

# Package ‘SurvivalClusteringTree’

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**Type** Package

**Title** Clustering Analysis Using Survival Tree and Forest Algorithms

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## Description

An outcome-guided algorithm is developed to identify clusters of samples with similar characteristics and survival rate. The algorithm first builds a random forest and then defines distances between samples based on the fitted random forest. Given the distances, we can apply hierarchical clustering algorithms to define clusters. Details about this method is described in <<https://github.com/luyouepiusf/SurvivalClusteringTree>>.

**License** GPL (>= 2)

**Suggests** knitr, rmarkdown, tinytest

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**NeedsCompilation** yes

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SurvivalClusteringTree-package

*Clustering Analysis Using Survival Tree and Forest Algorithms*

---

**Description**

An outcome-guided algorithm is developed to identify clusters of samples with similar characteristics and survival rate. The algorithm first builds a random forest and then defines distances between samples based on the fitted random forest. Given the distances, we can apply hierarchical clustering algorithms to define clusters. Details about this method is described in <<https://github.com/luyouepiusf/SurvivalClusteringTree>>

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**Maintainer**

Lu You <lu.you@epi.usf.edu>

**Author(s)**

NA

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plot\_survival\_tree     *Visualize the Fitted Survival Tree*

---

**Description**

Visualize the Fitted Survival Tree

**Usage**

```
plot_survival_tree(survival_tree, cex = 0.75)
```

**Arguments**

survival\_tree     a fitted survival tree object.  
cex                numeric character expansion factor.

**Value**

No return value, called for generating graphical outputs.

**Examples**

```
library(survival)
a_survival_tree<-
  survival_tree(
    survival_outcome=Surv(time,status==2)~1,
    numeric_predictor=~age+ph.ecog+ph.karno+pat.karno+meal.cal,
    factor_predictor=~as.factor(sex),
    data=lung)
plot_survival_tree(a_survival_tree)
```

---

predict\_distance\_forest

*Predict Distances Between Samples Based on a Survival Forest Fit  
(Data Supplied as a Dataframe)*

---

**Description**

The function `predict_distance_forest` predicts distances between samples based on a survival forest fit.

**Usage**

```
predict_distance_forest(
  survival_forest,
  numeric_predictor,
  factor_predictor,
  data,
  missing = "omit"
)
```

**Arguments**

`survival_forest` a fitted survival forest

`numeric_predictor` a formula specifying the numeric predictors. As in `~x1+x2+x3`, the three numeric variables `x1`, `x2`, and `x3` are included as numeric predictors. `x1[i]`, `x2[i]`, and `x3[i]` are the predictors of the *i*th sample. The best practice is to use the same variables names in the training and testing dataset.

`factor_predictor` a formula specifying the numeric predictors. As in `~z1+z2+z3`, the three character variables `z1`, `z2`, and `z3` are included as factor predictors. `z1[i]`, `z2[i]`, and `z3[i]` are the predictors of the *i*th sample. The best practice is to use the same variables names in the training and testing dataset.

`data` the dataframe (test data) that stores the outcome and predictor variables. Variables in the global environment will be used if `data` is missing.

**missing** a character value that specifies the handling of missing data. If `missing=="omit"`, samples with missing values in the splitting variables will be discarded. If `missing=="majority"`, samples with missing values in the splitting variables will be assigned to the majority node. If `missing=="weighted"`, samples with missing values in the splitting variables will be weighted by the weights of branch nodes. The best practice is to use the same method as the trained random forest.

## Details

Predict Distances Between Samples Based on a Survival Forest Fit (Data Supplied as a Dataframe)

## Value

A list. `mean_distance` is the mean distance matrix. `sum_distance` is the matrix that sums the distances between samples. `sum_non_na` is the matrix of the number of non NA distances being averaged.

## Examples

```
library(survival)
a_survival_forest<-
  survival_forest(
    survival_outcome=Surv(time,status==2)~1,
    numeric_predictor=~age+ph.ecog+ph.karno+pat.karno+meal.cal,
    factor_predictor=~as.factor(sex),
    data=lung,nboot=20)
a_distance<-
  predict_distance_forest(
    a_survival_forest,
    numeric_predictor=~age+ph.ecog+ph.karno+pat.karno+meal.cal,
    factor_predictor=~as.factor(sex),
    data=lung)
```

---

predict\_distance\_forest\_matrix

*Predict Distances Between Samples Based on a Survival Forest Fit  
(Data Supplied as Matrices)*

---

## Description

The function `predict_distance_forest_matrix` predicts distances between samples based on a survival forest fit.

