

Package ‘Minirand’

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Type Package

Title Minimization Randomization

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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)

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NeedsCompilation no

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blkrandomization *Blocked randomization*

Description

The function 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 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.

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
#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 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 | <i>Displays the number of randomized subjects at each level for all covariate factors.</i> |
|-------------|--|

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 | <i>Calculates the total imbalance measured by minimization algorithms.</i> |
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Description

The function to calculate the total imbalance measured by minimization algorithms

Usage

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

Arguments

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

Value

total imbalance

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