

# Package ‘iBST’

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**Type** Package

**Title** Improper Bagging Survival Tree

**Version** 1.1

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**Author** Cyprien Mbogning and Philippe Broet

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**Description** Fit a bagging survival tree on a mixture of population (susceptible and nonsusceptible) using either a pseudo R2 criterion or an adjusted Logrank criterion. The predictor is evaluated using the Out Of Bag Integrated Brier Score (IBS) and several scores of importance are computed for variable selection. The thresholds values for variable selection are computed using a nonparametric permutation test.  
See 'Cyprien Mbogning' and 'Philippe Broet' (2016)<[doi:10.1186/s12859-016-1090-x](https://doi.org/10.1186/s12859-016-1090-x)> for an overview about the methods implemented in this package.

**License** GPL (>= 2)

**LazyLoad** yes

**Depends** survival , rpart , parallel

**Imports** Rcpp (>= 1.0.8)

**LinkingTo** Rcpp

**NeedsCompilation** yes

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iBST-package	<i>improper Bagging Survival Tree</i>
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### Description

Fit a bagging survival tree on a mixture of population (susceptible and nonsusceptible) using either a pseudo R2 criterion or an adjusted Logrank criterion. The predictor is evaluated using the Out Of Bag Integrated Brier Score (IBS) and several scores of importance are computed for variable selection. The thresholds values for variable selection are computed using a nonparametric permutation test. See Cyprien Mbogning and Philippe Broet (2016) <doi:10.1186/s12859-016-1090-x> for an overview about the methods implemented in this package.

### Details

Package: iBST  
 Type: Package  
 Version: 1.1  
 Date: 2022-04-17  
 License: GPL(>=2.0)

### Author(s)

Cyprien Mbogning and Philippe Broet  
 Maintainer: Cyprien Mbogning <cyprien.mbogning@gmail.com>

### References

Mbogning, C. and Broet, P. (2016). Bagging survival tree procedure for variable selection and prediction in the presence of nonsusceptible patients. *BMC bioinformatics*, 17(1), 1.

### See Also

[Bagg\\_Surv](#) [Bagg\\_pred\\_Surv](#) [improper\\_tree](#)

### Examples

```
## Not run:
data(burn)
myarg = list(cp = 0, maxcompete = 0, maxsurrogate = 0, maxdepth = 2)
Y.names = c("T3", "D3")
P.names = 'Z2'
T.names = c("Z1", paste("Z", 3:11, sep = ''))
mybag = 40
```

```
set.seed(5000)

## fit an improper survival tree
burn.tree <- suppressWarnings(improper_tree(burn,
  Y.names,
  P.names,
  T.names,
  method = "R2",
  args.rpart = myarg))

plot(burn.tree)
text(burn.tree, cex = .7, xpd = TRUE)

## fit an improper Bagging survival tree with the adjusted Logrank criterion
burn.BagEssai0 <- suppressWarnings(Bagg_Surv(burn,
  Y.names,
  P.names,
  T.names,
  method = "LR",
  args.rpart = myarg,
  args.parallel = list(numWorkers = 1),
  Bag = mybag))

## fit an improper Bagging survival tree with the pseudo R2 criterion
burn.BagEssai1 <- suppressWarnings(Bagg_Surv(burn,
  Y.names,
  P.names,
  T.names,
  method = "R2",
  args.rpart = myarg,
  args.parallel = list(numWorkers = 1),
  Bag = mybag))

## Plot the variable importance scores
par(mfrow=c(1,3))
barplot(burn.BagEssai1$IIS,
  main = 'IIS',
  horiz = TRUE,
  las = 1,
  cex.names = .8,
  col = 'lightblue')

barplot(burn.BagEssai1$DIIS,
  main = 'DIIS',
  horiz = TRUE,
  las = 1,
  cex.names = .8,
  col = 'grey')

barplot(burn.BagEssai1$DEPTH,
  main = 'MinDepth',
  horiz = TRUE,
  las = 1,
```

```

cex.names = .8,
col = 'purple')

## evaluation of the Bagging predictors
pred0 <- suppressWarnings(Bagg_pred_Surv(burn,
  Y.names,
  P.names,
  burn.BagEssai0,
  args.parallel = list(numWorkers = 1),
  OOB = TRUE))

pred1 <- suppressWarnings(Bagg_pred_Surv(burn,
  Y.names,
  P.names,
  burn.BagEssai1,
  args.parallel = list(numWorkers = 1),
  OOB = TRUE))

## End(Not run)

```

---

Bagg\_pred\_Surv

*Bagging survival tree prediction*


---

### Description

Use the Bagging improper survival tree to predict on new features and to evaluate the predictor using Out Of Bag Integrated Brier Scores with either the Nelson Aalen estimator or the Breslow estimator. A permutation importance score is also computed using OOB observations.

