Package ‘PropScrRand’

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Type Package

Title Propensity Score Methods for Assigning Treatment in Randomized Trials

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Description Contains functions to run propensity-biased allocation to balance covariate distributions in sequential trials and propensity-constrained randomization to balance covariate distributions in trials with known baseline covariates at time of randomization. Currently only supports trials comparing two groups.

License GPL-3

NeedsCompilation no

Repository CRAN

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Contents

`genPerms` *Generate Treatment Permutations*

Description

Used within calls to `pcr` to generate a set of unique treatment permutations for randomization.

Usage

```
genPerms(n, n1, nPerms)
```

Arguments

`n`	Total number of units to be randomized.
`n1`	Number of units to receive treatment.
`nPerms`	Number of permutations to generate.

Details

This function randomly samples `nPerms` of the `choose(n, n1)` possible treatment permutations. If `nPerms` > `choose(n, n1)`, then all `choose(n, n1)` permutations are generated systematically. Also, in the case of 1-to-1 allocation, the complement treatment vectors are also produced, so the returned matrix has `2*nPerms` permutations. Uniqueness is checked throughout and duplicate permutations disgarded.

Value

The result is an `n1` x `nPerms` (or `n1` x `choose(n, n1)` or `n1` x `2*nPerms`) matrix. Each column represents one treatment permutation, with the values in the column giving the index of the treated units.

Author(s)

Travis M. Loux

Examples

```
genPerms(n=50, n1=25, nPerms=500)
genPerms(n=50, n1=35, nPerms=500)
```

`getVar` *Compute Propensity Score Variance*

Description

Given a data set and vector of indices for treated units, computes the variance of the propensity score fitted via logistic regression.

Usage

```
getVar(covs, tIndex)
```

Arguments

`covs`	A data frame of baseline covariates.
`tIndex`	A vector indicating which units are to receive treatment.

Value

Returns the variance of the fitted propensity scores.

Author(s)

Travis M. Loux

`pba` *Propensity-Biased Allocation*

Description

Performs propensity-biased allocation for assigning a new unit to treatment in a sequential design with two treatment levels (i.e., treatment and control).

Usage

```
pba(x, tr, newx, k = 1, global = 0.5)
pbaAgain(previous, newx, k = NA)
```

Arguments

`x`	A data frame of the covariate values of previously assigned units.
`tr`	A vector of treatment assignments (0 or 1) for previously assigned units.
`newx`	Data frame of covariate values of the new unit.
`k`	Balancing parameter.
`global`	Global target proportion to be treated.
`previous`	The output of a previous call to `pba` or `pbaAgain`

Details

The function `pba` generates a treatment assignment for a new unit. The steps of the process include regressesing `tr` on `x` by logistic regression, computeing the fitted value of the new unit using covarate values in `newx`, and transforming the fitted propensity score into the probability of treatment by a call to `piFunction` using `k` and `global` as parameters. The balancing parameter `k` must be one of `0`, `Inf`, or the ratio of two positive odd integers. Small values of `k` result in less restrictive randomization while larger values of `k` result in more forced balance. In particular, `k = 0` is equivalent to pure randomization and `k = Inf` results in deterministic allocation. Finally, a treatment assignment for the new unit is generated via a Bernoulli trial with probability from `piFunction`.

The function `pbaAgain` takes as input the output from a previous call to `pba` or `pbaAgain` and runs `pba` for the new unit using the values of `newx`. If `k = NA` (the default), the value of `k` from `previous` is used; otherwise, the provided value of `k` is used. The parameter `global` is assumed to stay the same throughout the trial. The output of `pbaAgain` contains the same information as `pba`.

Value

`results`	A list of results from the PBA procedure.
`phat`	The fitted propensity score for the new unit.
`ptreat`	The probability of assignment to the treatment group for the new unit.
`newtr`	Result of random assignment using `ptreat`.
`input`	A list of inputs to PBA procdure. Used in future calls to `pbaAgain`.
`x`	Input `x`.
`tr`	Input `tr`.
`newx`	Input `newx`.
`k`	Input `k`.
`global`	Input `global`.

Author(s)

Travis Loux

References

Loux, T.M. (2013) A simple, flexible, and effective covariate-adaptive treatment allocation procedure. Statistics in Medicine 32(22), 3775-3787. DOI: 10.1002/sim.5837

Examples

```
x0 = data.frame(matrix(rnorm(60), ncol=3))
t0 = rbinom(nrow(x0), size=1, prob=0.5)

x1 = data.frame(matrix(rnorm(3), ncol=3))
trial1 = pba(x=x0, tr=t0, newx=x1, k=Inf)

x2 = data.frame(matrix(rnorm(3), ncol=3))
trial2 = pbaAgain(previous=trial1, newx=x2)
```

```
x3 = data.frame(matrix(rnorm(3), ncol=3))
trial3 = pbaAgain(previous=trial2, newx=x3, k=5/3)
```

`pcr` *Propensity-Constrained Randomization*

Description

Performs propensity-contstrained randomization on a given data set with measured covariates on all units.

