized) residuals of the model estimating CVwR is performed.
print	If TRUE (default), the function prints its results to a file. If FALSE, returns a data.frame of results.
details	Defaults to FALSE. If TRUE, the function sends its results in full precision to a data.frame.
adjust	Defaults to FALSE. If TRUE, the empiric Type I Error is evaluated via simulations (by <a href="#">scABEL.ad</a> of library PowerTOST). Currently implemented designs are TRTR RTTR, TRT RTTR, and TRR RTTR RR. If the TIE exceeds the nominal level of the test $\alpha$ , $\alpha$ is iteratively adjusted until $TIE = \alpha \pm 1E - 6$ . If ola = TRUE and outlier(s) found – which lead to an always lower – recalculated CVwR, the assessment is repeated for its value.
verbose	Defaults to FALSE. If TRUE the ANOVA-table is send to the console. If ola = TRUE additional information about outliers are shown.
ask	Defaults to FALSE. If TRUE the user will be asked whether an already existing result file (and if outliers are found, the box plot) should be overwritten.
plot.bxp	Only observed if ola = TRUE and at least one outlier is found. If FALSE (default) the box plot will be shown in the graphics device. If TRUE the box plot will be saved in PNG format to path.out.
fence	Only observed if ola = TRUE. The limit for outlier detection as a multiplier of the interquartile range. Defaults to 2. Less outliers will be detected with higher values (not recommended).
data	Specification of one of the internal reference datasets (rds01–rds30). If given, path.in, file, set, and ext are ignored. For its use see the examples. If not given, defaults to NULL ( <i>i.e.</i> , import data from a file).

## Details

The model for the estimation of CVwR is

$\text{lm}(\log(\text{PK}) \sim \text{sequence} + \text{subject\%in\%sequence} + \text{period}, \text{data} = \text{data}[\text{data\$treatment} == "R",])$   
 where all effects are fixed.

The model for the treatment comparison is

$\text{lm}(\log(\text{PK}) \sim \text{sequence} + \text{subject\%in\%sequence} + \text{period} + \text{treatment}, \text{data} = \text{data})$   
 where all effects are fixed.

### Tested designs

- 4-period 2-sequence full replicates  
 TRTR | RTRT  
 TRRT | RTTR  
 TTRR | RRTT
- 2-period 4-sequence replicate  
 TR | RT | TT | RR (Balaam's design)
- 4-period 4-sequence full replicates  
 TRTR | RTRT | TRRT | RTTR  
 TRRT | RTTR | TTRR | RRTT
- 3-period 2-sequence full replicates  
 TRT | RTR  
 TRR | RTT
- 3-period (partial) replicates  
 TRR | RTR | RRT  
 TRR | RTR (extra-reference design)

### Data structure

- Columns must have the headers subject, period, sequence, treatment, PK, and/or logPK.  
 Any order of columns is acceptable.  
 Uppercase and mixed case headers will be internally converted to lowercase headers.
  - subject must be integer numbers or (any combination of) alphanumerics  
 [A-Z, a-z, -, \_, #, 0-9]
  - period must be integer numbers.
  - sequence must be contained in the tested designs (numbers or *e.g.*, ABAB are not acceptable).
  - The Test treatment must be coded T and the Reference R.

## Value

Prints results to a file if argument `print = TRUE` (default).

If argument `print = FALSE`, returns a data.frame with the elements:

Design	<i>e.g.</i> , TRTR RTRT
Method	A
n	total number of subjects
nTT	number of subjects with two treatments of T (full replicates only)



nRR	number of subjects with two treatments of R
Sub/seq	number of subjects per sequence
Miss/seq	if the design is unbalanced, number of missings per sequence
Miss/per	if the design is incomplete, number of missings per period
alpha	nominal level of the test
DF	degrees of freedom of the treatment comparison
CVwT(%)	intra-subject coefficient of variation of the test treatment (full replicates only)
CVwR(%)	intra-subject coefficient of variation of the reference treatment
sw.ratio	ratio of intrasubject variabilities of T and R (full replicates only)
sw.ratio.CL	upper confidence limit of sw.ratio (full replicates only)

- If reference-scaling is applicable (*i.e.*, CVwR(%) >30%):

L(%)	lower expanded limit of the acceptance range (AR)
U(%)	upper expanded limit of the acceptance range (AR)

- If reference-scaling is not applicable (*i.e.*, CVwR(%) ≤30%):

BE.lo(%)	lower limit of the conventional AR ( 80)
BE.hi(%)	upper limit of the conventional AR (125)

CL.lo(%)	lower confidence limit of the treatment comparison
CL.hi(%)	upper confidence limit of the treatment comparison
PE(%)	point estimate of the treatment comparison (aka GMR)
CI	assessment whether the $100(1 - 2\alpha)$ CI lies entirely within the acceptance range (pass/fail)
GMR	assessment whether the PE lies entirely within the GMR-restriction 80.00%–125.00% (pass/fail)
BE	mixed (aggregate) assessment whether the study demonstrates bioequivalence (pass/fail)
log.half-width	half-width of the confidence interval in log-scale

If ola = TRUE and at least one studentized outlier was detected:

outlier	outlying subject(s)
CVwR.rec(%)	intra-subject coefficient of variation of R; recalculated after exclusion of outlier(s)
sw.ratio.rec	ratio of intrasubject variabilities of T and R after exclusion of outlier(s); full replicates only
sw.ratio.rec.CL	upper confidence limit of sw.ratio.rec (full replicates only)

- If reference-scaling is applicable (*i.e.*, CVwR.rec(%) >30%):

L.rec(%)	recalculated lower expanded limit of the AR
U.rec(%)	recalculated upper expanded limit of the AR

- If reference-scaling is not applicable (*i.e.*, CVwR.rec(%) ≤30%):

BE.rec.lo(%)	lower limit of the conventional AR ( 80)
BE.rec.hi(%)	upper limit of the conventional AR (125)

CI.rec	assessment whether the $100(1 - 2\alpha)$ CI lies entirely within the new acceptance range (pass/fail)
--------	--------------------------------------------------------------------------------------------------------

GMR.rec	assessment whether the PE lies entirely within the GMR-restriction 80.00%–125.00% (pass/fail)
BE.rec	mixed (aggregate) assessment whether the study demonstrates bioequivalence (pass/fail)

## Warning

Files may contain a commentary header. If reading from a CSV-file, *each* line of the commentary header *must* start with "# " (hash space = ASCII 35 ASCII 32). If reading from an Excel-file all lines preceding the column headers are treated as a comment.

## Clarification

The ‘graphical’ presentation in the result file gives the confidence limits with filled black squares and the point estimate as a white rhombus. If a confidence limit exceeds the maximum possible expansion limit, it is shown as a triangle. Expanded limits are given as double vertical lines. Unscaled limits, the GMR restriction, and 100% are given with single vertical lines. The ‘resolution’ is approximately 0.5% and therefore, not all symbols might be shown. The CI and PE take precedence over the limits and the expanded limits over unscaled ones.

## Note

The EMA’s model specified as ‘Method B’ in *Annex I* assumes equal [*sic*] intra-subject variances of test and reference (like in  $2 \times 2 \times 2$  trials) – even if proven false in one of the full replicate designs (were *both*  $CV_{wT}$  and  $CV_{wR}$  can be estimated). Hence, amongst biostatisticians it is called the “crippled model” because the replicative nature of the study is ignored.

The half-width of the CI in log-scale allows a comparison of methods (B *v.s.* A) where a higher value *might* point towards a more conservative decision. In the provided reference datasets – with one exception – the conclusion of BE (based on the mixed CI and GMR criteria) agrees between ‘Method A’ and ‘Method B’. However, for the highly incomplete dataset 14 ‘Method A’ was *liberal* (passing by ANOVA but failing by the mixed effects model).

Reference-scaling is acceptable for  $C_{max}$  (immediate release products) and  $C_{max,ss}$ ,  $C_{\tau,ss}$ , and *partial* AUC (modified release products). However, quoting the BE guideline:

*The applicant should justify that the calculated intra-subject variability is a reliable estimate and that it is not the result of outliers.*

Quoting the Q&A on the Revised EMA Bioequivalence Guideline:

*... a study could be acceptable if the bioequivalence requirements are met both including the outlier subject (using the scaled average bioequivalence approach and the within-subject CV with this subject) and after exclusion of the outlier (using the within-subject CV without this subject).*

*An outlier test is not an expectation of the medicines agencies but outliers could be shown by a box plot. This would allow the medicines agencies to compare the data between them.*

The EMA’s method of reference-scaling for highly variable drugs / drug products is currently recommended in other jurisdictions as well (*e.g.*, the WHO; ASEAN States, Australia, Brazil, Egypt, the Russian Federation, the Eurasian Economic Union, the East African Community, New Zealand).

The WHO accepts reference-scaling for AUC (4-period full replicate studies are mandatory in order to assess the variability associated with each product). It is an open issue how this assessment should

be done. In Population Bioequivalence (PBE) and Individual Bioequivalence (IBE) the  $s_{wT}/s_{wR}$  ratio was assessed and similar variability was concluded for a ratio within 0.667–1.500. However, the power of comparing variabilities in a study designed to demonstrate ABE is low. This was one of the reasons why PBE and IBE were not implemented in regulatory practice. An alternative approach is given in the FDA's guidance on warfarin. Variabilities are considered comparable if the upper confidence limit of  $\sigma_{wT}/\sigma_{wR}$  is less than or equal to 2.5.