### Usage

```

Bagg_pred_Surv(xdata, Y.names, P.names, resBag, args.parallel = list(numWorkers = 1),
  new_data = data.frame(), OOB = FALSE)

```

### Arguments

xdata	The learning data frame
Y.names	A vector of the names of the two variables of interest (the time-to-event is follow by the event indicator)
P.names	The names of independant variables acting on the non-susceptible population (the plateau)
resBag	The result of the <a href="#">Bagg_Surv</a> function
args.parallel	a list containing the number of parallel computing arguments: The number of workers, the type of parallelization to achieve, ... see <a href="#">mclapply</a> for further details.

new_data	An optional data frame to validate the bagging procedure (the test dataset)
OOB	A value of TRUE or FALSE with TRUE indicating the computation of the OOB error using the Integrated Brier Score and also the computation of the permutation importance score.

**Value**

PREDNA	A matrix with Nelson Aalen predictions on all individuals of the learning sample
PREDBRE	A matrix with Breslow predictions on all individuals of the learning sample
tabhazNAa	A list of matrix with Nelson Aalen prediction of each tree of the bagging sequence with the leaf node prediction in each column
tabhazBRE	A list of matrix with Breslow prediction of each tree of the bagging sequence with the leaf node prediction in each column
OOB	A value of NULL if OOB is FALSE. A list of twelve elements otherwise: IBSKM: The Kaplan-Meier estimation of the Integrated Brier Score; IBSNAOOB: The OOB error using the Nelson-Aalen estimator; IBSBRE0OB: The OOB error using the Breslow estimator; vimpoobpbpna: The permutation variable importance using the Nelson-Aalen estimator; vimpoobpbpbre: The permutation variable importance using the Breslow estimator; oobibspbpna: The mean OOB error predictor by predictor using the Nelson-Aalen estimator; oobibspbpbre: The mean OOB error predictor by predictor using the Breslow estimator; SURVNAOOB: A matrix with the predicted OOB survival using the Nelson-Aalen estimator; SURVBRE0OB: A matrix with the predicted OOB survival using the Breslow estimator; BSTKM: The vector of Brier scores using the KM estimator; BSTNAOOB: The vector of Brier scores using the NA estimator; BSTBRE0OB: The vector of Brier scores using the BRE estimator.
Timediff	The execution time of the prediction procedure
TEST	A value of NULL if new_data is not available. A list of seven elements otherwise: IBSNAKMnew: The IBS using the NA estimator on the new dataset; IBSBRKMnew: The IBS using the BRE estimator on the new dataset; IBSKMnew: The IBS using the KM estimator on the new dataset; SURVNAnew: A matrix of predicted survival on the new dataset using the NA estimator; SURVBREnew: A matrix of predicted survival on the new dataset using the BRE estimator; SURV_NAnew: a vector of survival prediction on the testing dataset using the NA estimator; SURV_BREnew: a vector of survival prediction on the testing dataset using the BRE estimator.

**Author(s)**

Cyprien Mbogning and Philippe Broet

**References**

Mbogning, C. and Broet, P. (2016). Bagging survival tree procedure for variable selection and prediction in the presence of nonsusceptible patients. *BMC bioinformatics*, 17(1), 1.

