Package 'ncarbe'

September 22, 2017
Title Perform BE Test Using NonCompart Package
Version 0.1.0
Date 2017-09-22 KST
Maintainer Sungpil Han <shan@acp.kr></shan@acp.kr>
Description Performs a statistical analysis of 2x2 bioequivalence study using NonCompart package created by Kyun-Seop Bae. * Reference: Shein-Chung Chow, Jen-pei Liu. Design and Analysis of Bioavailability and Bioequivalence Studies, 3rd ed. 2008. (ISBN:9781584886686)
Depends R (>= $3.4.1$)
License GPL-3 file LICENSE
Encoding UTF-8
LazyData true
Imports NonCompart, dplyr
RoxygenNote 6.0.1
R topics documented: beNCA
Index
beNCA Performs a statistical analysis of 2x2 bioequivalence study
Description beNCA returns text output of a statistical analysis of 2x2 bioequivalence study. Analysis of varianc least square means, confidence interval, and sample size will be calculated for AUClast and Cmar Wilcoxon Signed-Rank Test and Hodges-Lehmann Estimate will be performed for Tmax.
Usage
beNCA(concData, SUBJ = "SUBJ", GRP = "GRP", PRD = "PRD", TRT = "TRT",

method = "kbe", ...)

beNCA

Arguments

SUBJ	Subject ID, any data type
GRP	column name in which information of "RT" or "TR" exists.
PRD	column name in which information of 1 or 2 exists.
TRT	column name in which information of "R" or "T" exists.
method	kbe by authors or nlme package uploaded on CRAN

Details

Reference: Shein-Chung Chow, Jen-pei Liu. Design and Analysis of Bioavailability and Bioequivalence Studies, 3rd ed. 2008. (ISBN:9781584886686)

Value

returns text results of statistical analysis of 2x2 bioequivalence study including and beNCAdataset.csv file in the working directory which can be run in SAS.

Examples

```
file <- system.file('example', 'beConc.csv', package = 'ncarbe')
concData <- read.csv(file, as.is = TRUE)
beNCA(concData)</pre>
```

Index

beNCA, 1