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Title Covariate-Adaptive Randomization for Clinical Trials

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Description Provides functions and command-line user interface to generate allocation sequence by covariate-adaptive randomization for clinical trials. The package currently supports six covariate-adaptive randomization procedures. Three hypothesis testing methods that are valid and robust under covariate-adaptive randomization are also available in the package to facilitate the inference for treatment effect under the included randomization procedures. Additionally, the package provides comprehensive and efficient tools to allow one to evaluate and compare the performance of randomization procedures and tests based on various criteria. See Ma W, Ye X, Tu F, and Hu F (2023) <doi:10.18637/jss.v107.i02> for details.

License GPL (>= 2)

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Contents

`carat-package` *carat-package: Covariate-Adaptive Randomization for Clinical Trials*

Description

Provides functions and a command-line user interface to generate allocation sequences for clinical trials with covariate-adaptive randomization methods. It currently supports six different covariate-adaptive randomization procedures, including stratified randomization, minimization, and a general family of designs proposed by Hu and Hu (2012) <doi:10.1214/12-AOS983>. Three hypothesis testing methods, all valid and robust under covariate-adaptive randomization are also included in the package to facilitate the inference for treatment effects under the included randomization procedures. Additionally, the package provides comprehensive and efficient tools for the performance evaluation and comparison of randomization procedures and tests based on various criteria.

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References

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Baldi Antognini A, Zagoraiou M. *The covariate-adaptive biased coin design for balancing clinical trials in the presence of prognostic factors*[J]. Biometrika, 2011, 98(3): 519-535. <doi:10.1093/biomet/asr021>

Hu Y, Hu F. *Asymptotic properties of covariate-adaptive randomization*[J]. The Annals of Statistics, 2012, 40(3): 1794-1815. <doi:10.1214/12-AOS983>

Ma W, Hu F, Zhang L. *Testing hypotheses of covariate-adaptive randomized clinical trials*[J]. Journal of the American Statistical Association, 2015, 110(510): 669-680. <doi:10.1080/01621459.2014.922469>

Ma W, Qin Y, Li Y, et al. *Statistical Inference for Covariate-Adaptive Randomization Procedures*[J]. Journal of the American Statistical Association, 2020, 115(531): 1488-1597. <doi:10.1080/01621459.2019.1635483>

Ma W, Ye X, Tu F, Hu F. *carat: Covariate-Adaptive Randomization for Clinical Trials*[J]. Journal of Statistical Software, 2023, 107(2): 1-47. <doi: 10.18637/jss.v107.i02>

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Shao J., Yu, X. *Validity of tests under covariate-adaptive biased coin randomization and generalized linear models*[J]. Biometrics, 2013, 69(4), 960-969. <doi:10.1111/biom.12062>

Shao J., Yu X, Zhong B. *A theory for testing hypotheses under covariate-adaptive randomization*[J]. Biometrika, 2010, 97(2): 347-360. <doi:10.1093/biomet/asq014>

Zelen M. *The randomization and stratification of patients to clinical trials*[J]. Journal of chronic diseases, 1974, 27(7): 365-375. <doi:10.1016/0021-9681(74)90015-0>

`AdjBCD` *Covariate-adjusted Biased Coin Design*

Description

Allocates patients to one of two treatments based on covariate-adjusted biased coin design as proposed by Baldi Antognini A, Zagoraiou M (2011) <doi:10.1093/biomet/asr021>.

Usage

```
AdjBCD(data, a = 3)
```

Arguments

data	a data frame. A row of the dataframe corresponds to the covariate profile of a patient.
a	a design parameter governing the degree of randomness. The default is 3.

Details

Consider I covaraites and m_i levels for the ith covariate, $i = 1, \ldots, I$. T_j is the assignment of the jth patient and $Z_j = (k_1, \ldots, k_I)$ indicates the covariate profile of the jth patient, $j = 1, \ldots, n$. For convenience, $(k_1, \ldots, k_I)$ and $(i; k_i)$ denote stratum and margin, respectively. $D_j(.)$ is the difference between numbers of patients assigned to treatment 1 and treatment 2 at the corresponding level after j patients have been assigned.

Let F^a be a decreasing and symmetric function of $D_j(.)$, which depends on a design parameter $a \geq 0$. Then, the probability of allocating the $(j+1)$th patient to treatment 1 is $F^a(D_j(.))$, where

$$F^a(x) = \frac{1}{x^a + 1},$$

for $x \geq 1$,

$$F^a(x) = 1/2,$$

for $x = 0$, and

$$F^a(x) = \frac{|x|^a}{|x|^a + 1},$$

for $x \leq -1$. As a goes to ∞, the design becomes more deteministic.

Details of the procedure can be found in Baldi Antognini and M. Zagoraiou (2011).

Value

It returns an object of class "carandom".

An object of class "carandom" is a list containing the following components:

datanumeric	a bool indicating whether the data is a numeric data frame.
covariates	a character string giving the name(s) of the included covariates.
strt_num	the number of strata.
cov_num	the number of covariates.
level_num	a vector of level numbers for each covariate.
n	the number of patients.
Cov_Assig	a (cov_num + 1) * n matrix containing covariate profiles for all patients and the corresponding assignments. The ith column represents the ith patient. The first cov_num rows include patients' covariate profiles, and the last row contains the assignments.

assignments	the randomization sequence.
All strata	a matrix containing all strata involved.
Diff	a matrix with only one column. There are final differences at the overall, within-stratum, and within-covariate-margin levels.
method	a character string describing the randomization procedure to be used.
Data Type	a character string giving the data type, Real or Simulated.
framework	the framework of the used randomization procedure: stratified randomization, or model-based method.
data	the data frame.

References

Baldi Antognini A, Zagoraiou M. *The covariate-adaptive biased coin design for balancing clinical trials in the presence of prognostic factors*[J]. Biometrika, 2011, 98(3): 519-535.

Ma W, Ye X, Tu F, Hu F. *carat: Covariate-Adaptive Randomization for Clinical Trials*[J]. Journal of Statistical Software, 2023, 107(2): 1-47.

See Also

See AdjBCD.sim for allocating patients with covariate data generating mechanism; See AdjBCD.ui for the command-line user interface.

Examples

```
# a simple use
## Real Data
## create a dataframe
df <- data.frame("gender" = sample(c("female", "male"), 1000, TRUE, c(1 / 3, 2 / 3)),
                 "age" = sample(c("0-30", "30-50", ">50"), 1000, TRUE),
                 "jobs" = sample(c("stu.", "teac.", "others"), 1000, TRUE),
                 stringsAsFactors = TRUE)
Res <- AdjBCD(df, a = 2)
## view the output
Res

  ## view all patients' profile and assignments
  Res$Cov_Assig


## Simulated Data
n <- 1000
cov_num <- 3
level_num <- c(2, 3, 5)
# Set pr to follow two tips:
#(1) length of pr should be sum(level_num);
#(2) sum of probabilities for each margin should be 1.
pr <- c(0.4, 0.6, 0.3, 0.4, 0.3, rep(0.2, times = 5))
# set the design parameter
a <- 1.8
```

```
# obtain result
Res.sim <- AdjBCD.sim(n, cov_num, level_num, pr, a)

  # view the assignments of patients
  Res.sim$Cov_Assig[cov_num + 1, ]
  # view the differences between treatment 1 and treatment 2 at all levels
  Res.sim$Diff
```

`AdjBCD.sim` *Covariate-adjusted Biased Coin Design with Covariate Data Generating Mechanism*

Description

Allocates patients to one of two treatments based on the covariate-adjusted biased coin design as proposed by Baldi Antognini A, Zagoraiou M (2011) <doi:10.1093/biomet/asr021>, by simulating the covariates-profile under the assumption of independence between covariates and levels within each covariate.

Usage

```
AdjBCD.sim(n = 1000, cov_num = 2, level_num = c(2, 2),
           pr = rep(0.5, 4), a = 3)
```

Arguments

`n`	the number of patients. The default is `1000`.
`cov_num`	the number of covariates. The default is `2`.
`level_num`	a vector of level numbers for each covariate. Hence the length of `level_num` should be equal to the number of covariates. The default is `c(2,2)`.
`pr`	a vector of probabilities. Under the assumption of independence between covariates, `pr` is a vector containing probabilities for each level of each covariate. The length of `pr` should correspond to the number of all levels, and the sum of the probabilities for each margin should be `1`. The default is `rep(0.5, 4)`, which corresponds to `cov_num = 2`, and `level_num = c(2, 2)`.
`a`	a design parameter governing the degree of randomness. The default is `3`.

Details

See `AdjBCD`.

Value

See `AdjBCD`.

References

Baldi Antognini A, Zagoraiou M. *The covariate-adaptive biased coin design for balancing clinical trials in the presence of prognostic factors*[J]. Biometrika, 2011, 98(3): 519-535.

Ma W, Ye X, Tu F, Hu F. *carat: Covariate-Adaptive Randomization for Clinical Trials*[J]. Journal of Statistical Software, 2023, 107(2): 1-47.

See Also

See `AdjBCD` for allocating patients with complete covariate data; See `AdjBCD.ui` for the command-line user interface.

`AdjBCD.ui` *Command-line User Interface Using Covariate-adjusted Biased Coin Design*

Description

A call to the user-interface function for allocation of patients to one of two treatments, using covariate-adjusted biased coin design, as proposed by Baldi Antognini A, Zagoraiou M (2011) <doi:10.1093/biomet/asr021>.

Usage

```
AdjBCD.ui(path, folder = "AdjBCD")
```

Arguments

`path`	the path in which a folder used to store variables will be created.
`folder`	name of the folder. If it is the default, a folder named `"AdjBCD"` will be created.

Details

See `AdjBCD`.

Value

It returns an object of `class` `"carseq"`.

The function `print` is used to obtain results. The generic accessor functions `assignment`, `covariate`, `cov_num`, `cov_profile` and others extract various useful features of the value returned by `AdjBCD.ui`.

Note

This function provides a command-line user interface, and users should follow the prompts to enter data including covariates as well as levels for each covariate, design parameter `a` and the covariate profile of the new patient.

References

Baldi Antognini A, Zagoraiou M. *The covariate-adaptive biased coin design for balancing clinical trials in the presence of prognostic factors*[J]. Biometrika, 2011, 98(3): 519-535.

Ma W, Ye X, Tu F, Hu F. *carat: Covariate-Adaptive Randomization for Clinical Trials*[J]. Journal of Statistical Software, 2023, 107(2): 1-47.

See Also

See `AdjBCD` for allocating patients with complete covariate data; See `AdjBCD.sim` for allocating patients with covariate data generating mechanism.

`boot.test` *Bootstrap t-test*

Description

Performs bootstrap t-test on treatment effects. This test is proposed by Shao et al. (2010) <doi:10.1093/biomet/asq014>.

Usage

```
boot.test(data, B = 200, method = c("HuHuCAR", "PocSimMIN", "StrBCD",
                                    "StrPBR", "DoptBCD", "AdjBCD"),
          conf = 0.95, ...)
```

Arguments

`data`	a data frame. It consists of patients' profiles, treatment assignments and outputs. See `getData`.
`B`	an integer. It is the number of bootstrap samples. The default is `200`.
`method`	the randomization procedure to be used for testing. This package provides tests for `"HuHuCAR"`, `"PocSimMIN"`, `"StrBCD"`, `"StrPBR"`, `"AdjBCD"`, and `"DoptBCD"`.
`conf`	confidence level of the interval. The default is `0.95`.
`...`	arguments to be passed to `method`. These arguments depend on the randomization method used and the following arguments are accepted: **omega** a vector of weights at the overall, within-stratum, and within-covariate-margin levels. It is required that at least one element is larger than 0. Note that `omega` is only needed when `HuHuCAR` is to be used. **weight** a vector of weights for within-covariate-margin imbalances. It is required that at least one element is larger than 0. Note that `weight` is only needed when `PocSimMIN` is to be used. **p** the biased coin probability. `p` should be larger than `1/2` and less than `1`. Note that `p` is only needed when `"HuHuCAR"`, `"PocSimMIN"` and `"StrBCD"` are to be used. **a** a design parameter governing the degree of randomness. Note that `a` is only needed when `"AdjBCD"` is to be used. **bsize** the block size for stratified randomization. It is required to be a multiple of 2. Note that `bsize` is only needed when `"StrPBR"` is to be used.

Details

The bootstrap t-test is described as follows:

1) Generate bootstrap data $(Y_1^*, Z_1^*), \ldots, (Y_n^*, Z_n^*)$ as a simple random sample with replacement from the original data $(Y_1, Z_1), \ldots, (Y_n, Z_n)$, where Y_i denotes the outcome and Z_i denotes the profile of the ith patient.

2) Perform covariate-adaptive procedures on the patients' profiles to obtain new treatment assignments $T_1^*, \ldots, T_n^*$, and define

$$\hat{\theta}^* = -\frac{1}{n_1^*}\sum_{i=1}^{n}(T_i^* - 2) \times Y_i^* - \frac{1}{n_0^*}\sum_{i=1}^{n}(T_i^* - 1) \times Y_i$$

where n_1^* is the number of patients assigned to treatment 1 and n_0^* is the number of patients assigned to treatment 2.

