

# Package ‘tmle.npvi’

May 22, 2015

**Type** Package

**Title** Targeted Learning of a NP Importance of a Continuous Exposure

**Version** 0.10.0

**Date** 2015-05-13

**Author** Antoine Chambaz, Pierre Neuvial

**Maintainer** Pierre Neuvial <pierre.neuvial@genopole.cnrs.fr>

**Description** Targeted minimum loss estimation (TMLE) of a non-parametric variable importance measure of a continuous exposure 'X' on an outcome 'Y', taking baseline covariates 'W' into account.

**License** GPL

**LazyLoad** yes

**LazyData** yes

**Depends** R (>= 2.10), R.utils (>= 1.4.1)

**Imports** R.methodsS3, R.oo, MASS, Matrix, geometry

**Suggests** SuperLearner (>= 2.0), e1071 (>= 1.5.24), randomForest (>= 4.5-35), polspline (>= 1.1.4), gam (>= 1.03), knitr

**VignetteBuilder** knitr

**NeedsCompilation** no

**Repository** CRAN

**Date/Publication** 2015-05-22 18:59:02

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---

as.character.NPVI      *Returns a Description*

---

**Description**

Returns a short string describing the NPVI object.

**Usage**

```
## S3 method for class 'NPVI'
as.character(x, ...)
```

**Arguments**

x                      An object of class TMLE.NPVI.  
 ...                    Not used.

**Value**

A character string summarizing the content of the object. The summary contains:

- The sample size of the data set involved in the TMLE procedure.
- The value of the TMLE and its estimated standard error.
- A reminder of the tuning of the stopping criteria, and a report on the convergence of the TMLE procedure (see [tmle.npvi](#)).
- A confidence interval with default level of 95% (the level can be changed by using [setConfLevel](#)).
- The  $p$ -value of the two-sided test of “ $\Psi(P_0) = 0$ ”.
- The  $p$ -value of the two-sided test of “ $\Psi(P_0) = \Phi(P_0)$ ”, with the estimated value of  $\Phi(P_0)$ .

**Author(s)**

Antoine Chambaz, Pierre Neuvial

**See Also**

[tmle.npvi](#)

**Examples**

```
FALSE
```

---

extractW

*Extracts W Columns from Matrix of Observations*

---

**Description**

Extracts the  $W$  column(s) from a `matrix` of observations.

**Usage**

```
extractW(mat)
```

**Arguments**

`mat` A `matrix` of observations, as the `obs` argument of function [tmle.npvi](#).

**Details**

Mainly for internal use.

**Value**

The `matrix` extracted from `mat` by removing the two `X` and `Y` columns.

**Author(s)**

Antoine Chambaz, Pierre Neuvial

---

extractXW	<i>Removes the Y Column from Matrix of Observations</i>
-----------	---

---

**Description**

Removes the Y column from a matrix of observations.

**Usage**

```
extractXW(mat)
```

**Arguments**

mat                    A matrix of observations, as the obs argument of function [tmle.npvi](#).

**Details**

Mainly for internal use.

**Value**

The matrix extracted from mat by removing the Y column in such a way that the first column is X.

**Author(s)**

Antoine Chambaz, Pierre Neuvial

---

getHistory.NPVI	<i>Returns History of TMLE Procedure</i>
-----------------	--

---

**Description**

Returns the 'history' of the TMLE procedure.

**Usage**

```
## S3 method for class 'NPVI'  
getHistory(this, ...)
```

**Arguments**

this                    An object of class TMLE.NPVI.  
...                      Not used.

**Value**

Returns a numeric matrix which encapsulates a summary of the TMLE procedure. If  $k$  successive updates were performed, then the matrix has either  $k + 1$  rows (if `cleverCovTheta` was set to `FALSE` in the call to `tmle.npvi`) or  $2k+1$  rows (otherwise). The matrix has 14 columns:

- "eps", values of the unique fluctuation parameter (if `cleverCovTheta` was set to `FALSE` in the call to `tmle.npvi`), or values of the parameter involved in the fluctuation of the joint distribution of  $(X, W)$  during each update (otherwise).
- "lli", increases in likelihood yielded by each update (if `cleverCovTheta` was set to `FALSE` in the call to `tmle.npvi`), or increases in likelihood yielded by the fluctuation of the joint distribution of  $(X, W)$  during each update (otherwise).
- "mic1", empirical means of the first component of the efficient influence curve at each step of the TMLE procedure.
- "epsT", values of the fluctuation parameter involved in the fluctuation of the conditional distribution of  $Y$  given  $(X, W)$  during each update (if `cleverCovTheta` was set to `TRUE` in the call to `tmle.npvi`), or NA (otherwise).
- "lliT", successive increases in likelihood yielded by the fluctuation of the conditional distribution of  $Y$  given  $(X, W)$  during each update (if `cleverCovTheta` was set to `TRUE` in the call to `tmle.npvi`), or NA (otherwise).
- "mic2", empirical means of the second component of the efficient influence curve at each step of the TMLE procedure.
- "psi", increasingly targeted estimators  $\Psi(P_n^k)$  of the parameter of interest. The last one is the TMLE. Their computation involves simulation of  $B$  iid copies of  $(X, W)$  under  $P_n^k$ .
- "psi.sd", estimated standard deviations of the increasingly targeted estimators of the parameter of interest. The last one corresponds to the TMLE. The computation involves the same  $B$  iid copies of  $(X, W)$  as above.
- "psiPn", same as "psi" except that the \*observed\*  $(X_i, W_i)$  are used instead of simulated copies drawn from  $P_n^k$ . Of course, "psi" must be favored.
- "psiPn.sd", same as "psi.sd" except that the \*observed\*  $(X_i, W_i)$  are used instead of simulated copies drawn from  $P_n^k$ . Of course, "psi.sd" must be favored.
- "mic", empirical means of the efficient influence curve at each step of the TMLE procedure. This column is the sum of the "mic1" and "mic2" columns.
- "div", total variation distances between each pair of successive distributions constructed in the course of the TMLE procedure.
- "sic", estimated standard deviations of the efficient influence curve at each step of the TMLE procedure.
- "phi", non-parametric substitution estimator of  $\phi = \Phi(P)$  where

$$\Phi(P) = \frac{E_P[f(X)Y]}{E_P[f(X)^2]},$$

with  $P$  the distribution of the random vector  $(W, X, Y)$ . The alternative parameter  $\phi$  should be interpreted as the counterpart of  $\psi$  which neglects  $W$ .

