Package ‘madr’

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Title Model Averaged Double Robust Estimation
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Description Estimates average treatment effects using model average double robust (MA-DR) estimation. The MA-DR estimator is defined as weighted average of double robust estimators, where each double robust estimator corresponds to a specific choice of the outcome model and the propensity score model. The MA-DR estimator extend the desirable double robustness property by achieving consistency under the much weaker assumption that either the true propensity score model or the true outcome model be within a specified, possibly large, class of models.
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add.to.dictionary

Worker function that fits propensity score models

Description
This function fits propensity score models and saves necessary information

Usage
add.to.dictionary(x, u, w, alpha)

Arguments
x vector of the treatment (0/1)
u matrix of covariates to be considered for inclusion/exclusion
w matrix of covariates that will be included in all models (optional)
alpha vector of inclusion indicators (which columns of U) to included in the propensity score model

Value
A list. The list contains the following named components:
out a list that contains the BIC and estimated propensity scores from propensity score models

add.to.dictionary.outcome
Worker function that fits outcome models

Description
This function fits outcome models and saves necessary information

Usage
add.to.dictionary.outcome(y, x, u, w, alpha, binary = F)
bic.to.prob

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>y</td>
<td>vector of the outcome</td>
</tr>
<tr>
<td>x</td>
<td>vector of the treatment (0/1)</td>
</tr>
<tr>
<td>u</td>
<td>matrix of covariates to be considered for inclusion/exclusion</td>
</tr>
<tr>
<td>w</td>
<td>matrix of covariates that will be included in all models (optional)</td>
</tr>
<tr>
<td>alpha</td>
<td>vector of inclusion indicators (which columns of U) to included in the propensity score model</td>
</tr>
<tr>
<td>binary</td>
<td>indicates if the outcome is binary</td>
</tr>
</tbody>
</table>

Value

A list. The list contains the following named components:

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>out</td>
<td>a list that contains the BIC, predicted values, and estimated treatment effect from each outcome model</td>
</tr>
</tbody>
</table>

bic.to.prob

*Convert BIC to model probabilities*

Description

This function transforms BIC to model probabilities

Usage

bic.to.prob(bic)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>bic</td>
<td>vector of BICs</td>
</tr>
</tbody>
</table>

Value

A vector of model probabilities of the same dimension of bic
expit  

*Expit (inverse logit) function*

**Description**

This function transforms the input using the expit function.

**Usage**

`expit(x)`

**Arguments**

- `x`  
  vector of values to apply the expit function

**Value**

A vector of the same dimension of `x`

--

madr  

*Calculate model averaged double robust estimate*

**Description**

This function estimates a model averaged double robust estimate.

**Usage**

`madr(Y, X, U, W = NULL, M = 1000, cut = 0.95, enumerate = F, tau = NULL, two.stage = NULL)`

**Arguments**

- `Y`  
  vector of the outcome

- `X`  
  vector of the treatment (0/1)

- `U`  
  matrix of covariates to be considered for inclusion/exclusion

- `W`  
  matrix of covariates that will be included in all models (optional)

- `M`  
  the number of MCMC iteration

- `cut`  
  cumulative probability of models to be retained for improved computational efficiency (1 retains all visited models)

- `enumerate`  
  indicator if all possible models should be enumerated (default: FALSE)

- `tau`  
  scalar value for the prior model dependence (1 is an independent prior; defaults to 0)

- `two.stage`  
  indicator if the two-stage procedure for calculating the model weights should be used (defaults to TRUE)
**Value**

A list. The list contains the following named components:

- `madr`: the model averaged double robust estimate
- `weight.ps`: a vector that contains the inclusion probability of each covariate in the propensity score model
- `weight.om`: a vector that contains the inclusion probability of each covariate in the outcome model