3) Repeat step 2 B times to generate B independent boostrap samples to obtain $\hat{\theta}_b^*$, $b = 1, \ldots, B$. The variance of $\bar{Y}_1 - \bar{Y}_0$ can then be approximated by the sample variance of $\hat{\theta}_b^*$.

Value

It returns an object of class `"htest"`.

An object of class `"htest"` is a list containing the following components:

`statistic`	the value of the t-statistic.
`p.value`	the p-value of the test,the null hypothesis is rejected if p-value is less than the pre-determined significance level.
`conf.int`	a confidence interval under the chosen level `conf` for the difference in treatment effect between treatment `1` and treatment `2`.
`estimate`	the estimated treatment effect difference between treatment `1` and treatment `2`.
`stderr`	the standard error of the mean (difference), used as denominator in the t-statistic formula.
`method`	a character string indicating what type of test was performed.
`data.name`	a character string giving the name(s) of the data.

References

Ma W, Ye X, Tu F, Hu F. *carat: Covariate-Adaptive Randomization for Clinical Trials*[J]. Journal of Statistical Software, 2023, 107(2): 1-47.

Shao J, Yu X, Zhong B. *A theory for testing hypotheses under covariate-adaptive randomization*[J]. Biometrika, 2010, 97(2): 347-360.

Examples

```
#Suppose the data used is patients' profile from real world,
#  while it is generated here. Data needs to be preprocessed
#  and then get assignments following certain randomization.
set.seed(100)
df<- data.frame("gender" = sample(c("female", "male"), 100, TRUE, c(1 / 3, 2 / 3)),
```

```
                "age" = sample(c("0-30", "30-50", ">50"), 100, TRUE),
               "jobs" = sample(c("stu.", "teac.", "other"), 100, TRUE, c(0.4, 0.2, 0.4)),
                stringsAsFactors = TRUE)
##data preprocessing
data.pd <- StrPBR(data = df, bsize = 4)$Cov_Assig

#Then we need to combine patients' profiles and outcomes after randomization and treatments.
outcome = runif(100)
data.combined = data.frame(rbind(data.pd,outcome), stringsAsFactors = TRUE)

#run the bootstrap t-test
B = 200
Strbt = boot.test(data.combined, B, "StrPBR", bsize = 4)
Strbt
```

`compPower` *Comparison of Powers for Different Tests under Different Randomization methods*

Description

Compares the power of tests under different randomization methods and treatment effects through matrices and plots.

Usage

```
compPower(powers, diffs, testname)
```

Arguments

`powers`	a list. Each argument consists the power generated by `evalPower()` in this package or by other sources. The length of each argument must match.
`diffs`	a vector. It contains values of group treatment effect differences. The length of this argument and the length of each argument of `powers` must match.
`testname`	a vector. Each element is the name of test and the randomization method used. For example, when applying `rand.test` and `corr.test` under `HuHuCAR`, it can be `c("HH.rand","HH.corr")`. The length of this argument must match the length of `diffs`.

Value

This function returns a list. The first element is a matrix consisting of powers of chosen tests under different values of treatment effects. The second element of the list is a plot of powers. `diffs` forms the vertical axis of the plot.

Examples

```
##settings
set.seed(100)
n = 1000
cov_num = 5
level_num = c(2,2,2,2,2)
pr = rep(0.5,10)
beta = c(1,4,3,2,5,5,4,3,2,1)
di = seq(0,0.5,0.1)
sigma = 1
type = "linear"
p=0.85
Iternum = 10 #<<for demonstration,it is suggested to be around 1000
sl = 0.05
weight = rep(0.1,5)

#comparison of corrected t-test under StrBCD and PocSim
##data generation
library("ggplot2")
Strctp=evalPower(n,cov_num,level_num,pr,type,beta,di,
                 sigma,Iternum,sl,"StrBCD","corr.test",FALSE,p)
PSctp=evalPower(n,cov_num,level_num,pr,type,beta,di,sigma,
                 Iternum,sl,"PocSimMIN","corr.test",FALSE,weight,p)
powers = list(Strctp,PSctp)
testname = c("StrBCD.corr","PocSimMIN.corr")

#get plot and matrix for comparison
cp = compPower(powers,di,testname)
cp
```

---

compRand *Compare Different Randomization Procedures via Tables and Plots*

Description

Compares randomization procedures based on several different quantities of imbalances. Among all included randomization procedures of class `"careval"`, two or more procedures can be compared in this function.

Usage

```
compRand(...)
```

Arguments

`...`	objects of class `"careval"`.

Details

The primary goal of using covariate-adaptive randomization in practice is to achieve balance with respect to the key covariates. We choose four rules to measure the absolute imbalances at overall, within-covariate-margin, and within-stratum levels, which are maximal, 95%quantile, median and mean of the absolute imbalances at different aspects. The Monte Carlo method is used to calculate the four types of imbalances. Let $D_{n,i}(\cdot)$ be the final difference at the corresponding level for ith iteration, $i = 1, \ldots,$ N, and N is the number of iterations.

(1) Maximal

$$\max_{i=1,\ldots,N} |D_{n,i}(\cdot)|.$$

(2) 95% quantile

$$|D_{n,\lceil 0.95N \rceil}(\cdot)|.$$

(3) Median

$$|D_{n,(N+1)/2}(\cdot)|$$

for N is odd, and

$$\frac{1}{2}(|D_{(N/2)}(\cdot)| + |D_{(N/2+1)}(\cdot)|)$$

for N is even.

(4) Mean

$$\frac{1}{N}\sum_{i=1}^{N} |D_{n,i}(\cdot)|.$$

Value

It returns an object of class "carcomp".

An object of class "carcomp" is a list containing the following components:

`Overall Imbalances`
: a matrix containing the maximum, 95%-quantile, median, and mean of the absolute overall imbalances for the randomization method(s) to be evaluated.

`Within-covariate-margin Imbalances Imbalances`
: a matrix containing the maximum, 95%-quantile, median, and mean of the absolute within-covariate-margin imbalances for the randomization method(s) to be evaluated.

`Within-stratum Imbalances`
: a matrix containing the maximum, 95%-quantile, median, and mean of the absolute within-stratum imbalances for the randomization method(s) to be evaluated.

`dfmm`
: a data frame containing the mean absolute imbalances at the overall, within-stratum, and within-covariate-margin levels for the randomization method(s) to be evaluated.

`df_abm`
: a data frame containing the absolute imbalances at the overall, within-stratum, and within-covariate-margin levels.

`mechanism`
: a character string giving the randomization method(s) to be evaluated.

`n`
: the number of patients.

`iteration`	the number of iterations.
`cov_num`	the number of covariates.
`level_num`	a vector of level numbers for each covariate.
`Data Type`	a character string giving the data type, `Real` or `Simulated`.
`DataGeneration`	a bool vector indicating whether the data used for all the iterations is the same for the randomization method(s) to be evaluated.

References

Atkinson A C. *Optimum biased coin designs for sequential clinical trials with prognostic factors*[J]. Biometrika, 1982, 69(1): 61-67.

Baldi Antognini A, Zagoraiou M. *The covariate-adaptive biased coin design for balancing clinical trials in the presence of prognostic factors*[J]. Biometrika, 2011, 98(3): 519-535.

Hu Y, Hu F. *Asymptotic properties of covariate-adaptive randomization*[J]. The Annals of Statistics, 2012, 40(3): 1794-1815.

Ma W, Ye X, Tu F, Hu F. *carat: Covariate-Adaptive Randomization for Clinical Trials*[J]. Journal of Statistical Software, 2023, 107(2): 1-47.

Pocock S J, Simon R. *Sequential treatment assignment with balancing for prognostic factors in the controlled clinical trial*[J]. Biometrics, 1975: 103-115.

Shao J, Yu X, Zhong B. *A theory for testing hypotheses under covariate-adaptive randomization*[J]. Biometrika, 2010, 97(2): 347-360.

Zelen M. *The randomization and stratification of patients to clinical trials*[J]. Journal of chronic diseases, 1974, 27(7): 365-375.

See Also

See `evalRand` or `evalRand.sim` to evaluate a specific randomization procedure.

Examples

```
## Compare stratified permuted block randomization and Hu and Hu's general CAR
cov_num <- 2
level_num <- c(2, 2)
pr <- rep(0.5, 4)
n <- 500
N <- 20 # <<adjust according to CPU
bsize <- 4
# set weight for Hu and Hu's method, it satisfies
# (1)Length should equal to cov_num
omega <- c(1, 2, 1, 1)
# Assess Hu and Hu's general CAR
Obj1 <- evalRand.sim(n = n, N = N, Replace = FALSE, cov_num = cov_num,
                     level_num = level_num, pr = pr, method = "HuHuCAR",
                     omega, p = 0.85)
# Assess stratified permuted block randomization
Obj2 <- evalRand.sim(n = n, N = N, Replace = FALSE, cov_num = cov_num,
                     level_num = level_num, pr = pr, method = "StrPBR",
```

```
                    bsize)

RES <- compRand(Obj1, Obj2)
```

`corr.test` *Corrected t-test*

Description

Performs corrected t-test on treatment effects. This test follows the idea of Ma et al. (2015) <doi:10.1080/01621459.2014.922469>.

Usage

```
corr.test(data, conf = 0.95)
```

Arguments

`data`	a data frame. It consists of patients' profiles, treatment assignments and outputs. See `getData`.
`conf`	confidence level of the interval. The default is `0.95`.

Details

When the working model is the true underlying linear model, and the chosen covariate-adaptive design achieves that the overall imbalance and marginal imbalances for all covariates are bounded in probability, we can derive the asymptotic distribution under the null distribution, where the treatment effect of each group is the same. Subsequently, we can replace the variance estimator in a simple two sample t-test with an adjusted variance estimator. Details can be found in Ma et al.(2015).

Value

It returns an object of class `"htest"`.

An object of class `"htest"` is a list containing the following components:

`statistic`	the value of the t-statistic.
`p.value`	the p-value of the test,the null hypothesis is rejected if p-value is less than the pre-determined significance level.
`conf.int`	a confidence interval under the chosen level `conf` for the difference in treatment effect between treatment `1` and treatment `2`.
`estimate`	the estimated treatment effect difference between treatment `1` and treatment `2`.
`stderr`	the standard error of the mean (difference), used as denominator in the t-statistic formula.
`method`	a character string indicating what type of test was performed.
`data.name`	a character string giving the name(s) of the data.

References

Ma W, Hu F, Zhang L. *Testing hypotheses of covariate-adaptive randomized clinical trials*[J]. Journal of the American Statistical Association, 2015, 110(510): 669-680.

Ma W, Ye X, Tu F, Hu F. *carat: Covariate-Adaptive Randomization for Clinical Trials*[J]. Journal of Statistical Software, 2023, 107(2): 1-47.

Examples

```
##generate data
set.seed(100)
n = 1000
cov_num = 5
level_num = c(2,2,2,2,2)
pr = rep(0.5,10)
beta = c(0.1,0.4,0.3,0.2,0.5,0.5,0.4,0.3,0.2,0.1)
omega = c(0.1, 0.1, rep(0.8 / 5, times = 5))
mu1 = 0
mu2 = 0.7
sigma = 1
type = "linear"
p = 0.85

dataH = getData(n,cov_num,level_num,pr,type,beta,
                mu1,mu2,sigma,"HuHuCAR",omega,p)

#run the corrected t-test
HHct=corr.test(dataH)
HHct
```

`DoptBCD` *Atkinson's D_A-optimal Biased Coin Design*

Description

Allocates patients to one of two treatments based on the D_A-optimal biased coin design in the presence of the prognostic factors proposed by Atkinson A C (1982) <doi:10.2307/2335853>.

Usage

```
DoptBCD(data)
```

Arguments

`data`	a data frame. A row of the dataframe corresponds to the covariate profile of a patient.

Details

Consider an experiment involving n patients. Assuming a linear model between response and covariates, Atkinson's D_A-optimal biased coin design sequentially assigns patients to minimize the variance of estimated treatment effects. Supposing j patients have been assigned, the probability of assigning the $(j+1)$th patient to treatment 1 is

$$\frac{[1-(1;\boldsymbol{x}_{j+1}^t)(\boldsymbol{F}_j^t\boldsymbol{F}_j)^{-1}\boldsymbol{b}_j]^2}{[1-(1;\boldsymbol{x}_{j+1}^t)(\boldsymbol{F}_j^t\boldsymbol{F}_j)^{-1}\boldsymbol{b}_j]^2+[1+(1;\boldsymbol{x}_{j+1}^t)(\boldsymbol{F}_j^t\boldsymbol{F}_j)^{-1}\boldsymbol{b}_j]^2},$$

where $\boldsymbol{X}=(\boldsymbol{x_i}, i=1,\ldots,j)$ and $\boldsymbol{x}_i=(x_{i1},\ldots,x_{ij})$ denote the covariate profile of the ith patient; and $\boldsymbol{F}_j=[\mathbf{1}_j;\boldsymbol{X}]$ is the information matrix; and $\boldsymbol{b}_j^T=(2\boldsymbol{T}_j-\mathbf{1}_j)^T\boldsymbol{F}_j$, $\boldsymbol{T}_j=(T_1,\ldots,T_j)$ is a sequence containing the first j patients' allocations.