**Usage**

```
predict_distance_forest_matrix(
  survival_forest,
  matrix_numeric,
  matrix_factor,
  missing = "omit"
)
```

**Arguments**

`survival_forest` a fitted survival forest

`matrix_numeric` numeric predictors, a numeric matrix. `matrix_numeric[i, j]` is the *j*th numeric predictor of the *i*th sample. The best practice is to have the same column names in the training and testing dataset.

`matrix_factor` factor predictors, a character matrix. `matrix_factor[i, j]` is the *j*th predictor of the *i*th sample. The best practice is to have the same column names in the training and testing dataset.

`missing` a character value that specifies the handling of missing data. If `missing=="omit"`, samples with missing values in the splitting variables will be discarded. If `missing=="majority"`, samples with missing values in the splitting variables will be assigned to the majority node. If `missing=="weighted"`, samples with missing values in the splitting variables will be weighted by the weights of branch nodes. The best practice is to use the same method as the trained random forest.

**Details**

Predict Distances Between Samples Based on a Survival Forest Fit (Data Supplied as Matrices)  
(Works for raw matrices)

**Value**

A list. `mean_distance` is the mean distance matrix. `sum_distance` is the matrix that sums the distances between samples. `sum_non_na` is the matrix of the number of non NA distances being averaged.

**Examples**

```
library(survival)
a_survival_forest<-
  survival_forest_matrix(
    time=lung$time,
    event=lung$status==2,
    matrix_numeric=data.matrix(lung[,c(4,6:9),drop=FALSE]),
    matrix_factor=data.matrix(lung[,5,drop=F]),
    nboot=20)
a_distance<-
```

```
predict_distance_forest_matrix(  
  a_survival_forest,  
  matrix_numeric=data.matrix(lung[,c(4,6:9),drop=FALSE]),  
  matrix_factor=data.matrix(lung[,5,drop=F]))
```

---

predict\_distance\_tree *Predict Distances Between Samples Based on a Survival Tree Fit (Data Supplied as a Dataframe)*

---

## Description

The function `predict_distance_tree` predicts distances between samples based on a survival tree fit.

## Usage

```
predict_distance_tree(  
  survival_tree,  
  numeric_predictor,  
  factor_predictor,  
  data,  
  missing = "omit"  
)
```

## Arguments

`survival_tree` a fitted survival tree

`numeric_predictor` a formula specifying the numeric predictors. As in  $\sim x_1+x_2+x_3$ , the three numeric variables  $x_1$ ,  $x_2$ , and  $x_3$  are included as numeric predictors.  $x_1[i]$ ,  $x_2[i]$ , and  $x_3[i]$  are the predictors of the  $i$ th sample. The best practice is to use the same variables names in the training and testing dataset.

`factor_predictor` a formula specifying the numeric predictors. As in  $\sim z_1+z_2+z_3$ , the three character variables  $z_1$ ,  $z_2$ , and  $z_3$  are included as factor predictors.  $z_1[i]$ ,  $z_2[i]$ , and  $z_3[i]$  are the predictors of the  $i$ th sample. The best practice is to use the same variables names in the training and testing dataset.

`data` the dataframe (test data) that stores the outcome and predictor variables. Variables in the global environment will be used if data is missing.

`missing` a character value that specifies the handling of missing data. If `missing=="omit"`, samples with missing values in the splitting variables will be discarded. If `missing=="majority"`, samples with missing values in the splitting variables will be assigned to the majority node. If `missing=="weighted"`, samples with missing values in the splitting variables will be weighted by the weights of branch nodes. The best practice is to use the same method as the trained random tree.

**Details**

Predict Distances Between Samples Based on a Survival Tree Fit (Data Supplied as a Dataframe)

**Value**

A list. `node_distance` gives the distance matrix between nodes. `ind_distance` gives the distance matrix between samples. `ind_weights` gives the weights of samples in each node.

**Examples**

```
library(survival)
a_survival_tree<-
  survival_tree(
    survival_outcome=Surv(time,status==2)~1,
    numeric_predictor=~age+ph.ecog+ph.karno+pat.karno+meal.cal,
    factor_predictor=~as.factor(sex),
    data=lung)
a_distance<-
  predict_distance_tree(
    a_survival_tree,
    numeric_predictor=~age+ph.ecog+ph.karno+pat.karno+meal.cal,
    factor_predictor=~as.factor(sex),
    data=lung)
```

---

predict\_distance\_tree\_matrix

*Predict Distances Between Samples Based on a Survival Tree Fit  
(Data Supplied as Matrices)*

---

**Description**

The function `predict_distance_tree_matrix` predicts distances between samples based on a survival tree fit.

