Package 'causalLearning'

December 3, 2017

Title Methods for heterogeneous treatment effect estimation

Version 1.0.0

Description The main functions are cv.causalBoosting and bagged.causalMARS, which build upon the simpler causalBoosting and causalMARS functions. All of these functions have their own predict methods.

Depends R (>= 3.3.0)

Imports ranger

License GPL-2

LazyData true

RoxygenNote 6.0.1

NeedsCompilation yes

Author Scott Powers [aut, cre],
Junyang Qian [aut],
Trevor Hastie [aut],
Robert Tibshirani [aut]

Maintainer Scott Powers <sspowers@stanford.edu>

R topics documented:

`bagged.causalMARS` *Fit a bag of causal MARS models*

Description

Fit a bag of causal MARS models

Usage

```
bagged.causalMARS(x, tx, y, nbag = 20, maxterms = 11, nquant = 5,
  degree = ncol(x), eps = 1, backstep = FALSE, propensity = FALSE,
  stratum = rep(1, nrow(x)), minnum = 5, verbose = FALSE)
```

Arguments

`x`	matrix of covariates
`tx`	vector of treatment indicators (0 or 1)
`y`	vector of response values
`nbag`	number of models to bag
`maxterms`	maximum number of terms to include in the regression basis (e.g. `maxterms = 11` means intercept + 5 pairs added)
`nquant`	number of quantiles used in splitting
`degree`	max number of different predictors that can interact in model
`eps`	shrinkage factor for new term added
`backstep`	logical: should out-of-bag samples be used to prune each model? otherwise full regression basis is used for each model
`propensity`	logical: should propensity score stratification be used?
`stratum`	optional vector giving propensity score stratum for each observation (only used if `propensity = TRUE`)
`minnum`	minimum number of observations in each arm of each propensity score stratum needed to estimate regression coefficients for basis (only used if `propensity = TRUE`)
`verbose`	logical: should progress be printed to console?

Value

an object of class `bagged.causalMARS`, which is itself a list of `causalMARS` objects

`causalBoosting` *Fit a causal boosting model*

Description

Fit a causal boosting model

Usage

```
causalBoosting(x, tx, y, num.trees = 500, maxleaves = 4, eps = 0.01,
  splitSpread = 0.1, x.est = NULL, tx.est = NULL, y.est = NULL,
  propensity = FALSE, stratum = NULL, stratum.est = NULL,
  isConstVar = TRUE)
```

Arguments

`x`	matrix of covariates
`tx`	vector of treatment indicators (0 or 1)
`y`	vector of response values
`num.trees`	number of shallow causal trees to build
`maxleaves`	maximum number of leaves per causal tree
`eps`	learning rate
`splitSpread`	how far apart should the candidate splits be for the causal trees? (e.g. `splitSpread = 0.1`) means we consider 10 quantile cutpoints as candidates for making split
`x.est`	optional matrix of estimation-set covariates used for honest re-estimation (ignored if `tx.est = NULL` or `y.est = NULL`)
`tx.est`	optional vector of estimation-set treatment indicators (ignored if `x.est = NULL` or `y.est = NULL`)
`y.est`	optional vector of estimation-set response values (ignored if `x.est = NULL` or `y.est = NULL`)
`propensity`	logical: should propensity score stratification be used?
`stratum`	optional vector giving propensity score stratum for each observation (only used if `propensity = TRUE`)
`stratum.est`	optional vector giving propensity score stratum for each estimation-set observation (ignored if `x.est = NULL` or `tx.est = NULL` or `y.est = NULL`)
`isConstVar`	logical: for the causal tree splitting criterion (T-statistc), should it be assumed that the noise variance is the same in treatment and control arms?

