Package 'BE'

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Version 0.1.0

Title Bioequivalence Study Data Analysis

Description Analyze bioequivalence study data in a industrial strength. Sample size could be determined for various crossover designs, such as 2x2 design, 2x4 design, 4x4 design, Balaam design, Two-sequence dual design, and William design.
Reference: Chow SC, Liu JP. Design and Analysis of Bioavailability and Bioequivalence Studies. 3rd ed. (2009, ISBN:978-1-58488-668-6).

Depends R (>= 3.0.0)

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NeedsCompilation no

LazyLoad yes

Repository CRAN

URL https://cran.r-project.org/package=BE

R topics documented:

be2x2 *Bioequivalence test of a 2x2 study*

Description

It performs conventional bioequivalence test for 2x2 study. Input is a file. Basic assumption is that the variable is distributed as log-normal distribution. This is SAS PROC GLM style. If you want PROC MIXED style, use `nlme:lme`.

Usage

```
be2x2(filename, Columns = c("AUClast", "Cmax", "Tmax"), Plot = TRUE)
```

Arguments

`filename`	Data file name. This should have at least the following columns and variable columns to be tested. AUC ans Cmax should be all positive values.
	`GRP : Group or Sequence, 'RT' or 'TR'`
	`PRD : Period, 1 or 2`
	`SUBJ : Subject ID`
	`TRT : Treatment or Drug, 'R' or 'T'`

`Columns`	Column names of variables to be tested. This is usaully c("AUClast", "Cmax", "Tmax") or c("AUClast", "AUCinf", "Cmax", "Tmax")
`Plot`	Whether plot on screen is to be done or not.

Details

It performs bioequivalency tests for severval variables of a 2x2 study in a data file.

Value

Returns text output of equivalence test result.

Author(s)

Kyun-Seop Bae <k@acr.kr>

See Also

`test2x2`, `plot2x2`

Examples

```
write.csv(NCAResult4BE, "temp.csv", quote=FALSE, row.names=FALSE)
print(be2x2("temp.csv", c("AUClast", "Cmax", "Tmax")), na.print="")
```

ci2cv — *Coefficient of variation (CV) from a confidence interval of previous 2x2 study*

Description

It calculates coefficient of variation (CV) from a confidence interval of previous 2x2 study.

Usage

```
ci2cv(n1, n2, LL, UL, Alpha = 0.1)
```

Arguments

n1	Subject count of group 1
n2	Subject count of group 2
LL	Lower limit of confidence interval of geometric mean ratio (Test/Reference)
UL	Upper limit of confidence interval of geometric mean ratio (Test/Reference)
Alpha	Alpha level. This means (1 - alpha/2)*100 % confidence interval is given

Details

It calculates coefficient of variation (CV) from a confidence interval of 2x2 bioequivalence study.

Value

Returns coefficient of variation (CV) in percent (%).

Author(s)

Kyun-Seop Bae <k@acr.kr>

Examples

```
ci2cv(12, 13, 0.85, 1.11)
```

ci2mse — *Mean squared error (MSE) from a confidence interval of previous 2x2 study*

Description

It calculates mean squared error (MSE) from a confidence interval of previous 2x2 study.

Usage

```
ci2mse(n1, n2, LL, UL, Alpha = 0.1)
```

Arguments

n1	Subject count of group 1
n2	Subject count of group 2
LL	Lower limit of confidence interval of geometric mean ratio (Test/Reference)
UL	Upper limit of confidence interval of geometric mean ratio (Test/Reference)
Alpha	Alpha level. This means (1 - alpha/2)*100 % confidence interval is given

Details

It calculates coefficient of variation (CV) from a confidence interval of 2x2 bioequivalence study.

Value

Returns mean squared error (MSE).

Author(s)

Kyun-Seop Bae <k@acr.kr>

Examples

```
ci2mse(12, 13, 0.85, 1.11)
```

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cv2mse *Mean squared error (MSE) from coefficient of variation (CV)*

Description

It alculates mean squared error (MSE) from oefficient of variation (CV).

Usage

```
cv2mse(cv)
```

Arguments

cv	Coefficient of variation (%) in original scale

Details

coefficient of variation (CV) is percent in original scale and mean squared error (MSE) is log scale.

Value

Returns mean squared error (MSE) in log scale).

Author(s)

Kyun-Seop Bae <k@acr.kr>

Examples

```
cv2mse(25)
```

hodges *Hodges-Lehmann estimation for a variable of a 2x2 study*

Description

It performs Hodges-Lehmann estimation for 2x2 study. This is usually for Tmax variable.