**Program offered for Use without any Guarantees and Absolutely No Warranty. No Liability is accepted for any Loss and Risk to Public Health Resulting from Use of this R-Code.**

#### Author(s)

Helmut Schütz, Michael Tomashevskiy, Detlew Labes

#### References

European Medicines Agency, Committee for Medicinal Products for Human Use. *Guideline on the Investigation of Bioequivalence*. London, 20 January 2010. [CPMP/EWP/QWP/1401/98 Rev. 1/ Corr \\*\\*](#)

3<sup>rd</sup> EGA Symposium on Bioequivalence. *Questions and Answers on the Revised EMA Bioequivalence Guideline*. London, 1 June 2010. [open access](#)

European Medicines Agency. *Clinical pharmacology and pharmacokinetics: questions and answers*. 3.1 Which statistical method for the analysis of a bioequivalence study does the Agency recommend? Annex I. London, 21 September 2016. [EMA/582648/2016](#)

European Medicines Agency, Committee for Medicinal Products for Human Use. *Guideline on the pharmacokinetic and clinical evaluation of modified release dosage forms*. London, 20 November 2014. [EMA/CPMP/EWP/280/96 Corr1](#)

World Health Organization, Prequalification Team: medicines. *Guidance Document: Application of reference-scaled criteria for AUC in bioequivalence studies conducted for submission to PQTm*. Geneva, 22 November 2018. [open access](#)

Food and Drug Administration, Office of Generic Drugs. *Draft Guidance on Warfarin Sodium*. Rockville, December 2012. [open access](#)

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

<a href="#">method.B</a>	evaluation by a linear mixed effects model (subjects random)
<a href="#">ABE</a>	evaluation for conventional (unscaled) Average Bioequivalence

#### Examples

```
# Importing from a CSV-file, using most of the defaults: variable
# separator colon, decimal separator period, no outlier-analysis,
# print to file.
```

```

# Note: You must adapt the path-variables. The example reads from
# the data provided by the library. Write-permissions must be granted
# for 'path.out' in order to save the result file. If 'path.out' is
# not specified, results are written to the home folder.

path.in <- paste0(find.package("replicateBE"), "/extdata/")
method.A(path.in = path.in, file = "DS", set = "01", ext = "csv")
# Should result in:
#   CVwT           : 35.16%
#   swT            : 0.34138
#   CVwR           : 46.96% (reference-scaling applicable)
#   swR            : 0.44645
#   Expanded limits : 71.23% ... 140.40% [100exp(±0.760·swR)]
#   swT / swR       : 0.7647 (similar variabilities of T and R)
#   sw-ratio (upper CL): 0.9324 (comparable variabilities of T and R)
#   Confidence interval: 107.11% ... 124.89% pass
#   Point estimate   : 115.66% pass
#   Mixed (CI & PE)  : pass
#
# Internal reference dataset 01 used and results to the home
# folder. Additional outlier-analysis and box plot saved as PNG
# (accidental overwriting prevented).
method.A(ola = TRUE, ask = TRUE, plot.bxp = TRUE, data = rds01)
# Should give the same as above. Additionally:
#   Outlier fence      : 2×IQR of studentized residuals.
#   Recalculation due to presence of 2 outliers (subj. 45|52)
#   CVwR (outl. excl.) : 32.16% (reference-scaling applicable)
#   swR (recalculated) : 0.31374
#   Expanded limits    : 78.79% ... 126.93% [100exp(±0.760·swR)]
#   swT / swR (recalc.): 1.0881 (similar variabilities of T and R)
#   sw-ratio (upper CL): 1.3282 (comparable variabilities of T and R)
#   Confidence interval: pass
#   Point estimate      : pass
#   Mixed (CI & PE)     : pass
# Same dataset. Show information about outliers and the ANOVA-table.
method.A(ola = TRUE, verbose = TRUE, data = rds01)
# Generate the data.frame of results (full precision) and show it
# in the console
x <- method.A(ola = TRUE, details = TRUE, print = FALSE, data = rds01)
print(x, row.names = FALSE)
#
# Assess the Type I Error and iteratively adjust alpha if necessary.
# Not run: due to timing policy of CRAN for examples

method.A(adjust = TRUE, data = rds01)
# Should give in the result file:
#   Assessment of the empiric Type I Error (TIE); 1,000,000 studies simulated.
#   TIE not > nominal 0.05; consumer risk is controlled.
#
# Same with recalculation based on outliers, iteratively adjust alpha
# if necessary

method.A(ola = TRUE, adjust = TRUE, data = rds01)

```

```

# Should give in the result file:
#   Assessment of the empiric Type I Error (TIE) based on original CVwR;
#   1,000,000 studies simulated.
#   TIE not > nominal 0.05; consumer risk is controlled.
#   Assessment of the empiric Type I Error (TIE) based on recalculated CVwR;
#   1,000,000 studies in each of the 8 iterations simulated.
#   TIE for alpha 0.050000      : 0.07018
#   TIE for adjusted alpha 0.033416: 0.05000
#
# Repeat the evaluation with the adjusted alpha.

method.A(alpha = 0.033416, ola = TRUE, adjust = TRUE, data = rds01)
# Should give in the result file:
#   alpha      : 0.033416 (93.3168% CI)
#   Confidence interval: 106.16% ... 126.00% pass
#   Point estimate   : 115.66% pass
#   Mixed (CI & PE)  : pass
#   Assessment based on recalculated CVwR 32.16%
#   Confidence interval: pass
#   Point estimate   : pass
#   Mixed (CI & PE)  : pass
#   Assessment of the empiric Type I Error (TIE) based on original CVwR;
#   1,000,000 studies simulated.
#   TIE not > nominal 0.05; consumer risk is controlled.
#   Assessment of empiric Type I Error (TIE) based on recalculated CVwR;
#   1,000,000 studies in each of the 8 iterations simulated.
#   TIE for alpha 0.033416      : 0.05000
#   TIE not > nominal 0.05; consumer risk is controlled.

```

method.B

*Comparative BA-calculation for Average Bioequivalence with Expanding Limits by the EMA's 'Method B'*

## Description

This function performs the required calculations for the mixed (or aggregate) BE decision via Average Bioequivalence with Expanding Limits (ABEL) based on a linear mixed effects model with subjects as a random effect ('Method B') as specified in *Annex I*.

## Usage

```

method.B(alpha = 0.05, path.in = "~/", path.out = "~/",
         file, set = "", ext, na = ".", sep = ",", dec = ".",
         logtrans = TRUE, ola = FALSE, print = TRUE, details = FALSE,
         verbose = FALSE, ask = FALSE, plot.bxp = FALSE,
         fence = 2, data = NULL, option = 2)

```

**Arguments**

<code>alpha</code>	Type I Error (TIE) probability (nominal level of the test). Conventionally set to 0.05, resulting in a $100(1 - 2\alpha)$ confidence interval.
<code>path.in</code>	Path to the data file for import. If missing or not existing the user's home folder "~/ " will be used.
<code>path.out</code>	Path to save the result file if <code>print=TRUE</code> . The user must have write-permission to the directory. If missing or not existing the user's home folder "~/ " will be used.
<code>file</code>	Name of the dataset for import ( <i>without</i> extension). Must be a string ( <i>i.e.</i> , enclosed in single or double quotation marks).
<code>set</code>	Name of the sheet of an Excel-file (mandatory). Must be a string ( <i>i.e.</i> , enclosed in single or double quotation marks).
<code>ext</code>	File-extension enclosed in single or double quotation marks. Acceptable are "csv" for comma delimited variables (CSV) or "xls", "xlsx" for Excel-files. The file-extension is not case-sensitive.
<code>na</code>	Character string denoting missing values. Acceptable are "NA" (not available), "ND" (not determined), "." (SAS), "Missing" (Phoenix WinNonlin), and "" (EXCEL; empty cell). Missings will be converted to NA in the imported data. Defaults to ".".
<code>sep</code>	Variable separator in the CSV-file. Acceptable are "," (comma = ASCII 44), ";" (semicolon = ASCII 59), and "\t" (tabulator = ASCII 9). Defaults to ",".
<code>dec</code>	Decimal separator in the CSV-file. Acceptable are "." (period = ASCII 46) or "," (comma = ASCII 44). Defaults to ".".
<code>logtrans</code>	If TRUE (default) the raw data (provided in column PK) will be internally log-transformed and used in the calculations. If FALSE the already log-transformed data (provided in the column logPK) will be used in the calculations.
<code>ola</code>	Defaults to FALSE. If TRUE an outlier analysis based on the studentized and standardized (aka internally studentized) residuals of the model estimating CVwR is performed.
<code>print</code>	If TRUE (default), the function prints its results to a file. If FALSE, returns a data.frame of results.
<code>details</code>	Defaults to FALSE. If TRUE, the function sends its results in full precision to a data.frame.
<code>verbose</code>	Defaults to FALSE. If TRUE the model-table is send to the console. If <code>ola = TRUE</code> additional information about outliers are shown.
<code>ask</code>	Defaults to FALSE. If TRUE the user will be asked whether an already existing result file (and if outliers are found, the box plot) should be overwritten.
<code>plot.bxp</code>	Only observed if <code>ola = TRUE</code> and at least one outlier is found. If FALSE (default) the box plot will be shown in the graphics device. If TRUE the box plot will be saved in PNG format to <code>path.out</code> .
<code>fence</code>	Only observed if <code>ola = TRUE</code> . The limit for outlier detection as a multiplier of the interquartile range. Defaults to 2. Less outliers will be detected with higher values (not recommended).

data	Specification of one of the internal reference datasets (rds01–rds30). If given, path.in, file, set, and ext are ignored. For its use see the examples. If not given, defaults to NULL ( <i>i.e.</i> , import data from a file).
option	If 2 (default), the model will be evaluated by lme() of package nlme. The degrees of freedom of the treatment comparison will be equivalent to SAS' DDFM=CONTAIN and Phoenix WinNonlin's Residual. If 1 or 3, the model will be evaluated by lmer() of package lmerTest. With 1 the degrees of freedom of the treatment comparison will be equivalent to SAS' DDFM=SATTERTHWAITE and Phoenix WinNonlin's Satterthwaite. 3 uses the Kenward-Roger approximation.

