

Package ‘icrf’

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Title Interval Censored Recursive Forests

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biocViews

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Description Implements interval censored recursive forests (ICRF) based on Cho, Jewell, and Kosorok (2021+).
ICRF is a variant of random forests where the outcome variable is interval censored survival data. It can be used for usual right censored data and current status data as well.
A recursion technique is used to improve accuracy and smoothed survival curves are provided.

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getTree.icrf	<i>Extract a single tree from an icrf object</i>
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Description

getTree 'extracts the structure of a tree from an icrf object.' Among nfold forests, the forest designated when implementing icrf will be considered. i.e., the kth tree of the last forest, when returnBest = FALSE or the tree of the best forest, when returnBest = TRUE, will be extracted. (Quoted statements are from randomForest by Liaw and Wiener unless otherwise mentioned.)

Usage

```
getTree(x, ...)

## S3 method for class 'icrf'
getTree(x, k = 1, labelVar = FALSE, ...)
```

Arguments

x	an icrf object.
...	not used.
k	'which tree to extract?'
labelVar	Splitting variables will be labelled with the original names when labelVar = TRUE. Otherwise they will be expressed as integers.

Details

'For numerical predictors, data with values of the variable less than or equal to the splitting point go to the left daughter node.'

'For categorical predictors, the splitting point is represented by an integer, whose binary expansion gives the identities of the categories that goes to left or right. For example, if a predictor has four

categories, and the split point is 13. The binary expansion of 13 is (1, 0, 1, 1) (because $13 = 1 \cdot 2^0 + 0 \cdot 2^1 + 1 \cdot 2^2 + 1 \cdot 2^3$), so cases with categories 1, 3, or 4 in this predictor get sent to the left, and the rest to the right.’

Value

’A matrix (or data frame, if labelVar=TRUE) with’ (5 + number of time points) ’columns and number of rows equal to total number of nodes in the tree. The columns are:’

- left daughter: ’the row where the left daughter node is; 0 if the node is terminal’
- right daughter: ’the row where the right daughter node is; 0 if the node is terminal’
- split var: ’which variable was used to split the node; 0 if the node is terminal’
- split point: ’where the best split is; see Details for categorical predictor’
- status: ’is the node terminal’ (-1) or not (-3)
- from the 6th to the last columns: the survival probability prediction for the node; each column represents the distinct time points. ’0 if the node is not terminal’

Examples

```
library(survival) # for Surv()
data(rat2)
L = ifelse(rat2$tumor, 0, rat2$survtime)
R = ifelse(rat2$tumor, rat2$survtime, Inf)
# Note that this is a toy example. Use a larger ntree and nfold in practice.

set.seed(1)
rats.icrf <-
  icrf(Surv(L, R, type = "interval2") ~ dose.lvl + weight + male + cage.no,
        data = rat2, ntree = 10, nfold = 3)
getTree(rats.icrf, k = 2)
```

Description

icrf implements the ICRF algorithm to estimate the conditional survival probability for interval censored survival data. (It can also be used for right-censored survival data and current status data.) icrf recursively builds random forests using the extremely randomized trees (ERT) algorithm and uses kernel smoothing in the time domain. This icrf package is built based on the randomForest package by Andy Liaw and Matthew Wiener. (Quoted statements are from randomForest by Liaw and Wiener unless otherwise mentioned.)