**Usage**

```
predict_distance_tree_matrix(
  survival_tree,
  matrix_numeric,
  matrix_factor,
  missing = "omit"
)
```

**Arguments**

`survival_tree` a fitted survival tree



matrix_numeric	numeric predictors, a numeric matrix. <code>matrix_numeric[i, j]</code> is the <i>j</i> th numeric predictor of the <i>i</i> th sample. The best practice is to have the same column names in the training and testing dataset.
matrix_factor	factor predictors, a character matrix. <code>matrix_factor[i, j]</code> is the <i>j</i> th predictor of the <i>i</i> th sample. The best practice is to have the same column names in the training and testing dataset.
missing	a character value that specifies the handling of missing data. If <code>missing=="omit"</code> , samples with missing values in the splitting variables will be discarded. If <code>missing=="majority"</code> , samples with missing values in the splitting variables will be assigned to the majority node. If <code>missing=="weighted"</code> , samples with missing values in the splitting variables will be weighted by the weights of branch nodes. The best practice is to use the same method as the trained random tree.

### Details

Predict Distances Between Samples Based on a Survival Tree Fit (Data Supplied as Matrices)  
(Works for raw matrices)

### Value

A list. `node_distance` gives the distance matrix between nodes. `ind_distance` gives the distance matrix between samples. `ind_weights` gives the weights of samples in each node.

### Examples

```
library(survival)
a_survival_tree<-
  survival_tree_matrix(
    time=lung$time,
    event=lung$status==2,
    matrix_numeric=data.matrix(lung[,c(4,6:9),drop=FALSE]),
    matrix_factor=data.matrix(lung[,5,drop=FALSE]))
a_distance<-
  predict_distance_tree_matrix(
    a_survival_tree,
    matrix_numeric=data.matrix(lung[,c(4,6:9),drop=FALSE]),
    matrix_factor=data.matrix(lung[,5,drop=FALSE]))
```

---

predict_weights	<i>Predict Weights of Samples in Terminal Nodes Based on a Survival Tree Fit (Data Supplied as a Dataframe)</i>
-----------------	---

---

### Description

The function `predict_weights` predicts weights of samples in terminal nodes based on a survival tree fit.

**Usage**

```
predict_weights(
  survival_tree,
  numeric_predictor,
  factor_predictor,
  data,
  missing = "omit"
)
```

**Arguments**

**survival\_tree** a fitted survival tree

**numeric\_predictor** a formula specifying the numeric predictors. As in  $\sim x1+x2+x3$ , the three numeric variables  $x1$ ,  $x2$ , and  $x3$  are included as numeric predictors.  $x1[i]$ ,  $x2[i]$ , and  $x3[i]$  are the predictors of the  $i$ th sample. The best practice is to use the same variables names in the training and testing dataset.

**factor\_predictor** a formula specifying the numeric predictors. As in  $\sim z1+z2+z3$ , the three character variables  $z1$ ,  $z2$ , and  $z3$  are included as factor predictors.  $z1[i]$ ,  $z2[i]$ , and  $z3[i]$  are the predictors of the  $i$ th sample. The best practice is to use the same variables names in the training and testing dataset.

**data** the dataframe (test data) that stores the outcome and predictor variables. Variables in the global environment will be used if data is missing.

**missing** a character value that specifies the handling of missing data. If `missing=="omit"`, samples with missing values in the splitting variables will be discarded. If `missing=="majority"`, samples with missing values in the splitting variables will be assigned to the majority node. If `missing=="weighted"`, samples with missing values in the splitting variables will be weighted by the weights of branch nodes. The best practice is to use the same method as the trained random tree.

**Details**

Predict Weights of Samples in Terminal Nodes Based on a Survival Tree Fit (Data Supplied as a Dataframe)

**Value**

A weight matrix representing the weights of samples in each node.

**Examples**

```
library(survival)
a_survival_tree<-
survival_tree(
  survival_outcome=Surv(time,status==2)~1,
  numeric_predictor=~age+ph.ecog+ph.karno+pat.karno+meal.cal,
```

```
    factor_predictor=~as.factor(sex),
    data=lung)
a_weight<-
predict_weights(
  a_survival_tree,
  numeric_predictor=~age+ph.ecog+ph.karno+pat.karno+meal.cal,
  factor_predictor=~as.factor(sex),
  data=lung)
```

---

predict\_weights\_matrix

*Predict Weights of Samples in Terminal Nodes Based on a Survival Tree Fit (Data Supplied as Matrices)*

---

### Description

The function `predict_weights_matrix` predicts weights of samples in terminal nodes based on a survival tree fit.