## Details

The model for the estimation of CVwR is

```
lm(log(PK) ~ sequence + subject%in%sequence + period, data = data[data$treatment == "R",])
```

where all effects are fixed.

The model for the treatment comparison is with the default option=2

```
lme(log(PK) ~ sequence + period + treatment, random = ~1|subject, data = data)
```

and with option=1, option=3

```
lmer(log(PK) ~ sequence + period + treatment + (1|subject), data = data)
```

where sequence, period, and treatment are fixed effects and subject(sequence) is a random effect.

## Tested designs

- 4-period 2-sequence full replicates  
TRTR | RTRT  
TRRT | RTTR  
TTRR | RRTT
- 2-period 4-sequence replicate  
TR | RT | TT | RR (Balaam's design)
- 4-period 4-sequence full replicates  
TRTR | RTRT | TRRT | RTTR  
TRRT | RTTR | TTRR | RRTT
- 3-period 2-sequence full replicates  
TRT | RTR  
TRR | RTT
- 3-period (partial) replicates  
TRR | RTR | RRT  
TRR | RTR (extra-reference design)

## Data structure

- Columns must have the headers subject, period, sequence, treatment, PK, and/or logPK. Any order of columns is acceptable.  
Uppercase and mixed case headers will be internally converted to lowercase headers.
  - subject must be integer numbers or (any combination of) alphanumerics [A-Z, a-z, -, \_, #, 0-9]

- period must be integer numbers.
- sequence must be contained in the tested designs (numbers or *e.g.*, ABAB are not acceptable).
- The Test treatment must be coded T and the Reference R.

## Value

Prints results to a file if argument `print = TRUE` (default).

If argument `print = FALSE`, returns a data.frame with the elements:

Design	<i>e.g.</i> , TRTR RTRT
Method	B-option (1, 2, or 3)
n	total number of subjects
nTT	number of subjects with two treatments of T (full replicates only)
nRR	number of subjects with two treatments of R
Sub/seq	number of subjects per sequence
Miss/seq	if the design is unbalanced, number of missings per sequence
Miss/per	if the design is incomplete, number of missings per period
alpha	nominal level of the test
DF	degrees of freedom of the treatment comparison
CVwT(%)	intra-subject coefficient of variation of the test treatment (full replicates only)
CVwR(%)	intra-subject coefficient of variation of the reference treatment
sw.ratio	ratio of intrasubject variabilities of T and R (full replicates only)
sw.ratio.CL	upper confidence limit of sw.ratio (full replicates only)

- If reference-scaling is applicable (*i.e.*,  $CVwR(\%) > 30\%$ ):

L(%)	lower expanded limit of the acceptance range (AR)
U(%)	upper expanded limit of the acceptance range (AR)

- If reference-scaling is not applicable (*i.e.*,  $\leq 30\%$ ):

BE.lo(%)	lower limit of the conventional AR ( 80)
BE.hi(%)	upper limit of the conventional AR (125)

CL.lo(%)	lower confidence limit of the treatment comparison
CL.hi(%)	upper confidence limit of the treatment comparison
PE(%)	point estimate of the treatment comparison (aka GMR)
CI	assessment whether the $100(1 - 2\alpha)$ CI lies entirely within the acceptance range (pass/fail)
GMR	assessment whether the PE lies entirely within the GMR-restriction 80.00%–125.00% (pass/fail)
BE	mixed (aggregate) assessment whether the study demonstrates bioequivalence (pass/fail)
log.half-width	half-width of the confidence interval in log-scale

If `ola = TRUE` and at least one studentized outlier was detected:

outlier	outlying subject(s)
CVwR.rec(%)	intra-subject coefficient of variation of R; recalculated after exclusion of outlier(s)
sw.ratio.rec	ratio of intrasubject variabilities of T and R after exclusion of outlier(s); full replicates only



sw.ratio.rec.CL upper confidence limit of sw.ratio.rec (full replicates only)

- If reference-scaling is applicable (*i.e.*, CVwR.rec(%) >30%):

L.rec(%)      recalculated lower expanded limit of the AR  
U.rec(%)      recalculated upper expanded limit of the AR

- If reference-scaling is not applicable (*i.e.*, CVwR.rec(%) ≤30%):

BE.rec.lo(%)      lower limit of the conventional AR ( 80)  
BE.rec.hi(%)      upper limit of the conventional AR (125)

CI.rec      assessment whether the  $100(1 - 2\alpha)$  CI lies entirely within the new acceptance range (pass/fail)  
GMR.rec      assessment whether the PE lies entirely within the GMR-restriction 80.00%–125.00% (pass/fail)  
BE.rec      mixed (aggregate) assessment whether the study demonstrates bioequivalence (pass/fail)

### Warning

Files may contain a commentary header. If reading from a CSV-file, *each* line of the commentary header *must* start with "# " (hash space = ASCII 35 ASCII 32). If reading from an Excel-file all lines preceding the column headers are treated as a comment.

### Clarification

The ‘graphical’ presentation in the result file gives the confidence limits with filled black squares and the point estimate as a white rhombus. If a confidence limit exceeds the maximum possible expansion limit, it is shown as a triangle. Expanded limits are given as double vertical lines. Unscaled limits, the GMR restriction, and 100% are given with single vertical lines. The ‘resolution’ is approximately 0.5% and therefore, not all symbols might be shown. The CI and PE take precedence over the limits and the expanded limits over unscaled ones.

### Note

The EMA’s model specified as ‘Method B’ in *Annex I* assumes equal [*sic*] intra-subject variances of test and reference (like in  $2 \times 2 \times 2$  trials) – even if proven false in one of the full replicate designs (were *both*  $CV_{wT}$  and  $CV_{wR}$  can be estimated). Hence, amongst biostatisticians it is called the “crippled model” because the replicative nature of the study is ignored.

The method for calculating the degrees of freedom is not specified in the SAS code provided by the EMA in *Annex I*. Hence, the default in PROC MIXED, namely DDFM=CONTAIN is applied.

For incomplete data (*i.e.*, missing periods) Satterthwaite’s approximation of the degrees of freedom (option=1) or Kenward-Roger (option=3) might be better choices – if stated as such in the statistical analysis plan.

The half-width of the confidence interval in log-scale allows a comparison of methods (B *v.s.* A) or options (2 *v.s.* 1). A higher value *might* point towards a more conservative decision. Quoting the Q&A-document:

*A simple linear mixed model, which assumes identical within-subject variability (Method B), may be acceptable as long as results obtained with the two methods do not lead to different regulatory*

decisions. However, in borderline cases [...] additional analysis using Method A might be required.

In the provided reference datasets – with one exception – the conclusion of BE (based on the mixed CI and GMR criteria) agrees between ‘Method A’ and ‘Method B’. However, for the highly incomplete dataset 14 ‘Method A’ was *liberal* (passing by ANOVA but failing by the mixed effects model).

Reference-scaling is acceptable for  $C_{max}$  (immediate release products) and  $C_{max,ss}$ ,  $C_{\tau,ss}$ , and *partial AUC* (modified release products). However, quoting the BE guideline:

*The applicant should justify that the calculated intra-subject variability is a reliable estimate and that it is not the result of outliers.*

Quoting the Q&A on the Revised EMA Bioequivalence Guideline:

*... a study could be acceptable if the bioequivalence requirements are met both including the outlier subject (using the scaled average bioequivalence approach and the within-subject CV with this subject) and after exclusion of the outlier (using the within-subject CV without this subject).*

*An outlier test is not an expectation of the medicines agencies but outliers could be shown by a box plot. This would allow the medicines agencies to compare the data between them.*

The EMA’s method of reference-scaling for highly variable drugs / drug products is currently recommended in other jurisdictions as well (*e.g.*, the WHO; ASEAN States, Australia, Brazil, Egypt, the Russian Federation, the Eurasian Economic Union, the East African Community, New Zealand).

The WHO accepts reference-scaling for AUC (4-period full replicate studies are mandatory in order to assess the variability associated with each product). It is an open issue how this assessment should be done. In Population Bioequivalence (PBE) and Individual Bioequivalence (IBE) the  $s_{wT}/s_{wR}$  ratio was assessed and similar variability was concluded for a ratio within 0.667–1.500. However, the power of comparing variabilities in a study designed to demonstrate ABE is low. This was one of the reasons why PBE and IBE were not implemented in regulatory practice. An alternative approach is given in the FDA’s guidance on warfarin. Variabilities are considered comparable if the upper confidence limit of  $\sigma_{wT}/\sigma_{wR}$  is less than or equal to 2.5.

