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Maintainer Michael Lingzhi Li <mlli@mit.edu>
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Author Michael Lingzhi Li [aut, cre], Kosuke Imai [aut]
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This function estimates AUPEC. The details of the methods for this design are given in Imai and Li (2019).

Usage

\[ \text{AUPEC}(T, \tau, Y, \text{centered} = \text{TRUE}) \]

Arguments

- \( T \): A vector of the unit-level binary treatment receipt variable for each sample.
- \( \tau \): A vector of the unit-level continuous score for treatment assignment. We assume those that have \( \tau < 0 \) should not have treatment. Conditional Average Treatment Effect is one possible measure.
- \( Y \): A vector of the outcome variable of interest for each sample.
- \( \text{centered} \): If \( \text{TRUE} \), the outcome variables would be centered before processing. This minimizes the variance of the estimator. Default is \( \text{TRUE} \).

Value

A list that contains the following items:

- \( \text{aupec} \): The estimated Area Under Prescription Evaluation Curve
- \( \text{sd} \): The estimated standard deviation of AUPEC.
- \( \text{vec} \): A vector of points outlining the AUPEC curve across each possible budget point for the dataset. Each step increases the budget by \( 1/n \) where \( n \) is the number of data points.
**AUPECcv**

**Author(s)**

Michael Lingzhi Li, Operations Research Center, Massachusetts Institute of Technology <mlli@mit.edu>, http://mlli.mit.edu;

**References**

Imai and Li (2019). “Experimental Evaluation of Individualized Treatment Rules”,

**Examples**

\[ T = c(1,0,1,0,1,0,1,0) \]
\[ \tau = c(0,0.1,0.2,0.3,0.4,0.5,0.6,0.7) \]
\[ Y = c(4,5,0,2,4,1,-4,3) \]
\[ \text{aupecclist <- AUPEC}(T,\tau,Y) \]
\[ \text{aupecclist}$aupec \]
\[ \text{aupecclist}$sd \]
\[ \text{aupecclist}$vec \]

**Description**

This function estimates AUPEC. The details of the methods for this design are given in Imai and Li (2019).

**Usage**

\[ \text{AUPECcv}(T, \tau, Y, \text{ind}, \text{centered} = \text{TRUE}) \]

**Arguments**

- **T**: A vector of the unit-level binary treatment receipt variable for each sample.
- **tau**: A matrix where the \( i \)th column is the unit-level continuous score for treatment assignment generated in the \( i \)th fold.
- **Y**: The outcome variable of interest.
- **ind**: A vector of integers (between 1 and number of folds inclusive) indicating which testing set does each sample belong to.
- **centered**: If TRUE, the outcome variables would be centered before processing. This minimizes the variance of the estimator. Default is TRUE.

**Value**

A list that contains the following items:

- **aupec**: The estimated AUPEC.
- **sd**: The estimated standard deviation of AUPEC.
consist.test

The Consistency Test for Grouped Average Treatment Effects (GATEs) in Randomized Experiments

Description

This function calculates statistics related to the test of treatment effect consistency across groups.

Usage

consist.test(T, tau, Y, ngates = 5, nsim = 10000)

Arguments

- **T**: A vector of the unit-level binary treatment receipt variable for each sample.
- **tau**: A vector of the unit-level continuous score. Conditional Average Treatment Effect is one possible measure.
- **Y**: A vector of the outcome variable of interest for each sample.
- **ngates**: The number of groups to separate the data into. The groups are determined by tau. Default is 5.
- **nsim**: Number of Monte Carlo simulations used to simulate the null distributions. Default is 10000.