Usage

```

icrf(x, ...)

## Default S3 method:
icrf(
  x,
  L,
  R,
  tau = max(R[is.finite(R)]) * 1.5,
  bandwidth = NULL,
  quasihonesty = TRUE,
  initialSmoothing = TRUE,
  timeSmooth = NULL,
  xtest = NULL,
  ytest = NULL,
  nfold = 5L,
  ntree = 500L,
  mtry = ceiling(sqrt(p)),
  split.rule = c("Wilcoxon", "logrank", "PetoWilcoxon", "PetoLogrank", "GWRS", "GLR",
    "SWRS", "SLR"),
  ERT = FALSE,
  uniformERT = ERT,
  returnBest = sampsize < n,
  imse.monitor = 1,
  replace = !ERT,
  sampsize = ifelse(ERT, 0.95, 0.632) * n,
  nodesize = 6L,
  maxnodes = NULL,
  importance = FALSE,
  nPerm = 1,
  proximity,
  oob.prox = ifelse(sampsize == n & !replace, FALSE, proximity),
  do.trace = FALSE,
  keep.forest = is.null(xtest),
  keep.inbag = FALSE,
  ...
)

## S3 method for class 'formula'
icrf(
  formula,
  data = NULL,
  data.type = c("interval", "right", "currentstatus"),
  interval.label = c("L", "R"),
  right.label = c("T", "status"),
  currentstatus.label = c("monitor", "status"),
  ...,
  na.action = na.fail,

```

```

    epsilon = NULL
  )

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

```

Arguments

<code>x</code>	a data frame or a matrix of predictors. <code>x</code> is not needed when <code>formula</code> is specified.
<code>...</code>	optional arguments to be passed to <code>icrf.default</code> .
<code>L, R</code>	the left and right end point of the interval. <code>R</code> should be greater than or equal to <code>L</code> . In case of equality, a small number <code>epsilon</code> (the smaller of minimum nonzero interval length and $1e-10$) is added.
<code>tau</code>	the study end time. ($[0, \tau]$ is the window for the analysis.)
<code>bandwidth</code>	a positive number. The bandwidth of the kernel smoothing. For faster computing, set <code>bandwidth = 0</code> for no smoothing.
<code>quasihonesty</code>	if TRUE, the terminal node prediction is given by the NPMLLE of the interval data. If FALSE, the terminal node prediction is given by the average of the conditional probabilities (exploitative).
<code>initialSmoothing</code>	if TRUE, the initial survival curve used for interval-conditional survival probability estimate is smoothed using the Gaussian kernel.
<code>timeSmooth</code>	a numeric vector of time points at which the smoothed survival curves are estimated. It should be in an increasing order. If null, a set of distinct interval end points is used.
<code>xtest</code>	a dataset or matrix of predictors for the test dataset.
<code>ytest</code>	a true survival curve for the test set in a form of the dataframe or matrix. The number of rows is the same as <code>xtest</code> and each column corresponds to the time points of <code>timeSmooth</code> .
<code>ifold</code>	Number of forests to iterate. In practice, numbers between 5 and 10 is reasonable.
<code>ntree</code>	Number of trees to build within each forest. 'This should not be set to too small a number, to ensure that every input row gets predicted at least a few times.'
<code>mtry</code>	Number of candidate predictors tried at each split. The default value is \sqrt{p} where p is number of variables in <code>x</code> .
<code>split.rule</code>	Splitting rules. See details. The default is "Wilcoxon", or equivalently "GWRs".
<code>ERT</code>	If <code>ERT=TRUE</code> ERT algorithm applies. If FALSE, a comprehensive greedy algorithm (Breiman's random forest algorithm) applies.
<code>uniformERT</code>	Only relevant when <code>ERT=TRUE</code> . If <code>uniformERT=TRUE</code> , random candidate cut-points are selected using uniform distribution. If FALSE, random candidate cut-points are chosen among the midpoints of two neighboring predictor values.