Usage

```
hodges(bedata, Var)
```

Arguments

bedata	Data table name. This should have at least the following columns and a variable column to be tested.
	`GRP : Group or Sequence, 'RT' or 'TR'`
	`PRD : Period, 1 or 2`
	`SUBJ : Subject ID`
	`TRT : Treatment or Drug, 'R' or 'T'`

Var	Variable to be estimated. This should be one of the column names in bedata table. Usually 'Tmax'

Details

It nonparametrically tests `Var` variable equivalency from a 2x2 study. This is done for a variable which we cannot assume log-normal distribution.

Value

`Wilcoxon Signed-Rank Test`
: A kind of nonparametric test

`Hodges-Lehmann Estimate`
: 90% confidence interval in orginal scale and percent scale

Author(s)

Kyun-Seop Bae <k@acr.kr>

Examples

```
hodges(NCAResult4BE, "Tmax")
```

mse2cv *Coefficient of variation (CV) from mean squared error (MSE)*

Description

It alculates coefficient of variation (CV) from mean squared error (MSE).

Usage

```
mse2cv(mse)
```

Arguments

mse	Mean square error (MSE) in log scale

Details

coefficient of variation (CV) is percent in original scale and mean squared error (MSE) is log scale.

Value

Returns coefficient of variation (CV) in percent (%).

Author(s)

Kyun-Seop Bae <k@acr.kr>

Examples

```
mse2cv(0.06062462)
```

NCAResult4BE *An Example of Noncompartmental Analysis Result for Bioequivalence Test*

Description

Contains Noncompartmental analysis result data from a concentration simulated bioequivalence study.

Usage

```
RptCfg
```

Format

A data frame with 48 observations on the following 10 variables.

`SUBJ` Subject ID

`GRP` Group or Sequence character code: 'RT' or 'TR"

`PRD` Period numeric value: 1 or 2

`TRT` Treatment or Drug code: 'R' or 'T'

`AUClast` AUClast positive numeric value

`Cmax` Cmax positive numeric value

`Tmax` Tmax positive numeric value

Details

This contains a simulated data for 2x2 bioequivalence study data analysis. Noncompartmental analysis results are from the `NonCompart` package.

`plot2x2` *Plot bioequivalence variable of a 2x2 study*

Description

It plots two 2x2 plots for a variable.

Usage

```
plot2x2(bedata, Var)
```

Arguments

`bedata`	Data table name. This should have at least the following columns and a variable column to be plotted.
	`GRP : Group or Sequence, 'RT' or 'TR'`
	`PRD : Period, 1 or 2`
	`SUBJ : Subject ID`
	`TRT : Treatment or Drug, 'R' or 'T'`

`Var`	Variable to be plotted. This should be one of the column names in bedata table.

Details

It plots `Var` column values according to GRP, PRD, TRT.

Value

It just draws two 2x2 plots for equivalence exploration.

Author(s)

Kyun-Seop Bae <k@acr.kr>

Examples

```
plot2x2(NCAResult4BE, "AUClast")
plot2x2(NCAResult4BE, "Cmax")
plot2x2(NCAResult4BE, "Tmax")
```

`pow2x2ci` *Power using a confidence interval of previous 2x2 study*

Description

It calculates power for the bioequivalence test on ratio using a confidence interval of previous 2x2 study.

Usage

```
pow2x2ci(n1, n2, LL, UL, Alpha = 0.1)
```

Arguments

`n1`	Subject count of group 1
`n2`	Subject count of group 2
`LL`	Lower limit of confidence interval of geometric mean ratio (Test/Reference)
`UL`	Upper limit of confidence interval of geometric mean ratio (Test/Reference)
`Alpha`	Alpha level. This means (1 - alpha/2)*100 % confidence interval is given

Details

It calculates power of sample size (n per group) with `CV`.

Value

Returns power [0, 1)

Author(s)

Kyun-Seop Bae <k@acr.kr>

Examples

```
pow2x2ci(12, 13, 0.85, 1.11)
```

pow2x2mse *Power using mean squared error (MSE) of previous 2x2 study*

Description

It calculates power for the bioequivalence test on ratio using mean squared error (MSE of previous 2x2 study.

Usage

```
pow2x2mse(n1, n2, mse, True.R = 1, Alpha = 0.1, ThetaL = 0.8, ThetaU = 1.25)
```

Arguments

n1	Subject count of group 1
n2	Subject count of group 2
mse	Mean squared error
True.R	True ratio of test/reference
Alpha	Alpha level. This means (1 - alpha/2)*100 % confidence interval is given
ThetaL	Lower limit of equivalence criteria
ThetaU	Upper limit of equivalence criteria

Details

It calculates power of sample size (n per group) with CV.