**Program offered for Use without any Guarantees and Absolutely No Warranty. No Liability is accepted for any Loss and Risk to Public Health Resulting from Use of this R-Code.**

#### Author(s)

Helmut Schütz, Michael Tomashevskiy, Detlew Labes

#### References

European Medicines Agency, Committee for Medicinal Products for Human Use. *Guideline on the Investigation of Bioequivalence*. London, 20 January 2010. [CPMP/EWP/QWP/1401/98 Rev. 1/ Corr \\*\\*](#)

3<sup>rd</sup> EGA Symposium on Bioequivalence. *Questions and Answers on the Revised EMA Bioequivalence Guideline*. London, 1 June 2010. [open access](#)

European Medicines Agency, Committee for Medicinal Products for Human Use. *Questions & Answers: positions on specific questions addressed to the Pharmacokinetics Working Party (PKWP)*. London, 19 November 2015. [EMA/618604/2008 Rev. 13](#)

European Medicines Agency. *Clinical pharmacology and pharmacokinetics: questions and answers. 3.1 Which statistical method for the analysis of a bioequivalence study does the Agency recommend? Annex I.* London, 21 September 2016. [EMA/582648/2016](#)

European Medicines Agency, Committee for Medicinal Products for Human Use. *Guideline on the pharmacokinetic and clinical evaluation of modified release dosage forms.* London, 20 November 2014. [EMA/CPMP/EWP/280/96 Corr1](#)

World Health Organization, Prequalification Team: medicines. *Guidance Document: Application of reference-scaled criteria for AUC in bioequivalence studies conducted for submission to PQTm.* Geneva, 22 November 2018. [open access](#)

Food and Drug Administration, Office of Generic Drugs. *Draft Guidance on Warfarin Sodium.* Rockville, December 2012. [open access](#)

## See Also

[method.A](#) evaluation by a fixed effects model (ANOVA)  
[ABE](#) evaluation for conventional (unscaled) Average Bioequivalence

## Examples

```
# Importing from a CSV-file, using most of the defaults: variable
# separator colon, decimal separator period, no outlier-analysis,
# print to file.
# Note: You must adapt the path-variables. The example reads from
# the data provided by the library. Write-permissions must be granted
# for 'path.out' in order to save the result file. If 'path.out' is
# not specified, results are written to the home folder.
path.in <- paste0(find.package("replicateBE"), "/extdata/")
method.B(path.in = path.in, file = "DS", set = "01", ext = "csv")
# Should result in:
#   CVwT           : 35.16%
#   swT            : 0.34138
#   CVwR           : 46.96% (reference-scaling applicable)
#   swR            : 0.44645
#   Expanded limits : 71.23% ... 140.40% [100exp(±0.760·swR)]
#   swT / swR       : 0.7647 (similar variabilities of T and R)
#   sw-ratio (upper CL): 0.9324 (comparable variabilities of T and R)
#   Confidence interval: 107.17% ... 124.97% pass
#   Point estimate   : 115.73% pass
#   Mixed (CI & PE)  : pass
#
# Internal reference dataset 01 used and results to the home
# folder. Additional outlier-analysis and box plot saved as PNG
# (accidental overwriting prevented).
method.B(ola = TRUE, ask = TRUE, plot.bxp = TRUE, data = rds01)
# Should give the same as above. Additionally:
#   Recalculation due to presence of 2 outliers (subj. 45|52)
```

```

# CVwR (outl. excl.) : 32.16% (reference-scaling applicable)
# swR (recalc.) : 0.31374
# Expanded limits : 78.79% ... 126.93% [100exp(±0.760·swR)]
# swT / swR (recalc.): 1.0881 (similar variabilities of T and R)
# sw-ratio (upper CL): 1.3282 (comparable variabilities of T and R)
# Confidence interval: pass
# Point estimate : pass
# Mixed (CI & PE) : pass
#
# Same dataset. Show information about outliers and the model-table.
method.B(ola = TRUE, verbose = TRUE, data = rds01)
# data.frame of results (full precision) shown in the console.
x <- method.B(ola = TRUE, print = FALSE, details = TRUE, data = rds01)
print(x, row.names = FALSE)
# Compare Method B with Method A for all reference datasets.

ds <- substr(grep("rds", unname(unlist(data(package="replicateBE"))),
value=TRUE), start=1, stop=5)
for (i in seq_along(ds)) {
  A <- method.A(print=FALSE, details=TRUE, data=eval(parse(text=ds[i])))$BE
  B <- method.B(print=FALSE, details=TRUE, data=eval(parse(text=ds[i])))$BE
  r <- paste0("A ", A, ", B ", B, " \u2013 ")
  cat(paste0(ds[i], ":"), r)
  if (A == B) {
    cat("Methods A and B agree.\n")
  } else {
    if (A == "fail" & B == "pass") {
      cat("Method A is conservative.\n")
    } else {
      cat("Method B is conservative.\n")
    }
  }
}
# should give
# rds01: A pass, B pass – Methods A and B agree.
# ...
# rds14: A pass, B fail – Method B is conservative.
# ...

```

refdata

*Reference Datasets***Description**

Datasets of replicate designs from the public domain, edited, or obtained by simulations to be evaluated by `method.A()`, `method.B()`, or `ABE()`.

**Details**

Design	Specification	Dataset	N	$CV_{wR}$ (%)	Evaluation
--------	---------------	---------	---	---------------	------------

TRTR RTRT	full	rds01	77	>30	method.A(), method.B()
TRTR RTRT	full	rds06	77	>30	method.A(), method.B()
TRTR RTRT	full	rds12	77	>30	method.A(), method.B()
TRTR RTRT	full	rds14	77	>30	method.A(), method.B()
TRTR RTRT	full	rds18	77	>30	method.A(), method.B()
TRTR RTRT	full	rds21	77	>30	method.A(), method.B()
TRTR RTRT	full	rds19	61	>30	method.A(), method.B()
TRTR RTRT	full	rds20	61	>30	method.A(), method.B()
TRTR RTRT	full	rds08	222	>30	method.A(), method.B()
TRTR RTRT	full	rds09	222	>30	method.A(), method.B()
TRTR RTRT	full	rds13	222	>30	method.A(), method.B()
TRTR RTRT	full	rds15	222	>30	method.A(), method.B()
TRTR RTRT	full	rds25	70	>30	method.A(), method.B()
TRTR RTRT	full	rds29	12	<30	method.A(), method.B(), ABE()
TRRT RTTR	full	rds26	54	>30	method.A(), method.B()
TRRT RTTR	full	rds05	26	<30	method.A(), method.B(), ABE()
TRRT RTTR	full	rds11	37	>30	method.A(), method.B()
TRRT RTTR	full	rds16	38	>30	method.A(), method.B()
TTRR RRTT	full	rds28	64	<30	method.A(), method.B(), ABE()
TRTR RTRT TRRT RTTR	full	rds23	22	>30	method.A(), method.B()
TRRT RTTR TTRR RRTT	full	rds24	39	>30	method.A(), method.B()
TRT RTTR	full	rds03	77	>30	method.A(), method.B()
TRT RTTR	full	rds17	19	>30	method.A(), method.B()
TTR RTT	full	rds10	18	<30	method.A(), method.B(), ABE()
TR RT TT RR	Balaam's	rds27	312	>30	method.A(), method.B()
TTR RTTR RR	partial	rds02	24	<30	method.A(), method.B(), ABE()
TTR RTTR RR	partial	rds04	51	>30	method.A(), method.B()
TTR RTTR RR	partial	rds07	360	>30	method.A(), method.B()
TTR RTTR RR	partial	rds30	14	<30	method.A(), method.B(), ABE()
TTR RTTR	partial	rds22	36	>30	method.A(), method.B()

In full replicate designs *both* R and T are administered twice (in 3-period designs to ½ of the subjects).

Balaam's design is a mixture of a conventional crossover (½ of the subjects) and a replicate design (¼ of the subjects receive *either* R or T twice).

In partial replicate designs *only* R is administered twice.

### Author(s)

Helmut Schütz (R-code for simulations by Detlew Labes), Michael Tomashevskiy (simulations in Phoenix NLME)

### Source

Dataset	Origin	Description
rds01	EMA	Data set in Annex II
rds06	rds01 edited	T and R switched
rds12	Phoenix NLME	Simulated with extreme variability

rds14	Phoenix NLME	Simulated with high variability and number of dropouts increasing with period
rds18	rds14 edited	Removed T data of subjects 63–78
rds21	rds01 edited	One extreme result of subjects 45 & 52 set to NA
rds19	rds18 edited	Removed data of subjects 63–78
rds20	rds19 edited	Outlier of R (subject 1) introduced: original value $\times 100$
rds08	R	Simulated with slight heteroscedasticity
rds09	rds08	Wide numeric range (data of last 37 subjects multiplied by 1,000,000)
rds13	rds08 edited	Highly incomplete (approx. 50% of period 4 data deleted)
rds15	rds08 edited	Highly incomplete (approx. 50% of period 4 data coded as missing 'NA')
rds25	R	Simulated with heteroscedasticity
rds29	R	Simulated with heteroscedasticity; imbalanced and incomplete
rds26	Patterson & Jones 2016	$C_{max}$ data given in Tables 4.30 & 4.31
rds05	Shumaker & Metzler	$C_{max}$ data given in the Appendix
rds11	Hauschke <i>et al.</i>	$C_{max}$ data given in Table 9.6.
rds16	FDA, CDER	$C_{max}$ data of Drug 14a
rds28	R	Simulated with homoscedasticity
rds23	FDA, CDER	$C_{max}$ data of Drug
rds24	FDA, CDER	$C_{max}$ data of Drug 1
rds03	rds01 edited	Period 4 removed
rds17	rds03 edited	Highly unbalanced (twelve subjects in RTR and seven in TRT)
rds10	Chow & Liu	AUC data given in Table 9.3.3.
rds27	R	Simulated with homoscedasticity
rds02	EMA	Data set in Annex III
rds04	Patterson & Jones 2012	$C_{max}$ data of Table II
rds07	R	Simulated with homoscedasticity
rds30	R	Simulated with heteroscedasticity; imbalanced and incomplete
rds22	R	Simulated with homoscedasticity