### Usage

```
predict_weights_matrix(
  survival_tree,
  matrix_numeric,
  matrix_factor,
  missing = "majority"
)
```

### Arguments

<code>survival_tree</code>	a fitted survival tree
<code>matrix_numeric</code>	numeric predictors, a numeric matrix. <code>matrix_numeric[i, j]</code> is the <i>j</i> th numeric predictor of the <i>i</i> th sample. The best practice is to have the same column names in the training and testing dataset.
<code>matrix_factor</code>	factor predictors, a character matrix. <code>matrix_factor[i, j]</code> is the <i>j</i> th predictor of the <i>i</i> th sample. The best practice is to have the same column names in the training and testing dataset.
<code>missing</code>	a character value that specifies the handling of missing data. If <code>missing=="omit"</code> , samples with missing values in the splitting variables will be discarded. If <code>missing=="majority"</code> , samples with missing values in the splitting variables will be assigned to the majority node. If <code>missing=="weighted"</code> , samples with missing values in the splitting variables will be weighted by the weights of branch nodes. The best practice is to use the same method as the trained tree.

### Details

Predict Weights of Samples in Terminal Nodes Based on a Survival Tree Fit (Data Supplied as Matrices)

**Value**

A weight matrix representing the weights of samples in each node.

**Examples**

```
library(survival)
a_survival_tree<-
  survival_tree_matrix(
    time=lung$time,
    event=lung$status==2,
    matrix_numeric=data.matrix(lung[,c(4,6:9),drop=FALSE]),
    matrix_factor=data.matrix(lung[,5,drop=FALSE]))
a_weight<-
  predict_weights_matrix(
    a_survival_tree,
    matrix_numeric=data.matrix(lung[,c(4,6:9),drop=FALSE]),
    matrix_factor=data.matrix(lung[,5,drop=FALSE]))
```

---

survival\_forest

*Build a Survival Forest (Data Supplied as a Dataframe)*


---

**Description**

The function `survival_forest` build a survival forest given the survival outcomes and predictors of numeric and factor variables.

**Usage**

```
survival_forest(
  survival_outcome,
  numeric_predictor,
  factor_predictor,
  weights = NULL,
  data,
  significance = 0.05,
  min_weights = 50,
  missing = "omit",
  test_type = "univariate",
  cut_type = 0,
  nboot = 100,
  seed = 0
)
```

**Arguments**

`survival_outcome`

a `Surv` object of right-censored outcomes. In `Surv(time,event)`, `time[i]` is the survival time of the *i*th sample. `event[i]` is the survival event of the *i*th sample.

<code>numeric_predictor</code>	a formula specifying the numeric predictors. As in <code>~x1+x2+x3</code> , the three numeric variables <code>x1</code> , <code>x2</code> , and <code>x3</code> are included as numeric predictors. <code>x1[i]</code> , <code>x2[i]</code> , and <code>x3[i]</code> are the predictors of the <i>i</i> th sample.
<code>factor_predictor</code>	a formula specifying the factor predictors. As in <code>~z1+z2+z3</code> , the three character variables <code>z1</code> , <code>z2</code> , and <code>z3</code> are included as factor predictors. <code>z1[i]</code> , <code>z2[i]</code> , and <code>z3[i]</code> are the predictors of the <i>i</i> th sample.
<code>weights</code>	sample weights, a numeric vector. <code>weights[i]</code> is the weight of the <i>i</i> th sample.
<code>data</code>	the dataframe that stores the outcome and predictor variables. Variables in the global environment will be used if <code>data</code> is missing.
<code>significance</code>	significance threshold, a numeric value. Stop the splitting algorithm when no splits give a p-value smaller than <code>significance</code> .
<code>min_weights</code>	minimum weight threshold, a numeric value. The weights in a node are greater than <code>min_weights</code> .
<code>missing</code>	a character value that specifies the handling of missing data. If <code>missing=="omit"</code> , samples with missing values in the splitting variables will be discarded. If <code>missing=="majority"</code> , samples with missing values in the splitting variables will be assigned to the majority node. If <code>missing=="weighted"</code> , samples with missing values in the splitting variables will be weighted by the weights of branch nodes.
<code>test_type</code>	a character value that specifies the type of statistical tests. If <code>test_type=="univariate"</code> , then it performs a log-rank test without p-value adjustments. If <code>test_type</code> is in <code>p.adjust.methods</code> , i.e., one of <code>holm</code> , <code>hochberg</code> , <code>hommel</code> , <code>bonferroni</code> , <code>BH</code> , <code>BY</code> , or <code>fdr</code> , then the p-values will be adjusted using the corresponding method.
<code>cut_type</code>	an integer value that specifies how to cut between two numeric values. If <code>cut_type==0</code> , then cut at the ends. If <code>cut_type==1</code> , then cut from the middle. If <code>cut_type==2</code> , then cut randomly between the two values.
<code>nboot</code>	an integer value that specifies the number of bootstrap replications.
<code>seed</code>	an integer value that specifies the seed.