Value

an object of class `causalBoosting` with attributes:

- CBM: a list storing the intercept, the causal trees and `eps`
- tauhat: matrix of treatment effects for each patient for each step
- G1: estimated-treatment conditional mean for each patient
- G0: estimated-control conditional mean for each patient
- err.y: training error at each step, in predicting response
- num.trees: number of trees specified by function call

`causalMARS` *Fit a causal MARS model*

Description

Fit a causal MARS model

Usage

```
causalMARS(x, tx, y, maxterms = 11, nquant = 5, degree = ncol(x),
  eps = 1, backstep = FALSE, x.val = NULL, tx.val = NULL,
  y.val = NULL, propensity = FALSE, stratum = rep(1, nrow(x)),
  stratum.val = NULL, minnum = 5)
```

Arguments

`x`	matrix of covariates
`tx`	vector of treatment indicators (0 or 1)
`y`	vector of response values
`maxterms`	maximum number of terms to include in the regression basis (e.g. `maxterms = 11` means intercept + 5 pairs added)
`nquant`	number of quantiles used in splitting
`degree`	max number of different predictors that can interact in model
`eps`	shrinkage factor for new term added
`backstep`	logical: after building out regression basis, should backward stepwise selection be used to create a sequence of models, with the criterion evaluated on a validation set to choose among the sequence?
`x.val`	optional matrix of validation-set covariates (only used if `backstep = TRUE`)
`tx.val`	optional vector of validation-set treatment indicators (only used if `backstep = TRUE`)
`y.val`	optional vector of validation-set response values (only used if `backstep = TRUE`)
`propensity`	logical: should propensity score stratification be used?
`stratum`	optional vector giving propensity score stratum for each observation (only used if `propensity = TRUE`)
`stratum.val`	optional vector giving propensity score stratum for each validation-set observation (only used if `propensity = backstep = TRUE`)
`minnum`	minimum number of observations in each arm of each propensity score stratum needed to estimate regression coefficients for basis (only used if `propensity = TRUE`)

Details

parallel arms mars with backward stepwise BOTH randomized case and propensity stratum. data structures: model terms (nodes) are numbered 1, 2, ... with 1 representing the intercept. forward stepwise: modmatrix contains basis functions as model is built up – two columns are added at each step. Does not include a column of ones for tidiness, we always add two terms, even when term added in linear (so that reflected version is just zero). backward stepwise: khat is the sequence of terms deleted at each step, based on deltahat = relative change in rss. rsstesthat is rss over test (validation) set achieved by each reduced model in sequence- used later for selecting a member of the sequence. active2 contains indices of columns with nonzero norm

Value

an object of class `causalMARS` with attributes:

- parent: indices of nodes that are parents at each stage
- childvar: index of predictor chosen at each forward step
- childquant: quantile of cutoff chosen at each forward step
- quant: quantiles of the columns of x
- active: indices of columns with nonzero norm
- allvars: list of variables appearing in each term
- khat: the sequence of terms deleted at each step
- deltahat: relative change in rss
- rsstesthat: validation-set rss achieved by each model in sequence
- setesthat: standard error for rsstesthat
- tim1: time elapsed during forward stepwise phase
- tim2: total time elapsed
- x
- tx
- y
- maxterms
- eps
- backstep
- propensity
- x.val
- tx.val
- y.val
- stratum
- stratum.val
- minnum

`cv.causalBoosting` *Fit a causal boosting model with cross validation*

Description

Fit a causal boosting model with cross validation

Usage

```
cv.causalBoosting(x, tx, y, num.trees = 500, maxleaves = 4, eps = 0.01,
  splitSpread = 0.1, type.measure = c("effect", "response"), nfolds = 5,
  foldid = NULL, propensity = FALSE, stratum = NULL, isConstVar = TRUE)
```

Arguments

x	matrix of covariates
tx	vector of treatment indicators (0 or 1)
y	vector of response values
num.trees	number of shallow causal trees to build
maxleaves	maximum number of leaves per causal tree
eps	learning rate
splitSpread	how far apart should the candidate splits be for the causal trees? (e.g. `splitSpread = 0.1`) means we consider 10 quantile cutpoints as candidates for making split
type.measure	loss to use for cross validation: 'response' returns mean-square error for predicting response in each arm. 'effect' returns MSE for treatment effect using honest over-fit estimation.
nfolds	number of cross validation folds
foldid	vector of fold membership
propensity	logical: should propensity score stratification be used?
stratum	optional vector giving propensity score stratum for each observation (only used if `propensity = TRUE`)
isConstVar	logical: for the causal tree splitting criterion (T-statistc), should it be assumed that the noise variance is the same in treatment and control arms?