**See Also**

[Bagg\\_Surv](#)

**Examples**

```
## Not run:
data(burn)
myarg = list(cp = 0, maxcompete = 0, maxsurrogate = 0, maxdepth = 2)
Y.names = c("T3" ,"D3")
P.names = 'Z2'
T.names = c("Z1", paste("Z", 3:11, sep = ''))
mybag = 40
set.seed(5000)

burn.BagEssai0 <- Bagg_Surv(burn, Y.names, P.names, T.names, method = "LR", args.rpart = myarg,
                           args.parallel = list(numWorkers = 1), Bag = mybag)

burn.BagEssai1 <- Bagg_Surv(burn, Y.names, P.names, T.names, method = "R2", args.rpart = myarg,
                           args.parallel = list(numWorkers = 1), Bag = mybag)

pred0 <- Bagg_pred_Surv(burn,
                        Y.names,
                        P.names,
                        burn.BagEssai0,
                        args.parallel = list(numWorkers = 1),
                        OOB = TRUE)

pred1 <- Bagg_pred_Surv(burn,
                        Y.names,
                        P.names,
                        burn.BagEssai1,
                        args.parallel = list(numWorkers = 1),
                        OOB = TRUE)

## End(Not run)
```

---

Bagg\_Surv

*Bagging improper survival trees*


---

**Description**

Bagging procedure to aggregate several improper trees using either the pseudo-R2 procedure or the adjusted Logrank procedure. Several scores for variables importance are computed.

**Usage**

```
Bagg_Surv(xdata,
          Y.names,
          P.names,
          T.names,
          method = "R2",
          args.rpart,
```

```
args.parallel = list(numWorkers = 1),
Bag = 100)
```

### Arguments

xdata	The learning data frame
Y.names	A vector of the names of the two variables of interest (the time-to-event is follow by the event indicator)
P.names	The names of independant variables acting on the non-susceptible population (the plateau)
T.names	The names of independant variables acting on the survival of the susceptible population
method	The choosen method (either "LR" for the Logrank or "R2" for the proposed pseudo-R2 criterion)
args.rpart	The improper survival tree parameters: a list of options that control details of the rpart algorithm. minbucket: the minimum number of observations in any terminal <leaf> node; cp: complexity parameter (Any split that does not decrease the overall lack of fit by a factor of cp is not attempted); maxdepth: the maximum depth of any node of the final tree, with the root node counted as depth 0. ... See <a href="#">rpart.control</a> for further details
args.parallel	a list containing the number of parallel computing arguments: The number of workers, the type of parallelization to achieve, ... see <a href="#">mclapply</a> for further details.
Bag	The number of Bagging samples to consider

### Details

For the Bagging procedure, it is mendatory to set `maxcompete = 0` and `maxsurrogate = 0` within the `args.rpart` arguments. This will ensured the correct calculation of the importance of variables and also a better computation time.

### Value

A list of ten elements

MaxTreeList	The list of improper survival trees computed during the bagging procedure
IIS	The Index Importance Score
DIIS	The Depth Index Importance Score
DEPTH	The minimum depth importance Score
IND_OOB	A list of length Bag containing the Out Of Bag (OOB) individuals for improper survival tree model
IIND_SAMP	The final list of length Bag of sample individuals used for each improper survival tree
IIND_SAMP	The initial list of sample individuals used for each improper survival tree at teh beginning

Bag	The number of bagging samples retained at the end of the procedure after removing the trees without leaves
indrpart	a vector of TRUE or FALSE with the value FALSE when the corresponding tree is removed from the final bagged predictor
Timediff	The elapsed time of the Bagging procedure

**Note**

This version of the code allows for the moment only one variable to have an impact on the cured population. The next version will allow more than one variable.

**Author(s)**

Cyprien Mbogning and Philippe Broet

**References**

Mbogning, C. and Broet, P. (2016). Bagging survival tree procedure for variable selection and prediction in the presence of nonsusceptible patients. *BMC bioinformatics*, 17(1), 1.

**See Also**

[Bagg\\_pred\\_Surv](#)

**Examples**

```
## Not run:
data(burn)
myarg = list(cp = 0, maxcompete = 0, maxsurrogate = 0, maxdepth = 2)
Y.names = c("T3" , "D3")
P.names = 'Z2'
T.names = c("Z1", paste("Z", 3:11, sep = ''))
mybag = 40
set.seed(5000)

burn.BagEssai0 <- Bagg_Surv(burn,
  Y.names,
  P.names,
  T.names,
  method = "LR",
  args.rpart = myarg,
  args.parallel = list(numWorkers = 1),
  Bag = mybag)

burn.BagEssai1 <- Bagg_Surv(burn,
  Y.names,
  P.names,
  T.names,
  method = "R2",
  args.rpart = myarg,
  args.parallel = list(numWorkers = 1),
```



```
Bag = mybag)
```

```
## End(Not run)
```

---

burn

*burn dataset*

---

### Description

The burn data frame has 154 rows and 17 columns.

