Package: madr (via r-universe)

October 31, 2024

Type Package

Title Model Averaged Double Robust Estimation

Version 1.0.0

Author Matthew Cefalu

Maintainer Matthew Cefalu <Matthew_Cefalu@rand.org>

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.

License GPL-3

LazyData TRUE

RoxygenNote 5.0.1

NeedsCompilation no

Date/Publication 2016-09-05 20:23:43

Repository https://mattcefalu.r-universe.dev

RemoteUrl https://github.com/cran/madr

RemoteRef HEAD

RemoteSha 904590d2d0d243f2a3468438f08409b1c77d0ce0

Contents

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)
```

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)
`alpha`	vector of inclusion indicators (which columns of U) to included in the propensity score model
`binary`	indicates if the outcome is binary

Value

A list. The list contains the following named components:

`out`	a list that contains the BIC, predicted values, and estimated treatment effect from each outcome model

bic.to.prob *Convert BIC to model probabilities*

Description

This function transforms BIC to model probabilities

Usage

```
bic.to.prob(bic)
```

Arguments

`bic`	vector of BICs

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

```
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 isnt 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

```
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 listcontains 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

`print.madr.mcmc` *Print function for madr.mcmc class*

Description

This function prints results from madr.mcmc class

Usage

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

Arguments

`x`	madr.mcmc object
`...`	ignored

`print.summary.madr.enumerate` *Print function for summary.madr.enumerate class*

Description

This function prints results from summary.madr.enumerate class

Usage

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

Arguments

`x`	summary.madr.enumerate object
`...`	ignored

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

```
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

```
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

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

```
## 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

Index