## References

- European Medicines Agency. London, 21 September 2016. *Annex II, Annex III*.
- Patterson SD, Jones B. *Viewpoint: observations on scaled average bioequivalence*. Pharm Stat. 2012; 11(1): 1–7. doi: [10.1002/pst.498](https://doi.org/10.1002/pst.498)
- Shumaker RC, Metzler CM. *The Phenytoin Trial is a Case Study of 'Individual' Bioequivalence*. Drug Inf J. 1998; 32(4): 1063–72. doi: [10.1177/009286159803200426](https://doi.org/10.1177/009286159803200426)
- Chow SC, Liu JP. *Design and Analysis of Bioavailability and Bioequivalence Studies*. Boca Raton: CRC Press; 3<sup>rd</sup> edition 2009. p275.
- Hauschke D, Steinijans VW, Pigeot I. *Bioequivalence Studies in Drug Development*. Chichester: John Wiley; 2007. p216.
- Patterson SD, Jones B. *Bioequivalence and Statistics in Clinical Pharmacology*. Boca Raton: CRC Press; 2<sup>nd</sup> edition 2016. p105–6.
- U.S. Food and Drug Administration, Center for Drug Evaluation and Research. *Bioequivalence Studies*. Rockville, 1997. [bioequivalence study files](#) (archived 2017-07-23)

See Also

4-period full replicates  
[TRTR.RTRT](#), [TRRT.RTTR](#), [TTRR.RRTT](#), [TRTR.RTRT.TRRT.RTTR](#), [TRRT.RTTR.TTRR.RRTT](#)  
2-period replicate (Balaam’s design)  
[TR.RT.TT.RR](#)  
3-period full replicates  
[TRT.RTR](#), [TRR.RTT](#)  
3-period partial replicates  
[TRR.RTR.RRT](#), [TRR.RTR](#)

Examples

```
# show structure of all data sets
ds <- substr(grep("rds", unname(unlist(data(package = "replicateBE"))),
               value = TRUE), start = 1, stop = 5)
for (i in seq_along(ds)) {
  cat(ds[i], "\n")
  str(eval(parse(text = ds[i])))
}
```

---

TR.RT.TT.RR	<i>Reference Dataset for TR RT TT RR Replicate Designs</i>
-------------	------------------------------------------------------------

---

Description

Dataset for Balaam’s design obtained by simulations to be evaluated by `method.A()`, `method.B()`.

Usage

`rds27`

Format

- Reference Dataset 27 (`rds27`)  
312 subjects. Balanced (78 subjects in each of the four sequences) and incomplete (T of subject 111 missing in period 2 of sequence RT). No outliers.  
A data frame with 624 observations on the following 5 variables:

subject	a factor with 312 levels: 1, 2, ..., 18
period	a factor with 2 levels: 1, 2
sequence	a factor with 4 levels: TR, RT, TT, RR
treatment	a factor with 2 levels: T, R
PK	a numeric vector of pharmacokinetic responses acceptable for reference-scaling (generally $C_{max}$ )

Details

Dataset	N	$CV_{wR}$ (%)	Evaluation
rds27	312	>30	method.A(), method.B()

**Note**

In software sequences and treatments are ranked in lexical order. Hence, executing `str()` or `summary()` will show sequence as "RR", "RT", "TR", "TT" and treatment as "R", "T". In BE – by convention – sequences are ordered with T first. The library follows this convention.

**Author(s)**

Helmut Schütz (R-code for simulations by Detlew Labes)

**Source**

Dataset	Origin	Description
rds27	R	Simulated with $CV_{wT} = CV_{wR} = 35\%$ , $CV_{bR} = CV_{bT} = 75\%$ , GMR 0.90.

**Examples**

```
str(rds27)
row <- c(1:2, 157:158, 313:314, 469:470)
rds27[row, ]
summary(rds27[2:5])
```

---

TRR.RTR	<i>Reference Dataset for TRR RTR (extra-reference) Designs</i>
---------	----------------------------------------------------------------

---

**Description**

Dataset simulated to be evaluated by `method.A()`, `method.B()`.

**Usage**

```
rds22
```

**Format**

- Reference dataset 22 (`rds22`)  
Simulated with  $CV_{wT} = CV_{wR} = 45\%$ ,  $CV_{bT} = CV_{bR} = 100\%$  GMR 0.90. 42 subjects.  
Balanced (21 subjects in each of the sequences) and complete (no missing data). No outliers.  
A data frame with 126 observations on the following 5 variables:



subject	a factor with 42 levels: 1, 2, ..., 42
period	a factor with 3 levels: 1, 2, 3
sequence	a factor with 2 levels: TRR, RTR
treatment	a factor with 2 levels: T, R
PK	a numeric vector of pharmacokinetic responses acceptable for reference-scaling (generally $C_{max}$ )
logPK	a numeric vector of the natural logarithms of PK

### Details

Dataset	N	$C_{wR}$ (%)	Evaluation
rds22	42	>30	method.A(), method.B()

### Note

In software sequences and treatments are ranked in lexical order. Hence, executing `str()` or `summary()` will show sequence as "RTR", "TRR" and treatment as "R", "T". In BE – by convention – sequences are ordered with T first. The library follows this convention.

This partial replicate design is also known as the ‘extra-reference design’. Since the Test is not administered in all periods, lacking period effects must be assumed. In the presence of *true* period effects the treatment comparison will be biased. Hence, this design is not recommended.

### Author(s)

Helmut Schütz (R-code for simulations by Detlew Labes)

### Source

Dataset	Origin	Description
rds22	R	Simulated with homoscedasticity.

### Examples

```
str(rds22)
rds22[61:66, ]
summary(rds22[2:5])
```

**Description**

Datasets from the public domain or simulated to be evaluated by method.A(), method.B(), or ABE().

**Format**

- Reference Dataset 02 (rds02)  
24 subjects.  
Balanced (eight subjects in each of the three sequences) and complete (no missing data). No outliers.  
A data frame with 72 observations on the following 6 variables:

subject	a factor with 24 levels: 1, 2, ..., 24
period	a factor with 3 levels: 1, 2, 3
sequence	a factor with 3 levels: TRR, RTR, RRT
treatment	a factor with 2 levels: T, R
PK	a numeric vector of pharmacokinetic responses acceptable for reference-scaling (generally $C_{max}$ )
logPK	a numeric vector of the natural logarithms of PK

In the source evaluated by SAS v9.1 for ABEL. Reported results:

CVwR	11.2%
PE	102.26% (Method A and B)
90% CI	97.32% – 107.46% (Method A and B)

- Reference Dataset 04 (rds04)  
Data set of Table II given by Patterson & Jones. 51 subjects.  
Balanced (17 subjects in each of the three sequences) and complete. No outliers.  
A data frame with 153 observations on the following 5 variables:

subject	a factor with 51 levels: 1, 2, ..., 56
period	a factor with 3 levels: 1, 2, 3
sequence	a factor with 3 levels: TRR, RTR, RRT
treatment	a factor with 2 levels: T, R
PK	a numeric vector of pharmacokinetic responses (here $C_{max}$ )

In the source evaluated by SAS with the FDA's mixed effects model (termed 'Method C' by the EMA; not compatible with the guideline). Reported results:

CVwR	61%
PE	137%
90% CI	119% – 159%

- Reference Dataset 07 (rds07)  
Simulated with  $CV_{wT} = CV_{wR} = 35\%$ , GMR 0.90. 360 subjects.

Balanced (120 subjects in each of the three sequences) and complete. No outliers.  
A data frame with 1,080 observations on the following 5 variables:

subject a factor with 360 levels: 1, 2, ..., 360  
 period a factor with 3 levels: 1, 2, 3  
 sequence a factor with 3 levels: TRR, RTR, RRT  
 treatment a factor with 2 levels: T, R  
 PK a numeric vector of pharmacokinetic responses (generally  $C_{max}$ )

- Reference Dataset 30 (rds30)

Simulated with heteroscedasticity ( $CV_{wT} = 14\%$ ,  $CV_{wR} = 28\%$ ), GMR = 0.90. 14 subjects. Imbalanced (six subjects in sequence TRR, five in RTR, and three RRT) and incomplete (two missings in sequences TRR and RTR and three in sequence RRT). Missings / period: 0/1, 0/2, 7/3. No outliers.