### Usage

```
data(burn)
```

### Format

A data frame with 154 observations on the following 17 variables.

Obs Observation number

Z1 Treatment: 0=routine bathing 1=Body cleansing

Z2 Gender (0=male 1=female)

Z3 Race: 0=nonwhite 1=white

Z4 Percentage of total surface area burned

Z5 Burn site indicator: head 1=yes, 0=no

Z6 Burn site indicator: buttock 1=yes, 0=no

Z7 Burn site indicator: trunk 1=yes, 0=no

Z8 Burn site indicator: upper leg 1=yes, 0=no

Z9 Burn site indicator: lower leg 1=yes, 0=no

Z10 Burn site indicator: respiratory tract 1=yes, 0=no

Z11 Type of burn: 1=chemical, 2=scald, 3=electric, 4=flame

T1 Time to excision or on study time

D1 Excision indicator: 1=yes 0=no

T2 Time to prophylactic antibiotic treatment or on study time

D2 Prophylactic antibiotic treatment: 1=yes 0=no

T3 Time to straphylococcus aureus infection or on study time

D3 Straphylococcus aureus infection: 1=yes 0=no

### Source

Klein and Moeschberger (1997) Survival Analysis Techniques for Censored and truncated data, Springer.

Ichida et al. Stat. Med. 12 (1993): 301-310.

**Examples**

```
data(burn)
## maybe str(burn) ;
```

---

```
improper_tree      imprper survival tree
```

---

**Description**

Fit an improper survival tree for the mixed population (susceptible and nonsusceptible) using either the proposed pseudo R2 criterion or an adjusted Logrank criterion

**Usage**

```
improper_tree(xdata,
              Y.names,
              P.names,
              T.names,
              method = "R2",
              args.rpart)
```

**Arguments**

xdata	The learning data frame
Y.names	A vector of the names of the two variables of interest (the time-to-event is follow by the event indicator)
P.names	The names of independant variables acting on the non-susceptible population (the plateau)
T.names	The names of independant variables acting on the survival of the susceptible population
method	The choosen method (either "LR" for the Logrank or "R2" for the proposed pseudo-R2 criterion)
args.rpart	The improper survival tree parameters: a list of options that control details of the rpart algorithm. minbucket: the minimum number of observations in any terminal <leaf> node; cp: complexity parameter (Any split that does not decrease the overall lack of fit by a factor of cp is not attempted); maxdepth: the maximum depth of any node of the final tree, with the root node counted as depth 0. ... See <a href="#">rpart.control</a> for further details

**Value**

An unpruned improper survival tree

**Author(s)**

Cyprien Mbogning and Philippe Broet

## References

Mbogning, C. and Broet, P. (2016). Bagging survival tree procedure for variable selection and prediction in the presence of nonsusceptible patients. *BMC bioinformatics*, 17(1), 1.

## See Also

[Bagg\\_Surv](#) [Bagg\\_pred\\_Surv](#)

## Examples

```
## Not run:
data(burn)
myarg = list(cp = 0, maxcompete = 0, maxsurrogate = 0, maxdepth = 3)
Y.names = c("T3" , "D3")
P.names = 'Z2'
T.names = c("Z1", paste("Z", 3:11, sep = ''))
burn.tree <- suppressWarnings(improper_tree(burn,
  Y.names,
  P.names,
  T.names,
  method = "R2",
  args.rpart = myarg))

plot(burn.tree)
text(burn.tree, cex = .7, xpd = TRUE)

## End(Not run)
```

---

permute\_select\_surv     *permutation variable selection*

---

## Description

Variable selection using the permutation test on several scores of importance: IIS, DIIS and DEPTH.

## Usage

```
permute_select_surv(xdata,
  Y.names,
  P.names,
  T.names,
  importance = "IIS",
  method = "R2",
  Bag,
  args.rpart,
  args.parallel = list(numWorkers = 1),
  nperm = 50)
```