Details of the procedure can be found in A.C.Atkinson (1982).

Value

It returns an object of `class` `"carandom"`.

An object of class `"carandom"` is a list containing the following components:

`datanumeric`	a bool indicating whether the data is a numeric data frame.
`covariates`	a character string giving the name(s) of the included covariates.
`strt_num`	the number of strata.
`cov_num`	the number of covariates.
`level_num`	a vector of level numbers for each covariate.
`n`	the number of patients.
`Cov_Assig`	a `(cov_num + 1) * n` matrix containing covariate profiles for all patients and the corresponding assignments. The ith column represents the ith patient. The first `cov_num` rows include patients' covariate profiles, and the last row contains the assignments.
`assignments`	the randomization sequence.
`All strata`	a matrix containing all strata involved.
`Diff`	a matrix with only one column. There are final differences at the overall, within-stratum, and within-covariate-margin levels.
`method`	a character string describing the randomization procedure to be used.
`Data Type`	a character string giving the data type, `Real` or `Simulated`.
`framework`	the framework of the used randomization procedure: stratified randomization, or model-based method.
`data`	the data frame.

References

Atkinson A C. *Optimum biased coin designs for sequential clinical trials with prognostic factors*[J]. Biometrika, 1982, 69(1): 61-67.

Ma W, Ye X, Tu F, Hu F. *carat: Covariate-Adaptive Randomization for Clinical Trials*[J]. Journal of Statistical Software, 2023, 107(2): 1-47.

See Also

See DoptBCD.sim for allocating patients with covariate data generating mechanism. See DoptBCD.ui for the command-line user interface.

Examples

```
# a simple use
## Real Data
df <- data.frame("gender" = sample(c("female", "male"), 100, TRUE, c(1 / 3, 2 / 3)),
                 "age" = sample(c("0-30", "30-50", ">50"), 100, TRUE),
                 "jobs" = sample(c("stu.", "teac.", "others"), 100, TRUE),
                 stringsAsFactors = TRUE)
Res <- DoptBCD(df)
## view the output
Res

## view all patients' profile and assignments
## Res$Cov_Assig

## Simulated Data
n <- 1000
cov_num <- 2

level_num <- c(2, 5)
# Set pr to follow two tips:
#(1) length of pr should be sum(level_num);
#(2)sum of probabilities for each margin should be 1.
pr <- c(0.4, 0.6, rep(0.2, times = 5))
Res.sim <- DoptBCD.sim(n, cov_num, level_num, pr)
## view the output
Res.sim

## view the difference between treatment 1 and treatment 2
##             at overall, within-strt. and overall levels
Res.sim$Diff


N <- 5
n <- 100
cov_num <- 2
level_num <- c(3, 5) # << adjust to your CPU and the length should correspond to cov_num
## Set pr to follow two tips:
## (1) length of pr should be sum(level_num);
## (2)sum of probabilities for each margin should be 1
pr <- c(0.3, 0.4, 0.3, rep(0.2, times = 5))
omega <- c(0.2, 0.2, rep(0.6 / cov_num, times = cov_num))

## generate a container to contain Diff
DH <- matrix(NA, ncol = N, nrow = 1 + prod(level_num) + sum(level_num))
DA <- matrix(NA, ncol = N, nrow = 1 + prod(level_num) + sum(level_num))
for(i in 1 : N){
  result <- HuHuCAR.sim(n, cov_num, level_num, pr, omega)
```

```
  resultA <- StrBCD.sim(n, cov_num, level_num, pr)
  DH[ , i] <- result$Diff; DA[ , i] <- resultA$Diff
}
## do some analysis
require(dplyr)

## analyze the overall imbalance
Ana_O <- matrix(NA, nrow = 2, ncol = 3)
rownames(Ana_O) <- c("HuHuCAR", "DoptBCD")
colnames(Ana_O) <- c("mean", "median", "95%quantile")
temp <- DH[1, ] %>% abs
tempA <- DA[1, ] %>% abs
Ana_O[1, ] <- c((temp %>% mean), (temp %>% median),
                (temp %>% quantile(0.95)))
Ana_O[2, ] <- c((tempA %>% mean), (tempA %>% median),
                (tempA %>% quantile(0.95)))

## analyze the within-stratum imbalances
tempW <- DH[2 : (1 + prod(level_num)), ] %>% abs
tempWA <- DA[2 : 1 + prod(level_num), ] %>% abs
Ana_W <- matrix(NA, nrow = 2, ncol = 3)
rownames(Ana_W) <- c("HuHuCAR", "DoptBCD")
colnames(Ana_W) <- c("mean", "median", "95%quantile")
Ana_W[1, ] = c((tempW %>% apply(1, mean) %>% mean),
               (tempW %>% apply(1, median) %>% mean),
               (tempW %>% apply(1, mean) %>% quantile(0.95)))
Ana_W[2, ] = c((tempWA %>% apply(1, mean) %>% mean),
               (tempWA %>% apply(1, median) %>% mean),
               (tempWA %>% apply(1, mean) %>% quantile(0.95)))

## analyze the marginal imbalance
tempM <- DH[(1 + prod(level_num) + 1) :
             (1 + prod(level_num) + sum(level_num)), ] %>% abs
tempMA <- DA[(1 + prod(level_num) + 1) :
               (1 + prod(level_num) + sum(level_num)), ] %>% abs
Ana_M <- matrix(NA, nrow = 2, ncol = 3)
rownames(Ana_M) <- c("HuHuCAR", "DoptBCD")
colnames(Ana_M) <- c("mean", "median", "95%quantile")
Ana_M[1, ] = c((tempM %>% apply(1, mean) %>% mean),
               (tempM %>% apply(1, median) %>% mean),
               (tempM %>% apply(1, mean) %>% quantile(0.95)))
Ana_M[2, ] = c((tempMA %>% apply(1, mean) %>% mean),
               (tempMA %>% apply(1, median) %>% mean),
               (tempMA %>% apply(1, mean) %>% quantile(0.95)))

AnaHP <- list(Ana_O, Ana_M, Ana_W)
names(AnaHP) <- c("Overall", "Marginal", "Within-stratum")

AnaHP
```

DoptBCD.sim *Atkinson's D_A-optimal Biased Coin Design with Covariate Data Generating Mechanism*

Description

Allocates patients generated by simulating covariates-profile under the assumption of independence between covariates and levels within each covariate, to one of two treatments based on the D_A-optimal biased coin design in the presence of prognostic factors, as proposed by Atkinson A C (1982) <doi:10.2307/2335853>.

Usage

```
DoptBCD.sim(n = 1000, cov_num = 2, level_num = c(2, 2),
            pr = rep(0.5, 4))
```

Arguments

n	the number of patients. The default is 1000.
cov_num	the number of covariates. The default is 2.
level_num	a vector of level numbers for each covariate. Hence the length of level_num should be equal to the number of covariates. The default is c(2,2).
pr	a vector of probabilities. Under the assumption of independence between covariates, pr is a vector containing probabilities for each level of each covariate. The length of pr should correspond to the number of all levels, and the sum of the probabilities for each margin should be 1. The default is rep(0.5, 4), which corresponds to cov_num = 2, and level_num = c(2, 2).

Details

See DoptBCD.

Value

See DoptBCD.

References

Atkinson A C. *Optimum biased coin designs for sequential clinical trials with prognostic factors*[J]. Biometrika, 1982, 69(1): 61-67.

Ma W, Ye X, Tu F, Hu F. *carat: Covariate-Adaptive Randomization for Clinical Trials*[J]. Journal of Statistical Software, 2023, 107(2): 1-47.

See Also

See DoptBCD for allocating patients with complete covariate data; See DoptBCD.ui for the command-line user interface.

DoptBCD.ui *Command-line User Interface Using Atkinson's D_A-optimal Biased Coin Design*

Description

A call to the user-interface function used to allocate patients to one of two treatments using Atkinson's D_A-optimal biased coin design proposed by Atkinson A C (1982) <doi:10.2307/2335853>.

Usage

```
DoptBCD.ui(path, folder = "DoptBCD")
```

Arguments

path	the path in which a folder used to store variables will be created.
folder	name of the folder. If default, a folder named "DoptBCD" will be created.

Details

See DoptBCD.

Value

It returns an object of class "carseq".

The function print is used to obtain results. The generic accessor functions assignment, covariate, cov_num, cov_profile and others extract various useful features of the value returned by that function.

Note

This function provides a command-line user interface and users should follow the prompts to enter data including covariates, as well as levels for each covariate and the covariate profile of the new patient.

References

Atkinson A C. *Optimum biased coin designs for sequential clinical trials with prognostic factors*[J]. Biometrika, 1982, 69(1): 61-67.

Ma W, Ye X, Tu F, Hu F. *carat: Covariate-Adaptive Randomization for Clinical Trials*[J]. Journal of Statistical Software, 2023, 107(2): 1-47.

See Also

See DoptBCD for allocating patients with complete covariate data; See DoptBCD.sim for allocating patients with covariate data generating mechanism.

`evalPower` *Evaluation of Tests and Randomization Procedures through Power*

Description

Returns powers and a plot of the chosen test and method under different treatment effects.

Usage

```
evalPower(n, cov_num, level_num, pr, type, beta, di = seq(0,0.5,0.1), sigma = 1,
      Iternum, sl = 0.05, method = c("HuHuCAR", "PocSimMIN", "StrBCD", "StrPBR",
                                     "DoptBCD","AdjBCD"),
         test = c("boot.test", "corr.test", "rand.test"), plot = TRUE, ...)
```

Arguments

`n`	the number of patients.
`cov_num`	the number of covariates.
`level_num`	a vector of level numbers for each covariate. Hence the length of `level_num` should be equal to the number of covariates.
`pr`	a vector of probabilities. Under the assumption of independence between covariates, `pr` is a vector containing probabilities for each level of each covariate. The length of `pr` should correspond to the number of all levels, and the sum of the probabilities for each margin should be `1`.
`type`	a data-generating method. Optional input: `"linear"` or `"logit"`.
`beta`	a vector of coefficients of covariates. The length of `beta` must correspond to the sum of all covariates' levels.
`di`	a value or a vector of values of difference in treatment effects. The default value is a sequence from `0` to `0.5` with increments of `0.1`. The value(s) forms the horizontal axis of the plot.
`sigma`	the error variance for the linear model. The default is 1. This should be a positive value and is only used when `type = linear`.
`Iternum`	an integer. It is the number of iterations required for power calculation.
`sl`	the significance level. If the p value returned by the test is less than `sl`, the null hypothesis will be rejected. The default value is `0.05`.
`method`	the randomization procedure to be used for power calculation. This package provides power calculation for `"HuHuCAR"`, `"PocSimMIN"`, `"StrBCD"`, `"StrPBR"`, `"AdjBCD"`, and `"DoptBCD"`.
`test`	a character string specifying the alternative tests used to verify hypothesis, must be one of `"boot.test"`, `"corr.test"` or `"rand.test"`, which are the bootstrap t test, the corrected t test, and the randomization test, respectively. The arguments associated with the testing function can be specified; otherwise, the default value will be used.

`plot` a bool. It indicates whether to plot or not. Optional input: `TRUE` or `FALSE`.

`...` arguments to be passed to `method`. These arguments depend on the randomization method used and the following arguments are accepted:

omega a vector of weights at the overall, within-stratum, and within-covariate-margin levels. It is required that at least one element is larger than 0. Note that `omega` is only needed when `HuHuCAR` is to be used.

weight a vector of weights for within-covariate-margin imbalances. It is required that at least one element is larger than 0. Note that `weight` is only needed when `PocSimMIN` is to be used.

p the biased coin probability. `p` should be larger than `1/2` and less than `1`. Note that `p` is only needed when `"HuHuCAR"`, `"PocSimMIN"` and `"StrBCD"` are to be used.

a a design parameter governing the degree of randomness. Note that `a` is only needed when `"AdjBCD"` is to be used.

bsize the block size for the stratified randomization. It is required to be a multiple of 2. Note that `bsize` is only needed when `"StrPBR"` is to be used.

B an integer. It is the number of bootstrap samples. It is needed only when `test` is `boot.test`.

Reps an integer. It is the number of randomized replications used in the randomization test. It is needed only when `test` is `rand.test`.

nthreads the number of threads to be used in parallel computation. This is needed only under `rand.test` and `boot.test`. The default is `1`.

Value

This function returns a list. The first element is a dataframe representing the powers of the chosen test under different values of treatment effects. The second element is the execution time. An optional element is the plot of power in which `di` forms the vertical axis.