<code>returnBest</code>	If <code>returnBest=TRUE</code> , the survival curve estimate at the best iteration is returned. If <code>FALSE</code> , the estimate at the last iteration is returned. The best iteration is determined by the type of IMSE measures specified in <code>imse.monitor</code> . By default, <code>returnBest=TRUE</code> when the out-of-bag sample is available (<code>sampsiz < n</code>).
<code>imse.monitor</code>	Which type of IMSE is used to monitor which fold is the best?
<code>replace</code>	Whether the cases are sampled with or without replacement?
<code>sampsiz</code>	Size of random sampling.
<code>nodesiz</code>	Each terminal node cannot be smaller than this value. 'Setting this number larger causes smaller trees to be grown (and thus take less time).'
<code>maxnodes</code>	Up to how many terminal nodes can a tree have? 'If not given, trees are grown to the maximum possible (subject to limits by <code>nodesiz</code>). If set larger than maximum possible, a warning is issued.'
<code>importance</code>	If <code>TRUE</code> , variable importance measure will be computed.
<code>nPerm</code>	How many permutations (of OOB data) to do for variable importance assessment? 'Number larger than 1 gives slightly more stable estimate, but not very effective. Currently only implemented for regression.'
<code>proximity</code>	If <code>TRUE</code> , proximity measure among the cases is calculated.
<code>oob.prox</code>	If <code>TRUE</code> , proximity is calculated only on "out-of-bag" data.
<code>do.trace</code>	If <code>TRUE</code> , intermediate outputs are printed during the tree building procedure. 'If set to some integer, then running output is printed for every <code>do.trace</code> trees.'
<code>keep.forest</code>	'If set to <code>FALSE</code> , the forest will not be retained in the output object. If <code>xtest</code> is given, defaults to <code>FALSE</code> .'
<code>keep.inbag</code>	'Should an <code>n</code> by <code>ntree</code> matrix be returned that keeps track of which samples are "in-bag" in which trees (but not how many times, if sampling with replacement)'
<code>formula</code> , <code>data.type</code> , <code>interval.label</code> , <code>right.label</code> , <code>currentstatus.label</code>	a formula object, with the response in a Surv 'interval2' or <code>cbind</code> . Alternatively, the survival outcome may be omitted in the formula and the labels relevant to the survival outcome can be entered in either <code>interval.label</code> , <code>right.label</code> , or <code>currentstatus.label</code> with the <code>data.type</code> being specified.
<code>data</code>	a data frame that includes the intervals and the predictor values.
<code>na.action</code>	'a function to specify the action to be taken if NAs are found. (NOTE: If given, this argument must be named.)'
<code>epsilon</code>	A small positive value needed to discriminate the left and right interval end points for the uncensored data.

Details

Four `split.rule` options are available: `Wilcoxon`, `logrank`, `PetoWilcoxon`, `PetoLogrank`. The aliases are `GWRS`, `GLR`, `SWRS`, and `SLR`, respectively. The first two are generalized Wilcoxon-rank-sum test and generalized log-rank test proposed in Cho et al (2020+), and the latter two are score-based Wilcoxon-rank-sum test and score-based log-rank test proposed by Peto and Peto (1972) "Asymptotically efficient rank invariant test procedures."

Value

An icrf class object which contains the following components in a list:

An icrf class object which contains the following components in a list:

- callthe original call to icrf
- methodThe input values of split.rule, ERT, quasihonest, bandwidth, and the subsample ratio (= sampsize / n)
- predictedthe estimated survival curves of the training set using out-of-bag samples.
- predictedNOthe estimated survival curves of the training set using non-out-of-bag samples.
- predictedNO.Smthe smoothed survival curves of the training set using non-out-of-bag samples.
- time.pointstime points at which the survival curves are estimated.
- time.points.smoothtime points at which the smoothed survival curves are estimated.
- imse.oobIntegrated mean squared error (IMSE) measured based on the out-of-bag samples
- imse.NOIntegrated mean squared error (IMSE) measured based on the non-out-of-bag samples
- oob.timesnumber of times for which each case was 'out-of-bag'
- importancean array of three matrices where each matrix has nfold columns and p (number of predictors) rows. The importance is measured based on increase in IMSE types 1 and 2, respectively, and the node impurity.
- importanceSD'The "standard errors" of the permutation-based importance measure.' A p by nfold by 2 array corresponding to the first two matrices of the importance array.
- nfoldnumber of forests iterated over.
- ntreenumber of trees built.
- mtrynumber of candidate predictors tried at each node.
- forest'a list that contains the entire forest;' NULL 'if keep. forest=FALSE.'
- intervalsn by 2 matrix of the intervals.
- proximityif proximity=TRUE if proximity=TRUE when icrf is called, a matrix of proximity measures among the input (based on the frequency that pairs of data points are in the same terminal nodes). inbagif keep.inbag=TRUE provides a matrix of in-bag indicators for the last forest iteration. runtimestart and end times and the elapsed time. testif test set is given (through the xtest or additionally ytest arguments), this component is a list which contains the corresponding predicted and error measures (IMSE's). If proximity=TRUE, there is also a component, proximity, which contains the proximity among the test set as well as proximity between test and training data.