Value

Returns power [0, 1)

Author(s)

Kyun-Seop Bae <k@acr.kr>

Examples

```
pow2x2mse(12, 13, 0.0756530)
```

powcv *Power using coefficient of variation (CV)*

Description

It calculates power for the bioequivalence test on ratio using coefficient of variation (CV).

Usage

```
powcv(n, CV, DesignNo = 1, True.R = 1, Alpha = 0.1, ThetaL = 0.8, ThetaU = 1.25)
```

Arguments

n	Sample size, n per group
CV	Coefficient of Variation (%)
DesignNo	Crossover design number.

```
Design Number (treatment x sequence x period)
1 2x2x2 : RT TR
2 2x4x2 (Balaam Design) : TT RR RT TR
3 2x2x3 (Two-sequence Dual Design): TRR RTT
4 2x2x4 : TRRT RTTR
5 2x4x4 : TTRR RRTT TRRT RTTR
6 3x6x3 (William Design for 3 treatments) + carry-over effect
        : RBA ARB BAR ABR BRA RAB
7 3x6x3 (William Design for 3 treatments) - carry-over effect
        : RBA ARB BAR ABR BRA RAB
8 4x4x4 (William Design for 4 treatments) + carry-over effect
        : RCAB ARBC BACR CBRA
9 4x4x4 (William Design for 4 treatments) - carry-over effect
        : RCAB ARBC BACR CBRA
```

True.R	True ratio of test/reference
Alpha	Alpha error level
ThetaL	Lower limit of equivalence criteria
ThetaU	Upper limit of equivalence criteria

Details

It calculates power of sample size (n per group) with CV.

Value

Returns power [0, 1)

Author(s)

Kyun-Seop Bae <k@acr.kr>

Examples

```
powcv(12, 25)
```

powmse *Power using mean squared error (MSE)*

Description

It calculates power for the bioequivalence test on ratio using mean squared error (MSE).

Usage

```
powmse(n, mse, DesignNo = 1, True.R = 1, Alpha = 0.1, ThetaL = 0.8, ThetaU = 1.25)
```

Arguments

n	Sample size, n per group
mse	Mean squared error
DesignNo	Crossover design number.

```
Design Number (treatment x sequence x period)
1 2x2x2 : RT TR
2 2x4x2 (Balaam Design) : TT RR RT TR
3 2x2x3 (Two-sequence Dual Design): TRR RTT
4 2x2x4 : TRRT RTTR
5 2x4x4 : TTRR RRTT TRRT RTTR
6 3x6x3 (William Design for 3 treatments) + carry-over effect
        : RBA ARB BAR ABR BRA RAB
7 3x6x3 (William Design for 3 treatments) - carry-over effect
        : RBA ARB BAR ABR BRA RAB
8 4x4x4 (William Design for 4 treatments) + carry-over effect
        : RCAB ARBC BACR CBRA
9 4x4x4 (William Design for 4 treatments) - carry-over effect
        : RCAB ARBC BACR CBRA
```

True.R	True ratio of test/reference
Alpha	Alpha error level
ThetaL	Lower limit of equivalence criteria
ThetaU	Upper limit of equivalence criteria

Details

It calculates power of sample size (n per group) with mse.

Value

Returns power [0, 1))

Author(s)

Kyun-Seop Bae <k@acr.kr>

Examples

```
powmse(12, 0.06)
```

ss2x2ci *Sample size using a confidence interval of previous 2x2 study*

Description

It calculates sample size for the bioequivalence test on ratio using a confidence interval of previous 2x2 study.

Usage

```
ss2x2ci(n1, n2, LL, UL, Alpha = 0.1)
```

Arguments

n1	Subject count of group 1
n2	Subject count of group 2
LL	Lower limit of confidence interval of geometric mean ratio (Test/Reference)
UL	Upper limit of confidence interval of geometric mean ratio (Test/Reference)
Alpha	Alpha level. This means (1 - alpha/2)*100 % confidence interval is given

Details

It calculates sample size (n per group) with CV, Alpha, and Beta for bioequivalence test.

Value

Returns sample size (n per group) for bioequivalence test with ratio criteria.

Author(s)

Kyun-Seop Bae <k@acr.kr>

Examples

```
ss2x2ci(12, 13, 0.85, 1.11)
```

sscv *Sample size using coefficient of variation (CV)*

Description

It calculates sample size for the bioequivalence test on ratio using coefficient of variation (CV).