Examples

```
##settings
set.seed(2019)
n = 100#<<for demonstration,it is suggested to be larger than 1000
cov_num = 5
level_num = c(2,2,2,2,2)
pr = rep(0.5,10)
beta = c(0.1,0.4,0.3,0.2,0.5,0.5,0.4,0.3,0.2,0.1)
omega = c(0.1, 0.1, rep(0.8 / 5, times = 5))
di = seq(0,0.5,0.1)
sigma = 1
type = "linear"
p = 0.85
Iternum = 10#<<for demonstration,it is suggested to be around 1000
sl = 0.05
Reps = 10#<<for demonstration,it is suggested to be 200

#Evaluation of Power
library("ggplot2")
```

```
Strtp=evalPower(n,cov_num,level_num,pr,type,beta,di,sigma,
                Iternum,sl,"HuHuCAR","rand.test",TRUE,omega,p,Reps, nthreads = 1)
Strtp
```

---

evalRand *Evaluation of Randomization Procedures*

Description

Evaluates a specific randomization procedure based on several different quantities of imbalances.

Usage

```
evalRand(data, method = "HuHuCAR", N = 500, ...)
```

Arguments

data	a data frame. A row of the dataframe corresponds to the covariate profile of a patient.
N	the iteration number. The default is 500.
method	the randomization procedure to be evaluated. This package provides assessment for "HuHuCAR", "PocSimMIN", "StrBCD", "StrPBR", "AdjBCD", and "DoptBCD".
...	arguments to be passed to method. These arguments depend on the randomization method assessed and the following arguments are accepted:

omega a vector of weights at the overall, within-stratum, and within-covariate-margin levels. It is required that at least one element is larger than 0. Note that omega is only needed when HuHuCAR is to be assessed.

weight a vector of weights for within-covariate-margin imbalances. It is required that at least one element is larger than 0. Note that weight is only needed when PocSimMIN is to be assessed.

p the biased coin probability. p should be larger than 1/2 and less than 1. Note that p is only needed when "HuHuCAR", "PocSimMIN" and "StrBCD" are to be assessed.

a a design parameter governing the degree of randomness. Note that a is only needed when "AdjBCD" is to be assessed.

bsize the block size for stratified permuted block randomization. It is required to be a multiple of 2. Note that bsize is only needed when "StrPBR" is to be assessed.

Details

The data is designed for N times using method.

Value

It returns an object of class "careval".

An object of class "careval" is a list containing the following components:

datanumeric	a bool indicating whether the data is a numeric data frame.
weight	a vector giving the weights imposed on each covariate.
bsize	the block size.
covariates	a character string giving the name(s) of the included covariates.
Assig	a n*N matrix containing assignments for each patient for N iterations.
strt_num	the number of strata.
All strata	a matrix containing all strata involved.
Imb	a matrix containing maximum, 95%-quantile, median, and mean of absolute imbalances at overall, within-stratum and within-covariate-margin levels. Note that, we refer users to the ith column of `All strata` for details of level $i, i = 1, \ldots,$strt_num.
SNUM	a matrix with N colunms containing the number of patients in each stratum for each iteration.
method	the randomization method to be evaluated.
cov_num	the number of covariates.
level_num	a vector of level numbers for each covariate.
n	the number of patients.
iteration	the number of iterations.
Data Type	the data type. Real or Simulated.
DIF	a matrix containing the final differences at the overall, within-stratum, and within-covariate-margin levels for each iteration.
data	the data frame.

References

Atkinson A C. *Optimum biased coin designs for sequential clinical trials with prognostic factors*[J]. Biometrika, 1982, 69(1): 61-67.

Baldi Antognini A, Zagoraiou M. *The covariate-adaptive biased coin design for balancing clinical trials in the presence of prognostic factors*[J]. Biometrika, 2011, 98(3): 519-535.

Hu Y, Hu F. *Asymptotic properties of covariate-adaptive randomization*[J]. The Annals of Statistics, 2012, 40(3): 1794-1815.

Ma W, Ye X, Tu F, Hu F. *carat: Covariate-Adaptive Randomization for Clinical Trials*[J]. Journal of Statistical Software, 2023, 107(2): 1-47.

Pocock S J, Simon R. *Sequential treatment assignment with balancing for prognostic factors in the controlled clinical trial*[J]. Biometrics, 1975: 103-115.

Shao J, Yu X, Zhong B. *A theory for testing hypotheses under covariate-adaptive randomization*[J]. Biometrika, 2010, 97(2): 347-360.

Zelen M. *The randomization and stratification of patients to clinical trials*[J]. Journal of chronic diseases, 1974, 27(7): 365-375.

See Also

See evalRand.sim to evaluate a randomization procedure with covariate data generating mechanism.

Examples

```
# a simple use
## Access by real data
## create a dataframe
df <- data.frame("gender" = sample(c("female", "male"), 1000, TRUE, c(1 / 3, 2 / 3)),
                 "age" = sample(c("0-30", "30-50", ">50"), 1000, TRUE),
                 "jobs" = sample(c("stu.", "teac.", "others"), 1000, TRUE),
                 stringsAsFactors = TRUE)
Res <- evalRand(data = df, method = "HuHuCAR", N = 500,
                omega = c(1, 2, rep(1, ncol(df))), p = 0.85)
## view the output
Res

  ## view all patients' assignments
  Res$Assig

## Assess by simulated data
cov_num <- 3
level_num <- c(2, 3, 5)
pr <- c(0.35, 0.65, 0.25, 0.35, 0.4, 0.25, 0.15, 0.2, 0.15, 0.25)
n <- 1000
N <- 50
omega = c(1, 2, 1, 1, 2)
# assess Hu and Hu's procedure with the same group of patients
Res.sim <- evalRand.sim(n = n, N = N, Replace = FALSE, cov_num = cov_num,
                        level_num = level_num, pr = pr, method = "HuHuCAR",
                        omega, p = 0.85)

  ## Compare four procedures
  cov_num <- 3
  level_num <- c(2, 10, 2)
  pr <- c(rep(0.5, times = 2), rep(0.1, times = 10), rep(0.5, times = 2))
  n <- 100
  N <- 200 # <<adjust according to CPU
  bsize <- 4
  ## set weights for HuHuCAR
  omega <- c(1, 2, rep(1, cov_num));
  ## set weights for PocSimMIN
  weight = rep(1, cov_num);
  ## set biased probability
  p = 0.80
  # assess Hu and Hu's procedure
  RH <- evalRand.sim(n = n, N = N, Replace = FALSE, cov_num = cov_num,
                     level_num = level_num, pr = pr, method = "HuHuCAR",
                     omega = omega, p = p)
  # assess Pocock and Simon's method
  RPS <- evalRand.sim(n = n, N = N, Replace = FALSE, cov_num = cov_num,
```

```
                    level_num = level_num, pr = pr, method = "PocSimMIN",
                    weight, p = p)
# assess Shao's procedure
RS <- evalRand.sim(n = n, N = N, Replace = FALSE, cov_num = cov_num,
                   level_num = level_num, pr = pr, method = "StrBCD",
                   p = p)
# assess stratified randomization
RSR <- evalRand.sim(n = n, N = N, Replace = FALSE, cov_num = cov_num,
                    level_num = level_num, pr = pr, method = "StrPBR",
                    bsize)

# create containers
C_M = C_O = C_WS = matrix(NA, nrow = 4, ncol = 4)
colnames(C_M) = colnames(C_O) = colnames(C_WS) =
  c("max", "95%quan", "med", "mean")
rownames(C_M) = rownames(C_O) = rownames(C_WS) =
  c("HH", "PocSim", "Shao", "StraRand")

# assess the overall imbalance
C_O[1, ] = RH$Imb[1, ]
C_O[2, ] = RPS$Imb[1, ]
C_O[3, ] = RS$Imb[1, ]
C_O[4, ] = RSR$Imb[1, ]
# view the result
C_O

# assess the marginal imbalances
C_M[1, ] = apply(RH$Imb[(1 + RH$strt_num) : (1 + RH$strt_num + sum(level_num)), ], 2, mean)
C_M[2, ] = apply(RPS$Imb[(1 + RPS$strt_num) : (1 + RPS$strt_num + sum(level_num)), ], 2, mean)
C_M[3, ] = apply(RS$Imb[(1 + RS$strt_num) : (1 + RS$strt_num + sum(level_num)), ], 2, mean)
C_M[4, ] = apply(RSR$Imb[(1 + RSR$strt_num) : (1 + RSR$strt_num + sum(level_num)), ], 2, mean)
# view the result
C_M

# assess the within-stratum imbalances
C_WS[1, ] = apply(RH$Imb[2 : (1 + RH$strt_num), ], 2, mean)
C_WS[2, ] = apply(RPS$Imb[2 : (1 + RPS$strt_num), ], 2, mean)
C_WS[3, ] = apply(RS$Imb[2 : (1 + RS$strt_num), ], 2, mean)
C_WS[4, ] = apply(RSR$Imb[2 : (1 + RSR$strt_num), ], 2, mean)
# view the result
C_WS

# Compare the four procedures through plots
meth = rep(c("Hu", "PS", "Shao", "STR"), times = 3)
shape <- rep(1 : 4, times = 3)
crt <- rep(1 : 3, each = 4)
crt_c <- rep(c("O", "M", "WS"), each = 4)
mean <- c(C_O[, 4], C_M[, 4], C_WS[, 4])
df_1 <- data.frame(meth, shape, crt, crt_c, mean,
                   stringsAsFactors = TRUE)

require(ggplot2)
p1 <- ggplot(df_1, aes(x = meth, y = mean, color = crt_c, group = crt,
```

```
                        linetype = crt_c, shape = crt_c)) +
  geom_line(size = 1) +
  geom_point(size = 2) +
  xlab("method") +
  ylab("absolute mean") +
  theme(plot.title = element_text(hjust = 0.5))
p1
```

`evalRand.sim` *Evaluation Randomization Procedures with Covariate Data Generating Mechanism*

Description

Evaluates randomization procedure based on several different quantities of imbalances by simulating patients' covariate profiles under the assumption of independence between covariates and levels within each covariate.

Usage

```
evalRand.sim(n = 1000, N = 500, Replace = FALSE, cov_num = 2,
             level_num = c(2, 2), pr = rep(0.5, 4), method = "HuHuCAR", ...)
```

Arguments

`N`	the iteration number. The default is 500.
`n`	the number of patients. The default is `1000`.
`Replace`	a bool. If `Replace = FALSE`, the function does clinical trial design for `N` iterations for one group of patients. If `Replace = TRUE`, the function dose clinical trial design for `N` iterations for `N` different groups of patients.
`cov_num`	the number of covariates. The default is `2`.
`level_num`	a vector of level numbers for each covariate. Hence the length of `level_num` should be equal to the number of covariates. The default is `c(2, 2)`.
`pr`	a vector of probabilities. Under the assumption of independence between covariates, `pr` is a vector containing probabilities for each level of each covariate. The length of `pr` should correspond to the number of all levels, and the sum of the probabilities for each margin should be `1`. The default is `rep(0.5, 4)`, which corresponds to `cov_num = 2`, and `level_num = c(2, 2)`.
`method`	the randomization procedure to be evaluated. This package provides assessment for `"HuHuCAR"`, `"PocSimMIN"`, `"StrBCD"`, `"StrPBR"`, `"AdjBCD"`, and `"DoptBCD"`.
`...`	arguments to be passed to `method`. These arguments depend on the randomization method assessed and the following arguments are accepted:
	omega a vector of weights at the overall, within-stratum, and within-covariate-margin levels. It is required that at least one element is larger than 0. Note that `omega` is only needed when `HuHuCAR` are to be assessed.

weight a vector of weights for within-covariate-margin imbalances. It is required that at least one element is larger than 0. Note that `weight` is only needed when `PocSimMIN` is to be assessed.

p the biased coin probability. `p` should be larger than `1/2` and less than `1`. Note that `p` is only needed when `"HuHuCAR"`, `"PocSimMIN"` and `"StrBCD"` is to be assessed.

a a design parameter governing the degree of randomness. Note that `a` is only needed when `"AdjBCD"` is to be assessed.

bsize the block size for stratified permuted block randomization. It is required to be a multiple of `2`. Note that `bsize` is only needed when `"StrPBR"` is to be assessed.

Details

See `evalRand`.

Value

See `evalRand`.

See Also

See `evalRand` to evaluate a randomization procedure with complete covariate data.

`getData` *Data Generation*

Description

Generates continuous or binary outcomes given patients' covariates, the underlying model and the randomization procedure.

Usage

```
getData(n, cov_num, level_num, pr, type, beta,
        mu1, mu2, sigma = 1, method = "HuHuCAR", ...)
```

Arguments

`n`	the number of patients.
`cov_num`	the number of covariates.
`level_num`	a vector of level numbers for each covariate. Hence the length of `level_num` should be equal to the number of covariates.
`pr`	a vector of probabilities. Under the assumption of independence between covariates, `pr` is a vector containing probabilities for each level of each covariate. The length of `pr` should correspond to the number of all levels, and the sum of the probabilities for each margin should be `1`.

`type` a data-generating method. Optional input: `"linear"` or `"logit"`.

`beta` a vector of coefficients of covariates. The length of `beta` must correspond to the sum of all covariates' levels.

`mu1`, `mu2` main effects of treatment 1 and treatment 2.