Usage

```
pcr(x, nTreat, M, m)
```

Arguments

`x`	Data frame of covariates.
`nTreat`	Number of units to be treated.
`M`	Number of candidate permutations to create.
`m`	Number of permutations to keep.

Details

Given the parameters, `pcr` generates `M` unique permutations by calling `genPerms`. For each permutation, the empirical propensity scores are computed and the variance returned by `getVar`. Finally, the `m` permutations with the smallest propensity score variance are found. The `m` permutations returned in `best` can then be used to perform randomization and randomization inference. We suggest `M` >= `10000` and `m/M` <= `0.10`.

Value

`treatments`	The (approximately) `M` permutations generated by `genPerms`.
`variance`	A vector of the propensity score variances for all `M` permutations in `treatments`.
`cutoff`	The calculated `m/M` quantile of propensity score variances.
`best`	The column indices of the permutations in `treatments` with propensity score variance below `cutoff`.

Author(s)

Travis Loux

References

Loux, T.M. (2015) Randomization, matching, and propensity scores in the design and analysis of experimental studies with known covariates. Statistics in Medicine. 34(4), 558-570. DOI: 10.1002/sim.6361

Examples

```
# 1:1 allocation, M small
dat1 = data.frame(x1=rnorm(50),
                  x2=rnorm(50),
                  x3=sample(c('a','b','c'), size=50, replace=TRUE))
trial1 = pcr(x=dat1, nTreat=25, M=500, m=50)

# 1:1 allocation, M large
dat2 = data.frame(x1=rnorm(10),
                  x2=rnorm(10),
                  x3=sample(c('a','b','c'), size=10, replace=TRUE))
trial2 = pcr(x=dat2, nTreat=5, M=200, m=20)

# non-1:1 allocation, M small
dat3 = data.frame(x1=rnorm(50),
                  x2=rnorm(50),
                  x3=sample(c('a','b','c'), size=50, replace=TRUE))
trial3 = pcr(x=dat3, nTreat=35, M=200, m=20)

# non-1:1 allocation, M large
dat4 = data.frame(x1=rnorm(10),
                  x2=rnorm(10),
                  x3=sample(c('a','b','c'), size=10, replace=TRUE))
trial4 = pcr(x=dat4, nTreat=6, M=300, m=30)
```

`piFunction` *Get PBA Treatment Probability*

Description

Used within calls to `pba` and `pbaAgain` to obtain the probability a unit is assigned treatment given its fitted propensity score.

Usage

```
piFunction(fit, kparam, qparam)
```

Arguments

`fit`	Fitted propensity score.
`kparam`	Balancing parameter.
`qparam`	Global target for proportion of units treated.

Details

The input `kparam` must be one of `0`, `Inf`, or the ratio of two positive odd integers. Both `fit` and `qparam` must be between 0 and 1.

Value

A numeric object. In the conext of PBA, the probability of assignment to treatment for the current unit.

Author(s)

Travis M. Loux

Examples

```
piFunction(fit=0.6, kparam=1, qparam=0.5)
piFunction(fit=0.6, kparam=5, qparam=0.5)
piFunction(fit=0.6, kparam=1/5, qparam=0.5)

piFunction(fit=0.6, kparam=1, qparam=2/3)
piFunction(fit=0.6, kparam=5, qparam=2/3)
piFunction(fit=0.6, kparam=1/5, qparam=2/3)
```

`plotpi` *Plots of piFunction*

Description

Can be used to investigate the strength of balance forced by various values of the tuning parameter `k`.

Usage

```
plotpi(k, global = 0.5)
addpi(k, global = 0.5, ...)
```

Arguments

`k`	Balancing parameter.
`global`	Global target for proportion of units treated.
`...`	Parameters in `addpi` passed to `lines` function.

Details

The function `plotpi` creates a plot of treatment probability against fitted propensity score for values of `k` and `global`. The function `addpi` adds a curve for a new combination of `k` and `global` to an existing plot.

Author(s)

Travis M. Loux

Examples

```
plotpi(k=3, global=0.5)
addpi(k=5/3, lty=2, col='red')
plotpi(k=1/3, global=2/3)
```

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