

Package: PropScrRand (via r-universe)

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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.

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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 discarded.

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 regressing `tr` on `x` by logistic regression, computing the fitted value of the new unit using covariate 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

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

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-constrained 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 $M \geq 10000$ and $m/M \leq 0.10$.

Value

treatments	The (approximately) M permutations generated by <code>genPerms</code> .
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

<code>fit</code>	Fitted propensity score.
<code>kparam</code>	Balancing parameter.
<code>qparam</code>	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 context 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

<code>k</code>	Balancing parameter.
<code>global</code>	Global target for proportion of units treated.
<code>...</code>	Parameters in <code>addpi</code> passed to <code>lines</code> 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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