- "sicAlt", estimated standard deviations of the efficient influence curve of  $\Psi - \Phi$  at each step of the TMLE procedure.

**Author(s)**

Antoine Chambaz, Pierre Neuvial

**See Also**

tmle.npvi

**Examples**

FALSE

---

getLightFit

*Makes Lighter Fitted Object*

---

**Description**

Makes a lighter version of a fitted object by removing elements containing data.

**Usage**

```
getLightFit(fit)
```

**Arguments**

`fit`            A fitted object.

**Details**

Most of the space used by a fitted object is not necessary for prediction. This concerns, for instance, the "residuals", "effects", "fitted.values", and "model" entries of a linear model fitted by `lm`. These entries can thus be removed from the object without affecting the model predictions. This function is currently only implemented for fitted objects that derive from class `'lm'` or `'rpart'`. It is mainly for internal use.

**Value**

Returns the same object as the input without the entries that contain data.

**Author(s)**

Antoine Chambaz, Pierre Neuvial

---

getObs.NPVI	<i>Retrieves the Observations</i>
-------------	-----------------------------------

---

**Description**

Retrieves the matrix of observations involved in the TMLE procedure.

**Usage**

```
## S3 method for class 'NPVI'  
getObs(this, tabulate, ...)
```

**Arguments**

<code>this</code>	An object of class <code>TMLE.NPVI</code> .
<code>tabulate</code>	A logical, to specify whether it is the original data set that is retrieved (if <code>FALSE</code> ) or a tabulated version of it (otherwise), for internal use only. If <code>tabulate</code> is missing then the value attached to the input object is used.
<code>...</code>	Not used.

**Value**

Either the original data set involved in the TMLE procedure or a tabulated version of it.

**Author(s)**

Antoine Chambaz, Pierre Neuvial

**See Also**

`tmle.npvi`

**Examples**

```
FALSE
```

---

getPsi.NPVI                      *Returns Current Estimator*

---

### Description

Returns the current value of the estimator.

### Usage

```
## S3 method for class 'NPVI'
getPsi(this, ...)
```

### Arguments

this	An object of class TMLE.NPVI.
...	Not used.

### Value

Retrieves the current value of the estimator  $\Psi(P_n^k)$  of the parameter of interest. Its computation involves simulation of a large number of iid copies of  $(X, W)$  under  $P_n^k$ .

### Author(s)

Antoine Chambaz, Pierre Neuvial

### See Also

tmle.npvi, getHistory, getPsiSd

### Examples

```
FALSE
```

---

getPsiSd.NPVI                      *Returns Current Estimated Standard Deviation of the Estimator*

---

### Description

Returns the current value of the estimated standard deviation of the current estimator.

### Usage

```
## S3 method for class 'NPVI'
getPsiSd(this, ...)
```



**Arguments**

`this`            An object of class `TMLE.NPVI`.  
`...`            Not used.

**Value**

Retrieves the estimated standard deviation of the current estimator  $\Psi(P_n^k)$  of the parameter of interest. Its computation involves simulation of a large number of iid copies of  $(X, W)$  under  $P_n^k$ .

**Author(s)**

Antoine Chambaz, Pierre Neuvial

**See Also**

`tmle.npvi`, `getHistory`, `getPsi`

**Examples**

```
FALSE
```

---

`getPValue.matrix`            *Calculates a p-value from a matrix object of type 'history'*

---

**Description**

Calculates a p-value from a matrix object of type 'history'

**Usage**

```
## S3 method for class 'matrix'
getPValue(this, wrt.phi = TRUE, nobs, ...)
```

**Arguments**

`this`            The history of a TMLE procedure.  
`wrt.phi`        A logical equal to `TRUE` by default, which means that  $psi_n$  is compared with  $phi_n$ . Otherwise,  $psi_n$  is compared with 0.  
`nobs`         An integer, the associated number of observations.  
`...`         Not used.

**Value**

Returns the p-value of the two-sided test of " $Psi(P_0) = Phi(P_0)$ " of " $Psi(P_0) = 0$ ", according to the value of `wrt.phi`.

**Author(s)**

Antoine Chambaz, Pierre Neuvial

**See Also**

tmle.npvi, getHistory.NPVI, as.character.NPVI

**Examples**

FALSE

---

getPValue.NPVI	<i>Calculates a p-value from a NPVI object</i>
----------------	--

---

**Description**

Calculates a p-value from a NPVI object

**Usage**

```
## S3 method for class 'NPVI'
getPValue(this, wrt.phi = TRUE, ...)
```

**Arguments**

<code>this</code>	An object of class <code>TMLE.NPVI</code> .
<code>wrt.phi</code>	A logical equal to <code>TRUE</code> by default, which means that $psi_n$ is compared with $phi_n$ . Otherwise, $psi_n$ is compared with 0.
<code>...</code>	Not used.

**Value**

Returns the p-value of the two-sided test of “ $Psi(P_0) = Phi(P_0)$ ” or “ $Psi(P_0) = 0$ ”, according to the value of `wrt.phi`.

**Author(s)**

Antoine Chambaz, Pierre Neuvial

**See Also**

tmle.npvi, getHistory, as.character.NPVI, getPValue.matrix

**Examples**

FALSE

---

getSample

*Generates Simulated Data*


---

**Description**

Generates a run of simulated observations of the form  $(W, X, Y)$  to investigate the "effect" of  $X$  on  $Y$  taking  $W$  into account.

