Package ‘gboost’

March 30, 2015

Type   Package

Title   High-dimensional Variable Selection in Survival Data via Gradient Boosting

Version 1.0.1

Date 2015-03-30

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Description This package implements a gradient boosting algorithm to perform automated variable selection in survival data analysis. It returns the coefficient estimates, indices of selected variables, optimal log partial likelihood and model size. Cross-validation can be enabled.

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R topics documented:

  gboost-package ........................................ 2
cv.gboost .............................................. 3
cv.gboost.default ..................................... 5
gboost .................................................. 6
gboost.default ......................................... 7
plot.cv.gboost ......................................... 9
print.cv.gboost ....................................... 9
print.gboost ......................................... 10
print.summary.cv.gboost ............................... 11
print.summary.gboost ................................. 12
summary.cv.gboost .................................... 13
summary.gboost ..................................... 13
Survl .................................................. 14

Index 16
Description

This package implements a gradient boosting algorithm to perform automated variable selection in survival data analysis. It returns the coefficient estimates, indices of selected variables, optimal log partial likelihood and model size. Cross-validation can be enabled.

Details

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Survival time, censoring indicator and covariates can be passed to the main functions as either vectors and matrices, or as data frames. The package includes four main functions:

- cv.gboost.default
- cv.gboost
- gboost.default
- gboost

Author(s)

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References


Examples

```r
require(mvtnorm)
N <- 600
p <- 50
true.beta <- array(0, c(p))
for(i in 1:p) { true.beta[(i-1)*10+1] <- (-1)^i*0.3*i }
rho <- 0.1
sigma_tmp <- matrix(0, ncol=10, nrow=10)
sigma.z <- matrix(0, ncol=p, nrow=p)
for(i in 1:10) {
  for(j in 1:10) {
    { }
```
sigma_tmp[i,j] <- rho^{abs(i-j)}
}
for(i in 1:5)
{
  sigma_z[(1+(i-1)*10):(i*10),(1+(i-1)*10):(i*10)] <- sigma_tmp
}
z <- rmvnorm(N, mean=rep(0,p), sigma=sigma_z)
U <- runif(N, 0, 1)
pre_time <- -log(U)/(1*exp(-0.3*z[,1]+0.6*z[,11]-0.9*z[,21]+1.2*z[,31]-1.5*z[,41]))
pre_censoring <- runif(N, 1, 30)
pre_censoring <- pre_censoring*(pre_censoring<3)+3*(pre_censoring>=3)
delta <- (pre_censoring>=pre_time)
time <- pre_time*(delta==1)+pre_censoring*(delta==0)

## Without formula ##
obj <- cv.gboost.default(time=time, delta=delta, z=z, nfold=5, track=3, rate=1e-4, tol=1e-4)
cbind(obj$select.var, round(obj$coefficients[obj$select.var],3))

## With formula ##

### test.data <- as.data.frame(cbind(z, time, delta))
### names(test.data[,1:5]) <- paste("V", 1:5, sep=")
obj1 <- gboost(formula=Surv(time, delta)~., data=test.data, cross.validation=TRUE)
summary(obj1)
obj2 <- cv.gboost(formula=Surv(time, delta)~ V1+ V2+ V11 + V12 + V21 + V22 + V31 + V32 + V41 + V42, data=test.data)
summary(obj2)
plot(obj2)

---

**cv.gboost**

*Function to implement cross-validation with data frame and formula as input*

**Description**

With survival time, censoring indicators and covariates input in a data frame, cv.gboost performs k fold cross validation to tune the parameter of updating steps.

**Usage**

cv.gboost(formula, data, nfold = 5, track = 5, rate = 0.01, tol = 1e-4)

**Arguments**

- **formula** specifies variables in the data frame to be responses or covariates. The responses, i.e. observed survival time and censoring indicators are specified by `Surv(time, delta)` with the first argument being the name of survival time and the second argument being the name of censoring indicators. Specifying covariate part is the same as in `lm()` for linear regression models. See the example for more details.

- **data** a data frame containing observed survival time, censoring indicators and covariates to select from.
cv.gboost

nfold  the number of folds in cross validation; default is 5.
track  the number of backtracking steps to examine cross validation risks; default is 5.
rate   a parameter specifying the learning rate; default is 0.01 to achieve slow learning.
tol    a parameter specifying the tolerance level in fitting tilde_beta_j; default is 1.0e-4.

Details

The input data should not contain missing values. Returns an object from class "cv.gboost", to which summary() and plot() can be applied to get selected variables and their estimated coefficients, model size and optimal number of updating steps, and plot the cross validation risks versus number of updating steps.

Value

Returned values can be directly accessed as in cv.gboost.default, including formula, coefficients, select.var, cv.risk, loglik, model.size, cv.m. summary() is recommended for displaying the fitted results.

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References


See Also

formula, cv.gboost.default, plot, summary.

