Package ‘SeqAlloc’

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Type Package

Title Sequential Allocation for Prospective Experiments

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Description Potential randomization schemes are prospectively evaluated when units are assigned to treatment arms upon entry into the experiment. The schemes are evaluated for balance on covariates and on predictability (i.e., how well could a site worker guess the treatment of the next unit enrolled).

Imports stats, graphics

License GPL-2

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Description

Potential randomization schemes are prospectively evaluated when units are assigned to treatment arms upon entry into the experiment. The schemes are evaluated for balance on covariates and on predictability (i.e., how well could a site worker guess the treatment of the next unit enrolled).

Details

- Package: SeqAlloc
- Type: Package
- Version: 1.0
- Date: 2016-08-03
- Imports: stats, graphics
- License: GPL-2

Author(s)

Xiaoshu Zhu <xiaoshuzhu@westat.com> and Sharon Lohr

References


**Description**

Allocates observations sequentially using a biased coin design. If equal numbers have been allocated to treatment and control, the next observation is allocated to treatment with probability 1/2. If there are more units assigned to treatment than control, the next observation is allocated to control with probability p; if there are more units assigned to control than treatment, the next observation is allocated to treatment with probability p.

**Usage**

```R
bcdalloc(n, pbcd, tol = 1e-06)
```

**Arguments**

- `n` number of observations
- `pbcd` probability p used for biased coin
- `tol` tolerance used for allocation

**Value**

Vector of zeroes and ones indicating the allocation of each unit to treatment (1) or control (0)

**Author(s)**

Xiaoshu Zhu <xiaoshuzhu@westat.com> and Sharon Lohr

**References**


**Examples**

```R
bcdalloc(20, 0.7)
```
Arguments

carwt_x1 matrix of dimension n x n, where n is the number of units to be randomly assigned to treatments. The (i,j) element of the matrix is the weighted match score of unit i and unit j. The matrix should be symmetric with diagonal elements of 1.

p probability the next unit should be allocated to the experiment arm that currently has fewer observations.

tol imbalance tolerance for deviation from equal allocation.

Value

Vector with the allocation to treatment (denoted by 1) and control (denoted by 0)

Note

This function works for categorical as well as binary covariates. The matrix carwt_x1 can be created from an X matrix by using the function weight_x in this package.

Author(s)

Xiaoshu Zhu <xiaoshuzhu@westat.com> and Sharon Lohr

References


See Also

weight_x

Examples

wtmat <- matrix(runif(10000), ncol=100)
wtmat <- (wtmat * lower.tri(wtmat)) + t(wtmat * lower.tri(wtmat))
diag(wtmat) <- 1

caitalloc(wtmat,1,3)
**Description**

Performs the sequential allocation for the covariate-adjusted randomization (CAR) method of allocating observations in a randomized experiment.

**Usage**

```r
caralloc(xmat, carwt, p, tol)
```

**Arguments**

- `xmat`: matrix or data frame of covariates for prospective enrollees in the experiment.
- `carwt`: vector of weights
- `p`: probability the next unit should be allocated to the experiment arm that currently has fewer observations. For CAR, use $0.5 < p < 1$.
- `tol`: tolerance for deviation from equal allocation. For CAR, set `tol` to be a small value, say 0.01. For CAIM, set `tol` to be the imbalance tolerance (d).

**Value**

Vector with the allocation to treatment (denoted by 1) and control (denoted by 0)

**Author(s)**

Xiaoshu Zhu <xiaoshuzhu@westat.com> and Sharon Lohr

**References**


**Examples**

```r
sampsize <- 200
percent <- c(0.5, 0.8, 0.2, 0.4)
carwt <- c(0.4, 0.3, 0.2, 0.1)

set.seed(5798)

xmat <- matrix(rbinom(sampsize*length(percent), 1, rep(percent, sampsize)),
           nrow=sampsize, ncol=length(percent), byrow=TRUE)
```

colnames(xmat) = c("C1","C2","C3","C4")
strat_factor = xmat[,1]*4 + xmat[,2]*2 + xmat[,4] + 1
caralloc(xmat,carwt,1,3)

---

cguess

### Evaluate Optimal Guess

#### Description

This function calculates the optimal guess for the allocation of the next observation in a sequential allocation scheme, and evaluates whether that guess is correct.

#### Usage

`cguess(alloc)`

#### Arguments

- **alloc**: vector of zeroes and ones, indicating the allocation to treatment (1) and control (0)

#### Details

Blackwell and Hodges (1957) proposed evaluating the predictability of a randomized allocation scheme by having an observer guess that the next unit would be allocated to the treatment arm that currently has fewer subjects. This function creates the guesses that would be generated by an observer following this strategy, then compares them with the actual allocation. If units 1 through j have more treatment than control units, then the observer guesses that observation j+1 is assigned to the control arm. If units 1 through j have more control than treatment units, then the observer guesses that observation j+1 is assigned to the treatment arm. If units 1 through j have the same number of control and treatment units, then the observer flips a coin with probability 0.5 for the allocation of the next unit. To reduce the variability in the percentage guessed correctly, this is recorded as a response of 0.5; however, the function is easily changed to allow the observer to guess treatment or control with probability 0.5 for that case.