`sigma` the error variance for the linear model. The default is 1. This should be a positive value and is only used when `type = linear`.

`method` the randomization procedure to be used for generating randomization sequences. This package provides data-generating function for `"HuHuCAR"`, `"PocSimMIN"`, `"StrBCD"`, `"StrPBR"`, `"AdjBCD"`, and `"DoptBCD"`.

`...` arguments to be passed to `method`. These arguments depend on the randomization method used and the following arguments are accepted:

omega a vector of weights at the overall, within-stratum, and within-covariate-margin levels. It is required that at least one element is larger than 0. Note that `omega` is only needed when `HuHuCAR` is to be used.

weight a vector of weights for within-covariate-margin imbalances. It is required that at least one element is larger than 0. Note that `weight` is only needed when `PocSimMIN` is to be used.

p the biased coin probability. `p` should be larger than `1/2` and less than `1`. Note that `p` is only needed when `"HuHuCAR"`, `"PocSimMIN"` and `"StrBCD"` are to be used.

a a design parameter governing the degree of randomness. Note that `a` is only needed when `"AdjBCD"` is to be used.

bsize the block size for stratified randomization. It is required to be a multiple of 2. Note that `bsize` is only needed when `"StrPBR"` is to be used.

Details

To generate continuous outcomes, we use the linear model:

$$y_i = \mu_j + x_i^T \beta + \epsilon_i,$$

to generate binary outcomes, we use the logit link function:

$$P(y_i = 1) = \frac{exp\{\mu_j + x_i^T \beta\}}{1 + exp\{\mu_j + x_i^T \beta}$$

,

where j indicates patient i belongs to treatment j.

Value

`getData` returns a size $cov_num + 2 \times n$ dataframe. The first `cov_num` rows represent patients' profile. The next row consists of patients' assignments and the final row consists of generated outcomes.

Examples

```
#Parameters' Setting
set.seed(100)
n = 1000
cov_num = 5
level_num = c(2,2,2,2,2)
beta = c(1,4,3,2,5,5,4,3,2,1)
mu1 = 0
mu2 = 0
sigma = 1
type = "linear"
p = 0.85
omega = c(0.1, 0.1, rep(0.8 / 5, times = 5))
pr = rep(0.5,10)

#Data Generation
dataH = getData(n, cov_num,level_num, pr, type, beta,
                mu1, mu2, sigma, "HuHuCAR", omega, p)
dataH[1:(cov_num+2),1:5]
```

HuHuCAR *Hu and Hu's General Covariate-Adaptive Randomization*

Description

Allocates patients to one of two treatments using Hu and Hu's general covariate-adaptive randomization proposed by Hu Y, Hu F (2012) <doi:10.1214/12-AOS983>.

Usage

```
HuHuCAR(data, omega = NULL, p = 0.85)
```

Arguments

data	a data frame. A row of the dataframe corresponds to the covariate profile of a patient.
omega	a vector of weights at the overall, within-stratum, and within-covariate-margin levels. It is required that at least one element is larger than 0. If omega = NULL (default), the overall, within-stratum, and within-covariate-margin imbalances are weighted with porportions 0.2, 0.3, and 0.5/cov_num for each covariate-margin, respectively, where cov_num is the number of covariates of interest.
p	the biased coin probability. p should be larger than 1/2 and less than 1. The default is 0.85.

Details

Consider I covariates and m_i levels for the ith covariate, $i = 1, \ldots, I$. T_j is the assignment of the jth patient and $Z_j = (k_1, \ldots, k_I)$ indicates the covariate profile of this patient, $j = 1, \ldots, n$. For convenience, $(k_1, \ldots, k_I)$ and $(i; k_i)$ denote the stratum and margin, respectively. $D_j(.)$ is the difference between the numbers of patients assigned to treatment 1 and treatment 2 at the corresponding levels after j patients have been assigned. The general covariate-adaptive randomization procedure is as follows:

(1) The first patient is assigned to treatment 1 with probability $1/2$;

(2) Suppose that $j-1$ patients have been assigned ($1 < j \leq n$) and the jth patient falls within $(k_1^*, \ldots, k_I^*)$;

(3) If the jth patient were assigned to treatment 1, then the potential overall, within-covariate-margin, and within-stratum differences between the two treatments would be

$$D_j^{(1)} = D_{j-1} + 1,$$

$$D_j^{(1)}(i; k_i^*) = D_{j-1}(i, k_i^*) + 1,$$

$$D_j^{(1)}(k_1^*, \ldots, k_I^*) = D_j(k_1^*, \ldots, k_I^*) + 1,$$

for margin $(i; k_i^*)$ and stratum $(k_1^*, \ldots, k_I^*)$. Similarly, the potential differences at the overall, within-covariate-margin, and within-stratum levels would be obtained if the jth patient were assigned to treatment 2;

(4) An imbalance measure is defined by

$$Imb_j^{(l)} = \omega_o [D_j^{(l)}]^2 + \sum_{i=1}^{I} \omega_{m,i} [D_j^{(l)}(i; k_i^*)]^2 + \omega_s [D_j^{(l)}(k_1^*, \ldots, k_I^*)]^2, l = 1, 2;$$

(5) Conditional on the assignments of the first $(j-1)$ patients as well as the covariate profiles of the first j patients, assign the jth patient to treatment 1 with probability

$$P(T_j = 1 | Z_j, T_1, \ldots, T_{j-1}) = q$$

for $Imb_j^{(1)} > Imb_j^{(2)}$,

$$P(T_j = 1 | Z_j, T_1, \ldots, T_{j-1}) = p$$

for $Imb_j^{(1)} < Imb_j^{(2)}$, and

$$P(T_j = 1 | Z_j, T_1, \ldots, T_{j-1}) = 0.5$$

for $Imb_j^{(1)} = Imb_j^{(2)}$.

Details of the procedure can be found in Hu and Hu (2012).

Value

It returns an object of `class "carandom"`.

An object of class `"carandom"` is a list containing the following components:

`datanumeric` a bool indicating whether the data is a numeric data frame.

covariates	a character string giving the name(s) of the included covariates.
strt_num	the number of strata.
cov_num	the number of covariates.
level_num	a vector of level numbers for each covariate.
n	the number of patients.
Cov_Assig	a (cov_num + 1) * n matrix containing covariate profiles for all patients and the corresponding assignments. The ith column represents the ith patient. The first cov_num rows include patients' covariate profiles, and the last row contains the assignments.
assignments	the randomization sequence.
All strata	a matrix containing all strata involved.
Diff	a matrix with only one column. There are final differences at the overall, within-stratum, and within-covariate-margin levels.
method	a character string describing the randomization procedure to be used.
Data Type	a character string giving the data type, Real or Simulated.
weight	a vector giving the weights imposed on each covariate.
framework	the framework of the used randomization procedure: stratified randomization, or model-based method.
data	the data frame.

References

Hu Y, Hu F. *Asymptotic properties of covariate-adaptive randomization*[J]. The Annals of Statistics, 2012, 40(3): 1794-1815.

Ma W, Ye X, Tu F, Hu F. *carat: Covariate-Adaptive Randomization for Clinical Trials*[J]. Journal of Statistical Software, 2023, 107(2): 1-47.

See Also

See HuHuCAR.sim for allocating patients with covariate data generating mechanism. See HuHuCAR.ui for the command-line user interface.

Examples

```
# a simple use
## Real Data
## create a dataframe
df <- data.frame("gender" = sample(c("female", "male"), 1000, TRUE, c(1 / 3, 2 / 3)),
                 "age" = sample(c("0-30", "30-50", ">50"), 1000, TRUE),
                 "jobs" = sample(c("stu.", "teac.", "others"), 1000, TRUE),
                 stringsAsFactors = TRUE)
omega <- c(1, 2, rep(1, 3))
Res <- HuHuCAR(data = df, omega)
## view the output
Res
```

```
## view all patients' profile and assignments
Res$Cov_Assig

## Simulated data
cov_num <- 3
level_num <- c(2, 3, 3)
pr <- c(0.4, 0.6, 0.3, 0.4, 0.3, 0.4, 0.3, 0.3)
omega <- rep(0.2, times = 5)
Res.sim <- HuHuCAR.sim(n = 100, cov_num, level_num, pr, omega)
## view the output
Res.sim

## view the detials of difference
Res.sim$Diff


N <- 100 # << adjust according to your CPU
n <- 1000
cov_num <- 3
level_num <- c(2, 3, 5) # << adjust to your CPU and the length should correspond to cov_num
# Set pr to follow two tips:
#(1) length of pr should be sum(level_num);
#(2)sum of probabilities for each margin should be 1.
pr <- c(0.4, 0.6, 0.3, 0.4, 0.3, rep(0.2, times = 5))
omega <- c(0.2, 0.2, rep(0.6 / cov_num, times = cov_num))
# Set omega0 = omegaS = 0
omegaP <- c(0, 0, rep(1 / cov_num, times = cov_num))

## generate a container to contain Diff
DH <- matrix(NA, ncol = N, nrow = 1 + prod(level_num) + sum(level_num))
DP <- matrix(NA, ncol = N, nrow = 1 + prod(level_num) + sum(level_num))
for(i in 1 : N){
  result <- HuHuCAR.sim(n, cov_num, level_num, pr, omega)
  resultP <- HuHuCAR.sim(n, cov_num, level_num, pr, omegaP)
  DH[ , i] <- result$Diff; DP[ , i] <- resultP$Diff
}

## do some analysis
require(dplyr)

## analyze the overall imbalance
Ana_O <- matrix(NA, nrow = 2, ncol = 3)
rownames(Ana_O) <- c("NEW", "PS")
colnames(Ana_O) <- c("mean", "median", "95%quantile")
temp <- DH[1, ] %>% abs
tempP <- DP[1, ] %>% abs
Ana_O[1, ] <- c((temp %>% mean), (temp %>% median),
                (temp %>% quantile(0.95)))
Ana_O[2, ] <- c((tempP %>% mean), (tempP %>% median),
                (tempP %>% quantile(0.95)))
## analyze the within-stratum imbalances
tempW <- DH[2 : (1 + prod(level_num)), ] %>% abs
tempWP <- DP[2 : 1 + prod(level_num), ] %>% abs
```

```
Ana_W <- matrix(NA, nrow = 2, ncol = 3)
rownames(Ana_W) <- c("NEW", "PS")
colnames(Ana_W) <- c("mean", "median", "95%quantile")
Ana_W[1, ] = c((tempW %>% apply(1, mean) %>% mean),
               (tempW %>% apply(1, median) %>% mean),
               (tempW %>% apply(1, mean) %>% quantile(0.95)))
Ana_W[2, ] = c((tempWP %>% apply(1, mean) %>% mean),
               (tempWP %>% apply(1, median) %>% mean),
               (tempWP %>% apply(1, mean) %>% quantile(0.95)))

## analyze the marginal imbalance
tempM <- DH[(1 + prod(level_num) + 1) : (1 + prod(level_num) + sum(level_num)), ] %>% abs
tempMP <- DP[(1 + prod(level_num) + 1) : (1 + prod(level_num) + sum(level_num)), ] %>% abs
Ana_M <- matrix(NA, nrow = 2, ncol = 3)
rownames(Ana_M) <- c("NEW", "PS"); colnames(Ana_M) <- c("mean", "median", "95%quantile")
Ana_M[1, ] = c((tempM %>% apply(1, mean) %>% mean),
               (tempM %>% apply(1, median) %>% mean),
               (tempM %>% apply(1, mean) %>% quantile(0.95)))
Ana_M[2, ] = c((tempMP %>% apply(1, mean) %>% mean),
               (tempMP %>% apply(1, median) %>% mean),
               (tempMP %>% apply(1, mean) %>% quantile(0.95)))

AnaHP <- list(Ana_O, Ana_M, Ana_W)
names(AnaHP) <- c("Overall", "Marginal", "Within-stratum")

AnaHP
```

`HuHuCAR.sim` *Hu and Hu's General Covariate-Adaptive Randomization with Covariate Data Generating Mechanism*

Description

Allocates patients to one of two treatments using general covariate-adaptive randomization proposed by Hu Y, Hu F (2012) <doi:10.1214/12-AOS983>, by simulating covariate profiles based on the assumption of independence between covariates and levels within each covariate.

Usage

```
HuHuCAR.sim(n = 1000, cov_num = 2, level_num = c(2, 2),
            pr = rep(0.5, 4), omega = NULL, p = 0.85)
```

Arguments

`n`	the number of patients. The default is `1000`.
`cov_num`	the number of covariates. The default is `2`.
`level_num`	a vector of level numbers for each covariate. Hence the length of `level_num` should be equal to the number of covariates. The default is `c(2, 2)`.

`pr`	a vector of probabilities. Under the assumption of independence between covariates, `pr` is a vector containing probabilities for each level of each covariate. The length of `pr` should correspond to the number of all levels, and the sum of the probabilities for each margin should be `1`. The default is `rep(0.5, 4)`, which corresponds to `cov_num = 2`, and `level_num = c(2, 2)`.
`omega`	a vector of weights at the overall, within-stratum, and within-covariate-margin levels. It is required that at least one element is larger than 0. If `omega = NULL` (default), the overall, within-stratum, and within-covariate-margin imbalances are weighted with porportions `0.2`, `0.3`, and `0.5/cov_num` for each covariate-margin, respectively, where `cov_num` is the number of covariates of interest.
`p`	the biased coin probability. `p` should be larger than `1/2` and less than `1`. The default is `0.85`.