Details

The details of the methods for this design are given in Imai and Li (2022).
Value

A list that contains the following items:

- **stat**: The estimated statistic for the test of consistency
- **pval**: The p-value of the null hypothesis (that the treatment effects are consistent)

Author(s)

Michael Lingzhi Li, Operations Research Center, Massachusetts Institute of Technology <mlli@mit.edu>, http://mlli.mit.edu;

References

Imai and Li (2022). “Statistical Inference for Heterogeneous Treatment Effects Discovered by Generic Machine Learning in Randomized Experiments”,

Examples

```r
T = c(1,0,1,0,1,0,1,0)
tau = c(0,0.1,0.2,0.3,0.4,0.5,0.6,0.7)
Y = c(4,5,0,2,4,1,-4,3)
consisttestlist <- consist.test(T,tau,Y,ngates=5)
consisttestlist$stat
consisttestlist$pval
```

**consistcv.test**

The Consistency Test for Grouped Average Treatment Effects (GATEs) under Cross Validation in Randomized Experiments

Description

This function calculates statistics related to the test of treatment effect consistency across groups under cross-validation.

Usage

```r
consistcv.test(T, tau, Y, ind, ngates = 5, nsim = 10000)
```

Arguments

- **T**: A vector of the unit-level binary treatment receipt variable for each sample.
- **tau**: A vector of the unit-level continuous score. Conditional Average Treatment Effect is one possible measure.
- **Y**: A vector of the outcome variable of interest for each sample.
- **ind**: A vector of integers (between 1 and number of folds inclusive) indicating which testing set does each sample belong to.
Description

This function estimates the Grouped Average Treatment Effects (GATEs) where the groups are determined by a continuous score. The details of the methods for this design are given in Imai and Li (2022).

Usage

GATE(T, tau, Y, ngates = 5)

ngates The number of groups to separate the data into. The groups are determined by tau. Default is 5.

nsim Number of Monte Carlo simulations used to simulate the null distributions. Default is 10000.

Details

The details of the methods for this design are given in Imai and Li (2022).

Value

A list that contains the following items:

stat The estimated statistic for the test of consistency under cross-validation.
pval The p-value of the null hypothesis (that the treatment effects are consistent)

Author(s)

Michael Lingzhi Li, Operations Research Center, Massachusetts Institute of Technology <mlli@mit.edu>, http://mlli.mit.edu;

References

Imai and Li (2022). “Statistical Inference for Heterogeneous Treatment Effects Discovered by Generic Machine Learning in Randomized Experiments”.

Examples

T = c(1,0,1,0,1,0,1,0)
tau = matrix(c(0,0.1,0.2,0.3,0.4,0.5,0.6,0.7,-0.5,-0.3,-0.1,0.1,0.3,0.5,0.7,0.9),nrow = 8, ncol = 2)
Y = c(4,5,0,2,4,1,-4,3)
ind = c(rep(1,4),rep(2,4))
consisttestlist <- consistcv.test(T,tau,Y,ind,ngates=2)
consisttestlist$stat
consisttestlist$pval

GATE

Estimation of the Grouped Average Treatment Effects (GATEs) in Randomized Experiments

Description

This function estimates the Grouped Average Treatment Effects (GATEs) where the groups are determined by a continuous score. The details of the methods for this design are given in Imai and Li (2022).

Usage

GATE(T, tau, Y, ngates = 5)
Arguments

T  A vector of the unit-level binary treatment receipt variable for each sample.

tau  A vector of the unit-level continuous score. Conditional Average Treatment Effect is one possible measure.

Y  A vector of the outcome variable of interest for each sample.

ngates  The number of groups to separate the data into. The groups are determined by tau. Default is 5.

Value

A list that contains the following items:

gate  The estimated vector of GATEs of length ngates arranged in order of increasing tau.

sd  The estimated vector of standard deviation of GATEs.

Author(s)

Michael Lingzhi Li, Operations Research Center, Massachusetts Institute of Technology <mlli@mit.edu>, http://mlli.mit.edu;

References

Imai and Li (2022). “Statistical Inference for Heterogeneous Treatment Effects Discovered by Generic Machine Learning in Randomized Experiments”.