A data frame with 35 observations on the following 5 variables:

subject a factor with 14 levels: 1, 2, ..., 39  
 period a factor with 3 levels: 1, 2, 3  
 sequence a factor with 3 levels: TRR, RTR, RRT  
 treatment a factor with 2 levels: T, R  
 PK a numeric vector of pharmacokinetic responses (generally  $C_{max}$ )

## Details

Dataset	N	$CV_{wR}$ (%)	Evaluation
rds02	24	<30	method.A(), method.B(), ABE()
rds04	51	>30	method.A(), method.B()
rds07	360	>30	method.A(), method.B()
rds30	14	<30	method.A(), method.B(), ABE()

## Note

In software sequences and treatments are ranked in lexical order. Hence, executing `str()` or `summary()` will show sequence as "RRT", "RTR", "TRR" and treatment as "R", "T". In BE – by convention – sequences are ordered with T first. The library follows this convention.

## Author(s)

Helmut Schütz (R-code for simulations by Detlew Labes)

## Source

Dataset	Origin	Description
rds02	EMA	Annex III.
rds04	Patterson & Jones	$C_{max}$ data of Table II.
rds07	R	Large simulated data set with homoscedasticity.
rds30	R	Simulated with heteroscedasticity; imbalanced and incomplete.

## References

European Medicines Agency. London, 21 September 2016. *Annex I, Annex III*.

Patterson SD, Jones B. *Viewpoint: observations on scaled average bioequivalence*. Pharm Stat. 2012; 11(1): 1–7. doi: [10.1002/pst.498](https://doi.org/10.1002/pst.498)

## Examples

```
str(rds02)
row <- c(10:12, 1:3, 16:18)
rds02[row, ]
summary(rds02[2:6])
```

---

TRR.RTT

---

Reference Dataset for TRR\RTT Replicate Designs

---

## Description

Dataset from the public domain to be evaluated by `method.A()`, `method.B()`, or `ABE()`.

## Usage

```
rds10
```

## Format

- Reference Dataset 10 (`rds10`)  
18 subjects.  
Balanced (nine subjects in both sequences) and complete. No outliers.  
A data frame with 54 observations on the following 5 variables:

subject	a factor with 18 levels: 1, 2, ..., 18
period	a factor with 3 levels: 1, 2, 3
sequence	a factor with 2 levels: TRR, RTT
treatment	a factor with 2 levels: T, R
PK	a numeric vector of pharmacokinetic responses (here AUC)

**Details**

Dataset	N	$CV_{wR}$ (%)	Evaluation
rds10	36	<30	method.A(), method.B(), ABE()

**Note**

In software sequences and treatments are ranked in lexical order. Hence, executing `str()` or `summary()` will show sequence as "RTT", "TRR" and treatment as "R", "T". In BE – by convention – sequences are ordered with T first. The library follows this convention.

In analogy to the EMA's Q&A: Uncertain estimate of CVwR since less than twelve subjects in sequence TRR.

**Source**

Dataset	Origin	Description
rds10	Chow & Liu	AUC data given in Table 9.3.3.

**References**

Chow SC, Liu JP. *Design and Analysis of Bioavailability and Bioequivalence Studies*. Boca Raton: CRC Press; 3<sup>rd</sup> edition 2009. p275.

**Examples**

```
str(rds10)
row <- c(1:3, 28:30)
rds10[row, ]
summary(rds10[2:5])
```

---

TRRT.RTTR

---

*Reference Datasets for TRRT\RTTR Replicate Designs*


---

**Description**

Datasets from the public domain to be evaluated by `method.A()`, `method.B()`, or `ABE()`.

**Format**

- Reference Dataset 05 (rds05)  
26 subjects.  
Balanced (13 subjects in both sequences) and complete. No outliers.  
A data frame with 104 observations on the following 5 variables:

subject	a factor with 26 levels: 1, 2, ..., 26
period	a factor with 4 levels: 1, 2, 3, 4
sequence	a factor with 2 levels: TRRT, RTTR
treatment	a factor with 2 levels: T, R
PK	a numeric vector of pharmacokinetic responses (here $C_{max}$ )

In the source evaluated by SAS with the FDA's mixed effects model (termed 'Method C' by the EMA; not compatible with the guideline). Reported results:

CVwR	5.47%
CVwT	6.75%
PE	107.90%
90% CI	103.66% – 112.2%

- Reference Dataset 11 (rds11)

37 subjects.

Unbalanced (18 subjects in sequence TRRT and 19 subjects in RTTR) and complete. No outliers.

A data frame with 148 observations on the following 5 variables

subject	a factor with 37 levels: 1, 2, ..., 37
period	a factor with 4 levels: 1, 2, 3, 4
sequence	a factor with 2 levels: TRRT, RTTR
treatment	a factor with 2 levels: T, R
PK	a numeric vector of pharmacokinetic responses (here $C_{max}$ )

In the source evaluated by SAS with the FDA's mixed effects model (termed 'Method C' by the EMA; not compatible with the guideline). Reported results:

PE	90.0%
90% CI	79.6% – 101.7%

- Reference Dataset 16 (rds16)

38 subjects.

Unbalanced (18 subjects in sequence TRRT and 20 in RTTR) and complete. No outliers.

A data frame with 152 observations on the following 5 variables:

subject	a factor with 38 levels: 1, 2, ..., 38
period	a factor with 4 levels: 1, 2, 3, 4
sequence	a factor with 2 levels: TRRT, RTTR
treatment	a factor with 2 levels: T, R
PK	a numeric vector of pharmacokinetic responses (here $C_{max}$ )

**Details**

Dataset	N	$CV_{wR}$ (%)	Evaluation
rds05	26	<30	method.A(), method.B(), ABE()
rds11	37	>30	method.A(), method.B()
rds16	38	>30	method.A(), method.B()

**Note**

In software sequences and treatments are ranked in lexical order. Hence, executing `str()` or `summary()` will show sequence as "RTTR", "TRRT" and treatment as "R", "T". In BE – by convention – sequences are ordered with T first. The library follows this convention.

**Source**

Dataset	Origin	Description
rds05	Shumaker & Metzler	$C_{max}$ data given in the Appendix.
rds11	Hauschke <i>et al.</i>	$C_{max}$ data given in Table 9.6.
rds16	FDA, CDER	$C_{max}$ data of Drug 14a.

**References**

- Shumaker RC, Metzler CM. *The Phenytoin Trial is a Case Study of ‘Individual’ Bioequivalence*. Drug Inf J. 1998; 32(4): 1063–72. doi: [10.1177/009286159803200426](https://doi.org/10.1177/009286159803200426)
- Hauschke D, Steinijans VW, Pigeot I. *Bioequivalence Studies in Drug Development*. Chichester: John Wiley; 2007. p216.
- U.S. Food and Drug Administration, Center for Drug Evaluation and Research. *Bioequivalence Studies*. Rockville, 1997. [bioequivalence study files](#) (archived 2017-07-23)

**Examples**

```
str(rds05)
summary(rds05[2:5])
head(rds11, 8)
```

---

TRRT.RTTR.TTRR.RRTT      *Reference Dataset for TRRT\RTTR\TTRR\RRTT Designs*

---

**Description**

Dataset from the public domain to be evaluated by `method.A()` and/or `method.B()`.

**Format**

- Reference Dataset 24 (rds24)  
40 subjects (one completely missing).  
Unbalanced (nine subjects in sequence TRRT and ten in each of the other three) and complete.  
Two outliers (subject 3 in sequence RTTR and subject 30 in sequence TTRR).  
A data frame with 160 observations on the following 5 variables:

subject	a factor with 40 levels: 1, 2, ..., 932
period	a factor with 4 levels: 1, 2, 3, 4
sequence	a factor with 4 levels: TRRT, RTTR, TTRR, RRTT
treatment	a factor with 2 levels: T, R
PK	a numeric vector of pharmacokinetic responses acceptable for reference-scaling (here $C_{max}$ )

**Details**

Dataset	N	$CV_{wR}$ (%)	Evaluation
rds24	39	>30	method.A(), method.B()

**Note**

In software sequences and treatments are ranked in lexical order. Hence, executing `str()` or `summary()` will show sequence as "RRTT", "RTTR", "TRRT", "TTRR" and treatment as "R", "T".  
In BE – by convention – sequences are ordered with T first. The library follows this convention.

**Source**

Dataset	Origin	Description
rds24	FDA, CDER	$C_{max}$ data of Drug 1.

**References**

U.S. Food and Drug Administration, Center for Drug Evaluation and Research. *Bioequivalence Studies*. Rockville, 1997. [bioequivalence study files](#) (archived 2017-07-23)

**Examples**

```
str(rds24)
row <- c(13:16, 9:12, 1:4, 5:8)
rds24[row, ]
summary(rds24[2:5])
```



TRT.RTR

*Reference Datasets for TRT\RTR Replicate Designs***Description**

Datasets from the public domain and edited to be evaluated by method.A() and/or method.B().

**Format**

- Reference dataset 03 (rds03)

Based on rds01. Removed all data of period 4. 77 subjects.

Unbalanced (39 subjects in sequence TRT and 38 in RTR) and incomplete (six missings in sequence TRT and two in RTR). Missings / period: 0/1, 1/2, 7/3. Two outliers (subjects 45 and 52) in sequence RTR.

A data frame with 223 observations on the following 6 variables:

subject	a factor with 77 levels: 1, 2, ..., 78
period	a factor with 3 levels: 1, 2, 3
sequence	a factor with 2 levels: TRT, RTR
treatment	a factor with 2 levels: T, R
PK	a numeric vector of pharmacokinetic responses acceptable for reference-scaling (generally $C_{max}$ )

- Reference dataset 17 (rds17)

Based on rds03. 19 subjects.

Unbalanced (seven subjects in sequence TRT and twelve in RTR) and incomplete (one missing in sequence TRT). Missings / period: 0/1, 0/2, 1/3. One outlier (subject 18) in sequence RTR.