Value

an object of class `cv.causalBoosting` which is an object of class `causalBoosting` with these additional attributes:

- num.trees.min: number of trees with lowest CV error
- cvm: vector of mean CV error for each number of trees
- cvsd: vector of standard errors for mean CV errors

`pollinated.ranger` *Pollinate a fitted ranger random forest model*

Description

Pollinate a fitted ranger random forest model

Usage

```
pollinated.ranger(object, x, y)
```

Arguments

object	a fitted `ranger` object
x	matrix of covariates
y	vector of response values

Value

an object of class `pollinated.ranger` which is a `ranger` object that has been pollinated with the data in (x, y)

predict.bagged.causalMARS

Make predictions from a bag of fitted causal MARS models

Description

Make predictions from a bag of fitted causal MARS models

Usage

```
## S3 method for class 'bagged.causalMARS'
predict(object, newx, type = c("average", "all"),
  ...)
```

Arguments

object	a fitted bagged.causalMARS object
newx	matrix of new covariates for which estimated treatment effects are desired
type	type of prediction required: 'average' returns a vector of the averages of the bootstrap estimates. 'all' returns a matrix of all of the bootstrap estimates.
...	ignored

Value

a vector of estimated personalized treatment effects corresponding to the rows of newx

predict.causalBoosting

Make predictions from a fitted causal boosting model

Description

Make predictions from a fitted causal boosting model

Usage

```
## S3 method for class 'causalBoosting'
predict(object, newx, newtx = NULL,
  type = c("treatment.effect", "conditional.mean", "response"),
  num.trees = 1:object$num.trees, honest = FALSE, naVal = 0, ...)
```

Arguments

object	a fitted causalBoosting object
newx	matrix of new covariates for which estimated treatment effects are desired
newtx	option vector of new treatment assignments (only used if type = 'response')
type	type of prediction required: 'treatment.effect' returns estimated treatment effect. 'conditional.mean' returns two predictions, one for each arm. 'response' returns prediction for arm corresponding to newtx.
num.trees	number(s) of shallow causal trees to use for prediction
honest	logical: should honest re-estimates of leaf means be used for prediction? This requires that x.est, tx.est, y.est were specified when the causal boosting model was fit
naVal	value with which to replace NA predictions
...	ignored

Value

a vector or matrix of predictions corresponding to the rows of newx

---

predict.causalMARS *Make predictions from a fitted causal MARS model*

Description

Make predictions from a fitted causal MARS model

Usage

```
## S3 method for class 'causalMARS'
predict(object, newx, active, ...)
```

Arguments

object	a fitted causalMARS object
newx	matrix of new covariates for which estimated treatment effects are desired
active	indices of columns with nonzero norm (defaults to model selected via backward stepwise phase, or the full model if backstep = FALSE)
...	ignored

Value

a vector of estimated personalized treatment effects corresponding to the rows of newx

predict.causalTree *Make predictions from a fitted causal tree model*

Description

Make predictions from a fitted causal tree model

Usage

```
## S3 method for class 'causalTree'
predict(object, newx, newtx = NULL,
  type = c("treatment.effect", "conditional.mean", "response"),
  honest = FALSE, naVal = 0, ...)
```

Arguments

object	a fitted causalTree object
newx	matrix of new covariates for which estimated treatment effects are desired
newtx	option vector of new treatment assignments (only used if type = 'response')
type	type of prediction required: 'treatment.effect' returns estimated treatment effect. 'conditional.mean' returns two predictions, one for each arm. 'response' returns prediction for arm corresponding to newtx.
honest	logical: should honest re-estimates of leaf means be used for prediction? This requires that x.est, tx.est, y.est were specified when the causal boosting model was fit
naVal	value with which to replace NA predictions
...	ignored