**Examples**

```r
set.seed(122)
## generate data
n = 100 # number of observations
k = 4  # number of covariates
U = matrix(rnorm(n*k),n,k)
colnames(U) = paste0("U",1:k)
A = rbinom(n,1,expit(-1+.5*rowSums(U)))
Y = rnorm(n,1+A+.25*rowSums(U))

## A is confounded -- true effect is 1
lm(Y~A)

## fit ma-dr -- can enumerate models if k isn't too big
res = madr(y=Y,x=A,u=U,enumerate=TRUE,tau=1,two.stage=FALSE) # independent prior
res

res = madr(y=Y,x=A,u=U,enumerate=TRUE,tau=0,two.stage=TRUE) # tau=0 and using two-stage weights
res

## no need to refit madr each time when enumerating -- use summarize and specify different taus
summary(res,tau=1,two.stage=FALSE) # independent prior
summary(res,tau=0,two.stage=FALSE)
summary(res,tau=0,two.stage=TRUE) # two-stage procedure for calculating weights

## use mcmc instead of enumerating (the default)
madr(Y=Y,X=A,U=U,M=1000,cut=1) # should approximate tau=0 and two.stage=TRUE
```

---

**madr.enumerate**  
*Model averaged double robust estimate with enumeration of all possible models (linear terms only)*

**Description**

This function enumerates all possible models and estimates a model averaged double robust estimate.

**Usage**

```r
madr.enumerate(Y, X, U, W = NULL, tau = 1, two.stage = F)
```
Arguments

- **Y**: vector of the outcome
- **X**: vector of the treatment indicator (0/1)
- **U**: matrix of covariates to be considered for inclusion/exclusion
- **W**: matrix of covariates that will be included in all models (optional)
- **tau**: scalar value for the prior model dependence (1 is an independent prior)
- **two.stage**: indicator if the two-stage procedure for calculating the model weights should be used

Value

A object of class madr.enumerate. The object contains the following named components:

- **out**: a matrix that contains the BIC and estimated treatment from each outcome model
- **ps**: a matrix that contains the BIC from each propensity score model
- **dr**: a matrix that contains the model-specific double robust estimates
- **U.names**: the column names of U

---

**madr.mcmc**

*Calculate model averaged double robust estimate using a pseudo-MC3 algorithm*

---

Description

This function uses a pseudo-MC3 algorithm to search the model space, then estimate a model averaged double robust estimate using the two-stage procedure for estimating model weights with tau=0.

Usage

```
madr.mcmc(Y, X, U, W = NULL, M = 1000, cut = 0.95)
```

Arguments

- **Y**: vector of the outcome
- **X**: vector of the treatment (0/1)
- **U**: matrix of covariates to be considered for inclusion/exclusion
- **W**: matrix of covariates that will be included in all models (optional)
- **M**: the number of MCMC iteration
- **cut**: cumulative probability of models to be retained for improved computational efficiency (1 retains all visited models)
Value

A list. The list contains the following named components:

- madr: the model averaged double robust estimate
- weight.ps: a vector that contains the inclusion probability of each covariate in the propensity score model
- weight.om: a vector that contains the inclusion probability of each covariate in the outcome model

OM.MA

*Calculate model probabilities for the outcome models using a pseudo-MC3 algorithm*

Description

This function uses a pseudo-MC3 algorithm to search the outcome model space.

Usage

`OM.MA(y, x, u, w = NULL, m = 1000, alpha = NULL, binary = F)`

Arguments

- `y`: vector of the outcome
- `x`: vector of the treatment (0/1)
- `u`: matrix of covariates to be considered for inclusion/exclusion
- `w`: matrix of covariates that will be included in all models (optional)
- `m`: the number of MCMC iteration
- `alpha`: vector of inclusion indicators (which columns of `U`) to start MCMC algorithm (optional)
- `binary`: indicator if the outcome is binary (optional)

Value

A list. The list contains the following named components:

- `dict`: a list that contains the BIC, predicted values, and estimated treatment effect from each outcome model
- `alpha`: the last model visited by the algorithm
- `out.table`: a matrix that contains the BIC and estimated treatment effect from each outcome model
OM.MA.enumerate

Enumerates all possible outcome models (linear terms only)

Description

This function enumerates and fits all possible outcome models.