**Usage**

```
getSample(n, 0, lambda0, p = rep(1/3, 3), omega = rep(1/2, 3),
  Sigma1 = matrix(c(1, 1/sqrt(2), 1/sqrt(2), 1), 2, 2), sigma2 = omega[2]/5,
  Sigma3 = Sigma1, f = identity, verbose = FALSE)
```

**Arguments**

n	An integer, the number of observations to be generated.
0	A 3x3 numeric matrix or data.frame. Rows are 3 baseline observations used as "class centers" for the simulation. Columns are: <ul style="list-style-type: none"> <li>• <math>W</math>, baseline covariate (e.g. DNA methylation), or "confounder" in a causal model.</li> <li>• <math>X</math>, continuous exposure variable (e.g. DNA copy number), or "cause" in a causal model, with a reference value <math>x_0</math> equal to 0[2, "X"].</li> <li>• <math>Y</math>, outcome variable (e.g. gene expression level), or "effect" in a causal model.</li> </ul>
lambda0	A function that encodes the relationship between $W$ and $Y$ in observations with levels of $X$ equal to the reference value $x_0$ .
p	A vector of length 3 whose entries sum to 1. Entry $p[k]$ is the probability that each observation belong to class $k$ with class center 0[k, ]. Defaults to rep(1/3, 3).
omega	A vector of length 3 with positive entries. Entry $\omega[k]$ is the standard deviation of $W$ in class $k$ (on a logit scale). Defaults to rep(1/2, 3).
Sigma1	A 2x2 covariance matrix of the random vector $(X, Y)$ in class $k=1$ , assumed to be bivariate Gaussian with mean 0[1, c("X", "Y")]. Defaults to matrix(c(1, 1/sqrt(2), 1/sqrt(2), 1/sqrt(2)), 2, 2).
sigma2	A positive numeric, the variance of the random variable $Y$ in class $k=2$ , assumed to be univariate Gaussian with mean 0[2, "Y"]. Defaults to omega[2]/5.
Sigma3	A 2x2 covariance matrix of the random vector $(X, Y)$ in class $k=3$ , assumed to be bivariate Gaussian with mean 0[3, c("X", "Y")]. Defaults to Sigma1.
f	A function involved in the definition of the parameter of interest $\psi$ , which must satisfy $f(0) = 0$ (see Details). Defaults to identity.
verbose	Prescribes the amount of information output by the function. Defaults to FALSE.

## Details

The parameter of interest is defined as  $\psi = \Psi(P)$  with

$$\Psi(P) = \frac{E_P[f(X - x_0) * (\theta(X, W) - \theta(x_0, W))]}{E_P[f(X - x_0)^2]},$$

with  $P$  the distribution of the random vector  $(W, X, Y)$ ,  $\theta(X, W) = E_P[Y|X, W]$ ,  $x_0$  the reference value for  $X$ , and  $f$  a user-supplied function such that  $f(0) = 0$  (e.g.,  $f = \textit{identity}$ , the default value). The value  $\psi$  is obtained using the **known**  $\theta$  and the joint empirical distribution of  $(X, W)$  based on the same run of observations as in `obs`. Seeing  $W, X, Y$  as DNA methylation, DNA copy number and gene expression, respectively, the simulation scheme implements the following constraints:

- There are two or three copy number classes: normal regions ( $k=2$ ), and regions of copy number gains and/or losses ( $k=1$  and/or  $k=3$ ).
- In normal regions, gene expression levels are negatively correlated with DNA methylation.
- In regions of copy number alteration, copy number and expression are positively correlated.

## Value

Returns a list with the following tags:

<code>obs</code>	A matrix of $n$ observations. The $c(W, X, Y)$ columns of <code>obs</code> have the same interpretation as the columns of the input argument <code>O</code> .
<code>psi</code>	A numeric, approximated value of the true parameter $\psi$ obtained using the <b>known</b> $\theta$ and the joint empirical distribution of $(X, W)$ based on the same run of observations as in <code>obs</code> . The larger the sample size, the more accurate the approximation.
<code>g</code>	A function, the <b>known</b> positive conditional probability $P(X = x_0 W)$ .
<code>mu</code>	A function, the <b>known</b> conditional expectation $E_P(X W)$ .
<code>muAux</code>	A function, the <b>known</b> conditional expectation $E_P(X X \neq x_0, W)$ .
<code>theta</code>	A function, the <b>known</b> conditional expectation $E_P(Y X, W)$ .
<code>theta0</code>	A function, the <b>known</b> conditional expectation $E_P(Y X = x_0, W)$ .
<code>sigma2</code>	A positive numeric, the <b>known</b> expectation $E_P(f(X - x_0)^2)$ .
<code>effIC</code>	A function, the <b>known</b> efficient influence curve of the functional $\Psi$ at $P$ , <b>assuming</b> that the reference value $x_0 = 0$ .
<code>varIC</code>	A positive numeric, approximated value of the variance of the efficient influence curve of the functional $\Psi$ at $P$ and evaluated at $O$ , obtained using the same run of observations as in <code>obs</code> . The larger the sample size, the more accurate the approximation.

## Author(s)

Antoine Chambaz, Pierre Neuvial

## References

Chambaz, A., Neuvial, P., & van der Laan, M. J. (2012). Estimation of a non-parametric variable importance measure of a continuous exposure. *Electronic journal of statistics*, 6, 1059–1099.