A data frame with 56 observations on the following 6 variables:

subject	a factor with 19 levels: 1, 2, ..., 22
period	a factor with 3 levels: 1, 2, 3
sequence	a factor with 2 levels: TRT, RTR
treatment	a factor with 2 levels: T, R
PK	a numeric vector of pharmacokinetic responses acceptable for reference-scaling (generally $C_{max}$ )

**Details**

Dataset	N	$CV_{wR}$ (%)	Evaluation
rds03	77	>30	method.A(), method.B()
rds17	19	>30	method.A(), method.B()

**Note**

In software sequences and treatments are ranked in lexical order. Hence, executing `str()` or `summary()` will show sequence as "RTR", "TRT" and treatment as "R", "T". In BE – by convention – sequences are ordered with T first. The library follows this convention.

**Author(s)**

Helmut Schütz

**Source**

Dataset	Origin	Description
rds03	rds01 edited	Period 4 removed.
rds17	rds03 edited	Highly unbalanced (seven subjects in TRT and twelve in RTR).

**Examples**

```
head(rds03, 6)
summary(rds03[2:5])
```

---

TRTR.RTRT

---

*Reference Datasets for TRTR\RTT Designs*


---

**Description**

Datasets from the public domain, edited, or obtained by simulations to be evaluated by method.A() and/or method.B().

**Format**

- Reference dataset 01 (rds01)  
77 subjects.  
Unbalanced (39 subjects in sequence TRTR and 38 in RTRT) and incomplete (seven missings in sequence TRTR and three in sequence RTRT). Missings / period: 0/1, 1/2, 7/3, 2/4. Two outliers (subjects 45 and 52) in sequence RTRT.  
A data frame with 298 observations on the following 6 variables:

subject	a factor with 77 levels: 1, 2, ..., 78
period	a factor with 4 levels: 1, 2, 3, 4
sequence	a factor with 2 levels: TRTR, RTRT
treatment	a factor with 2 levels: T, R
PK	a numeric vector of pharmacokinetic responses acceptable for reference-scaling (generally $C_{max}$ )
logPK	a numeric vector of the natural logarithms of PK

In the source evaluated by SAS v9.1 for ABEL. Reported results:

CV <sub>wR</sub>	47.0%
PE	115.66% (Method A)
	115.73% (Method B)
90% CI	107.11% – 124.89% (Method A)
	107.17% – 124.97% (Method B)

- Reference dataset 06 (rds06)

Based on rds01. 77 subjects. Responses of T and R switched.

Unbalanced (39 subjects in sequence TRTR and 38 in RTRT) and incomplete (seven missings in sequence TRTR and three in sequence RTRT). Missings / period: 0/1, 1/2, 7/3, 2/4. No outliers.

A data frame with 298 observations on the following 6 variables:

subject	a factor with 77 levels: 1, 2, ..., 78
period	a factor with 4 levels: 1, 2, 3, 4
sequence	a factor with 2 levels: TRTR, RTRT
treatment	a factor with 2 levels: T, R
PK	a numeric vector of pharmacokinetic responses acceptable for reference-scaling (generally $C_{max}$ )

- Reference dataset 08 (rds08)

Simulated with slight heteroscedasticity ( $CV_{wT} = 70\%$ ,  $CV_{wR} = 80\%$ ),  $CV_{bT} = CV_{bR} = 150\%$ , GMR = 0.85. 222 subjects.

Balanced (222 subjects in both sequences) and complete. No outliers.

The extreme sample size results from high variability, an assumed true GMR 0.85, and target power 90%.

A data frame with 888 observations on the following 5 variables:

subject	a factor with 222 levels: 1, 2, ..., 222
period	a factor with 4 levels: 1, 2, 3, 4
sequence	a factor with 2 levels: TRTR, RTRT
treatment	a factor with 2 levels: T, R
PK	a numeric vector of pharmacokinetic responses acceptable for reference-scaling (generally $C_{max}$ )

- Reference dataset 09 (rds09)

Based on rds08. Wide numeric range (data of last 37 subjects multiplied by 1,000,000). 222 subjects.

Balanced (222 subjects in both sequences) and complete. No outliers.

A data frame with 888 observations on the following 5 variables:

subject	a factor with 222 levels: 1, 2, ..., 222
period	a factor with 4 levels: 1, 2, 3, 4

sequence	a factor with 2 levels: TRTR, RTRT
treatment	a factor with 2 levels: T, R
PK	a numeric vector of pharmacokinetic responses acceptable for reference-scaling (generally $C_{max}$ )

- Reference dataset 12 (rds12)  
Simulated with extreme intra- and intersubject variability, GMR = 1.6487. 77 subjects.  
Unbalanced (39 subjects in sequence TRTR and 38 in RTRT) and incomplete (seven missings in sequence TRTR and three in sequence RTRT). Missings / period: 0/1, 1/2, 7/3, 2/4. No outliers.  
A data frame with 298 observations on the following 6 variables:

subject	a factor with 77 levels: 1, 2, ..., 78
period	a factor with 4 levels: 1, 2, 3, 4
sequence	a factor with 2 levels: TRTR, RTRT
treatment	a factor with 2 levels: T, R
PK	a numeric vector of pharmacokinetic responses acceptable for reference-scaling (generally $C_{max}$ )

- Reference dataset 13 (rds13)  
Based on rds08. Highly incomplete (approx. 50% of period 4 data deleted). 222 subjects.  
Balanced (111 subjects in both sequences) and incomplete (56 missings in both sequences).  
Missings / period: 0/0, 0/0, 0/0, 112/4. No outliers.  
A data frame with 776 observations on the following 5 variables:

subject	a factor with 222 levels: 1, 2, ..., 222
period	a factor with 4 levels: 1, 2, 3, 4
sequence	a factor with 2 levels: TRTR, RTRT
treatment	a factor with 2 levels: T, R
PK	a numeric vector of pharmacokinetic responses acceptable for reference-scaling (generally $C_{max}$ )

- Reference dataset 14 (rds14)  
Simulated with high variability, GMR = 1. Dropouts as a hazard function growing with period.  
77 subjects.  
Unbalanced (39 subjects in sequence TRTR and 38 in RTRT) and incomplete (18 missings in sequence TRTR and 17 in sequence RTRT). Missings / period: 0/1, 4/2, 12/3, 19/4. No outliers.  
A data frame with 273 observations on the following 6 variables:

subject	a factor with 77 levels: 1, 2, ..., 78
period	a factor with 4 levels: 1, 2, 3, 4
sequence	a factor with 2 levels: TRTR, RTRT
treatment	a factor with 2 levels: T, R
PK	a numeric vector of pharmacokinetic responses acceptable for reference-scaling (generally $C_{max}$ )

- Reference dataset 15 (rds15)  
Based on ref08. Highly incomplete (approx. 50% of period 4 data coded as missing 'NA'). 222 subjects.  
Balanced (111 subjects in both sequences) and incomplete (56 missings in both sequences).  
Missings / period: 0/1, 0/2, 0/3, 112/4. No outliers.  
A data frame with 888 observations (112 NA) on the following 5 variables

subject      a factor with 222 levels: 1, 2, ..., 222  
 period      a factor with 4 levels: 1, 2, 3, 4  
 sequence    a factor with 2 levels: TRTR, RTRT  
 treatment   a factor with 2 levels: T, R  
 PK           a numeric vector of pharmacokinetic responses acceptable for reference-scaling (generally  $C_{max}$ )

- Reference dataset 18 (rds18)  
Data set based on rds14. Removed T data of subjects 63–78. 77 subjects.  
Unbalanced (39 subjects in sequence TRTR and 38 in RTRT) and incomplete (32 missings in sequence TRTR and 31 in sequence RTRT). Missings / period: 8/1, 12/2, 18/3, 25/4. No outliers.  
A data frame with 245 observations on the following 6 variables:

subject      a factor with 77 levels: 1, 2, ..., 78  
 period      a factor with 4 levels: 1, 2, 3, 4  
 sequence    a factor with 2 levels: TRTR, RTRT  
 treatment   a factor with 2 levels: T, R  
 PK           a numeric vector of pharmacokinetic responses acceptable for reference-scaling (generally  $C_{max}$ )

- Reference dataset 19 (rds19)  
Data set based on rds18. Removed data of subjects 63–78. 61 subjects.  
Unbalanced (31 subjects in sequence TRTR and 30 in RTRT) and incomplete (14 missings in both sequences). Missings / period: 0/1, 4/2, 9/3, 15/4. Two outliers (subjects 18 and 51 in sequence RTRT).  
A data frame with 216 observations on the following 6 variables:

subject      a factor with 61 levels: 1, 2, ..., 62  
 period      a factor with 4 levels: 1, 2, 3, 4  
 sequence    a factor with 2 levels: TRTR, RTRT  
 treatment   a factor with 2 levels: T, R  
 PK           a numeric vector of pharmacokinetic responses acceptable for reference-scaling (generally  $C_{max}$ )

- Reference dataset 20 (rds20)  
Data set based on rds19. Extreme outlier of R (subject 1) introduced: original value  $\times 100$ . 61 subjects.  
Unbalanced (31 subjects in sequence TRTR and 30 in RTRT) and incomplete (14 missings in both sequences). Missings / period: 0/1, 4/2, 9/3, 15/4. Two outliers (subjects 1 and 51 in

sequence RTRT).