#### Value

Vector of length `length(alloc)` containing values 0, 0.5, and 1. A value is 1 if the guess is correct, 0 if it is incorrect, and 0.5 if the allocation preceding the observation in question was equal.

#### Author(s)

Xiaoshu Zhu <xiaoshuzhu@westat.com> and Sharon Lohr
covimbal

References


Examples

alloc <- rbinom(50,1,.5)
cguess(alloc)

covimbal

Evaluate covariate imbalance using R-squared.

Description

Evaluate imbalance in the covariates from the allocation by finding R-squared for a centered regression through the origin.

Usage

covimbal(y, xmatc)

Arguments

y vector of 0’s and 1’s representing allocation
xmatc centered X matrix

Value

Value of R-squared from centered regression

Author(s)

Xiaoshu Zhu <xiaoshuzhu@westat.com> and Sharon Lohr

References

Examples

```r
alloc <- rbinom(60,1,.5)
xmat <- matrix(rbinom(240,1,.4),ncol=4)
xmatc <- scale(xmat,center=TRUE,scale=FALSE)
covimbalm(alloc,xmatc)
```

---

**MAICimbalm**

*Maximum Allocation Imbalance for Covariates*

Description

Evaluate maximum of the allocation imbalance for all covariates

Usage

```r
MAICimbalm(alloc, xmat)
```

Arguments

- `alloc` vector of allocations to treatment (1) or control (0)
- `xmat` matrix describing covariates for each prospective observation

Value

maximum of covariate imbalances

Author(s)

Xiaoshu Zhu <xiaoshuzhu@westat.com> and Sharon Lohr

References


See Also

- `WAICimbalm`

Examples

```r
alloc <- rbinom(60,1,.5)
xmat <- matrix(rbinom(240,1,.4),ncol=4)
MAICimbalm(alloc, xmat)
```
**SeqAlloc**  
*Sequential Allocation for Prospective Experiments*

**Description**
Simulates results of allocations using complete randomization (CR), random allocation rule (RAR), biased coin design (BCD), permuted block design (PBD), stratified permuted block design (SPBD), covariate-adaptive randomization (CAR), big stick design (BSD), and covariate-adjusted imbalance tolerance (CAIT) designs. The order of the prospective enrollees is permuted for a preset number of iterations; for each iteration, the allocations are determined for each of the methods listed above. The allocations are then evaluated for balance on the covariates and for predictability (i.e., how well an observer could guess the next treatment assignment).

**Usage**
```r
SeqAlloc(xmat, carwt, strata = NULL, blksize, pbcd, pcar, bsdtol, caittol, niter, seed = 12345)
```

**Arguments**
- **xmat**: matrix or data frame of covariates for prospective enrollees in the experiment. This matrix is to be used in CAR/CAIT methods, and should include strata or marginals of strata as columns
- **carwt**: vector of weights to be used for CAR and CAIT methods
- **strata**: vector of planned strata for study (if none, should be NULL)
- **blksize**: vector of block sizes for PBDs and SPBDs
- **pbcd**: probability for biased coin design (BCD) method
- **pcar**: probability for CAR method
- **bsdtol**: tolerance (d value) for BSD method
- **caittol**: tolerance (d value) for CAIM method
- **niter**: number of iterations for simulation
- **seed**: random number seed, allows the allocation to be reproduced later

**Value**
List containing summary statistics (minimum, 25th percentile, median, mean, 75th percentile, 90th percentile, 95th percentile, maximum) for evaluation measures, including AI, Rsquared, MAIC, WAIC, perccorr, and perccorr_strat.

- **schemes**: names of schemes evaluated
- **AI**: value of overall allocation imbalance defined as | Proportion of observations that are allocated to the treatment group - 0.5 |
- **Rsquared**: value of R-squared from regression through the origin
- **MAIC**: maximum of allocation imbalance for all covariates
SeqAlloc

WAIC  weighted average of allocation imbalance for all covariates
perccorr  percentage of allocations that an observer could guess correctly using the Blackwell-Hodges rule
perccorr_strat  percentage of allocations that an observer could guess correctly using the Blackwell-Hodges rule within each stratum
carwt  weights used in CAR and CAIM procedures

Note
Because the program allows for sequential allocation methods, it can be slow when the data set and/or number of iterations is large.

Author(s)
Xiaoshu Zhu <xiaoshuzhu@westat.com> and Sharon Lohr

References

Examples
sampsize <- 200
percent <- c(0.5,0.8,0.2,0.4)
set.seed(200)

xmat <- matrix(rbinom(sampsize*length(percent),1,rep(percent,sampsize)),
nrow=sampsize,ncol=length(percent),byrow=TRUE)
colnames(xmat) <- c("C1","C2","C3","C4")
strat_factor <- xmat[,2]*2 + xmat[,4] + 1

SeqAlloc(xmat,carwt=c(.4,.3,.2,.1),strata=strat_factor,blksize=c(2,6),
pbcd=.7,pcar=.8,bsdtol=2,caittol=5,niter=10, seed = 20850)
SeqAllocplot

Plot the evaluation criteria for the designs

Description

Provides boxplots and scatterplots of balance and predictability measures for candidate sequential allocations.