## Examples

```
## Parameters for the simulation (case 'f=identity')
O <- cbind(W=c(0.05218652, 0.01113460),
           X=c(2.722713, 9.362432),
           Y=c(-0.4569579, 1.2470822))
O <- rbind(NA, O)
lambda0 <- function(W) {-W}
p <- c(0, 1/2, 1/2)
omega <- c(0, 3, 3)
S <- matrix(c(10, 1, 1, 0.5), 2, 2)

## Simulating a data set of 200 i.i.d. observations
sim <- getSample(2e2, 0, lambda0, p=p, omega=omega, sigma2=1, Sigma3=S)
str(sim)

obs <- sim$obs
head(obs)
pairs(obs)

## Adding (dummy) baseline covariates
V <- matrix(runif(3*nrow(obs)), ncol=3)
colnames(V) <- paste("V", 1:3, sep="")
obsV <- cbind(V, obs)
head(obsV)

## True psi and confidence intervals (case 'f=identity')
sim01 <- getSample(1e4, 0, lambda0, p=p, omega=omega, sigma2=1, Sigma3=S)
truePsi1 <- sim01$psi

confInt01 <- truePsi1+c(-1, 1)*qnorm(.975)*sqrt(sim01$varIC/nrow(sim01$obs))
confInt1 <- truePsi1+c(-1, 1)*qnorm(.975)*sqrt(sim01$varIC/nrow(obs))
msg <- "\nCase f=identity:\n"
msg <- c(msg, "\ttrue psi is: ", paste(signif(truePsi1, 3)), "\n")
msg <- c(msg, "\t95%-confidence interval for the approximation is: ",
        paste(signif(confInt01, 3)), "\n")
msg <- c(msg, "\toptimal 95%-confidence interval is: ",
        paste(signif(confInt1, 3)), "\n")
cat(msg)

## True psi and confidence intervals (case 'f=atan')
f2 <- function(x) {1*atan(x/1)}
sim02 <- getSample(1e4, 0, lambda0, p=p, omega=omega, sigma2=1, Sigma3=S, f=f2);
truePsi2 <- sim02$psi;

confInt02 <- truePsi2+c(-1, 1)*qnorm(.975)*sqrt(sim02$varIC/nrow(sim02$obs))
confInt2 <- truePsi2+c(-1, 1)*qnorm(.975)*sqrt(sim02$varIC/nrow(obs))
```

```

msg <- "\nCase f=atan:\n"
msg <- c(msg, "\ttrue psi is: ", paste(signif(truePsi2, 3)), "\n")
msg <- c(msg, "\t95%-confidence interval for the approximation is: ",
        paste(signif(confInt02, 3)), "\n")
msg <- c(msg, "\toptimal 95%-confidence interval is: ",
        paste(signif(confInt2, 3)), "\n")
cat(msg)

```

---

learnCondExpX2givenW *Estimation of Cond. Expect. of  $X^2$  Given  $W$*

---

### Description

Function for the estimation of the conditional expectation of  $X^2$  given  $W$  when flavor is set to "learning".

### Arguments

obs	The matrix of observations, see for instance the obs argument of the function <code>tmle.npvi</code> .
light	A logical, kept for compatibility, which should be set to TRUE (its default value). This requires that the result of each fit be reduced in size (for a faster execution). Currently implemented only for flavor learning.

### Value

Returns the fitted object.

### Author(s)

Antoine Chambaz, Pierre Neuvial

### See Also

`learnG`, `learnMuAux`, `learnTheta`, `learnCondExpXYgivenW`, `learnDevG`, `learnDevMu`, `learnDevTheta`

---

learnCondExpXYgivenW    *Estimation of Cond. Expect. of XY Given W*

---

**Description**

Function for the estimation of the conditional expectation of  $XY$  given  $W$  when flavor is set to "learning".

**Arguments**

obs	The matrix of observations, see for instance the obs argument of the function <code>tmle.npvi</code> .
light	A logical, kept for compatibility, which should be set to TRUE (its default value). This requires that the result of each fit be reduced in size (for a faster execution). Currently implemented only for flavor learning.

**Value**

Returns the fitted object.

**Author(s)**

Antoine Chambaz, Pierre Neuvial

**See Also**

learnG, learnMuAux, learnTheta, learnCondExpX2givenW, learnDevG, learnDevMu, learnDevTheta

---

learnDevG    *Estimation of Cond. Expect. of  $((X==0)-gW)*effIC1$  Given W*

---

**Description**

Function for the estimation of the conditional expectation of  $((X==0)-gW)*effIC1$  given  $W$  when flavor is set to "learning".

**Arguments**

obs	The matrix of observations, see for instance the obs argument of the function <code>tmle.npvi</code> .
effIC1	The vector <code>effIC1</code> of the first component of the efficient influence curve, as currently estimated, evaluated at our observations.
gW	The vector <code>gW</code> of the conditional probability that $X = 0$ given $W$ , as currently estimated, evaluated at our observations.

light	A logical, kept for compatibility, which should be set to TRUE (its default value). This requires that the result of each fit be reduced in size (for a faster execution). Currently implemented only for flavor learning.
verbose	Prescribes the amount of information output by the function. Defaults to FALSE.
...	Additional arguments possibly needed.

**Value**

Returns the fitted object.

**Author(s)**

Antoine Chambaz, Pierre Neuvial

**See Also**

learnG, learnMuAux, learnTheta, learnCondExpX2givenW, learnCondExpXYgivenW, learnDevMu, learnDevTheta

---

learnDevMu

*Estimation of Cond. Expect. of  $(X-\mu_W)*effIC1$  Given  $W$*

---

**Description**

Function for the estimation of the conditional expectation of  $(X-\mu_W)*effIC1$  given  $W$  when flavor is set to "learning".

**Arguments**

obs	The matrix of observations, see for instance the obs argument of the function <code>tmle.npvi</code> .
effIC1	The vector <code>effIC1</code> of the first component of the efficient influence curve, as currently estimated, evaluated at our observations.
muW	The vector <code>muW</code> of the conditional expectation of $X$ given $W$ , as currently estimated, evaluated at our observations.
light	A logical, kept for compatibility, which should be set to TRUE (its default value). This requires that the result of each fit be reduced in size (for a faster execution). Currently implemented only for flavor learning.
verbose	Prescribes the amount of information output by the function. Defaults to FALSE.
...	Additional arguments possibly needed.