Examples

T = c(1,0,1,0,1,0,1,0)
tau = c(0,0.1,0.2,0.3,0.4,0.5,0.6,0.7)
Y = c(4,5,0,2,4,1,-4,3)
gatelist <- GATE(T,tau,Y,ngates=5)
gatelist$gate

GATEcv  Estimation of the Grouped Average Treatment Effects (GATEs) in Randomized Experiments Under Cross Validation

Description

This function estimates the Grouped Average Treatment Effects (GATEs) under cross-validation where the groups are determined by a continuous score. The details of the methods for this design are given in Imai and Li (2022).

Usage

GATEcv(T, tau, Y, ind, ngates = 5)
**Arguments**

- **T**: A vector of the unit-level binary treatment receipt variable for each sample.
- **tau**: A vector of the unit-level continuous score. Conditional Average Treatment Effect is one possible measure.
- **Y**: A vector of the outcome variable of interest for each sample.
- **ind**: A vector of integers (between 1 and number of folds inclusive) indicating which testing set does each sample belong to.
- **ngates**: The number of groups to separate the data into. The groups are determined by tau. Default is 5.

**Value**

A list that contains the following items:

- **gate**: The estimated vector of GATEs under cross-validation of length ngates arranged in order of increasing tau.
- **sd**: The estimated vector of standard deviation of GATEs under cross-validation.

**Author(s)**

Michael Lingzhi Li, Operations Research Center, Massachusetts Institute of Technology <mlli@mit.edu>, [http://mlli.mit.edu](http://mlli.mit.edu);

**References**

Imai and Li (2022). “Statistical Inference for Heterogeneous Treatment Effects Discovered by Generic Machine Learning in Randomized Experiments”.

**Examples**

```r
T = c(1,0,1,0,1,0,1,0)
tau = matrix(c(0,0.1,0.2,0.3,0.4,0.5,0.6,0.7,-0.5,-0.3,-0.1,0.1,0.3,0.5,0.7,0.9),nrow = 8, ncol = 2)
Y = c(4,5,0,2,4,1,-4,3)
ind = c(rep(1,4),rep(2,4))
gatelist <- GATEcv(T, tau, Y, ind, ngates = 2)
gatelist$gate
gatelist$sd
```

**Description**

This function calculates statistics related to the test of heterogeneous treatment effects across groups.
Usage
het.test(T, tau, Y, ngates = 5)

Arguments
- **T**: A vector of the unit-level binary treatment receipt variable for each sample.
- **tau**: A vector of the unit-level continuous score. Conditional Average Treatment Effect is one possible measure.
- **Y**: A vector of the outcome variable of interest for each sample.
- **ngates**: The number of groups to separate the data into. The groups are determined by tau. Default is 5.

Details
The details of the methods for this design are given in Imai and Li (2022).

Value
A list that contains the following items:
- **stat**: The estimated statistic for the test of heterogeneity.
- **pval**: The p-value of the null hypothesis (that the treatment effects are homogeneous)

Author(s)
Michael Lingzhi Li, Operations Research Center, Massachusetts Institute of Technology <mlli@mit.edu>, http://mlli.mit.edu;

References
Imai and Li (2022). “Statistical Inference for Heterogeneous Treatment Effects Discovered by Generic Machine Learning in Randomized Experiments”.

Examples
```R
T = c(1,0,1,0,1,0,1,0)
tau = c(0,0.1,0.2,0.3,0.4,0.5,0.6,0.7)
Y = c(4,5,0,2,4,1,-4,3)
hettestlist <- het.test(T,tau,Y,ngates=5)
hettestlist$stat
hettestlist$pval
```
**Description**

This function calculates statistics related to the test of heterogeneous treatment effects across groups under cross-validation.

