Package ‘bujar’

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Type Package
Title Buckley-James Regression for Survival Data with High-Dimensional Covariates
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Author Zhu Wang and others (see COPYRIGHTS)
Maintainer Zhu Wang <wangz1@uthscsa.edu>
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>.
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**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**

```r
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)
```

**Arguments**

- `y`: survival time
- `cens`: censoring indicator, must be 0 or 1 with 0=alive, 1=dead
- `x`: covariate matrix
- `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
vimprint 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 learner="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
ncore 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

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
ctype  0 (converged), 1, not converged but cycle found, 2, not converged and max iteration reached.

Author(s)
Zhu Wang

References


**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)
supply(fit)
## End(Not run)

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**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


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 chematherapy 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

Examples
```r
data(rchop)
str(rchop)
```
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