Examples

### With formula ###

```r
# test.data <- as.data.frame(cbind(z, time, delta))
# names(test.data[,1:50]) <- paste("V", 1:50, sep="")
# obj2 <- cv.gboost(formula=Surv(time, delta)~ V1+ V2+ V11 + V12 + V21 +
# V22 + V31 + V32 + V41 + V42, data=test.data)
# summary(obj2)
# plot(obj2)
# obj3 <- cv.gboost(formula=Surv(time, delta)~ ., data=test.data)
```
cv.gboost.default  

Function to implement cross-validation with input covariate matrices

Description

With survival time, censoring indicators and covariates input as vectors or matrices, `cv.gboost.default` performs k fold cross validation to tune the parameter of updating steps.

Usage

```r
cv.gboost.default(time, delta, z, nfold = 5, track = 5, rate = 0.01, tol = 1e-04)
```

Arguments

- `time`: a numerical vector of observed survival time.
- `delta`: a numerical vector of censoring indicators. 0 stands for censored and 1 for observed event.
- `z`: a numeric matrix of observed covariates, with columns corresponding to covariates and rows to subjects.
- `nfold`: the number of folds in cross validation; default is 5.
- `track`: the number of backtracking steps to examine cross validation risks; default is 5.
- `rate`: a parameter specifying the learning rate; default is 0.01 to achieve slow learning.
- `tol`: a parameter specifying the tolerance level in fitting tilde_beta_j; default is 1.0e-4.

Details

The input data should not contain missing values. Returns a list.

Value

- `coefficients`: a vector of estimated coefficients corresponding to all covariates in `z`.
- `loglik`: the optimal log partial likelihood.
- `model.size`: the number of covariates that have non-zero coefficient estimates.
- `select.var`: the vector of indices of selected variables, i.e. covariates with non-zero coefficient estimates.
- `cv.risk`: the vector of cross validation risks at each iteration step.
- `cv.m`: the number of updating steps giving the optimal risk

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References

gboost

Function to implement proposed gradient boosting algorithm with
data frame input

Description

With survival time, censoring indicators and covariates input as a data frame, gboost.default performs variable selection using the proposed gradient boosting algorithm. The option of k fold cross validation to tune the parameter of updating steps can be enabled (default).

Usage

gboost(formula, data, cross.validation = TRUE, nfold = 5, track = 5, m.stop = 500, rate = 0.01, tol = 1e-4)

Arguments

formula specifies variables in the data frame to be responses or covariates. The responses, i.e. observed survival time and censoring indicators are specified by Surv(,) with the first argument being the name of survival time and the second argument being the name of censoring indicators. Specifying covariate part is the same as in lm() for linear regression models. See the example for more details.
data a data frame containing observed survival time, censoring indicators and covariates to select from.
cross.validation a logical value for whether cross validation is enabled or disabled; default is TRUE.
nfold the number of folds in cross validation; default is 5.
track the number of backtracking steps to examine cross validation risks; default is 5.
m.stop pre-specified number of updating steps. Only useful when cross.validation=FALSE.
rate a parameter specifying the learning rate; default is 0.01 to achieve slow learning.
tol a parameter specifying the tolerance level in fitting tilde_beta_j; default is 1.0e-4.

Details

The input data should not contain missing values. Returns an object of class "gboost".

See Also

cv.gboost, gboost.default and gboost.

Examples

# obj <- cv.gboost.default(time=time, delta=delta, z=z,
# nfold=5, track=3, rate=0.01, tol=1.0e-4)
# cbind(obj$select.var, round(obj$coefficients[obj$select.var],3))
gboost.default

Value

coefficients a vector of estimated coefficients with each element corresponding to a covariate
likelihood the estimated maximum log-likelihood.
model.size the number of covariates that have non-zero coefficients.
select.var the vector of indices of selected variables.
m.stop the number of updating steps, as pre-specified if cross.validation=FALSE, or
giving the optimal risk if cross.validation=TRUE

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References

variable selection with error control for genome-wide association studies.

See Also

summary, formula, gboost.default, cv.gboost.

Examples

# test.data <- as.data.frame(cbind(z, time, delta))
# names(test.data[,1:50]) <- paste("V", 1:50, sep="")
# obj1 <- gboost(formula=Surv(time, delta)~., data=test.data, cross.validation=T)
# summary(obj1)

---

**gboost.default**  
*Function to implement proposed gradient boosting algorithm with co-
variate matrices*

**Description**

With survival time, censoring indicators and covariates input as vectors and matrices, gboost.default
performs variable selection using the proposed gradient boosting algorithm. The option of k fold
cross validation to tune the parameter of updating steps can be enabled (default).