**Usage**

```r
hetcv.test(T, tau, Y, ind, ngates = 5)
```

**Arguments**

- `T`: A vector of the unit-level binary treatment receipt variable for each sample.
- `tau`: A vector of the unit-level continuous score. Conditional Average Treatment Effect is one possible measure.
- `Y`: A vector of the outcome variable of interest for each sample.
- `ind`: A vector of integers (between 1 and number of folds inclusive) indicating which testing set does each sample belong to.
- `ngates`: The number of groups to separate the data into. The groups are determined by `tau`. Default is 5.

**Details**

The details of the methods for this design are given in Imai and Li (2022).

**Value**

A list that contains the following items:

- `stat`: The estimated statistic for the test of heterogeneity under cross-validation.
- `pval`: The p-value of the null hypothesis (that the treatment effects are homogeneous)

**Author(s)**

Michael Lingzhi Li, Operations Research Center, Massachusetts Institute of Technology <mlli@mit.edu>,
http://mlli.mit.edu;

**References**

Imai and Li (2022). “Statistical Inference for Heterogeneous Treatment Effects Discovered by Generic Machine Learning in Randomized Experiments”,

Examples

```r
T = c(1,0,1,0,1,0,1,0)
tau = matrix(c(0,0.1,0.2,0.3,0.4,0.5,0.6,0.7,-0.5,-0.3,-0.1,0.1,0.3,0.5,0.7,0.9), nrow = 8, ncol = 2)
Y = c(4,5,0,2,4,1,-4,3)
ind = c(rep(1,4), rep(2,4))
hettestlist <- hetcv.test(T, tau, Y, ind, ngates = 2)
hettestlist$stat
hettestlist$pval
```

**PAPD**

*Estimation of the Population Average Prescription Difference in Randomized Experiments*

**Description**

This function estimates the Population Average Prescription Difference with a budget constraint. The details of the methods for this design are given in Imai and Li (2019).

**Usage**

```r
PAPD(T, Thatfp, Thatgp, Y, plim, centered = TRUE)
```

**Arguments**

- **T**
  A vector of the unit-level binary treatment receipt variable for each sample.

- **Thatfp**
  A vector of the unit-level binary treatment that would have been assigned by the first individualized treatment rule. Please ensure that the percentage of treatment units of That is lower than the budget constraint.

- **Thatgp**
  A vector of the unit-level binary treatment that would have been assigned by the second individualized treatment rule. Please ensure that the percentage of treatment units of That is lower than the budget constraint.

- **Y**
  A vector of the outcome variable of interest for each sample.

- **plim**
  The maximum percentage of population that can be treated under the budget constraint. Should be a decimal between 0 and 1.

- **centered**
  If TRUE, the outcome variables would be centered before processing. This minimizes the variance of the estimator. Default is TRUE.

**Value**

A list that contains the following items:

- **papd**
  The estimated Population Average Prescription Difference

- **sd**
  The estimated standard deviation of PAPD.
Author(s)
Michael Lingzhi Li, Operations Research Center, Massachusetts Institute of Technology <mlli@mit.edu>, http://mlli.mit.edu;

References
Imai and Li (2019). “Experimental Evaluation of Individualized Treatment Rules”,

Examples

```r
T = c(1,0,1,0,1,0,1,0)
That = c(0,1,1,0,0,1,1,0)
That2 = c(1,0,0,1,1,0,0,1)
Y = c(4,5,0,2,4,1,-4,3)
papdlist <- PAPD(T,That,That2,Y,plim = 0.5)
papdlist$papd
papdlist$sd
```

PAPDcv

Estimation of the Population Average Prescription Difference in Randomized Experiments Under Cross Validation

Description
This function estimates the Population Average Prescription Difference. The details of the methods for this design are given in Imai and Li (2019).

