Package ‘Minirand’
January 22, 2020

Type Package
Title Minimization Randomization
Version 0.1.3
Date 2020-01-22
Author Man Jin [aut, cre],
      Adam Polis [aut],
      Jonathan Hartzel [aut]
Maintainer Man Jin <mj2149@gmail.com>
Description Randomization schedules are generated in the schemes with k \(k \geq 2\) treatment groups and any allocation ratios by minimization algorithms.
License GPL (>= 2)
Encoding UTF-8
RoxygenNote 6.1.0
NeedsCompilation no
Repository CRAN
Date/Publication 2020-01-22 22:30:02 UTC

R topics documented:

blkrandomization .................................................. 2
Minirand ................................................................. 2
randbalance ........................................................... 4
totimbal ............................................................... 4

Index

1
Minirand

Minimization randomization to k treatment groups

Description

The function is used to generate treatment assignment by minimization algorithms.

Usage

Minirand(covmat = covmat, j, covwt = covwt, ratio = ratio, 
ntrt = ntrt, trtseq = trtseq, method = "Range", result = res, p)
Minirand

Arguments

covmat matrix or data frame of covariate factors
j the jth subject in the randomization sequence
covwt vector of weights of the covariate factors
ratio vector of randomization ratios for each treatment
ntrt numeric number of treatment groups
trtseq vector of a sequence of treatment groups
method the method or algorithm for the minimization randomization
result the treatment assignments in subjects achieved so far
p the high probability for new assignment

Value

treatment assignment for the jth subject

References

Pocock and Simon (1975), Sequential Treatment Assignment with Balancing for Prognostic Factors in the Controlled Clinical Trial. Biometrics; 103-115.

Examples

ntrt <- 3
nsample <- 120
trtseq <- c(1, 2, 3)
ratio <- c(2, 2, 1)
c1 <- sample(seq(1, 0), nsample, replace = TRUE, prob = c(0.4, 0.6))
c2 <- sample(seq(1, 0), nsample, replace = TRUE, prob = c(0.3, 0.7))
c3 <- sample(c(2, 1, 0), nsample, replace = TRUE, prob = c(0.33, 0.2, 0.5))
c4 <- sample(seq(1, 0), nsample, replace = TRUE, prob = c(0.33, 0.67))
covmat <- cbind(c1, c2, c3, c4) # generate the matrix of covariate factors for the subjects
# label of the covariates
colnames(covmat) = c("Gender", "Age", "Hypertension", "Use of Antibiotics")
covwt <- c(1/4, 1/4, 1/4, 1/4) # equal weights
res <- rep(100, nsample) # result is the treatment needed from minimization method
# generate treatment assignment for the 1st subject
res[1] = sample(trtseq, 1, replace = TRUE, prob = ratio/sum(ratio))
for (j in 2:nsample)
{
  # get treatment assignment sequentially for all subjects
  res[j] <- Minirand(covmat=covmat, j, covwt=covwt, ratio=ratio, ntrt=ntrt, trtseq=trtseq, method="Range", result=res, p = 0.9)
}
trt1 <- res
# Display the number of randomized subjects at covariate factors
balance1 <- randbalance(trt1, covmat, ntrt, trtseq)


**totimbal**

totimbal(trt = trt, covmat = covmat, covwt = covwt, ratio = ratio, ntrt = ntrt, trtseq = trtseq, method = "Range")

**randbalance**

Displays the number of randomized subjects at each level for all covariate factors.

**Description**

The function to count the number of randomized subjects at each level for all covariate factors.

**Usage**

randbalance(trt, covmat, ntrt, trtseq)

**Arguments**

- trt: treatment sequence for all the randomized subjects
- covmat: matrix or data frame of covariate factors
- ntrt: numeric number of treatment groups
- trtseq: vector of a sequence of treatment groups

**Value**

the number of randomized subjects at each level for all covariate factors

**totimbal**

Calculates the total imbalance measured by minimization algorithms.

**Description**

The function to calculates the total imbalance measured by minimization algorithms.

**Usage**

totimbal(trt = trt, covmat = covmat, covwt = covwt, ratio = ratio, ntrt = ntrt, trtseq = trtseq, method = "Range")
Arguments

- **trt**: treatment sequence for all the randomized subjects
- **covmat**: matrix or data frame of covariate factors
- **covwt**: vector of weights of the covariate factors
- **ratio**: vector of randomization ratios for each treatment
- **ntrt**: numeric number of treatment groups
- **trtseq**: vector of a sequence of treatment groups
- **method**: the method or algorithm for the minimization randomization

Value

total imbalance
Index

blkrandomization, 2
Minirand, 2
randbalance, 4
totimbal, 4