A data frame with 216 observations on the following 6 variables:

subject	a factor with 61 levels: 1, 2, ..., 62
period	a factor with 4 levels: 1, 2, 3, 4
sequence	a factor with 2 levels: TRTR, RTRT
treatment	a factor with 2 levels: T, R
PK	a numeric vector of pharmacokinetic responses acceptable for reference-scaling (generally $C_{max}$ )

- Reference dataset 21 (rds21)

Based on ds01. 77 subjects. One extreme result of subjects 45 & 52 set to NA.

Unbalanced (39 subjects in sequence TRTR and 38 in RTRT) and incomplete (seven missings in sequence TRTR and five in sequence RTRT). Missings / period: 1/1, 1/2, 8/3, 2/4. No outliers.

A data frame with 298 observations (2 NA) on the following 6 variables:

subject	a factor with 61 levels: 1, 2, ..., 62
period	a factor with 4 levels: 1, 2, 3, 4
sequence	a factor with 2 levels: TRTR, RTRT
treatment	a factor with 2 levels: T, R
PK	a numeric vector of pharmacokinetic responses acceptable for reference-scaling (generally $C_{max}$ )

- Reference dataset 25 (rds25)

Simulated with heteroscedasticity ( $CV_{wT} = 50\%$ ,  $CV_{wR} = 80\%$ ),  $CV_{bT} = CV_{bR} = 130\%$ , GMR = 0.85. 70 subjects.

Balanced (70 subjects in both sequences) and complete. No outliers.

A data frame with 280 observations on the following 5 variables:

subject	a factor with 70 levels: 1, 2, ..., 70
period	a factor with 4 levels: 1, 2, 3, 4
sequence	a factor with 2 levels: TRTR, RTRT
treatment	a factor with 2 levels: T, R
PK	a numeric vector of pharmacokinetic responses acceptable for reference-scaling (generally $C_{max}$ )

- Reference dataset 26 (rds26)

54 subjects.

Balanced (27 subjects in both sequences) and incomplete (two missings in both sequences).

Missings / period: 0/1, 0/2, 2/3, 2/4. One outlier (subject 49) in sequence RTRT.

A data frame with 216 observations on the following 5 variables:

subject	a factor with 54 levels: 1, 2, ..., 57
period	a factor with 4 levels: 1, 2, 3, 4
sequence	a factor with 2 levels: TRTR, RTRT
treatment	a factor with 2 levels: T, R

PK a numeric vector of pharmacokinetic responses acceptable for reference-scaling (here  $C_{max}$ )

In the source evaluated by SAS for ABEL. Reported results (Method A):

CV <sub>wR</sub>	60.25%
PE	151.3%
90% CI	133.5% – 171.4%

- Reference dataset 29 (rds29)

Simulated with heteroscedasticity ( $CV_{wT} = 14\%$ ,  $CV_{wR} = 28\%$ ,  $CV_{bT} = 28\%$ ,  $CV_{bR} = 56\%$ ), GMR = 0.90. 12 subjects.

Imbalanced (five subjects in sequence TRTR and seven in sequence RTRT) and incomplete (three missings in sequence TRTR and four in sequence RTRT). Missings / period: 0/1, 1/2, 2/3, 4/4. One outlier (subject 11) in sequence RTRT.

A data frame with 41 observations on the following 5 variables:

subject	a factor with 12 levels: 1, 2, ..., 20
period	a factor with 4 levels: 1, 2, 3, 4
sequence	a factor with 2 levels: TRTR, RTRT
treatment	a factor with 2 levels: T, R
PK	a numeric vector of pharmacokinetic responses acceptable for reference-scaling (generally $C_{max}$ )

## Details

Dataset	N	$CV_{wR}$ (%)	Evaluation
rds01	77	>30	method.A(), method.B()
rds06	77	>30	method.A(), method.B()
rds08	222	>30	method.A(), method.B()
rds09	222	>30	method.A(), method.B()
rds12	77	>30	method.A(), method.B()
rds13	222	>30	method.A(), method.B()
rds14	77	>30	method.A(), method.B()
rds15	222	>30	method.A(), method.B()
rds18	77	>30	method.A(), method.B()
rds19	61	>30	method.A(), method.B()
rds20	61	>30	method.A(), method.B()
rds21	77	>30	method.A(), method.B()
rds25	70	>30	method.A(), method.B()
rds26	54	>30	method.A(), method.B()
rds29	12	<30	method.A(), method.B(), ABE()

**Note**

In software sequences and treatments are ranked in lexical order. Hence, executing `str()` or `summary()` will show sequence as "RTRT", "TRTR" and treatment as "R", "T". In BE – by convention – sequences are ordered with T first. The library follows this convention.

**Author(s)**

Helmut Schütz (R-code for simulations by Detlew Labes), Michael Tomashevskiy (simulations in Phoenix NLME)

**Source**

Dataset	Origin	Description
rds01	EMA	Annex II.
rds06	rds01 edited	T and R switched.
rds08	R	Large simulated data set with slight heteroscedasticity.
rds09	rds08	Wide numeric range (data of last 37 subjects multiplied by 1,000,000).
rds12	Phoenix NLME	Simulated with extreme intra- and intersubject variability.
rds13	rds08 edited	Highly incomplete (approx. 50% of period 4 data deleted).
rds14	Phoenix NLME	Simulated with high intra- and intersubject and number of dropouts increasing with period.
rds15	rds08 edited	Highly incomplete (approx. 50% of period 4 data coded as missing 'NA').
rds18	rds14 edited	Removed T data of subjects 63–78.
rds19	rds18 edited	Removed data of subjects 63–78.
rds20	rds19 edited	Outlier of R (subject 1) introduced: original value $\times 100$ .
rds21	rds01 edited	One extreme result of subjects 45 & 52 set to NA.
rds25	R	Simulated with heteroscedasticity.
rds26	Patterson & Jones	$C_{max}$ data given in Tables 4.40 and 4.31.
rds29	R	Simulated with heteroscedasticity; imbalanced and incomplete.

**References**

European Medicines Agency. London, 21 September 2016. *Annex I, Annex II*.

Patterson SD, Jones B. *Bioequivalence and Statistics in Clinical Pharmacology*. Boca Raton: CRC Press; 2<sup>nd</sup> edition 2016. p105–6.

**Examples**

```
str(rds01)
summary(rds01[2:6])
```



---

TRTR.RTRT.TRRT.RTTR      *Reference Dataset for TRTR\RTTR\TRRT\RTTR Designs*

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### Description

Dataset from the public domain to be evaluated by method.A() and/or method.B().

### Format

- Reference Dataset 23 (rds23)  
22 subjects.  
Unbalanced (four subjects in sequence RTRT and six in each of the other three) and complete.  
Two outliers (subjects 8 and 17) in sequence TRTR.  
A data frame with 88 observations on the following 5 variables:

subject	a factor with 22 levels: 1, 2, ..., 27
period	a factor with 4 levels: 1, 2, 3, 4
sequence	a factor with 4 levels: TRTR, RTRT, TRRT, RTTR
treatment	a factor with 2 levels: T, R
PK	a numeric vector of pharmacokinetic responses acceptable for reference-scaling (here $C_{max}$ )

### Details

Dataset	N	$CV_{wR}$ (%)	Evaluation
rds23	22	>30	method.A(), method.B()

### Note

In software sequences and treatments are ranked in lexical order. Hence, executing str() or summary() will show sequence as "RTRT", "RTTR", "TRRT", "TRTR" and treatment as "R", "T".  
In BE – by convention – sequences are ordered with T first. The library follows this convention.

### Source

Data-set	Origin	Description
rds23	FDA, CDER	$C_{max}$ data of Drug 7.

## References

U.S. Food and Drug Administration, Center for Drug Evaluation and Research. *Bioequivalence Studies*. Rockville, 1997. [bioequivalence study files](#) (archived 2017-07-23)

## Examples

```
str(rds23)
row <- c(25:28, 5:8, 9:12, 1:4)
rds23[row, ]
summary(rds23[2:5])
```

---

TTRR.RRTT

---

*Reference Datasets for TTRR\RTT Designs*


---

## Description

Dataset obtained by simulations to be evaluated by method.A() and/or method.B().

## Format

- Reference Dataset 28 (rds28)  
64 subjects. Balanced (64 subjects in both sequences) and complete. No outliers.  
A data frame with 256 observations on the following 5 variables:

subject	a factor with 64 levels: 1, 2, ..., 64
period	a factor with 4 levels: 1, 2, 3, 4
sequence	a factor with 2 levels: TTRR, RRTT
treatment	a factor with 2 levels: T, R
PK	a numeric vector of pharmacokinetic responses acceptable for reference-scaling (generally $C_{max}$ )

## Details

Dataset	N	$CV_{wR}$ (%)	Evaluation
rds28	64	<30	method.A(), method.B()

## Note

In software sequences and treatments are ranked in lexical order. Hence, executing str() or summary() will show sequence as "RRTT", "TTRR" and treatment as "R", "T". In BE – by convention – sequences are ordered with T first. The library follows this convention.

**Author(s)**

Helmut Schütz (R-code for simulations by Detlew Labes)

**Source**

Dataset	Origin	Description
rds28	R	Simulated with $CV_{wT} = CV_{wR} = 35\%$ , $CV_{bR} = CV_{bR} = 75\%$ , GMR 0.90.

**Examples**

```
str(rds28)
summary(rds28[1:5])
```

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