Usage

```r
PAPDcv(T, Thatfp, Thatgp, Y, ind, plim, centered = TRUE)
```

Arguments

- **T** A vector of the unit-level binary treatment receipt variable for each sample.
- **Thatfp** A matrix where the i-th column is the unit-level binary treatment that would have been assigned by the first individualized treatment rule generated in the i-th fold. Please ensure that the percentage of treatment units of That is lower than the budget constraint.
- **Thatgp** A matrix where the i-th column is the unit-level binary treatment that would have been assigned by the second individualized treatment rule generated in the i-th fold. Please ensure that the percentage of treatment units of That is lower than the budget constraint.
- **Y** The outcome variable of interest.
- **ind** A vector of integers (between 1 and number of folds inclusive) indicating which testing set does each sample belong to.
PAPE

plim The maximum percentage of population that can be treated under the budget constraint. Should be a decimal between 0 and 1.
centered If TRUE, the outcome variables would be centered before processing. This minimizes the variance of the estimator. Default is TRUE.

Value

A list that contains the following items:
papd The estimated Population Average Prescription Difference.
sd The estimated standard deviation of PAPD.

Author(s)

Michael Lingzhi Li, Operations Research Center, Massachusetts Institute of Technology <mlli@mit.edu>, http://mlli.mit.edu;

References

Imai and Li (2019). “Experimental Evaluation of Individualized Treatment Rules”,

Examples

```
T = c(1,0,1,0,1,0,1,0)
That = matrix(c(0,1,1,0,1,0,1,0,1,0,1,0,1,0,1,0), nrow = 8, ncol = 2)
That2 = matrix(c(0,0,1,1,0,0,1,1,1,1,0,0,1,1,0,0), nrow = 8, ncol = 2)
Y = c(4,5,0,2,4,1,-4,3)
ind = c(rep(1,4),rep(2,4))
papdlist <- PAPDcv(T, That, That2, Y, ind, plim = 0.5)
papdlist$papd
papdlist$sd
```

Description

This function estimates the Population Average Prescription Effect with and without a budget constraint. The details of the methods for this design are given in Imai and Li (2019).

Usage

```
PAPE(T, That, Y, plim = NA, centered = TRUE)
```
Arguments

T
A vector of the unit-level binary treatment receipt variable for each sample.

That
A vector of the unit-level binary treatment that would have been assigned by
the individualized treatment rule. If plim is specified, please ensure that the
percentage of treatment units of That is lower than the budget constraint.

Y
A vector of the outcome variable of interest for each sample.

plim
The maximum percentage of population that can be treated under the budget
constraint. Should be a decimal between 0 and 1. Default is NA which assumes
no budget constraint.

centered
If TRUE, the outcome variables would be centered before processing. This mini-
mizes the variance of the estimator. Default is TRUE.

Value

A list that contains the following items:

pape
The estimated Population Average Prescription Effect.

sd
The estimated standard deviation of PAPE.

Author(s)

Michael Lingzhi Li, Operations Research Center, Massachusetts Institute of Technology <mlli@mit.edu>,
http://mlli.mit.edu;

References


Examples

T = c(1,0,1,0,1,0,1,0)
That = c(0,1,1,0,0,1,1,0)
Y = c(4,5,0,2,4,1,-4,3)
papelist <- PAPE(T,That,Y)
papelist$pape
papelist$sd

Description

This function estimates the Population Average Prescription Effect with and without a budget con-
straint. The details of the methods for this design are given in Imai and Li (2019).
Usage

`PAPEcv(T, That, Y, ind, plim = NA, centered = TRUE)`

Arguments

T
A vector of the unit-level binary treatment receipt variable for each sample.

That
A matrix where the i-th column is the unit-level binary treatment that would have been assigned by the individualized treatment rule generated in the i-th fold. If `plim` is specified, please ensure that the percentage of treatment units of `That` is lower than the budget constraint.

Y
The outcome variable of interest.

ind
A vector of integers (between 1 and number of folds inclusive) indicating which testing set does each sample belong to.

plim
The maximum percentage of population that can be treated under the budget constraint. Should be a decimal between 0 and 1. Default is NA which assumes no budget constraint.

centered
If TRUE, the outcome variables would be centered before processing. This minimizes the variance of the estimator. Default is TRUE.