Author(s)

Hunyoung Cho, Nicholas P. Jewell, and Michael R. Kosorok.

References

Cho H., Jewell N. J., and Kosorok M. R. (2020+). "Interval censored recursive forests"

See Also

[predict.icrf](#), [plot.icrf](#), [survplot](#), [importance.icrf](#)

Examples

```
# rats data example.
# The type of this dataset is current status data.
# Note that this is a toy example. Use a larger ntree and nfold in practice.
data(rat2)

set.seed(2)
# 1. formula (currentstatus)
rats.icrf <-
  icrf(~ dose.lvl + weight + male + cage.no, data = rat2,
       data.type = "currentstatus", currentstatus.label = c("survtime", "tumor"),
       returnBest = TRUE, ntree=10, nfold=3)

# 2. formula containing the interval
# Alternatively, create the interval endpoints and use the Surv object.
L = ifelse(rat2$tumor, 0, rat2$urvtime)
R = ifelse(rat2$tumor, rat2$urvtime, Inf)
library(survival) # for Surv function
icrf(Surv(L, R, type = "interval2") ~ dose.lvl + weight + male + cage.no, data = rat2,
     ntree=10, nfold=3)

# Or, 3. formula (interval)
rat2b <- cbind(rat2, L = L, R = R)
set.seed(1)
icrf( ~ dose.lvl + weight + male + cage.no, data = rat2b,
     data.type = "interval", interval.label = c("L", "R"),
     ntree=10, nfold=3)

# 4. default method
set.seed(1)
icrf(rat2[, c("dose.lvl", "weight", "male", "cage.no")], L = L, R = R,
     ntree=10, nfold=3)
```

importance.icrf	<i>'Extract variable importance measure'</i>
-----------------	--

Description

'This is the extractor function for variable importance measures as produced by' icrf. (Quoted statements are from randomForest by Liaw and Wiener unless otherwise mentioned.)

Usage

```
importance(x, ...)

## Default S3 method:
importance(x, ...)

## S3 method for class 'icrf'
importance(x, type = NULL, ...)
```

Arguments

x	'an object of class' icrf
...	'not used'
type	either 1, 2, 3, or any combination of them, 'specifying the type of importance measure' (1 = mean increase in IMSE1, 2 = mean increase in IMSE2, 3 = mean decrease in node impurity). If not specified, all available types of importances are returned.

Details

'Here are the definitions of the variable importance measures. The first two measures are computed from permuting OOB data: For each tree, the prediction error on the out-of-bag portion of the data is recorded' (IMSE1 and IMSE2). 'Then the same is done after permuting each predictor variable.' 'The difference between the two are then averaged over all trees' The normalization by the standard deviation of the differences is not supported in this version. The third measure 'is the total decrease in node impurities from splitting on the variable, averaged over all trees.' 'For regression, it is measured by residual sum of squares.'

Value

An array of importance measure matrices, one row for each predictor variable.' Each column corresponds to the forest iteration. Each matrix corresponds to the type of the measure.

Author(s)

Hunyoung Cho, Nicholas P. Jewell, and Michael R. Kosorok.