Details

See `HuHuCAR`.

Value

See `HuHuCAR`.

References

Hu Y, Hu F. *Asymptotic properties of covariate-adaptive randomization*[J]. The Annals of Statistics, 2012, 40(3): 1794-1815.

Ma W, Ye X, Tu F, Hu F. *carat: Covariate-Adaptive Randomization for Clinical Trials*[J]. Journal of Statistical Software, 2023, 107(2): 1-47.

See Also

See `HuHuCAR` for allocating patients with complete covariate data; See `HuHuCAR.ui` for the command-line user interface.

`HuHuCAR.ui` *Command-line User Interface Using Hu and Hu's General Covariate-adaptive Randomization*

Description

A call to the user-iterface function used to allocate patients to one of two treatments using Hu and Hu's general covariate-adaptive randomization method as proposed by Hu Y, Hu F (2012) <doi:10.1214/12-AOS983>.

Usage

```
HuHuCAR.ui(path, folder = "HuHuCAR")
```

Arguments

path	the path in which a folder used to store variables will be created.
folder	name of the folder. If default, a folder named "HuHuCAR" will be created.

Details

See HuHuCAR

Value

It returns an object of class "carseq".

The function print is used to obtain results. The generic accessor functions assignment, covariate, cov_num, cov_profile and others extract various useful features of the value returned by HuHuCAR.ui.

Note

This function provides a command-line interface so that users should follow the prompts to enter data, including covariates as well as levels for each covariate, weights omega, biased probability p and the covariate profile of the new patient.

References

Hu Y, Hu F. *Asymptotic properties of covariate-adaptive randomization*[J]. The Annals of Statistics, 2012, 40(3): 1794-1815.

Ma W, Ye X, Tu F, Hu F. *carat: Covariate-Adaptive Randomization for Clinical Trials*[J]. Journal of Statistical Software, 2023, 107(2): 1-47.

See Also

See HuHuCAR for allocating patients with complete covariate data; See HuHuCAR.sim for allocating patients with covariate data generating mechanism.

---

pats *Data of Covariate Profile of Patients*

Description

Gives the simulated covariate profile of patients for clincal trials.

Usage

```
data(pats)
```

Arguments

pats	a data frame. Each row contains an individual's covariate profile and each column corresponds to a covariate. It contains the following columns: **gender** Options are male and female. **employment status** Options are "unemployment" (unemp), "part time" (part.), and "full time" (full.). **income** Options are >= 1w, <= 0.5w, and 0.5~1w. **marriage status** Options are unmarried, married, and divorced

---

PocSimMIN *Pocock and Simon's Method in the Two-Arms Case*

Description

Allocates patients to one of two treatments using Pocock and Simon's method proposed by Pocock S J, Simon R (1975) <doi:10.2307/2529712>.

Usage

```
PocSimMIN(data, weight = NULL, p = 0.85)
```

Arguments

data	a data frame. A row of the dataframe corresponds to the covariate profile of a patient.
weight	a vector of weights for within-covariate-margin imbalances. It is required that at least one element is larger than 0. If weight = NULL (default), the within-covariate-margin imbalances are weighted with an equal proportion, 1/cov_num, for each covariate-margin.
p	the biased coin probability. p should be larger than 1/2 and less than 1. The default is 0.85.

Details

Consider I covariates and m_i levels for the ith covariate, $i = 1, \ldots, I$. T_j is the assignment of the jth patient and $Z_j = (k_1, \ldots, k_I)$ indicates the covariate profile of this patient, $j = 1, \ldots, n$. For convenience, $(k_1, \ldots, k_I)$ and $(i; k_i)$ denote the stratum and margin, respectively. $D_j(.)$ is the difference between the numbers of patients assigned to treatment 1 and treatment 2 at the corresponding levels after j patients have been assigned. The Pocock and Simon's minimization procedure is as follows:

(1) The first patient is assigned to treatment 1 with probability $1/2$;

(2) Suppose that $j - 1$ patients have been assigned ($1 < j \leq n$) and the jth patient falls within $(k_1^*, \ldots, k_I^*)$;

(3) If the jth patient were assigned to treatment 1, then the potential within-covariate-margin differences between the two treatments would be

$$D_j^{(1)}(i;k_i^*) = D_{j-1}(i,k_i^*) + 1$$

for margin $(i;k_i^*)$. Similarly, the potential differences would be obtained in the same way if the jth patient were assigned to treatment 2;

(4) An imbalance measure is defined by

$$Imb_j^{(l)} = \sum_{i=1}^{I} \omega_{m,i}[D_j^{(l)}(i;k_i^*)]^2, l = 1,2;$$

(5) Conditional on the assignments of the first $(j-1)$ patients as well as the covariate profiles of the first j patients, assign the jth patient to treatment 1 with the probability

$$P(T_j = 1|Z_j, T_1, \ldots, T_{j-1}) = q$$

for $Imb_j^{(1)} > Imb_j^{(2)}$,

$$P(T_j = 1|Z_j, T_1, \ldots, T_{j-1}) = p$$

for $Imb_j^{(1)} < Imb_j^{(2)}$, and

$$P(T_j = 1|Z_j, T_1, \ldots, T_{j-1}) = 0.5$$

for $Imb_j^{(1)} = Imb_j^{(2)}$.

Details of the procedure can be found in Pocock S J, Simon R (1975).

Value

It returns an object of `class` `"carandom"`.

An object of class `"carandom"` is a list containing the following components:

`datanumeric`	a bool indicating whether the data is a numeric data frame.
`covariates`	a character string giving the name(s) of the included covariates.
`strt_num`	the number of strata.
`cov_num`	the number of covariates.
`level_num`	a vector of level numbers for each covariate.
`n`	the number of patients.
`Cov_Assig`	a `(cov_num + 1) * n` matrix containing covariate profiles for all patients and the corresponding assignments. The ith column represents the ith patient. The first `cov_num` rows include patients' covariate profiles, and the last row contains the assignments.
`assignments`	the randomization sequence.
`All strata`	a matrix containing all strata involved.
`Diff`	a matrix with only one column. There are final differences at the overall, within-stratum, and within-covariate-margin levels.
`method`	a character string describing the randomization procedure to be used.

Data Type	a character string giving the data type, Real or Simulated.
weight	a vector giving the weights imposed on each covariate.
framework	the framework of the used randomization procedure: stratified randomization, or model-based method.
data	the data frame.

References

Ma W, Ye X, Tu F, Hu F. *carat: Covariate-Adaptive Randomization for Clinical Trials*[J]. Journal of Statistical Software, 2023, 107(2): 1-47.

Pocock S J, Simon R. *Sequential treatment assignment with balancing for prognostic factors in the controlled clinical trial*[J]. Biometrics, 1975: 103-115.

See Also

See PocSimMIN.sim for allocating patients with covariate data generating mechanism. See PocSimMIN.ui for the command-line user interface.

Examples

```
# a simple use
## Real Data
## creat a dataframe
df <- data.frame("gender" = sample(c("female", "male"), 1000, TRUE, c(1 / 3, 2 / 3)),
                 "age" = sample(c("0-30", "30-50", ">50"), 1000, TRUE),
                 "jobs" = sample(c("stu.", "teac.", "others"), 1000, TRUE),
                 stringsAsFactors = TRUE)
weight <- c(1, 2, 1)
Res <- PocSimMIN(data = df, weight)
## view the output
Res

## view all patients' profile and assignments
Res$Cov_Assig

## Simulated Data
cov_num = 3
level_num = c(2, 3, 3)
pr = c(0.4, 0.6, 0.3, 0.3, 0.4, 0.4, 0.3, 0.3)
Res.sim <- PocSimMIN.sim(n = 1000, cov_num, level_num, pr)
## view the output
Res.sim

## view the detials of difference
Res.sim$Diff


N <- 5
n <- 1000
cov_num <- 3
```

```
level_num <- c(2, 3, 5)
# Set pr to follow two tips:
# (1) length of pr should be sum(level_num);
# (2)sum of probabilities for each margin should be 1.
pr <- c(0.4, 0.6, 0.3, 0.4, 0.3, rep(0.2, times = 5))
omega <- c(0.2, 0.2, rep(0.6 / cov_num, times = cov_num))
weight <- c(2, rep(1, times = cov_num - 1))

## generate a container to contain Diff
DH <- matrix(NA, ncol = N, nrow = 1 + prod(level_num) + sum(level_num))
DP <- matrix(NA, ncol = N, nrow = 1 + prod(level_num) + sum(level_num))
for(i in 1 : N){
  result <- HuHuCAR.sim(n, cov_num, level_num, pr, omega)
  resultP <- PocSimMIN.sim(n, cov_num, level_num, pr, weight)
  DH[ , i] <- result$Diff; DP[ , i] <- resultP$Diff
}

## do some analysis
require(dplyr)

## analyze the overall imbalance
Ana_O <- matrix(NA, nrow = 2, ncol = 3)
rownames(Ana_O) <- c("NEW", "PS")
colnames(Ana_O) <- c("mean", "median", "95%quantile")
temp <- DH[1, ] %>% abs
tempP <- DP[1, ] %>% abs
Ana_O[1, ] <- c((temp %>% mean), (temp %>% median),
                (temp %>% quantile(0.95)))
Ana_O[2, ] <- c((tempP %>% mean), (tempP %>% median),
                (tempP %>% quantile(0.95)))

## analyze the within-stratum imbalances
tempW <- DH[2 : (1 + prod(level_num)), ] %>% abs
tempWP <- DP[2 : 1 + prod(level_num), ] %>% abs
Ana_W <- matrix(NA, nrow = 2, ncol = 3)
rownames(Ana_W) <- c("NEW", "PS")
colnames(Ana_W) <- c("mean", "median", "95%quantile")
Ana_W[1, ] = c((tempW %>% apply(1, mean) %>% mean),
               (tempW %>% apply(1, median) %>% mean),
               (tempW %>% apply(1, mean) %>% quantile(0.95)))
Ana_W[2, ] = c((tempWP %>% apply(1, mean) %>% mean),
               (tempWP %>% apply(1, median) %>% mean),
               (tempWP %>% apply(1, mean) %>% quantile(0.95)))

## analyze the marginal imbalance
tempM <- DH[(1 + prod(level_num) + 1) :
             (1 + prod(level_num) + sum(level_num)), ] %>% abs
tempMP <- DP[(1 + prod(level_num) + 1) :
               (1 + prod(level_num) + sum(level_num)), ] %>% abs
Ana_M <- matrix(NA, nrow = 2, ncol = 3)
rownames(Ana_M) <- c("NEW", "PS")
colnames(Ana_M) <- c("mean", "median", "95%quantile")
Ana_M[1, ] = c((tempM %>% apply(1, mean) %>% mean),
```

```
               (tempM %>% apply(1, median) %>% mean),
               (tempM %>% apply(1, mean) %>% quantile(0.95)))
Ana_M[2, ] = c((tempMP %>% apply(1, mean) %>% mean),
               (tempMP %>% apply(1, median) %>% mean),
               (tempMP %>% apply(1, mean) %>% quantile(0.95)))

AnaHP <- list(Ana_O, Ana_M, Ana_W)
names(AnaHP) <- c("Overall", "Marginal", "Within-stratum")

AnaHP
```

`PocSimMIN.sim` *Pocock and Simon's Method in the Two-Arms Case with Covariate Data Generating Mechanism*

Description

Allocates patients to one of two treatments using Pocock and Simon's method proposed by Pocock S J, Simon R (1975) <doi:10.2307/2529712>, by simulating covariate profiles under the assumption of independence between covariates and levels within each covariate.

Usage

```
PocSimMIN.sim(n = 1000, cov_num = 2, level_num = c(2, 2),
              pr = rep(0.5, 4), weight = NULL, p = 0.85)
```

Arguments

`n`	the number of patients. The default is `1000`.
`cov_num`	the number of covariates. The default is `2`.
`level_num`	a vector of level numbers for each covariate. Hence the length of `level_num` should be equal to the number of covariates. The default is `c(2, 2)`.
`pr`	a vector of probabilities. Under the assumption of independence between covariates, `pr` is a vector containing probabilities for each level of each covariate. The length of `pr` should correspond to the number of all levels, and the sum of the probabilities for each margin should be `1`. The default is `rep(0.5, 4)`, which corresponds to `cov_num` = `2`, and `level_num` = `c(2, 2)`.
`weight`	a vector of weights for within-covariate-margin imbalances. It is required that at least one element is larger than 0. If `weight` = `NULL` (default), the within-covariate-margin imbalances are weighted with an equal proportion, `1/cov_num`, for each covariate-margin.
`p`	the biased coin probability. `p` should be larger than `1/2` and less than `1`. The default is `0.85`.

Details

See `PocSimMIN`.

