Package ‘Minirand’

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Type Package

Title Minimization Randomization

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Description Randomization schedules are generated in the schemes with k (k>=2) treatment groups and any allocation ratios by minimization algorithms.

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Encoding UTF-8

RoxygenNote 6.1.0

NeedsCompilation no

Repository CRAN

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R topics documented:

`blkrandomization` *Blocked randomization*

Description

The fuction is used to generate treatment assignments based on blocked randomization.

Usage

```
blkrandomization(n, blocksize, block)
```

Arguments

`n`	numeric number of subjects who will be randomized
`blocksize`	numeric value of block size used for blocked randomization
`block`	vector of treatment blocks used for blocked randomization

Value

trt a sequence of treatment assignments

Examples

```
blocksize <- 4
block <- c(1, 2, 3, 4) # treatment 1, 2, 3, 4
n <- 35
blkrandomization(n, blocksize, block)
```

`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)
```

Arguments

`covmat`	matrix or data frame of covariate factors
`j`	the jth subject in the randomization sequence
`covwt`	vector of weights of the covaraite 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 subjetcs 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.

Jin, Polis, and Hartzel (2019), "Algorithms for minimization randomization and the implementation with an R package". Communications in Statistics-Simulation and Computation; May 2019.

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
#gernerate 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 sequentiall 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)
```

```
balance1
totimbal(trt = trt1, 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 fuction to cound 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

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`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 covaraite 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

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