[Cho H., Jewell N. J., and Kosorok M. R. \(2020+\). "Interval censored recursive forests"](#)

See Also

icrf, varImpPlot

Examples

```
# rats data example.
# Note that this is a toy example. Use a larger ntree and nfold in practice.
data(rat2)

set.seed(1)
```

```
rats.icrf <-
  icrf(~ dose.lvl + weight + male + cage.no, data = rat2,
       data.type = "currentstatus", currentstatus.label = c("survtime", "tumor"),
       returnBest = TRUE, ntree=10, nfold=3)
importance(rats.icrf)
```

 measure

Prediction error measures

Description

This function measures the prediction errors including the IMSE (integrated mean squared error) of type 1 and 2, the integrated absolute error, and the supremum absolute error. When the true survival curve is unknown but the observed interval is available, IMSE is used. When the true survival curve is known, the integrated and supremum absolute errors are used.

Usage

```
measure(
  surv.hat,
  timepoints,
  tau,
  method = c("all", "imse", "int.error"),
  L = NULL,
  R = NULL,
  surv.true = NULL
)
```

Arguments

surv.hat	the estimated survival curve matrix with rows representing the observations and the columns representing the time points at which the survival curve is estimated.
timepoints	a vector of time points at which the survival curve is estimated.
tau	the study end time. ([0, tau] is the window for the analysis.)
method	Which measure will be used? Either <code>imse</code> , <code>int.error</code> (<code>int.error</code> returns both integrated and supremum absolute errors), or <code>all</code> (both) should be entered.
L, R	the left and right interval endpoints. These are required when <code>method == "imse"</code> or <code>"all"</code> .
surv.true	the true survival curve matrix with rows representing the observations and the columns representing the time points at which the survival curve is evaluated. This is required when <code>method == "int.error"</code> or <code>"all"</code> .

Details

For details of the error measures, see Cho H., Jewell N. J., and Kosorok M. R. (2020+). "Interval censored recursive forest"

Value

A vector of prediction errors:

- `imse.type1` and `imse.type2` when `method == "imse"`
- `int.error` and `sup.error` when `method == "int.error"`
- `imse.type1`, `imse.type2`, `int.error`, and `sup.error` when `method == "all"`

Author(s)

Hunyong Cho hunycho@live.unc.edu, based on the code and the documents of `randomForest` by Andy Liaw and Matthew Wiener.

References

[Cho H., Jewell N. J., and Kosorok M. R. \(2020+\). "Interval censored recursive forests"](#)

Examples

```
# rats data example.
# Note that this is a toy example. Use a larger ntree and nfold in practice.
library(survival) # for Surv()
data(rat2)
L = ifelse(rat2$tumor, 0, rat2$survtime)
R = ifelse(rat2$tumor, rat2$survtime, Inf)

set.seed(1)
rats.icrf <-
  icrf(Surv(L, R, type = "interval2") ~ dose.lvl + weight + male + cage.no,
        data = rat2, ntree = 10, nfold = 3)

measure(rats.icrf$predicted.Sm, timepoints = rats.icrf$time.points,
        tau = rats.icrf$tau, method = "imse", L = L, R = R)
```

plot

icrf IMSE rate plot

Description

'Plot the error rates or MSE of a `randomForest` object' (Quoted statements are from `randomForest` by Liaw and Wiener unless otherwise mentioned.)

Usage

```
## S3 method for class 'icrf'
plot(x, type = "l", main = deparse(substitute(x)), oob = FALSE, ...)
```

Arguments

x	an object of icrf class.
type	'type of plot.'
main	'main title of the plot.'
oob	Whether the out-of-bag error should be returned?
...	'other graphical parameters.'

Value

The IMSE (integrated mean squared error) of the `icrf` object is invisibly returned. 'If the object has a non-null test component, then the returned object is a matrix where the first' (two) column is the IMSE measure (types 1 and 2), 'and the second column is for the test set.' The rows represent the forest iterations.

