Package 'bujar'

June 25, 2023

Type Package

Title Buckley-James Regression for Survival Data with High-Dimensional Covariates

Version 0.2-11

Date 2023-06-23

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Description Buckley-James regression for right-censoring survival data with high-dimensional covariates. Implementations for survival data include boosting with componentwise linear least squares, componentwise smoothing splines, regression trees and MARS. Other high-dimensional tools include penalized regression for survival data. See Wang and Wang (2010) <doi:10.2202/1544-6115.1550>.

Imports mda, mpath, mboost, gbm, earth, elasticnet, rms, methods, modeltools, bst, parallel, survival

Depends R (>= 3.5.0)

Suggests TH.data, R.rsp, gridExtra

VignetteBuilder R.rsp

License GPL-2

LazyLoad yes

NeedsCompilation no

Repository CRAN

Date/Publication 2023-06-25 02:40:02 UTC

R topics documented:

bujar *Buckley-James Regression*

Description

Buckley-James regression for right-censoring survival data with high-dimensional covariates. Including L_2 boosting with componentwise linear least squares, componentwise P-splines, regression trees. Other Buckley-James methods including elastic net, MCP, SCAD, MARS and ACOSSO (ACOSSO not supported for the current version).

Usage

```
bujar(y, cens, x, valdata = NULL, degree = 1, learner = "linear.regression",
center=TRUE, mimpu = NULL, iter.bj = 20, max.cycle = 5, nu = 0.1, mstop = 50,
twin = FALSE, mstop2= 100, tuning = TRUE, cv = FALSE, nfold = 5, method = "corrected",
vimpint = TRUE,gamma = 3, lambda=NULL, whichlambda=NULL, lamb = 0, s = 0.5, nk = 4,
wt.pow = 1, theta = NULL, rel.inf = FALSE, tol = .Machine$double.eps, n.cores= 2,
rng=123, trace = FALSE)
## S3 method for class 'bujar'
print(x, ...)
## S3 method for class 'bujar'
predict(object, newx=NULL, ...)
## S3 method for class 'bujar'
plot(x, ...)
## S3 method for class 'bujar'
coef(object, ...)
## S3 method for class 'bujar'
summary(object, ...)
```

Arguments

y	survival time
cens	censoring indicator, must be 0 or 1 with 0=alive, 1=dead
x	covariate matrix
object	an object of class "bujar"
newx	covariate matrix for prediction
valdata	test data, which must have the first column as survival time, second column as censoring indicator, and the remaining columns similar to same x.
degree	mars/tree/linear regression degree of interaction; if 2, second-order interaction, if degree=1, additive model;
learner	methods used for BJ regression.
center	center covariates
mimpu	initial estimate. If TRUE, mean-imputation; FALSE, imputed with the marginal best variable linear regression; if NULL, 0.

iter.bj	number of B-J iteration
max.cycle	max cycle allowed
nu	step-size boosting parameter
mstop	boosting tuning parameters. It can be one number or have the length iter.bj+max.cycle. If cv=TRUE, then mstop is the maximum number of tuning parameter
twin	logical, if TRUE, twin boosting
mstop2	twin boosting tuning parameter
tuning	logical value. if TRUE, the tuning parameter will be selected by cv or AIC/BIC methods. Ignored if twin=TRUE for which no tuning parameter selection is implemented
cv	logical value. if TRUE, cross-validation for tuning parameter, only used if tuning=TRUE. If tuning=FALSE or twin=TRUE, then ignored
nfold	number of fold of cv
method	boosting tuning parameter selection method in AIC
vimpint	logical value. If TRUE, compute variable importance and interaction measures for MARS if learner="mars" and degree > 1.
gamma	MCP, or SCAD gamma tuning parameter
lambda	MCP, or SCAD lambda tuning parameter
whichlambda	which lambda used for MCP or SCAD lambda tuning parameter
lamb	elastic net lambda tuning parameter, only used if learner="enet"
s	the second enet tuning parameter, which is a fraction between (0, 1), only used if learne="enet"
nk	number of basis function for learner="mars"
wt.pow	not used but kept for historical reasons, only for learner=ACOSSO. This is a parameter (power of weight). It might be chosen by CV from c(0, 1.0, 1.5, 2.0, 2.5, 3.0). If wt.pow=0, then this is COSSO method
theta	For learner="acosso", not used now. A numerical vector with 0 or 1. 0 means the variable not included and 1 means included. See Storlie et al. (2009).
rel.inf	logical value. if TRUE, variable importance measure and interaction importance measure computed
tol	convergency criteria
n.cores	The number of CPU cores to use. The cross-validation loop will attempt to send different CV folds off to different cores. Used for learner="tree"
rng	a number to be used for random number generation in boosting trees
trace	logical value. If TRUE, print out interim computing results
...	additional arguments used in estimation methods, for instance, trees.

Details

Buckley-James regression for right-censoring survival data with high-dimensional covariates. Including L_2 boosting with componentwise linear least squares, componentwise P-splines, regression trees. Other Buckley-James methods including elastic net, SCAD and MCP. learner="enet" and learner="enet2" use two different implementations of LASSO. Some of these methods are discussed in Wang and Wang (2010) and the references therein. Also see the references below.