**Value**

Returns the fitted object.



**Author(s)**

Antoine Chambaz, Pierre Neuvial

**See Also**

learnG, learnMuAux, learnTheta, learnCondExpX2givenW, learnCondExpXYgivenW, learnDevG, learnDevTheta

---

learnDevTheta	<i>Estimation of Cond. Expect. of <math>(Y - \text{theta}XW)^2</math> Given <math>(X, W)</math></i>
---------------	---

---

**Description**

Function for the estimation of the conditional expectation of  $(Y - \text{theta}XW)^2$  given  $(X, W)$  when flavor is set to "learning".

**Arguments**

obs	The matrix of observations, see for instance the obs argument of the function <code>tmle.npvi</code> .
thetaXW	The vector <code>thetaXW</code> of the conditional expectation of $Y$ given $(X, W)$ , as currently estimated, evaluated at our observations.
light	A logical, kept for compatibility, which should be set to TRUE (its default value). This requires that the result of each fit be reduced in size (for a faster execution). Currently implemented only for flavor learning.
verbose	Prescribes the amount of information output by the function. Defaults to FALSE.
...	Additional arguments possibly needed.

**Value**

Returns the fitted object.

**Author(s)**

Antoine Chambaz, Pierre Neuvial

**See Also**

learnG, learnMuAux, learnTheta, learnCondExpX2givenW, learnCondExpXYgivenW, learnDevG, learnDevMu

---

 learnG

*Estimation of Cond. Prob. of  $X=x_0$  Given  $W$* 


---

**Description**

Function for the estimation of the conditional probability that  $X = x_0$  (the reference value for  $X$ ) given  $W$ , version based on 'glm'.

**Arguments**

obs	The matrix of observations, see for instance the obs argument of the function <code>tmle.npvi</code> .
theX0	The reference value for $X$ .
light	A logical, kept for compatibility, which should be set to TRUE (its default value). This requires that the result of each fit be reduced in size (for a faster execution). Currently implemented only for flavor learning.
...	Additional arguments possibly needed.

**Value**

Returns the fitted object.

**Author(s)**

Antoine Chambaz, Pierre Neuvial

**See Also**

`learnMuAux`, `learnTheta`, `learnCondExpX2givenW`, `learnCondExpXYgivenW`, `learnDevG`, `learnDevMu`, `learnDevTheta`

---

 learningLib

*learningLib*


---

**Description**

List of default learning algorithms to use in `tmle.npvi` when `flavor` is set to "learning".

---

learnMuAux	<i>Estimation of Cond. Expect. of X Given (<math>X \neq x_0</math>, W)</i>
------------	--

---

**Description**

Function for the estimation of the conditional expectation of  $X$  given  $(X \neq x_0, W)$ , version based on 'glm'.

**Arguments**

obs	The matrix of observations, see for instance the obs argument of the function <code>tmle.npvi</code> , where only observations with $X \neq 0$ are kept.
light	A logical, kept for compatibility, which should be set to TRUE (its default value). This requires that the result of each fit be reduced in size (for a faster execution). Currently implemented only for flavor learning.
...	Additional arguments possibly needed.

**Value**

Returns the fitted object.

**Author(s)**

Antoine Chambaz, Pierre Neuvial

**See Also**

learnG, learnTheta, learnCondExpX2givenW, learnCondExpXYgivenW, learnDevG, learnDevMu, learnDevTheta

---

learnTheta	<i>Estimation of Cond. Expect. of Y given (X, W)</i>
------------	--

---

**Description**

Function for the estimation of the conditional expectation of  $Y$  given  $(X, W)$ , version based on 'glm'.

**Arguments**

obs	The matrix of observations, see for instance the obs argument of the function <code>tmle.npvi</code> , where only observations with $X \neq 0$ are kept.
light	A logical, kept for compatibility, which should be set to TRUE (its default value). This requires that the result of each fit be reduced in size (for a faster execution). Currently implemented only for flavor learning.
...	Additional arguments possibly needed.

**Value**

Returns the fitted object.

**Author(s)**

Antoine Chambaz, Pierre Neuvial

**See Also**

learnG, learnMuAux, learnCondExpX2givenW, learnCondExpXYgivenW, learnDevG, learnDevMu, learnDevTheta

---

`predict.SL.glm.condExpX2givenW`

*SL Wrapper for Estimation of Cond. Expect. of  $X^2$  Given  $W$*

---

**Description**

Prediction algorithm wrapper for SuperLearner, for the estimation of the conditional expectation of  $X^2$  given  $W$ .

**Arguments**

object

newdata

...

**Value**

Returns a prediction.

**Author(s)**

Antoine Chambaz, Pierre Neuvial

**See Also**

SL.glm.condExpX2givenW

---

`predict.SL.glm.condExpXYgivenW`

*SL Wrapper for Estimation of Cond. Expect. of XY Given W*

---

**Description**

Prediction algorithm wrapper for SuperLearner.

**Arguments**

object  
newdata  
...

**Value**

Returns a prediction.

**Author(s)**

Antoine Chambaz, Pierre Neuvial

**See Also**

`SL.glm.condExpXYgivenW`

---

`predict.SL.glm.g`

*SL Wrapper for Estimation of Cond. Prob. of X=0 Given W*

---

**Description**

Prediction algorithm wrapper for SuperLearner.

**Arguments**

object  
newdata  
...

**Value**

Returns a prediction.

**Author(s)**

Antoine Chambaz, Pierre Neuvial

**See Also**

SL.glm.g

---

predict.SL.glm.theta *SL Wrapper for Estimation of Cond. Expect. of Y Given (X,W)*

---

**Description**

Prediction algorithm wrapper for SuperLearner.

**Arguments**

object  
newdata  
...

**Value**

Returns a prediction.