Note

'If the x has a non-null test component, then the test set errors are also plotted.'

Author(s)

Hunyoung Cho, Nicholas P. Jewell, and Michael R. Kosorok.

References

Cho H., Jewell N. J., and Kosorok M. R. (2020+). "Interval censored recursive forests"

Examples

```
# rats data example
# Note that this is a toy example. Use a larger ntree and nfold in practice.
data(rat2)
set.seed(1)
samp <- sample(1:dim(rat2)[1], 200)
rats.train <- rat2[samp, ]
rats.test <- rat2[-samp, ]
# Note that this is a toy example. Use a larger ntree and nfold in practice.
set.seed(2)

rats.icrf.small <-
  icrf(~ dose.lvl + weight + male + cage.no, data = rat2,
       data.type = "currentstatus", currentstatus.label = c("survtime", "tumor"),
       returnBest = TRUE, ntree=10, nfold=3)
plot(rats.icrf.small)
```

predict.icrf	<i>icrf predictions</i>
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Description

Prediction method of test data using interval censored recursive forest. (Quoted statements are from randomForest by Liaw and Wiener unless otherwise mentioned.)

Usage

```
## S3 method for class 'icrf'
predict(
  object,
  newdata,
  predict.all = FALSE,
  proximity = FALSE,
  nodes = FALSE,
  smooth = TRUE,
  ...
)
```

Arguments

object	an object of icrf class generated by the function icrf.
newdata	'a data frame or matrix containing new data. (Note: If not given, the predicted survival estimate of the training data set in the object is returned.)'
predict.all	'Should the predictions of all trees be kept?'
proximity	'Should proximity measures be computed?'
nodes	'Should the terminal node indicators (an n by ntree matrix) be returned? If so, it is in the "nodes" attribute of the returned object.'
smooth	Should smoothed curve be returned?
...	'not used currently.'

Value

A matrix of predicted survival probabilities is returned where the rows represent the observations and the columns represent the time points. 'If predict.all=TRUE, then the returned object is a list of two components: aggregate, which is the vector of predicted values by the forest, and individual, which is a matrix where each column contains prediction by a tree in the forest.' The forest is either the last forest or the best forest as specified by returnBest argument in icrf function.

'If proximity=TRUE, the returned object is a list with two components: pred is the prediction (as described above) and proximity is the proximity matrix.'

'If nodes=TRUE, the returned object has a "nodes" attribute, which is an n by ntree matrix, each column containing the node number that the cases fall in for that tree.'

Author(s)

Hunyoung Cho, Nicholas P. Jewell, and Michael R. Kosorok.

References

Cho H., Jewell N. J., and Kosorok M. R. (2020+). "Interval censored recursive forests"

Examples

```
# rats data example
# Note that this is a toy example. Use a larger ntree and nfold in practice.
library(survival) # for Surv()
data(rat2)
set.seed(1)
samp <- sample(1:dim(rat2)[1], 200)
rats.train <- rat2[samp, ]
rats.test <- rat2[-samp, ]
L = ifelse(rats.train$tumor, 0, rats.train$survtime)
R = ifelse(rats.train$tumor, rats.train$survtime, Inf)

set.seed(2)
rats.icrf.small <-
  icrf(survival::Surv(L, R, type = "interval2") ~ dose.lvl + weight + male + cage.no,
       data = rats.train, ntree = 10, nfold = 3, proximity = TRUE)

# predicted survival curve for the training data
predict(rats.icrf.small)
predict(rats.icrf.small, smooth = FALSE) # non-smoothed

# predicted survival curve for new data
predict(rats.icrf.small, newdata = rats.test)
predict(rats.icrf.small, newdata = rats.test, proximity = TRUE)

# time can be extracted using attr()
newpred = predict(rats.icrf.small, newdata = rats.test)
attr(newpred, "time")

newpred2 = predict(rats.icrf.small, newdata = rats.test, proximity = TRUE)
attr(newpred2$predicted, "time")
```

Description

This is the ‘Rat tumor data’ data from Dinse and Lagakos (1984). 112 female and 207 male rats. This data can be considered as a current status data where the time (T) from birth to the onset of the tumor is the main variable of interest but is never observed, but can only be guessed by the set of the death time (survtime) and the tumor indicator (tumor). Quotes are from Dinse and Lagakos (1984).