Value

See PocSimMIN.

References

Ma W, Ye X, Tu F, Hu F. *carat: Covariate-Adaptive Randomization for Clinical Trials*[J]. Journal of Statistical Software, 2023, 107(2): 1-47.

Pocock S J, Simon R. *Sequential treatment assignment with balancing for prognostic factors in the controlled clinical trial*[J]. Biometrics, 1975: 103-115.

See Also

See PocSimMIN for allocating patients with complete covariate data; See PocSimMIN.ui for the command-line user interface.

`PocSimMIN.ui` *Command-line User Interface Using Pocock and Simon's Procedure with Two-Arms Case*

Description

A call to the user-iterface function used to allocate patients to one of two treatments using Pocock and Simon's method proposed by Pocock S J, Simon R (1975) <doi:10.2307/2529712>.

Usage

```
PocSimMIN.ui(path, folder = "PocSimMIN")
```

Arguments

`path`	the path in which a folder used to storage variables will be created.
`folder`	name of the folder. If default, a folder named `"PocSimMIN"` will be created.

Details

See PocSimMIN.

Value

It returns an object of `class` `"carseq"`.

The function `print` is used to obtain results. The generic accessor functions `assignment`, `covariate`, `cov_num`, `cov_profile` and others extract various useful features of the value returned by `PocSimMIN.ui`.

Note

This function provides a command-line interface and users should follow the prompts to enter data including covariates as well as levels for each covariate, `weight`, biased probability `p` and the covariate profile of the new patient.

References

Ma W, Ye X, Tu F, Hu F. *carat: Covariate-Adaptive Randomization for Clinical Trials*[J]. Journal of Statistical Software, 2023, 107(2): 1-47.

Pocock S J, Simon R. *Sequential treatment assignment with balancing for prognostic factors in the controlled clinical trial*[J]. Biometrics, 1975: 103-115.

See Also

See `PocSimMIN` for allocating a given completely collected data; See `PocSimMIN.sim` for allocating patients with covariate data generating mechanism.

`rand.test` *Randomization Test*

Description

Performs randomization test on treatment effects.

Usage

```
rand.test(data, Reps = 200, method = c("HuHuCAR", "PocSimMIN", "StrBCD",
                                       "StrPBR", "DoptBCD", "AdjBCD"),
          conf = 0.95, binwidth = 30, ...)
```

Arguments

`data`	a data frame. It consists of patients' profiles, treatment assignments and outputs. See `getData`.
`Reps`	an integer. It is the number of randomized replications used in the randomization test. The default is `200`.
`method`	the randomization procedure to be used for testing. This package provides tests for `"HuHuCAR"`, `"PocSimMIN"`, `"StrBCD"`, `"StrPBR"`, `"AdjBCD"`, and `"DoptBCD"`.
`conf`	confidence level of the interval. The default is `0.95`.
`binwidth`	the number of bins for each bar in histogram. The default is 30.
`...`	arguments to be passed to `method`. These arguments depend on the randomization method used and the following arguments are accepted: **omega** a vector of weights at the overall, within-stratum, and within-covariate-margin levels. It is required that at least one element is larger than 0. Note that `omega` is only needed when `HuHuCAR` is to be used. **weight** a vector of weights for within-covariate-margin imbalances. It is required that at least one element is larger than 0. Note that `weight` is only needed when `PocSimMIN` is to be used. **p** the biased coin probability. `p` should be larger than `1/2` and less than `1`. Note that `p` is only needed when `"HuHuCAR"`, `"PocSimMIN"` and `"StrBCD"` are to be used.

a a design parameter governing the degree of randomness. Note that `a` is only needed when `"AdjBCD"` is to be used.

bsize the block size for stratified randomization. It is required to be a multiple of 2. Note that `bsize` is only needed when `"StrPBR"` is to be used.

Details

The randomization test is described as follows: 1) For the observed responses $Y_1, \ldots, Y_n$ and the treatment assignments $T_1, T_2, \ldots, T_n$, compute the observed test statistic

$$S_{obs} = \frac{-\sum_{i=1}^{n} Y_i * (T_i - 2)}{n_1} - \frac{\sum_{i=1}^{n} Y_i * (T_i - 1)}{n_0}$$

where n_1 is the number of patients assigned to treatment 1 and n_0 is the number of patients assigned to treatment 2;

2) Perform the covariate-adaptive randomization procedure to obtain the new treatment assignments and calculate the corresponding test statistic S_i. And repeat this process L times;

3) Calculate the two-sided Monte Carlo p-value estimator

$$p = \frac{\sum_{l=1}^{L} I(|S_l| \geq |S_{obs}|)}{L}$$

Value

It returns an object of class `"htest"`.

An object of class `"htest"` is a list containing the following components:

`p.value`	p-value of the test, the null hypothesis is rejected if the p-value is less than `sl`.
`estimate`	the estimated difference in treatment effects between treatment `1` and treatment `2`.
`conf.int`	a confidence interval under the chosen level `conf` for the difference in treatment effect between treatment `1` and treatment `2`.
`method`	a character string indicating what type of test was performed.
`data.name`	a character string giving the name(s) of the data.
`statistic`	the value of the t-statistic. As the randomization test is a nonparametric method, we cannot calculate the t-statistic, so it is hidden in this result.

References

Ma W, Ye X, Tu F, Hu F. *carat: Covariate-Adaptive Randomization for Clinical Trials*[J]. Journal of Statistical Software, 2023, 107(2): 1-47.

Rosenberger W F, Lachin J M. Randomization in clinical trials: *theory and practice*[M]. John Wiley & Sons, 2015.

Examples

```
##generate data
set.seed(100)
n = 1000
cov_num = 5
level_num = c(2,2,2,2,2)
pr = rep(0.5,10)
beta = c(0.1,0.4,0.3,0.2,0.5,0.5,0.4,0.3,0.2,0.1)
mu1 = 0
mu2 = 0.01
sigma = 1
type = "linear"
p = 0.85

dataS = getData(n, cov_num, level_num, pr, type,
               beta, mu1, mu2, sigma, "StrBCD", p)

#run the randomization test
library("ggplot2")
Strt = rand.test(data = dataS, Reps = 200,method = "StrBCD",
                conf = 0.95, binwidth = 30,
                p = 0.85)
Strt
```

StrBCD *Shao's Method in the Two-Arms Case*

Description

Allocates patients to one of the two treatments using Shao's method proposed by Shao J, Yu X, Zhong B (2010) <doi:10.1093/biomet/asq014>.

Usage

```
StrBCD(data, p = 0.85)
```

Arguments

`data`	a data frame. A row of the dataframe corresponds to the covariate profile of a patient.
`p`	the biased coin probability. `p` should be larger than `1/2` and less than `1`. The default is `0.85`.

Details

Consider I covariates and m_i levels for the ith covariate, $i = 1, \ldots, I$. T_j is the assignment of the jth patient and $Z_j = (k_1, \ldots, k_I)$ indicates the covariate profile of this patient, $j = 1, \ldots, n$. For convenience, $(k_1, \ldots, k_I)$ and $(i; k_i)$ denote the stratum and margin, respectively. $D_j(.)$ is the

difference between the numbers of patients assigned to treatment 1 and treatment 2 at the corresponding levels after j patients have been assigned. The stratified biased coin design is as follows:

(1) The first patient is assigned to treatment 1 with probability $1/2$;

(2) Suppose $j-1$ patients have been assigned ($1 < j \leq n$) and the jth patient falls within $(k_1^*, \ldots, k_I^*)$;

(3) If the jth patient were assigned to treatment 1, then the potential within-stratum difference between the two treatments would be

$$D_j^{(1)}(k_1^*, \ldots, k_I^*) = D_j(k_1^*, \ldots, k_I^*) + 1$$

for stratum $(k_1^*, \ldots, k_I^*)$. Similarly, the potential difference would be obtained in the same way if the jth patient were assigned to treatment 2;

(4) An imbalance measure is defined by

$$Imb_j^{(l)} = [D_j^{(l)}(k_1^*, \ldots, k_I^*)]^2, l = 1, 2;$$

(5) Conditional on the assignments of the first $(j-1)$ patients as well as the covariates'profiles of the first j patients, assign the jth patient to treatment 1 with probability

$$P(T_j = 1 | Z_j, T_1, \ldots, T_{j-1}) = q$$

for $Imb_j^{(1)} > Imb_j^{(2)}$,

$$P(T_j = 1 | Z_j, T_1, \ldots, T_{j-1}) = p$$

for $Imb_j^{(1)} < Imb_j^{(2)}$, and

$$P(T_j = 1 | Z_j, T_1, \ldots, T_{j-1}) = 0.5$$

for $Imb_j^{(1)} = Imb_j^{(2)}$.

Details of the procedure can be found in Shao J, Yu X, Zhong B (2010).

Value

It returns an object of class "carandom".

An object of class "carandom" is a list containing the following components:

datanumeric	a bool indicating whether the data is a numeric data frame.
covariates	a character string giving the name(s) of the included covariates.
strt_num	the number of strata.
cov_num	the number of covariates.
level_num	a vector of level numbers for each covariate.
n	the number of patients.
Cov_Assig	a (cov_num + 1) * n matrix containing covariate profiles for all patients and the corresponding assignments. The ith column represents the ith patient. The first cov_num rows include patients' covariate profiles, and the last row contains the assignments.
assignments	the randomization sequence.

`All strata`	a matrix containing all strata involved.
`Diff`	a matrix with only one column. There are final differences at the overall, within-stratum, and within-covariate-margin levels.
`method`	a character string describing the randomization procedure to be used.
`Data Type`	a character string giving the data type, `Real` or `Simulated`.
`framework`	the framework of the used randomization procedure: stratified randomization, or model-based method.
`data`	the data frame.

References

Ma W, Ye X, Tu F, Hu F. *carat: Covariate-Adaptive Randomization for Clinical Trials*[J]. Journal of Statistical Software, 2023, 107(2): 1-47.

Shao J, Yu X, Zhong B. *A theory for testing hypotheses under covariate-adaptive randomization*[J]. Biometrika, 2010, 97(2): 347-360.

See Also

See `StrBCD.sim` for allocating patients with covariate data generating mechanism. See `StrBCD.ui` for command-line user interface.

Examples

```
# a simple use
## Real Data
## creat a dataframe
df <- data.frame("gender" = sample(c("female", "male"), 1000, TRUE, c(1 / 3, 2 / 3)),
                 "age" = sample(c("0-30", "30-50", ">50"), 1000, TRUE),
                 "jobs" = sample(c("stu.", "teac.", "others"), 1000, TRUE),
                 stringsAsFactors = TRUE)
Res <- StrBCD(data = df)
## view the output
Res

## view all patients' profile and assignments
Res$Cov_Assig

## Simulated Data
cov_num = 3
level_num = c(2, 3, 3)
pr = c(0.4, 0.6, 0.3, 0.4, 0.3, 0.4, 0.3, 0.3)
Res.sim <- StrBCD.sim(n = 1000, cov_num, level_num, pr)
## view the output
Res.sim

## view the detials of difference
Res.sim$Diff


N <- 5
```

```
n <- 1000
cov_num <- 3
level_num <- c(2, 3, 5)
# Set pr to follow two tips:
# (1) length of pr should be sum(level_num);
# (2)sum of probabilities for each margin should be 1
pr <- c(0.4, 0.6, 0.3, 0.4, 0.3, rep(0.2, times = 5))
omega <- c(0.2, 0.2, rep(0.6 / cov_num, times = cov_num))

## generate a container to contain Diff
DH <- matrix(NA, ncol = N, nrow = 1 + prod(level_num) + sum(level_num))
DS <- matrix(NA, ncol = N, nrow = 1 + prod(level_num) + sum(level_num))
for(i in 1 : N){
  result <- HuHuCAR.sim(n, cov_num, level_num, pr, omega)
  resultS <- StrBCD.sim(n, cov_num, level_num, pr)
  DH[ , i] <- result$Diff; DS[ , i] <- resultS$Diff
}

## do some analysis
require(dplyr)

## analyze the overall imbalance
Ana_O <- matrix(NA, nrow = 2, ncol = 3)
rownames(Ana_O) <- c("NEW", "Shao")
colnames(Ana_O) <- c("mean", "median", "95%quantile")
temp <- DH[1, ] %>% abs
tempS <- DS[1, ] %>% abs
Ana_O[1, ] <- c((temp %>% mean), (temp %>% median),
                (temp %>% quantile(0.95)))
Ana_O[2, ] <- c((tempS %>% mean), (tempS %>% median),
                (tempS %>% quantile(0.95)))

## analyze the within-stratum imbalances
tempW <- DH[2 : (1 + prod(level_num)), ] %>% abs
tempWS <- DS[2 : 1 + prod(level_num), ] %>% abs
Ana_W <- matrix(NA, nrow = 2, ncol = 3)
rownames(Ana_W) <- c("NEW", "Shao")
colnames(Ana_W) <- c("mean", "median", "95%quantile")
Ana_W[1, ] = c((tempW %>% apply(1, mean) %>% mean),
               (tempW %>% apply(1, median) %>% mean),
               (tempW %>% apply(1, mean) %>% quantile(0.95)))
Ana_W[2, ] = c((tempWS %>% apply(1, mean) %>% mean),
               (tempWS %>% apply(1, median) %>% mean),
               (tempWS %>% apply(1, mean) %>% quantile(0.95)))

## analyze the marginal imbalance
tempM <- DH[(1 + prod(level_num) + 1) :
              (1 + prod(level_num) + sum(level_num)), ] %>% abs
tempMS <- DS[(1 + prod(level_num) + 1) :
               (1 + prod(level_num) + sum(level_num)), ] %>% abs
Ana_M <- matrix(NA, nrow = 2, ncol = 3)
rownames(Ana_M) <- c("NEW", "Shao")
colnames(Ana_M) <- c("mean", "median", "95%quantile")
```

```
Ana_M[1, ] = c((tempM %>% apply(1, mean) %>% mean),
               (tempM %>% apply(1, median) %>% mean),
               (tempM %>% apply(1, mean) %>% quantile(0.95)))
Ana_M[2, ] = c((tempMS %>% apply(1, mean) %>% mean),
               (tempMS %>% apply(1, median) %>% mean),
               (tempMS %>% apply(1, mean) %>% quantile(0.95)))

AnaHP <- list(Ana_O, Ana_M, Ana_W)
names(AnaHP) <- c("Overall", "Marginal", "Within-stratum")

AnaHP
```

`StrBCD.sim` *Shao's Method in the Two-Arms Case with Covariate Data Generating Mechanism*

Description

Allocates patients to one of two treatments using Shao's method proposed by Shao J, Yu X, Zhong B (2010) <doi:10.1093/biomet/asq014>, by simulating covariate profiles under the assumption of independence between covariates and levels within each covariate.