**Author(s)**

Antoine Chambaz, Pierre Neuvial

**See Also**

SL.glm.theta

---

setConfLevel.NPVI *Sets Confidence Level*

---

**Description**

Sets the confidence level of a TMLE.NPVI object.

**Usage**

```
## S3 method for class 'NPVI'  
setConfLevel(this, confLevel, ...)
```

**Arguments**

<code>this</code>	An object of class <code>TMLE.NPVI</code> .
<code>confLevel</code>	A numeric, confidence interval level.
<code>...</code>	Not used.

**Author(s)**

Antoine Chambaz, Pierre Neuvial

**See Also**

`as.character.NPVI`

**Examples**

```
FALSE
```

---

`SL.glm.condExpX2givenW`

*SL Wrapper for Estimation of Cond. Expect. of  $X^2$  Given  $W$*

---

**Description**

Prediction algorithm wrapper for SuperLearner, for the estimation of the conditional expectation of  $X^2$  given  $W$ .

**Arguments**

```
Y
X
newX
family
obsWeights
...
```

**Value**

Returns a fitted object.

**Author(s)**

Antoine Chambaz, Pierre Neuvial

**See Also**

`learnCondExpX2givenW`, `predict.SL.glm.condExpX2givenW`

SL.glm.condExpXYgivenW

*SL Wrapper for Estimation of Cond. Expect. of XY Given W*

---

**Description**

Prediction algorithm wrapper for SuperLearner, for the estimation of the conditional expectation of  $XY$  given  $W$ .

**Arguments**

Y  
X  
newX  
family  
obsWeights  
...

**Value**

Returns a fitted object.

**Author(s)**

Antoine Chambaz, Pierre Neuvial

**See Also**

learnCondExpXYgivenW, predict.SL.glm.condExpXYgivenW

---

SL.glm.g

*SL Wrapper for Estimation of Cond. Prob. of  $X=0$  Given W*

---

**Description**

Prediction algorithm wrapper for SuperLearner, for the estimation of the conditional probability of  $X = 0$  given  $W$ .

**Arguments**

Y  
X  
newX  
family  
obsWeights  
...



**Value**

Returns a fitted object.

**Author(s)**

Antoine Chambaz, Pierre Neuvial

**See Also**

learnG, predict.SL.glm.g

---

SL.glm.theta

*SL Wrapper for Estimation of Cond. Prob. of  $X=0$  Given  $W$*

---

**Description**

Prediction algorithm wrapper for SuperLearner, for the estimation of the conditional expectation of  $Y$  given  $(X, W)$ .

**Arguments**

Y  
X  
newX  
family  
obsWeights  
...

**Value**

Returns a fitted object.

**Author(s)**

Antoine Chambaz, Pierre Neuvial

**See Also**

learnTheta, predict.SL.glm.theta

---

superLearningLib

*superLearningLib*

---

**Description**

List of default libraries of algorithms to use in `tmle.npvi` when `flavor` is set to "superLearning".

---

`tcga2012brca`*Sample breast cancer data from TCGA*

---

**Description**

Expression, DNA copy number, and DNA methylation data of 125 genes of chromosome 21 for 463 breast cancer samples from TCGA.

**Usage**`tcga2012brca`**Format**

A list of matrices. Each matrix corresponds to a particular gene and has the following columns:

$Y$  gene expression level (outcome variable)

$X$  DNA copy number (continuous exposure variable)

$W_1 \dots W_k$  DNA methylation (k baseline covariates)

**Details**

These data were obtained using the scripts located in `testScripts/tcga2012brca`. See the `tmle-npvi.pdf` vignette for more details on the preparation of the data set.

Gene names and genomic coordinates are stored in the names of the list.

**Author(s)**

Antoine Chambaz, Pierre Neuvial

**Source**

Raw data may be retrieved from [https://tcga-data.nci.nih.gov/docs/publications/brca\\_2012/](https://tcga-data.nci.nih.gov/docs/publications/brca_2012/)

**methylation** [http://tcga-data.nci.nih.gov/docs/publications/brca\\_2012/BRCA.methylation.27k.450k.466.zip](http://tcga-data.nci.nih.gov/docs/publications/brca_2012/BRCA.methylation.27k.450k.466.zip)

**copy number data** [http://tcga-data.nci.nih.gov/docs/publications/brca\\_2012/BRCA.GISTIC2.tar.gz](http://tcga-data.nci.nih.gov/docs/publications/brca_2012/BRCA.GISTIC2.tar.gz)

**expression** [http://tcga-data.nci.nih.gov/docs/publications/brca\\_2012/BRCA.exp.466.med.txt](http://tcga-data.nci.nih.gov/docs/publications/brca_2012/BRCA.exp.466.med.txt)

**annotation data for methylation probes** [http://supportres.illumina.com/documents/myillumina/b78d361a-def5-4adb-ab38-e8990625f053/humanmethylation450\\_15017482\\_v1-2.csv](http://supportres.illumina.com/documents/myillumina/b78d361a-def5-4adb-ab38-e8990625f053/humanmethylation450_15017482_v1-2.csv)

## References

Chambaz, A., Neuvial, P., & van der Laan, M. J. (2012). Estimation of a non-parametric variable importance measure of a continuous exposure. *Electronic journal of statistics*, 6, 1059–1099.

Cancer Genome Atlas Network. (2012). Comprehensive molecular portraits of human breast tumours. *Nature*, 490(7418), 61-70.

## Examples

```
data(tcga2012brca)
nms <- names(tcga2012brca)
ii <- grep("TP53", nms)
obs <- tcga2012brca[[ii]]
pairs(obs, main=nms[ii])

thr <- 0.02
whichSmall <- which(abs(obs[, "X"]) <= thr)
obs[whichSmall, "X"] <- 0

## the code below takes ~20s to run
## Not run: res <- tmle.npvi(obs)
```

---

tmle.npvi

*Targeted Minimum Loss Estimation of NPVI*


---

## Description

Carries out the targeted minimum loss estimation (TMLE) of a non-parametric variable importance measure of a continuous exposure.