Usage

```
data(rat2)
```

Format

A data frame with 319 rows and 6 variables:

dose.lvl ‘dose level of PBB (coded 0-5).’

weight ‘initial weight in grams.’

cage.no ‘number of the cage tier.’

survtime ‘survival time (age) in weeks.’

tumor ‘response indicator (1 = hyperplasia present, 0 = hyperplasia absent).’

male The gender (0 = female, 1 = male).

References

Dinse, G. E., & Lagakos, S. W. (1983). Regression analysis of tumour prevalence data. *Journal of the Royal Statistical Society: Series C (Applied Statistics)*, 32(3), 236-248.

Dinse, G. E., & Lagakos, S. W. (1984). Correction: Regression analysis of tumour prevalence data. *Journal of the Royal Statistical Society: Series C (Applied Statistics)*, 33(1), 79-80.

survplot	<i>‘Plotting individual survival curves’</i>
----------	--

Description

Plotting individual survival curves.

Usage

```
survplot(
  x,
  i,
  smooth = TRUE,
  timepoints = NULL,
  title = "Estimated survival curve",
  suppress.inf.time = TRUE,
  ...
)
```

Arguments

x	an object of class <code>icrf</code> or a survival matrix with rows representing subjects and columns representing times
i	subject index
smooth	which curve of an <code>icrf</code> object to be plotted? smoothed or non-smoothed. Ignored when x is a matrix.
timepoints	A numeric vector. needed when the time attribute is missing.
title	Title of the plot.
suppress.inf.time	Do not draw the curve at timepoints being infinity?
...	'Other graphical parameters to be passed on to' <code>ggplot</code> .

Value

'Invisibly,' the vector of survival probabilities that are plotted.

Author(s)

Hunyoung Cho, Nicholas P. Jewell, and Michael R. Kosorok.

References

Cho H., Jewell N. J., and Kosorok M. R. (2020+). "Interval censored recursive forests"

Examples

```
# rats data example.
# Note that this is a toy example. Use a larger ntree and nfold in practice.
data(rat2)

set.seed(1)
rats.icrf <-
  icrf(~ dose.lvl + weight + male + cage.no, data = rat2,
        data.type = "currentstatus", currentstatus.label = c("survtime", "tumor"),
        returnBest = TRUE, ntree=10, nfold=3)
survplot(rats.icrf, c(1,3,5))
```

treesize.icrf *Size of trees in an icrf ensemble*

Description

'Size of trees (number of nodes)' in the returned forest of icrf. The returned forest depends on the returnBest argument of the icrf function; It is either the last forest, when returnBest = FALSE or the the best forest, when returnBest = TRUE. (Quoted statements are from randomForest by Liaw and Wiener unless otherwise mentioned.)

Usage

```
treesize(x, ...)  
  
## S3 method for class 'icrf'  
treesize(x, terminal = TRUE, ...)
```

Arguments

x	an object of class icrf, 'which contains a forest component.'
...	'not used.'
terminal	'count terminal nodes only (TRUE) or all nodes (FALSE)'

Value

'A vector containing number of nodes for the trees' in the icrf object.

Note

The icrf 'object must contain the forest component; i.e., created with' `icrf(..., keep.forest=TRUE)`.

Author(s)

Hunyoung Cho, Nicholas P. Jewell, and Michael R. Kosorok.

