

# Package ‘evalITR’

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**Version** 0.2.2

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**Title** Evaluating Individualized Treatment Rules

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**Depends** stats, 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](https://arxiv.org/abs/1905.05389)>.

**License** GPL (>= 2)

**URL** <https://github.com/MichaelLLi/evalITR>

**BugReports** <https://github.com/MichaelLLi/evalITR/issues>

**RoxygenNote** 7.1.1

**Suggests** testthat

**NeedsCompilation** no

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**Repository** CRAN

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## R topics documented:

AUPEC	2
AUPECcv	3
PAPD	4
PAPDcv	5
PAPE	6
PAPEcv	7
PAV	9
PAVcv	10

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

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### 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
```

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AUPECcv	<i>Estimation of the Area Under Prescription Evaluation Curve (AU-PEC) in Randomized Experiments Under Cross Validation</i>
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**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 <i>i</i> th column is the unit-level continuous score for treatment assignment generated in the <i>i</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.

**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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PAPD

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

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## 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*

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**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 <i>i</i> th column is the unit-level binary treatment that would have been assigned by the first individualized treatment rule generated in the <i>i</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>i</i> th column is the unit-level binary treatment that would have been assigned by the second individualized treatment rule generated in the <i>i</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.

<code>plim</code>	The maximum percentage of population that can be treated under the budget constraint. Should be a decimal between 0 and 1.
<code>centered</code>	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:

<code>papd</code>	The estimated Population Average Prescription Difference.
<code>sd</code>	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
```

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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
```

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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 <i>i</i> th column is the unit-level binary treatment that would have been assigned by the individualized treatment rule generated in the <i>i</i> th fold. If <i>plim</i> is specified, please ensure that the percentage of treatment units of <i>That</i> 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
```



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PAV	<i>Estimation of the Population Average Value in Randomized Experiments</i>
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### 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 <code>plim</code> is specified, please ensure that the percentage of treatment units of <code>That</code> 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 $i$ 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 <code>plim</code> is specified, please ensure that the percentage of treatment units of <code>That</code> 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
```

# Index

## \* **evaluation**

- AUPEC, [2](#)
- AUPECcv, [3](#)
- PAPD, [4](#)
- PAPDcv, [5](#)
- PAPE, [6](#)
- PAPEcv, [7](#)
- PAV, [9](#)
- PAVcv, [10](#)

- AUPEC, [2](#)
- AUPECcv, [3](#)

- PAPD, [4](#)
- PAPDcv, [5](#)
- PAPE, [6](#)
- PAPEcv, [7](#)
- PAV, [9](#)
- PAVcv, [10](#)