## Usage

```
tmle.npvi(obs, f = identity, nMax = 30L, flavor = c("learning",
  "superLearning"), lib = list(), nodes = 1L, cvControl = NULL,
  family = c("parsimonious", "gaussian"), cleverCovTheta = FALSE,
  bound = 1, B = 1e+05, trueGMu = NULL, iter = 5L, stoppingCriteria = list(mic = 0.01,
  div = 0.01, psi = 0.1), gmin = 0.05, gmax = 0.95, mumax = quantile(f(obs[obs[,
  "X"] != 0, "X"]), type = 1, probs = 0.01), mumax = quantile(f(obs[obs[,
  "X"] != 0, "X"]), type = 1, probs = 0.99), verbose = FALSE,
  tabulate = TRUE, exact = TRUE, light = TRUE)
```

## Arguments

**obs**                    A  $n \times p$  matrix or data frame of observations, with  $p \geq 3$ .

- Column "X" corresponds to the continuous exposure variable (e.g. DNA copy number), or "cause" in a causal model, with a reference value  $x_0$  equal to 0.

	<ul style="list-style-type: none"> <li>• Column "Y" corresponds to the outcome variable (e.g. gene expression level), or "effect" in a causal model.</li> <li>• All other columns are interpreted as baseline covariates <math>W</math> taken into account in the definition of the "effect" of <math>X</math> on <math>Y</math>.</li> </ul>
f	A function involved in the definition of the parameter of interest $\psi$ , which must satisfy $f(0) = 0$ (see Details). Defaults to identity.
nMax	An integer (defaults to 30L; 10L is the smallest authorized value and we recommend a value less than 50L for reasonable computational time) indicating the maximum number of observed values of $X \neq 0$ which are used to create the supports of the conditional distributions of $X$ given $W$ and $X \neq 0$ involved in the simulation under $P_n^k$ when family is set to "parsimonious".
flavor	Indicates whether the construction of the relevant features of $P_n^0$ and $P_n^k$ , the (non-targeted yet) initial and (targeted) successive updated estimators of the true distribution of $(W, X, Y)$ relies on the Super Learning methodology (option "superLearning") or not (option "learning", default value). In the former case, the SuperLearner package is loaded.
lib	A list providing the function tmle.npvi with the necessary algorithms involved in the estimation of the features of interest. If empty (default) then the default algorithms are used. See Details.
nodes	An integer, which indicates how many nodes should be involved in the computation of the TMLE when it relies on the "superLearning" flavor. Defaults to 1. If larger than 1, then the parallel package is loaded and a cluster with nodes nodes is created and exploited.
cvControl	'NULL' (default value) or an integer indicating how many folds are involved in the Super Learning procedure. If flavor and cvControl are simultaneously set to "superLearning" and NULL then the Super Learning procedure relies on 10-fold cross-validation.
family	Indicates whether the simulation of the conditional distribution of $X$ given $W$ under $P_n^k$ (the initial estimator if $k = 0$ or its $k$ th update if $k \geq 1$ ) should be based on a weighted version of the empirical measure (case "parsimonious", default value and faster execution) or on a Gaussian model (case "gaussian").
cleverCovTheta	A logical, indicating whether the one-step (if FALSE, default value) or the two-step (if TRUE) updating procedure should be carried out.
bound	A positive numeric (defaults to 1), upper-bound on the absolute value of the fluctuation parameter.
B	An integer (defaults to 1e5) indicating the sample size of the data set simulated under each $P_n^k$ to compute an approximated value of $\Psi(P_n^k)$ , the parameter of interest at $P_n^k$ . The larger B, the more accurate the approximation.
trueGMu	Either NULL (default value) if the <b>true</b> conditional probability $g(W) = P(X = 0 W)$ and conditional expectation $muAux(W) = E_P(X X \neq 0, W)$ are not both known beforehand. Otherwise, a list with tags g and muAux and respective values the two respective functions (see the related outputs of getSample).
iter	An integer (defaults to 5) indicating a maximal number of updates.
stoppingCriteria	A list providing tuning parameters for the stopping criteria. Defaults to list(mic=0.01, div=0.01, see Details).

gmin	A positive numeric, lower-bound on the range of values of the estimated probabilities $P_n^k(X = 0 W)$ that $X$ be equal to its reference value $\theta$ given $W$ . Defaults to $5e-2$ , and must be smaller than gmax.
gmax	A positive numeric smaller than 1, upper-bound on the range of values of the estimated probabilities $P_n^k(X = 0 W)$ that $X$ be equal to its reference value $\theta$ given $W$ . Defaults to $95e-2$ , and must be larger than gmin.
mumin	A numeric, lower-bound on the range of values of the estimated conditional expectation $E_{P_n^k}(X X \neq 0, W)$ of $X$ given $X \neq 0$ and $W$ . Defaults to the first percentile of $X$ , and must be smaller than mumax.
mumax	A numeric, upper-bound on the range of values of the estimated conditional expectation $E_{P_n^k}(X X \neq 0, W)$ of $X$ given $X \neq 0$ and $W$ . Defaults to the 99th percentile of $X$ , and must be larger than mumin.
verbose	Prescribes the amount of information output by the function. Defaults to FALSE.
tabulate	A logical, kept for compatibility, which should be set to TRUE (its default value). This requires that the joint distribution of $(X, W)$ under $P_n^k$ be a weighted version of the empirical measure (for a faster execution).
exact	A logical, kept for compatibility, which should be set to TRUE (its default value). This requires that the successive updates of the estimators of the relevant features of the true distribution of $(W, X, Y)$ be derived from the current estimators based on exact formulas rather than on their first-order approximations.
light	A logical, kept for compatibility, which should be set to TRUE (its default value). This requires that the result of each fit be reduced in size (for a faster execution). Currently implemented only for flavor learning.