**Arguments**

xdata	The learning data frame
Y.names	A vector of the names of the two variables of interest (the time-to-event is follow by the event indicator)
P.names	The names of independant variables acting on the non-susceptible population (the plateau)
T.names	The names of independant variables acting on the survival of the susceptible population
importance	The importance score to consider: either IIS, DIIS or DEPTH
method	The splitting method: either "R2" for the proposed pseudo-R2 criterion or "LR" for the adjusted Logrank criterion
Bag	The number of Bagging samples to consider
args.rpart	The improper survival tree parameters: a list of options that control details of the rpart algorithm. minbucket: the minimum number of observations in any terminal <leaf> node; cp: complexity parameter (Any split that does not decrease the overall lack of fit by a factor of cp is not attempted); maxdepth: the maximum depth of any node of the final tree, with the root node counted as depth 0. ... See <a href="#">rpart.control</a> for further details
args.parallel	a list containing the number of parallel computing arguments: The number of workers, the type of parallelization to achieve, ... see <a href="#">mclapply</a> for further details.
nperm	The number of permutation samples to consider for the permutation test

**Details**

Testing weither the importance score is null or not.

**Value**

A list of five elements:

pvalperm1	The permutation test P-values ranking in decreasing order
pvalperm2	The permutation test P-values ranking in decreasing order considering an approximate gaussian distribution under the null hypothesis
pvalKS	The Kolmogorov-Smirnov P-values of the comparisons between the observed importance under the null hypothesis and a theoretical gaussian distribution
IMPH1	The observed importance score
PERMH0	A matrix with the importance scores for each permutation sample in each column

**Author(s)**

Cyprien Mbogning and Philippe Broet

## References

Mbogning, C. and Broet, P. (2016). Bagging survival tree procedure for variable selection and prediction in the presence of nonsusceptible patients. *BMC bioinformatics*, 17(1), 1.

## See Also

[Bagg\\_Surv](#) [Bagg\\_pred\\_Surv](#)

## Examples

```
## Not run:
myarg = list(cp = 0, maxcompete = 0, maxsurrogate = 0, maxdepth = 2)
Y.names = c("T3" ,"D3")
P.names = 'Z2'
T.names = c("Z1", paste("Z", 3:11, sep = ''))
mybag = 40
set.seed(5000)

data(burn)
resperm0 <- suppressWarnings(permute_select_surv(xdata = burn,
  Y.names,
  P.names,
  T.names,
  method = "LR",
  Bag = mybag,
  args.rpart = myarg,
  args.parallel = list(numWorkers = 1),
  nperm = 150))

## End(Not run)
```

---

PseudoR2.Cure

*Pseudo R2 criterion*

---

## Description

Pseudo R2 criterion for a mixture of population (susceptible and nonsusceptible populations)

## Usage

```
PseudoR2.Cure(ygene, ydelai, yetat, strate, ordered = FALSE)
```

## Arguments

ygene	The main variable of interest
ydelai	The right censored delay until the event
yetat	The censoring indicator
strate	The variables acting on the nonsusceptible or cured population
ordered	A value of TRUE or FALSE indicating whether or not the times to event are ordered

**Value**

A pseudo R2 value lying between 0 and 1.

**Author(s)**

Cyprien Mbogning and Philippe Broet

**References**

Mbogning, C. and Broet, P. (2016). Bagging survival tree procedure for variable selection and prediction in the presence of nonsusceptible patients. *BMC bioinformatics*, 17(1), 1.

**See Also**

[Bagg\\_Surv](#) [Bagg\\_pred\\_Surv](#) [improper\\_tree](#)

**Examples**

```
data(burn)
PseudoR2.Cure(ygene = burn$Z3,
  ydelai = burn$T3,
  yetat = burn$D3,
  strate = burn$Z2)
```

```
PseudoR2.Cure(ygene = burn$Z2,
  ydelai = burn$T3,
  yetat = burn$D3,
  strate = burn$Z2)
```

---

rcpp\_hello\_world      *Simple function using Rcpp*

---

**Description**

Simple function using Rcpp

**Usage**

```
rcpp_hello_world()
```

**Examples**

```
## Not run:
rcpp_hello_world()

## End(Not run)
```

---

tree2indicators      *From a tree to indicators (or dummy variables)*

---

**Description**

Coerces a given tree structure inheriting from rpart to binary covariates.

**Usage**

```
tree2indicators(fit)
```

**Arguments**

fit                    a tree structure inheriting to the rpart method

**Value**

a list of indicators defining the leaf nodes of the fitted tree from left to right

**Author(s)**

Cyprien Mbogning

**Examples**

```
fit <- rpart(Kyphosis ~ Age + Number + Start, data = kyphosis)
tree2indicators(fit)
```

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