Usage

```
sscv(CV, DesignNo = 1, True.R = 1, Alpha = 0.1, Beta = 0.2,
     ThetaL = 0.8, ThetaU = 1.25, nMax = 999999)
```

Arguments

CV	Coefficient of Variation (%)
DesignNo	Crossover design number.

```
Design Number (treatment x sequence x period)
1 2x2x2 : RT TR
2 2x4x2 (Balaam Design) : TT RR RT TR
3 2x2x3 (Two-sequence Dual Design): TRR RTT
4 2x2x4 : TRRT RTTR
5 2x4x4 : TTRR RRTT TRRT RTTR
6 3x6x3 (William Design for 3 treatments) + carry-over effect
        : RBA ARB BAR ABR BRA RAB
7 3x6x3 (William Design for 3 treatments) - carry-over effect
        : RBA ARB BAR ABR BRA RAB
8 4x4x4 (William Design for 4 treatments) + carry-over effect
        : RCAB ARBC BACR CBRA
9 4x4x4 (William Design for 4 treatments) - carry-over effect
        : RCAB ARBC BACR CBRA
```

True.R	True ratio of test/reference
Alpha	Alpha error level
Beta	Beta error level
ThetaL	Lower limit of equivalence criteria
ThetaU	Upper limit of equivalence criteria
nMax	Maximum subject number (sample size) per group

Details

It calculates sample size (n per group) with CV, Alpha, and Beta for bioequivalence test.

Value

Returns sample size (n per group) for bioequivalence test with ratio criteria.

Author(s)

Kyun-Seop Bae <k@acr.kr>

Examples

```
sscv(25)
```

ssmse *Sample size using mean squared error (MSE)*

Description

It calculates sample size for the bioequivalence test on ratio using mean squared error (MSE).

Usage

```
ssmse(mse, DesignNo = 1, True.R = 1, Alpha = 0.1, Beta = 0.2,
      ThetaL = 0.8, ThetaU = 1.25, nMax = 999999)
```

Arguments

mse	Mean squared error
DesignNo	Crossover design number.

```
Design Number (treatment x sequence x period)
1 2x2x2 : RT TR
2 2x4x2 (Balaam Design) : TT RR RT TR
3 2x2x3 (Two-sequence Dual Design): TRR RTT
4 2x2x4 : TRRT RTTR
5 2x4x4 : TTRR RRTT TRRT RTTR
6 3x6x3 (William Design for 3 treatments) + carry-over effect
        : RBA ARB BAR ABR BRA RAB
7 3x6x3 (William Design for 3 treatments) - carry-over effect
        : RBA ARB BAR ABR BRA RAB
8 4x4x4 (William Design for 4 treatments) + carry-over effect
        : RCAB ARBC BACR CBRA
9 4x4x4 (William Design for 4 treatments) - carry-over effect
        : RCAB ARBC BACR CBRA
```

True.R	True ratio of test/reference
Alpha	Alpha error level
Beta	Beta error level
ThetaL	Lower limit of equivalence criteria
ThetaU	Upper limit of equivalence criteria
nMax	Maximum subject number (sample size) per group

Details

It calculates sample size (n per group) with mse, Alpha, and Beta for bioequivalence test.

Value

Returns sample size (n per group) for bioequivalence test with ratio criteria.

Author(s)

Kyun-Seop Bae <k@acr.kr>

Examples

```
ssmse(0.06)
```

`test2x2` *Bioequivalence test for a variable of a 2x2 study*

Description

It performs conventional bioequivalence test for 2x2 study. Basic assumption is that the variable is distributed as log-normal distribution. This is SAS PROC GLM style. If you want PROC MIXED style use `nlme:lme`.

Usage

```
test2x2(bedata, Var)
```

Arguments

`bedata`	Data table name. This should have at least the following columns and a variable column to be tested. `Var` column values should be all positive values.
	`GRP : Group or Sequence, 'RT' or 'TR'`
	`PRD : Period, 1 or 2`
	`SUBJ : Subject ID`
	`TRT : Treatment or Drug, 'R' or 'T'`

`Var`	Variable to be tested. This should be one of the column names in bedata table. Usually 'AUClast' or 'Cmax'

Details

It tests `Var` variable equivalency from a 2x2 study. Current regulatory requirements is 90% confidence interval of gemotric mean ratio (Test/Reference) should be within [0.8, 1.25].

Value

`Analysis of Variance (log scale)`	Analysis of Variance in log scale
`Betwwen and Within Subject Variability`	Variance in log scale and coefficient of variance in original scale
`Least Square Means`	Geomtric means
`90% Confidence Interval`	90% confidence interval of geometric mean ratio (T/R)
`Sample Size`	Sample size for the replication of this study

Author(s)

Kyun-Seop Bae <k@acr.kr>

Examples

```
print(test2x2(NCAResult4BE, "AUClast"), na.print="")
print(test2x2(NCAResult4BE, "Cmax"), na.print="")
```

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