## Details

The parameter of interest is defined as  $\psi = \Psi(P)$  with

$$\Psi(P) = \frac{E_P[f(X) * (\theta(X, W) - \theta(0, W))]}{E_P[f(X)^2]},$$

with  $P$  the distribution of the random vector  $(W, X, Y)$ ,  $\theta(X, W) = E_P[Y|X, W]$ ,  $0$  **the reference value for  $X$** , and  $f$  a user-supplied function such that  $f(0) = 0$  (e.g.,  $f = \text{identity}$ , the default value).

The TMLE procedure stops when the maximal number of iterations, `iter`, is reached or when at least one of the following criteria is met:

- The empirical mean  $P_n \text{effIC}(P_n^{k+1})$  of the efficient influence curve at  $P_n^{k+1}$  scaled by the estimated standard deviation of the efficient influence curve at  $P_n^{k+1}$  is smaller, in absolute value, than `mic`.
- The total variation (TV) distance between  $P_n^k$  and  $P_n^{k+1}$  is smaller than `div`.
- The change between the successive values  $Psi(P_n^k)$  and  $Psi(P_n^{k+1})$  is smaller than `psi`.

If `lib` is an empty list (`list()`, default value) then the default algorithms for the chosen flavor are loaded (`learningLib` when flavor is set to "learning" or `superLearningLib` when flavor is

set to "superLearning"). A valid `lib` argument must mimic the structure of either `learningLib` or `superLearningLib`, depending on flavor.

The "superLearning" flavor requires the `SuperLearner` package and, by default, the `e1071`, `gam`, `glmnet`, `polyspline` and `randomForest` packages.

If `family` is set to "parsimonious" (recommended) then the packages `sgeostat` and `geometry` are required.

## Value

Returns an object of class "NPVI" summarizing the different steps of the TMLE procedure. The method `getHistory` outputs the "history" of the procedure (see `getHistory`). The object notably includes the following information:

<code>obs</code>	The matrix of observations used to carry out the TMLE procedure. Use the method <code>getObs</code> to retrieve it.
<code>psi</code>	The TMLE of the parameter of interest. Use the method <code>getPsi</code> to retrieve it.
<code>psi.sd</code>	The estimated standard deviation of the TMLE of the parameter of interest. Use the method <code>getPsiSd</code> to retrieve it.

## Author(s)

Antoine Chambaz, Pierre Neuvial

## References

Chambaz, A., Neuvial, P., & van der Laan, M. J. (2012). Estimation of a non-parametric variable importance measure of a continuous exposure. *Electronic journal of statistics*, 6, 1059–1099.

Chambaz, A., Neuvial, P. (2015). `tmle.npvi`: targeted, integrative search of associations between DNA copy number and gene expression, accounting for DNA methylation. To appear in *Bioinformatics Applications Notes*.

## See Also

`getSample`, `getHistory`

## Examples

```
set.seed(12345)
##
## Simulating a data set and computing the true value of the parameter
##

## Parameters for the simulation (case 'f=identity')
O <- cbind(W=c(0.05218652, 0.01113460),
           X=c(2.722713, 9.362432),
           Y=c(-0.4569579, 1.2470822))
O <- rbind(NA, O)
lambda0 <- function(W) {-W}
p <- c(0, 1/2, 1/2)
```

```

omega <- c(0, 3, 3)
S <- matrix(c(10, 1, 1, 0.5), 2, 2)

## Simulating a data set of 200 i.i.d. observations
sim <- getSample(2e2, 0, lambda0, p=p, omega=omega, sigma2=1, Sigma3=S)
obs <- sim$obs

## Adding (dummy) baseline covariates
V <- matrix(runif(3*nrow(obs)), ncol=3)
colnames(V) <- paste("V", 1:3, sep="")
obs <- cbind(V, obs)

## Caution! MAKING '0' THE REFERENCE VALUE FOR 'X'
X0 <- 0[2,2]
obsC <- obs
obsC[, "X"] <- obsC[, "X"] - X0
obs <- obsC

## True psi and confidence intervals (case 'f=identity')
sim <- getSample(1e4, 0, lambda0, p=p, omega=omega, sigma2=1, Sigma3=S)
truePsi <- sim$psi

confInt0 <- truePsi + c(-1, 1)*qnorm(.975)*sqrt(sim$varIC/nrow(sim$obs))
confInt <- truePsi + c(-1, 1)*qnorm(.975)*sqrt(sim$varIC/nrow(obs))
cat("\nCase f=identity:\n")
msg <- paste("\ttrue psi is: ", signif(truePsi, 3), "\n", sep="")
msg <- paste(msg, "\t95%-confidence interval for the approximation is: ",
             signif(confInt0, 3), "\n", sep="")
msg <- paste(msg, "\toptimal 95%-confidence interval is: ",
             signif(confInt, 3), "\n", sep="")
cat(msg)

##
## TMLE procedure
##

## Running the TMLE procedure
npvi <- tmle.npvi(obs, f=identity, flavor="learning", B=5e4, nMax=10)

## Summarizing its results
npvi
setConfLevel(npvi, 0.9)
npvi

history <- getHistory(npvi)
print(round(history, 4))

hp <- history[, "psi"]
hs <- history[, "sic"]
hs[1] <- NA
ics <- c(-1,1) %*% t(qnorm(0.975)*hs/sqrt(nrow(getObs(npvi))))

pch <- 20

```

```
ylim <- range(c(confInt, hp, ics+hp), na.rm=TRUE)

xs <- (1:length(hs))-1
plot(xs, hp, ylim=ylim, pch=pch, xlab="Iteration", ylab=expression(psi[n]),
      xaxp=c(0, length(hs)-1, length(hs)-1))
dummy <- sapply(seq(along=xs), function(x) lines(c(xs[x],xs[x]), hp[x]+ics[, x]))

abline(h=confInt, col=4)
abline(h=confInt0, col=2)
```



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