Usage

```
StrBCD.sim(n = 1000, cov_num = 2, level_num = c(2, 2),
           pr = rep(0.5, 4), p = 0.85)
```

Arguments

`n`	the number of patients. The default is `1000`.
`cov_num`	the number of covariates. The default is `2`.
`level_num`	a vector of level numbers for each covariate. Hence the length of `level_num` should be equal to the number of covariates. The default is `c(2, 2)`.
`pr`	a vector of probabilities. Under the assumption of independence between covariates, `pr` is a vector containing probabilities for each level of each covariate. The length of `pr` should correspond to the number of all levels, and the sum of the probabilities for each margin should be `1`. The default is `rep(0.5, 4)`, which corresponds to `cov_num` = `2`, and `level_num` = `c(2, 2)`.
`p`	the biased coin probability. `p` should be larger than `1/2` and less than `1`. The default is `0.85`.

Details

See `StrBCD`.

Value

See StrBCD.

References

Ma W, Ye X, Tu F, Hu F. *carat: Covariate-Adaptive Randomization for Clinical Trials*[J]. Journal of Statistical Software, 2023, 107(2): 1-47.

Shao J, Yu X, Zhong B. *A theory for testing hypotheses under covariate-adaptive randomization*[J]. Biometrika, 2010, 97(2): 347-360.

See Also

See StrBCD for allocating patients with complete covariate data; See StrBCD.ui for the command-line user interface.

StrBCD.ui *Command-line User Interface Using Shao's Method*

Description

A call to the user-interface function used to allocate patients to one of two treatments using Shao's method proposed by Shao J, Yu X, Zhong B (2010) <doi:10.1093/biomet/asq014>.

Usage

```
StrBCD.ui(path, folder = "StrBCD")
```

Arguments

path	the path in which a folder used to storage variables will be created.
folder	name of the folder. If default, a folder named "StrBCD" will be created.

Details

See StrBCD.

Value

It returns an object of class "carseq".

The function print is used to obtain results. The generic accessor functions assignment, covariate, cov_num, cov_profile and others extract various useful features of the value returned by StrBCD.ui.

Note

This function provides a command-line interface and users should follow the prompts to enter data including covariates as well as levels for each covariate, biased probability p and the covariate profile of the new patient.

References

Ma W, Ye X, Tu F, Hu F. *carat: Covariate-Adaptive Randomization for Clinical Trials*[J]. Journal of Statistical Software, 2023, 107(2): 1-47.

Shao J, Yu X, Zhong B. *A theory for testing hypotheses under covariate-adaptive randomization*[J]. Biometrika, 2010, 97(2): 347-360.

See Also

See `StrBCD` for allocating patients with complete covariate data; See `StrBCD.sim` for allocating patients with covariate data generating mechanism.

`StrPBR` *Stratified Permuted Block Randomization*

Description

Allocates patients to one of two treatments using stratified permuted block randomization proposed by Zelen M (1974) <doi:10.1016/0021-9681(74)90015-0>.

Usage

```
StrPBR(data, bsize = 4)
```

Arguments

`data`	a data frame. A row of the dataframe corresponds to the covariate profile of a patient.
`bsize`	the block size for stratified randomization. It is required to be a multiple of 2. The default is `4`.

Details

Different covariate profiles are defined to be strata, and then permuted block randomization is applied to each stratum. It works efficiently when the number of strata is small. However, when the number of strata increases, the stratified permuted block randomization fails to obtain balance between two treatments.

Permuted block randomization, or blocking, is used to balance treatments within a block so that there are the same number of subjects in each treatment. A block contains the same number of each treatment and blocks of different sizes are combined to make up the randomization list.

Details of the procedure can be found in Zelen M (1974).

Value

It returns an object of class "carandom".

An object of class "carandom" is a list containing the following components:

datanumeric	a bool indicating whether the data is a numeric data frame.
covariates	a character string giving the name(s) of the included covariates.
strt_num	the number of strata.
cov_num	the number of covariates.
level_num	a vector of level numbers for each covariate.
n	the number of patients.
Cov_Assig	a (cov_num + 1) * n matrix containing covariate profiles for all patients and the corresponding assignments. The ith column represents the ith patient. The first cov_num rows include patients' covariate profiles, and the last row contains the assignments.
assignments	the randomization sequence.
All strata	a matrix containing all strata involved.
Diff	a matrix with only one column. There are final differences at the overall, within-stratum, and within-covariate-margin levels.
method	a character string describing the randomization procedure to be used.
Data Type	a character string giving the data type, Real or Simulated.
framework	the framework of the used randomization procedure: stratified randomization, or model-based method.
data	the data frame.
bsize	the block size.
numbers of pats for each stratum	a vector giving the numbers of patients for each stratum.

References

Ma W, Ye X, Tu F, Hu F. *carat: Covariate-Adaptive Randomization for Clinical Trials*[J]. Journal of Statistical Software, 2023, 107(2): 1-47.

Zelen M. *The randomization and stratification of patients to clinical trials*[J]. Journal of chronic diseases, 1974, 27(7): 365-375.

See Also

See StrPBR.sim for allocating patients with covariate data generating mechanism. See StrPBR.ui for the command-line user interface.

Examples

```
# a simple use
## Real Data
## creat a dataframe
df <- data.frame("gender" = sample(c("female", "male"), 100, TRUE, c(1 / 3, 2 / 3)),
                 "age" = sample(c("0-30", "30-50", ">50"), 100, TRUE),
                 "jobs" = sample(c("stu.", "teac.", "others"), 100, TRUE),
                 stringsAsFactors = TRUE)
Res <- StrPBR(data = df, bsize = 4)
## view the output
Res

## view all patients' profile and assignments
Res$Cov_Assig

## Simulated data
cov_num <- 3
level_num <- c(2, 3, 3)
pr <- c(0.4, 0.6, 0.3, 0.4, 0.3, 0.4, 0.3, 0.3)
Res.sim <- StrPBR.sim(n = 100, cov_num, level_num, pr)
## view the output
Res.sim

## view the detials of difference
Res.sim$Diff


N <- 5
n <- 1000
cov_num <- 3
level_num <- c(2, 3, 5)
# Set pr to follow two tips:
#(1) length of pr should be sum(level_num);
#(2)sum of probabilities for each margin should be 1.
pr <- c(0.4, 0.6, 0.3, 0.4, 0.3, rep(0.2, times = 5))
omega <- c(0.2, 0.2, rep(0.6 / cov_num, times = cov_num))
# Set block size for stratified randomization
bsize <- 4

## generate a container to contain Diff
DS <- matrix(NA, ncol = N, nrow = 1 + prod(level_num) + sum(level_num))
for(i in 1 : N){
  rtS <- StrPBR.sim(n, cov_num, level_num, pr, bsize)
  DS[ , i] <- rtS$Diff
}

## do some analysis
require(dplyr)

## analyze the overall imbalance
Ana_O <- matrix(NA, nrow = 1, ncol = 3)
rownames(Ana_O) <- c("Str.R")
```

```
colnames(Ana_O) <- c("mean", "median", "95%quantile")
tempS <- DS[1, ] %>% abs
Ana_O[1, ] <- c((tempS %>% mean), (tempS %>% median),
                (tempS %>% quantile(0.95)))
## analyze the within-stratum imbalances
tempWS <- DS[2 : 1 + prod(level_num), ] %>% abs
Ana_W <- matrix(NA, nrow = 1, ncol = 3)
rownames(Ana_W) <- c("Str.R")
colnames(Ana_W) <- c("mean", "median", "95%quantile")
Ana_W[1, ] = c((tempWS %>% apply(1, mean) %>% mean),
               (tempWS %>% apply(1, median) %>% mean),
               (tempWS %>% apply(1, mean) %>% quantile(0.95)))

## analyze the marginal imbalance
tempMS <- DS[(1 + prod(level_num) + 1) : (1 + prod(level_num) + sum(level_num)), ] %>% abs
Ana_M <- matrix(NA, nrow = 1, ncol = 3)
rownames(Ana_M) <- c("Str.R");
colnames(Ana_M) <- c("mean", "median", "95%quantile")
Ana_M[1, ] = c((tempMS %>% apply(1, mean) %>% mean),
               (tempMS %>% apply(1, median) %>% mean),
               (tempMS %>% apply(1, mean) %>% quantile(0.95)))

AnaHP <- list(Ana_O, Ana_M, Ana_W)
names(AnaHP) <- c("Overall", "Marginal", "Within-stratum")

AnaHP
```

`StrPBR.sim` *Stratified Permuted Block Randomization with Covariate Data Generating Mechanism*

Description

Allocates patients to one of two treatments using stratified randomization proposed by Zelen M (1974) <doi:10.1016/0021-9681(74)90015-0>, by simulating covariates-profile on assumption of independence between covariates and levels within each covariate.

Usage

```
StrPBR.sim(n = 1000, cov_num = 2, level_num = c(2, 2),
           pr = rep(0.5, 4), bsize = 4)
```

Arguments

`n`	the number of patients. The default is `1000`.
`cov_num`	the number of covariates. The default is `2`.
`level_num`	a vector of level numbers for each covariate. Hence the length of `level_num` should be equal to the number of covariates. The default is `c(2, 2)`.

pr	a vector of probabilities. Under the assumption of independence between covariates, pr is a vector containing probabilities for each level of each covariate. The length of pr should correspond to the number of all levels, and the sum of the probabilities for each margin should be 1. The default is rep(0.5, 4), which corresponds to cov_num = 2, and level_num = c(2, 2).
bsize	the block size for the stratified randomization. It is required to be a multiple of 2. The default is 4.

Details

See StrPBR.

Value

See StrPBR.

References

Ma W, Ye X, Tu F, Hu F. *carat: Covariate-Adaptive Randomization for Clinical Trials*[J]. Journal of Statistical Software, 2023, 107(2): 1-47.

Zelen M. *The randomization and stratification of patients to clinical trials*[J]. Journal of chronic diseases, 1974, 27(7): 365-375.

See Also

See StrPBR for allocating patients with complete covariate data; See StrPBR.ui for the command-line user interface.

StrPBR.ui *Command-line User Interface Using Stratified Permuted Block Randomization with Two-Arms Case*

Description

A call to the user-iterface function used to allocate patients to one of two treatments using stratified permuted block randomization proposed by Zelen M (1974) <doi: 10.1016/0021-9681(74)90015-0>.

Usage

```
StrPBR.ui(path, folder = "StrPBR")
```

Arguments

path	the path in which a folder used to storage variables will be created.
folder	name of the folder. If default, a folder named "StrPBR" will be created.

Details

See StrPBR.

Value

It returns an object of class "carseq".

The function print is used to obtain results. The generic accessor functions assignment, covariate, cov_num, cov_profile and others extract various useful features of the value returned by StrPBR.ui.

Note

This function provides a command-line interface and users should follow the prompts to enter data including covariates as well as levels for each covariate, block size bsize and the covariate profile of the new patient.

References

Ma W, Ye X, Tu F, Hu F. *carat: Covariate-Adaptive Randomization for Clinical Trials*[J]. Journal of Statistical Software, 2023, 107(2): 1-47.

Zelen M. *The randomization and stratification of patients to clinical trials*[J]. Journal of chronic diseases, 1974, 27(7): 365-375.

See Also

See StrPBR for allocating patients with complete covariate data; See StrPBR.sim for allocating patients with covariate data generating mechanism.

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