Usage

SeqAllocplot(mysim, bporder = NULL, stratum = F, cexsize = 0.7)

Arguments

- **mysim**: output from function SeqAlloc
- **bporder**: vector giving the randomization methods to be plotted, corresponding to the positions in mysim$schemes
- **stratum**: logical variable of whether PBD designs should be plotted, default is FALSE
- **cexsize**: size of characters in plot and axis, default is 0.7

Value

Produces selected plots of predictability and balance for randomization schemes. Requires user to click window or press "enter" to progress through plots.

Note

These are example plots; the plotting code can be extracted from this function or the function is easily modified if different plots are desired.

Author(s)

Xiaoshu Zhu <xiaoshuzhu@westat.com> and Sharon Lohr

References


See Also

SeqAlloc
Examples

```r
sampsize <- 200
percent <- c(0.5, 0.8, 0.2, 0.4)
set.seed(200)

xmat <- matrix(rbinom(sampsize*length(percent), 1, rep(percent, sampsize)),
    nrow = sampsize, ncol = length(percent), byrow = TRUE)
colnames(xmat) <- c("C1", "C2", "C3", "C4")
strat_factor <- xmat[, 1] * 4 + xmat[, 2] * 2 + xmat[, 4] + 1

mysim <- SeqAlloc(xmat, carwt = c(.4, .3, .2, .1), strata = strat_factor, blksize = c(2, 6),
    pbc = .7, pcar = .67, bsdtol = 2, caittol = 3, niter = 10, seed = 30924)

SeqAllocplot(mysim, bporder = c(3, 4, 7, 8), stratum = FALSE, cexsize = 0.6)
```

stratblockalloc  

Stratified permuted block allocation

Description

Allocates observations to treatment (1) or control (0) within strata

Usage

```r
stratblockalloc(n, blksize)
```

Arguments

- `n`: number of observations
- `blksize`: size of each block: must be even number

Details

Allocates observations within each block of size `blksize` so that half of the observations in each block are in the treatment group and the other half are in the control group.

Value

vector of allocations to treatment (1) or control (0) group

Author(s)

Xiaoshu Zhu <xiaoshuzhu@westat.com> and Sharon Lohr

References

**summary95**

**Examples**

```r
stratblockalloc(20, 2)
```

---

**Description**

Finds the Minimum, 25th percentile, Median, Mean, 75th percentile, 90th percentile, 95th percentile, and Maximum of the vector

**Usage**

```r
summary95(x)
```

**Arguments**

- `x` vector for which summary statistics are desired

**Details**

The code from the `summary` function in R is modified to include the 90th and 95th percentiles

**Value**

vector of summary statistics for data

**Author(s)**

Xiaoshu Zhu <xiaoshuzhu@westat.com> and Sharon Lohr, adapted from 'summary' function in R.

**Examples**

```r
summary95(rnorm(40))
```
WAICimbal

Weighted Average of Allocation Imbalance for Covariates

Description

Evaluate weighted average of the allocation imbalance for all covariates

Usage

WAICimbal(alloc, xmat, carwt)

Arguments

<table>
<thead>
<tr>
<th>alloc</th>
<th>vector of allocations to treatment (1) or control (0)</th>
</tr>
</thead>
<tbody>
<tr>
<td>xmat</td>
<td>matrix describing covariates for each prospective observation</td>
</tr>
<tr>
<td>carwt</td>
<td>vector of weights to be accorded to respective covariates</td>
</tr>
</tbody>
</table>

Value

Weighted average of covariate imbalances

Author(s)

Xiaoshu Zhu <xiaoshuzhu@westat.com> and Sharon Lohr

References


See Also

MAICimbal

Examples

alloc <- rbinom(60,1,.5)
xmat <- matrix(rbinom(240,1,.4),ncol=4)
carwt <- c(.1,.3,.2,.4)

WAICimbal(alloc, xmat, carwt)
weight_x

Calculate weight matrix from matrix of covariates

Description

Calculate a vector of weights relating vector xrow with the rows of xmat, according to the weights in vector carwt. For each row in xmat, the positions of agreement with xrow are found. The weight for that row of xmat is then the sum of the elements of carwt corresponding to the matches.

Usage

weight_x(xrow, xmat, carwt)

Arguments

xrow vector used for matching
xmat matrix of covariates
carwt vector of weight for each match

Value

Vector of weights relating vector xrow to the rows of xmat

Author(s)

Xiaoshu Zhu <xiaoshuzhu@westat.com> and Sharon Lohr

References


Examples

xrow <- c(1,0,1,1)
xmat <- matrix(rbinom(60,1,.4),ncol=4)
carwt <- c(.6,.4,.2,.1)

weight_x(xrow, xmat, carwt)
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