Value

A list that contains the following items:

pape
The estimated Population Average Prescription Effect.

sd
The estimated standard deviation of PAPE.

Author(s)

Michael Lingzhi Li, Operations Research Center, Massachusetts Institute of Technology <mlli@mit.edu>, http://mlli.mit.edu;

References


Examples

T = c(1,0,1,0,1,0,1,0)
That = matrix(c(0,1,1,0,1,0,1,0,0,1,0,1,0,1,0,0,1), nrow = 8, ncol = 2)
Y = c(4,5,0,2,4,1,-4,3)
ind = c(rep(1,4),rep(2,4))
papelist <- PAPEcv(T, That, Y, ind)
papelist$pape
papelist$sd
Description

This function estimates the Population Average Value. The details of the methods for this design are given in Imai and Li (2019).

Usage

`PAV(T, That, Y, centered = TRUE)`

Arguments

- `T` A vector of the unit-level binary treatment receipt variable for each sample.
- `That` A vector of the unit-level binary treatment that would have been assigned by the individualized treatment rule. If `plim` is specified, please ensure that the percentage of treatment units of `That` is lower than the budget constraint.
- `Y` A vector of the outcome variable of interest for each sample.
- `centered` If `TRUE`, the outcome variables would be centered before processing. This minimizes the variance of the estimator. Default is `TRUE`.

Value

A list that contains the following items:

- `pav` The estimated Population Average Value.
- `sd` The estimated standard deviation of PAV.

Author(s)

Michael Lingzhi Li, Operations Research Center, Massachusetts Institute of Technology <mlli@mit.edu>, [http://mlli.mit.edu](http://mlli.mit.edu);

References


Examples

```r
t = c(1,0,1,0,1,0,1,0)
That = c(0,1,1,0,0,1,1,0)
y = c(4,5,0,2,4,1,-4,3)
pavlist <- PAV(t,That,y)
pavlist$pav
pavlist$sd
```
PAVcv

Estimation of the Population Average Value in Randomized Experiments Under Cross Validation

Description

This function estimates the Population Average Value. The details of the methods for this design are given in Imai and Li (2019).

Usage

PAVcv(T, That, Y, ind, centered = TRUE)

Arguments

T
A vector of the unit-level binary treatment receipt variable for each sample.

That
A matrix where the i-th column is the unit-level binary treatment that would have been assigned by the individualized treatment rule generated in the i-th fold. If plim is specified, please ensure that the percentage of treatment units of That is lower than the budget constraint.

Y
The outcome variable of interest.

ind
A vector of integers (between 1 and number of folds inclusive) indicating which testing set does each sample belong to.

centered
If TRUE, the outcome variables would be centered before processing. This minimizes the variance of the estimator. Default is TRUE.

Value

A list that contains the following items:

pav
The estimated Population Average Value.

sd
The estimated standard deviation of PAV.

Author(s)

Michael Lingzhi Li, Operations Research Center, Massachusetts Institute of Technology <mlli@mit.edu>, http://mlli.mit.edu;

References

Imai and Li (2019). “Experimental Evaluation of Individualized Treatment Rules”,

Examples

\[ T = c(1,0,1,0,1,0,1,0) \]
\[ \text{That} = \text{matrix}(c(0,1,1,0,0,1,0,0,0,0,1,0,1,0,0,1), \text{nrow} = 8, \text{ncol} = 2) \]
\[ Y = c(4,5,0,2,4,1,-4,3) \]
\[ \text{ind} = \text{c(rep}(1,4),\text{rep}(2,4)) \]
\[ \text{pavlist} \leftarrow \text{PAVcv}(T, \text{That}, Y, \text{ind}) \]
\[ \text{pavlist}\$\text{pav} \]
\[ \text{pavlist}\$\text{sd} \]
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