References

[Cho H., Jewell N. J., and Kosorok M. R. \(2020+\). "Interval censored recursive forests"](#)

Examples

```
# rats data example.  
# Note that this is a toy example. Use a larger ntree and nfold in practice.  
data(rat2)  
  
set.seed(1)  
rats.icrf <-  
  icrf(~ dose.lvl + weight + male + cage.no, data = rat2,
```

```

data.type = "currentstatus", currentstatus.label = c("survtime", "tumor"),
returnBest = TRUE, ntree=10, nfold=3)
treesize(rats.icrf)

```

varImpPlot.icrf *'Variable Importance Plot'*

Description

'Dotchart of variable importance as measured by' icrf. (Quoted statements are from randomForest by Liaw and Wiener unless otherwise mentioned.)

Usage

```

varImpPlot(x, ...)

## S3 method for class 'icrf'
varImpPlot(
  x,
  sort = TRUE,
  n.var = min(30, nrow(x$importance)),
  type = NULL,
  forest = NULL,
  main = deparse(substitute(x)),
  ...
)

```

Arguments

x	'an object of class' icrf
...	'Other graphical parameters to be passed on to dotchart.'
sort	'Should the variables be sorted in decreasing order of importance?'
n.var	'How many variables to show? (Ignored if sort=FALSE.)'
type	'arguments to be passed on to importance'
forest	The forest for which the importance is plotted. If NULL, the best forest is plotted.
main	'plot title'

Value

'Invisibly, the importance of the variables that were plotted.'

Author(s)

Hunyoung Cho, Nicholas P. Jewell, and Michael R. Kosorok.

References

Cho H., Jewell N. J., and Kosorok M. R. (2020+). "Interval censored recursive forests"

Examples

```
# rats data example.
# Note that this is a toy example. Use a larger ntree and nfold in practice.
data(rat2)

set.seed(1)
rats.icrf <-
  icrf(~ dose.lvl + weight + male + cage.no, data = rat2,
       data.type = "currentstatus", currentstatus.label = c("survtime", "tumor"),
       returnBest = TRUE, ntree=10, nfold=3)
varImpPlot(rats.icrf)
```

varUsed.icrf	<i>'Variables used in' an icrf ensemble</i>
--------------	---

Description

'Find out which predictor variables are actually used in' the returned forest of the icrf. The returned forest depends on the returnBest argument of the icrf function; It is either the last forest, when returnBest = FALSE or the the best forest, when returnBest = TRUE. (Quoted statements are from randomForest by Liaw and Wiener unless otherwise mentioned.)

Usage

```
varUsed(x, ...)

## S3 method for class 'icrf'
varUsed(x, by.tree = FALSE, count = TRUE, ...)
```

Arguments

x	'an object of class' icrf.
...	not used.
by.tree	'Should the list of variables used be broken down by trees in the forest?'
count	'Should the frequencies that variables appear in trees be returned?'

Value

'A vector containing number of nodes for the trees' in the icrf object.

'If count=TRUE and by.tree=FALSE, an integer vector containing frequencies that variables are used in the forest. If by.tree=TRUE, a matrix is returned, breaking down the counts by tree (each column corresponding to one tree and each row to a variable).'

'If count=FALSE and by.tree=TRUE, a list of integer indices is returned giving the variables used in the trees, else if by.tree=FALSE, a vector of integer indices giving the variables used in the entire forest.'

Author(s)

Hunyoung Cho, Nicholas P. Jewell, and Michael R. Kosorok.

References

[Cho H., Jewell N. J., and Kosorok M. R. \(2020+\). "Interval censored recursive forests"](#)

Examples

```
# rats data example.  
# Note that this is a toy example. Use a larger ntree and nfold in practice.  
data(rat2)  
  
set.seed(1)  
rats.icrf <-  
  icrf(~ dose.lvl + weight + male + cage.no, data = rat2,  
       data.type = "currentstatus", currentstatus.label = c("survtime", "tumor"),  
       returnBest = TRUE, ntree=10, nfold=3)  
varUsed(rats.icrf)
```

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