Value

a vector or matrix of predictions corresponding to the rows of newx

predict.cv.causalBoosting *Make predictions from a fitted cross-validated causal boosting model*

Description

Make predictions from a fitted cross-validated causal boosting model

Usage

```
## S3 method for class 'cv.causalBoosting'
predict(object, newx, newtx = NULL,
  type = c("treatment.effect", "conditional.mean", "response"),
  num.trees = object$num.trees.min.effect, naVal = 0, ...)
```

Arguments

object	a fitted cv.causalBoosting object
newx	matrix of new covariates for which estimated treatment effects are desired
newtx	option vector of new treatment assignments (only used if type = 'individual')
type	type of prediction required: 'treatment.effect' returns estimated treatment effect. 'conditional.mean' returns two predictions, one for each arm. 'response' returns prediction for arm corresponding to newtx.
num.trees	number of shallow causal trees to use for prediction
naVal	value with which to replace NA predictions
...	ignored

Value

a vector or matrix of predictions corresponding to the rows of newx

---

predict.pollinated.ranger

Make predictions from a pollinated ranger random forest model

---

Description

Make predictions from a pollinated ranger random forest model

Usage

```
## S3 method for class 'pollinated.ranger'
predict(object, newx, predict.all = FALSE,
  na.treatment = c("omit", "replace", "NA"), ...)
```

Arguments

object	a fitted pollinated.ranger object
newx	matrix of new covariates for which predictions are desired
predict.all	logical: should predictions from all trees be returned? Otherwise the average across trees is returned
na.treatment	how to treat NA predictions from individual trees: 'omit' only uses trees for which the prediction is not NA. 'replace' replaces NA predictions with the overall mean response. 'NA' returns NA if any tree prediction is NA.
...	additional arguments passed on to predict.ranger

Value

a vector of predicted treatment effects corresponding to the rows of newx

predict.PTOforest *Make predictions from a fitted PTO forest model*

Description

Make predictions from a fitted PTO forest model

Usage

```
## S3 method for class 'PTOforest'
predict(object, newx, ...)
```

Arguments

object	a fitted PTOforest object
newx	matrix of new covariates for which estimated treatment effects are desired
...	ignored

Value

a vector of predictions corresponding to the rows of newx

PTOforest *Fit a pollinated transformed outcome (PTO) forest model*

Description

Fit a pollinated transformed outcome (PTO) forest model

Usage

```
PTOforest(x, tx, y, pscore = rep(0.5, nrow(x)), num.trees = 500,
  mtry = ncol(x), min.node.size = max(25, nrow(x)/40), postprocess = TRUE,
  verbose = FALSE)
```

Arguments

x	matrix of covariates
tx	vector of treatment indicators (0 or 1)
y	vector of response values
pscore	vector of propensity scores
num.trees	number of trees for transformed outcome forest
mtry	number of variables to possibly split at in each node
min.node.size	minimum node size for transformed outcome forest
postprocess	logical: should optional post-processing random forest be fit at end?
verbose	logical: should progress be printed to console?

Value

an object of class `PTOforest` with attributes:

- x: matrix of covariates supplied by function call
- pscore: vector of propensity score supplied by function call
- postprocess: logical supplied by function call
- TOfit: fitted random forest on transformed outcomes
- PTOfit1: TOfit pollinated with treatment-arm outcomes
- PTOfit0: TOfit pollinated with control-arm outcomes
- postfit: post-processing random forest summarizing results

`stratify` *Get propensity strata from propensity scores*

Description

Get propensity strata from propensity scores

Usage

```
stratify(pscore, tx, min.per.arm = 30)
```

Arguments

`pscore`	vector of propensity scores
`tx`	vector of treatment indicators
`min.per.arm`	minimum number of observations for each arm within each stratum

Value

a vector of integers with length equal to the length of pscore, reporting the propensity stratum corresponding to each propensity score

Index