Package 'evalITR'

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Title Evaluating Individualized Treatment Rules

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Depends stats, MASS (>= 7.0), quadprog (>= 1.0), Matrix (>= 1.0), dplyr (>= 1.0), R (>= 3.5.0)

Description Provides various statistical methods for evaluating Individualized Treatment Rules under randomized data. The provided metrics include Population Average Value (PAV), Population Average Prescription Effect (PAPE), Area Under Prescription Effect Curve (AUPEC). It also provides the tools to analyze Individualized Treatment Rules under budget constraints. Detailed reference in Imai and Li (2019) <arXiv:1905.05389>.

License GPL (>= 2)

URL https://github.com/MichaelLLi/evalITR

BugReports https://github.com/MichaelLLi/evalITR/issues

RoxygenNote 7.1.2

Encoding UTF-8

Suggests testthat

NeedsCompilation no

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R topics documented:

AUPEC *Estimation of the Area Under Prescription Evaluation Curve (AUPEC) in Randomized Experiments*

Description

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

Usage

```
AUPEC(T, tau, Y, centered = 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.
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 Area Under Prescription Evaluation Curve
sd	The estimated standard deviation of AUPEC.
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.

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)
aupeclist <- AUPEC(T,tau,Y)
aupeclist$aupec
aupeclist$sd
aupeclist$vec
```

AUPECcv *Estimation of the Area Under Prescription Evaluation Curve (AUPEC) in Randomized Experiments Under Cross Validation*

Description

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

Usage

```
AUPECcv(T, tau, Y, ind, centered = TRUE)
```

Arguments

T	A vector of the unit-level binary treatment receipt variable for each sample.
tau	A matrix where the ith column is the unit-level continuous score for treatment assignment generated in the ith 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.

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 = 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))
aupeclist <- AUPECcv(T, tau, Y, ind)
aupeclist$aupec
aupeclist$sd
```

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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

```
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

```
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.

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$gate
gatelist$sd
```

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;

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))
gatelist <- GATEcv(T, tau, Y, ind, ngates = 2)
gatelist$gate
gatelist$sd
```

---

het.test *The Heterogeneity Test for Grouped Average Treatment Effects (GATEs) in Randomized Experiments*

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

```
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
```

`hetcv.test` *The Heterogeneity Test for Grouped Average Treatment Effects (GATEs) under Cross Validation in Randomized Experiments*

Description

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

Usage

```
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

```
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

```
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

```
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

```
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 ith column is the unit-level binary treatment that would have been assigned by the first individualized treatment rule generated in the ith fold. Please ensure that the percentage of treatment units of That is lower than the budget constraint.
Thatgp	A matrix where the ith column is the unit-level binary treatment that would have been assigned by the second individualized treatment rule generated in the ith 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.

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(0,1,1,0,0,1,1,0,1,0,0,1,1,0,0,1), 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
```

PAPE *Estimation of the Population Average Prescription Effect in Randomized Experiments*

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 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

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

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
```

PAPEcv *Estimation of the Population Average Prescription Effect in Randomized Experiments Under Cross Validation*

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

```
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 ith column is the unit-level binary treatment that would have been assigned by the individualized treatment rule generated in the ith 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

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

Examples

```
T = c(1,0,1,0,1,0,1,0)
That = matrix(c(0,1,1,0,0,1,1,0,1,0,0,1,1,0,0,1), 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
```

PAV *Estimation of the Population Average Value in Randomized Experiments*

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;

References

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

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)
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 ith column is the unit-level binary treatment that would have been assigned by the individualized treatment rule generated in the ith 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)
That = matrix(c(0,1,1,0,0,1,1,0,1,0,0,1,1,0,0,1), nrow = 8, ncol = 2)
Y = c(4,5,0,2,4,1,-4,3)
ind = c(rep(1,4),rep(2,4))
pavlist <- PAVcv(T, That, Y, ind)
pavlist$pav
pavlist$sd
```

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