Value

x	original covariates
y	survival time
cens	censoring indicator
ynew	imputed y
yhat	estimated y from ynew
pred.bj	estimated y from the testing sample
res.fit	model fitted with the learner
learner	original learner used
degree	=1, additive model, degree=2, second-order interaction
mse	MSE at each BJ iteration, only available in simulations, or when valdata provided
mse.bj	MSE from training data at the BJ termination
mse.bj.val	MSE with valdata
mse.all	a vector of MSE for uncensoring data at BJ iteration
nz.bj.iter	number of selected covariates at each BJ iteration
nz.bj	number of selected covariates at the claimed BJ termination
xselect	a vector of dimension of covariates, either 1 (covariate selected) or 0 (not selected)
coef.bj	estimated coefficients with linear model
vim	a vector of length of number of column of x, variable importance, between 0 to 100
interactions	measure of strength of interactions
ybstdiff	largest absolute difference of estimated y. Useful to monitor convergency
ybstcon	a vector with length of BJ iteration each is a convergency measure
cycleperiod	number of cycle of BJ iteration
cycle.coef.diff	within cycle of BJ, the maximum difference of coefficients for BJ boosting
nonconv	logical value. if TRUE, non-convergency
fnorm2	value of L_2 norm, can be useful to access convergency
mselect	a vector of length of BJ iteration, each element is the tuning parameter mstop
contype	0 (converged), 1, not converged but cycle found, 2, not converged and max iteration reached.

Author(s)

Zhu Wang

References

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Peter Buhlmann (2006), Boosting for high-dimensional linear models. *The Annals of Statistics*, **34**(2), 559–583.

Peter Buhlmann and Torsten Hothorn (2007), Boosting algorithms: regularization, prediction and model fitting. *Statistical Science*, **22**(4), 477–505.

J. Friedman (1991), Multivariate Adaptive Regression Splines (with discussion) . *Annals of Statistics*, **19**/1, 1–141.

J.H. Friedman, T. Hastie and R. Tibshirani (2000), Additive Logistic Regression: a Statistical View of Boosting. *Annals of Statistics* **28**(2):337-374.

C. Storlie, H. Bondell, B. Reich and H. H. Zhang (2009), Surface Estimation, Variable Selection, and the Nonparametric Oracle Property. *Statistica Sinica*, to appear.

Sijian Wang, Bin Nan, Ji Zhu, and David G. Beer (2008), Doubly penalized Buckley-James Method for Survival Data with High-Dimensional Covariates. *Biometrics*, **64**:132-140.

H. Zou and T. Hastie (2005), Regularization and variable selection via the elastic net. *Journal of the Royal Statistical Society*, Series B, **67**, 301-320.

Examples

```
data("wpbc", package = "TH.data")
wpbc2 <- wpbc[, 1:12]
wpbc2$status <- as.numeric(wpbc2$status) - 1
fit <- bujar(y=log(wpbc2$time),cens=wpbc2$status, x= wpbc2[, -(1:2)])
print(fit)
coef(fit)
pr <- predict(fit)
plot(fit)
fit <- bujar(y=log(wpbc2$time),cens=wpbc2$status, x= wpbc2[, -(1:2)], tuning = TRUE)
## Not run:
fit <- bujar(y=log(wpbc2$time),cens=wpbc2$status, x=wpbc2[, -(1:2)], learner="pspline")
fit <- bujar(y=log(wpbc2$time),cens=wpbc2$status, x=wpbc2[, -(1:2)],
 learner="tree", degree=2)
### select tuning parameter for "enet"
tmp <- gcv.enet(y=log(wpbc2$time), cens=wpbc2$status, x=wpbc2[, -(1:2)])
fit <- bujar(y=log(wpbc2$time),cens=wpbc2$status, x=wpbc2[, -(1:2)], learner="enet",
lamb = tmp$lambda, s=tmp$s)

fit <- bujar(y=log(wpbc2$time),cens=wpbc2$status, x=wpbc2[, -(1:2)], learner="mars",
degree=2)
summary(fit)

## End(Not run)
```

chop *Survival of CHOP for diffuse large B cell lymphoma*

Description

Microarray data for DLBCL patients undergoing CHOP treatment.

Usage

```
data(chop)
```

Format

The format is: num [1:181, 1:3835]

Details

Microarray data of DLBCL of 181 patients treated with a combination chemotherapy with cyclophosphamide, doxorubicin, vincristine and prednisone (CHOP). The original data have 54675 probe sets or covariates. Due to the nature of high-dimensional data, a preselection procedure was conducted to filter out the genes with lower variations if a sample variance for a gene was smaller than the 10th percentile for that gene. The first column if the survival times. The second column is an indicator whether an the survival time was observed or right censoring occurred. 0=alive, 1=dead. There are 3833 genes after the filtering process.

Source

Lenz, et al. (2008). Stromal gene signatures in large-B-cell lymphomas. *New England Journal of Medicine*, **359(22)**, 2313–2323

Examples

```
data(chop)
str(chop)
```

rchop *Survival of R-CHOP for diffuse large B cell lymphoma*

Description

Microarray data for DLBCL patients undergoing R-CHOP treatment.

Usage

```
data(rchop)
```

Format

The format is: num [1:233, 1:3835]

Details

Microarray data of DLBCL of 233 patients treated with the current gold standard R-CHOP including rituxima immunotherapy in addition to the chemotherapy CHOP. The original data have 54675 probe sets or covariates. Due to the nature of high-dimensional data, a preselection procedure was conducted to filter out the genes to match those in chop. The first column if the survival times. The second column is an indicator whether an the survival time was observed or right censoring occurred. 0=alive, 1=dead. There are 3833 same genes as in chop. The data set is used to validate the prediction accuracy for models developed using training data chop.

Source

Lenz, et al. (2008). Stromal gene signatures in large-B-cell lymphomas. *New England Journal of Medicine*, **359(22)**, 2313–2323

Examples

```
data(rchop)
str(rchop)
```

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