Usage

OM.MA.enumerate(y, x, u, w = NULL)

Arguments

Y          vector of the outcome
X          vector of the treatment indicator (0/1)
U          matrix of covariates to be considered for inclusion/exclusion
W          matrix of covariates that will be included in all models (optional)

Value

A list. The list contains the following named components:
dict      a list that contains the BIC, predicted values, and estimated treatment effect from each outcome model
out.table a matrix that contains the BIC and estimated treatment effect from each outcome model

print.madr.enumerate

Print function for madr.enumerate class

Description

This function prints results from madr.enumerate class.

Usage

## S3 method for class 'madr.enumerate'
print(x, ...)

Arguments

x          madr.enumerate object
...        ignored
\textit{print.madr.mcmc} \hspace{1cm} \textit{Print function for madr.mcmc class}

\section*{Description}
This function prints results from madr.mcmc class

\section*{Usage}
\begin{verbatim}
## S3 method for class 'madr.mcmc'
print(x, ...)
\end{verbatim}

\section*{Arguments}
\begin{verbatim}
x       madr.mcmc object
...
     ignored
\end{verbatim}

\section*{print.summary.madr.enumerate} \hspace{1cm} \textit{Print function for summary.madr.enumerate class}

\section*{Description}
This function prints results from summary.madr.enumerate class

\section*{Usage}
\begin{verbatim}
## S3 method for class 'summary.madr.enumerate'
print(x, ...)
\end{verbatim}

\section*{Arguments}
\begin{verbatim}
x       summary.madr.enumerate object
...
     ignored
\end{verbatim}
PS.MA

*Calculate model probabilities for the propensity score model using a pseudo-MC3 algorithm*

**Description**

This function uses a pseudo-MC3 algorithm to search the propensity score model space.

**Usage**

```r
PS.MA(X, U, W = NULL, M = 1000, alpha = NULL, master.index = NULL, master.dict = list())
```

**Arguments**

- `X` vector of the treatment (0/1)
- `U` matrix of covariates to be considered for inclusion/exclusion
- `W` matrix of covariates that will be included in all models (optional)
- `M` the number of MCMC iteration
- `alpha` vector of inclusion indicators (which columns of U) to start MCMC algorithm (optional)
- `master.index` indexes which columns of U should be considered for inclusion in the propensity score model (optional)
- `master.dict` list containing information from previous propensity score model fits (optional)

**Value**

A list. The list contains the following named components:

- `dict` a list that contains the BIC and estimated propensity scores from propensity score models
- `alpha` the last model visited by the algorithm
- `out.table` a matrix that contains the BIC from each propensity score model
**PS.MA.enumerate**

*Enumerates all possible propensity score models (linear terms only)*

**Description**

This function enumerates and fits all possible propensity score models.

**Usage**

```r
PS.MA.enumerate(x, u, w = NULL)
```

**Arguments**

- `x`: vector of the treatment indicator (0/1)
- `u`: matrix of covariates to be considered for inclusion/exclusion
- `w`: matrix of covariates that will be included in all models (optional)

**Value**

A list. The list contains the following named components:

- `dict`: a list that contains the BIC and estimated propensity scores from propensity score models
- `out.table`: a matrix that contains the BIC from each propensity score model

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**summary.madr.enumerate**

*Provides model averaged double robust estimate for different values of tau*

**Description**

This function estimates model averaged double robust estimate for different values of tau using a `madr.enumerate` object.

**Usage**

```r
## S3 method for class 'madr.enumerate'
summary(object, tau = NULL, two.stage = NULL, ...)
```
Arguments

- **object**: madr.enumerate object
- **tau**: scalar value for the prior model dependence (1 is an independent prior; defaults to value used in madr.enumerate)
- **two.stage**: indicator if the two-stage procedure for calculating the model weights should be used (defaults to value used in madr.enumerate)
- **...**: ignored

Value

A list. The list contains the following named components:

- **madr**: the model averaged double robust estimate
- **weight.ps**: a vector that contains the inclusion probability of each covariate in the propensity score model
- **weight.om**: a vector that contains the inclusion probability of each covariate in the outcome model
- **tau**: value of tau used in estimation
- **two.stage**: indicator if the two-stage procedure for calculating the model weights was used
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