**Usage**

gboost.default(time, delta, z, cross.validation = TRUE, nfold = 5, track = 5, m.stop = 500, tol
Arguments

time a numerical vector of observed survival time.
delta a numerical vector of censoring indicators. 0 stands for censored and 1 for observed event.
z a numeric matrix of observed covariates, with columns corresponding to covariates and rows to subjects.
cross.validation a logical value for whether cross validation is enabled or disabled; default is TRUE.
nfold the number of folds in cross validation; default is 5. Only valid when cross.validation=TRUE.
track the number of backtracking steps to examine cross validation risks; default is 5. Only valid when cross.validation=TRUE.
m.stop a pre-specified number of updating steps; only useful when cross.validation=FALSE.
tol a parameter specifying the tolerance level in fitting tilde_beta_j; default is 1.0e-4.
rate a parameter specifying the learning rate; default is 0.01 to achieve slow learning.

Details

The input data should not contain missing values. Returns a list.

Value

coefficients a vector of estimated coefficients corresponding to all covariates in z.
loglik the optimal log partial likelihood.
model.size the number of covariates that have non-zero coefficient estimates.
select.var the vector of indices of selected variables, i.e. covariates with non-zero coefficient estimates.
m.stop the number of updating steps, as pre-specified if cross.validation=FALSE, or giving the optimal risk if cross.validation=TRUE.

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References


See Also
cv.gboost.default, cv.gboost and gboost.

Examples

# obj <- gboost.default(time=time, delta=delta, z=z, cross.validation=T,
#                        nfold=5, track=3, rate=0.01, tol=1.0e-4)
plot.cv.gboost  

Plotting an object of class 'cv.gboost'.

Description

For an object of class 'cv.gboost' from function cv.gboost, plot cross validation risks versus number of updating steps.

Usage

# S3 method for class 'cv.gboost' object
plot(obj, ...)

Arguments

obj an object of class 'cv.gboost'.
...
other arguments of plot().

Author(s)

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References


See Also

plot.

print.cv.gboost  

Print a 'cv.gboost' object

Description

Print a 'cv.gboost' object

Usage

## S3 method for class 'cv.gboost'
print(x, ...)

Arguments

x fitted cv.gboost object.
...
additional print arguments.
print.gboost

Value
Returns the call and formula of cv.gboost object.

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References

See Also
cv.gboost, print.

print.gboost  Print a 'gboost' object.

Description
Print a 'gboost' object.

Usage
print(x, ...)

Arguments
x a fitted object of class 'gboost'.
...
additional arguments for print.

Value
Returns the call and formula of a 'gboost' object.

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References

See Also
print.
Print the summary of a `cv.gboost` object.

**Description**

Print the summary of a `cv.gboost` object with a standard function `summary()`.

**Usage**

```r
# S3 method for summarizing a 'cv.gboost' object
summary(x, ...)
```

**Arguments**

- `x` : fitted `cv.gboost` object
- `...` : additional arguments for `summary()`.

**Value**

Returns the formula, log partial likelihood, model size, number of updating steps, selected variables and corresponding coefficient estimates.

**Author(s)**

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**References**


**See Also**

cv.gboost, summary.

**Examples**

```r
# summary(obj2)
```
Summarize a 'gboost' object.

Description

Print the summary of a 'gboost' object with a standard function `summary()`.

Usage

```r
# S3 method for printing the summary of a 'gboost' object
summary(x, ...)
```

Arguments

- `x`: fitted 'gboost' object.
- `...`: additional arguments for `summary()`.

Value

Returns the formula, log partial likelihood, model size, number of updating steps, selected variables and corresponding coefficient estimates.

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References


See Also

`gboost`, `summary`.

Examples

```r
# summary(obj1)
```
summary.cv.gboost

Summarize a 'cv.gboost' object.

Description

Summarize a 'cv.gboost' object.

Usage

summary.cv.gboost(x, ...)

Arguments

x  
fitted 'cv.gboost' object.

...  
additional arguments

Value

Returns an object of class 'summary.cv.gboost'.

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References


See Also
cv.gboost
Value
Returns an object of class ‘summary.gboost’.

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References

See Also
gboost

table

<table>
<thead>
<tr>
<th>Survl</th>
<th>Combining observed survival time and censoring indicators</th>
</tr>
</thead>
</table>

Description
Combining observed survival time and censoring indicators for further use in cv.gboost and gboost.

Usage

```r
Survl(time, delta)
```

Arguments

time a vector of observed survival time
delta a vector of censoring indicators of the same length as time.

Value

Returns a matrix with two columns, time and delta.

Author(s)
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References

See Also
cv.gboost
Examples

# Surv1(time,delta)
Index

cv.gboost, 3
 cv.gboost.default, 5

formula, 4, 7

gboost, 6
gboost (gboost-package), 2
gboost-package, 2
gboost.default, 7

plot, 4, 9
 plot.cv.gboost, 9
 print, 10
 print.cv.gboost, 9
 print.gboost, 10
 print.summary.cv.gboost, 11
 print.summary.gboost, 12

summary, 4, 7, 11, 12
 summary.cv.gboost, 13
 summary.gboost, 13
 Surv1, 14