## Details

Build a Survival Forest (Data Supplied as a Dataframe)

## Value

A list containing the information of the survival forest fit.

## Examples

```
library(survival)
a_survival_forest<-
survival_forest(
  survival_outcome=Surv(time,status==2)~1,
  numeric_predictor=~age+ph.ecog+ph.karno+pat.karno+meal.cal,
```

```
factor_predictor=~as.factor(sex),
data=lung,nboot=20)
```

---

survival\_forest\_matrix

*Build a Survival Forest (Data Supplied as Matrices)*

---

### Description

The function `survival_forest_matrix` build a survival forest given the survival outcomes and predictors of numeric and factor variables.

### Usage

```
survival_forest_matrix(
  time,
  event,
  matrix_numeric,
  matrix_factor,
  weights = rep(1, length(time)),
  significance = 0.05,
  min_weights = 50,
  missing = "omit",
  test_type = "univariate",
  cut_type = 0,
  nboot = 100,
  seed = 0
)
```

### Arguments

<code>time</code>	survival times, a numeric vector. <code>time[i]</code> is the survival time of the <i>i</i> th sample.
<code>event</code>	survival events, a logical vector. <code>event[i]</code> is the survival event of the <i>i</i> th sample.
<code>matrix_numeric</code>	numeric predictors, a numeric matrix. <code>matrix_numeric[i, j]</code> is the <i>j</i> th numeric predictor of the <i>i</i> th sample.
<code>matrix_factor</code>	factor predictors, a character matrix. <code>matrix_factor[i, j]</code> is the <i>j</i> th predictor of the <i>i</i> th sample.
<code>weights</code>	sample weights, a numeric vector. <code>weights[i]</code> is the weight of the <i>i</i> th sample.
<code>significance</code>	significance threshold, a numeric value. Stop the splitting algorithm when no splits give a p-value smaller than <code>significance</code> .
<code>min_weights</code>	minimum weight threshold, a numeric value. The weights in a node are greater than <code>min_weights</code> .

missing	a character value that specifies the handling of missing data. If <code>missing=="omit"</code> , samples with missing values in the splitting variables will be discarded. If <code>missing=="majority"</code> , samples with missing values in the splitting variables will be assigned to the majority node. If <code>missing=="weighted"</code> , samples with missing values in the splitting variables will be weighted by the weights of branch nodes.
test_type	a character value that specifies the type of statistical tests. If <code>test_type=="univariate"</code> , then it performs a log-rank test without p-value adjustments. If <code>test_type</code> is in <code>p.adjust.methods</code> , i.e., one of <code>holm</code> , <code>hochberg</code> , <code>hommel</code> , <code>bonferroni</code> , <code>BH</code> , <code>BY</code> , or <code>fdr</code> , then the p-values will be adjusted using the corresponding method.
cut_type	an integer value that specifies how to cut between two numeric values. If <code>cut_type==0</code> , then cut at the ends. If <code>cut_type==1</code> , then cut from the middle. If <code>cut_type==2</code> , then cut randomly between the two values.
nboot	an integer value that specifies the number of bootstrap replications.
seed	an integer value that specifies the seed.

## Details

Build a Survival Forest (Data Supplied as Matrices)

## Value

A list containing the information of the survival forest fit.

## Examples

```
library(survival)
a_survival_forest<-
  survival_forest_matrix(
    time=lung$time,
    event=lung$status==2,
    matrix_numeric=data.matrix(lung[,c(4,6:9),drop=FALSE]),
    matrix_factor=data.matrix(lung[,5,drop=FALSE]),
    nboot=20)
```

---

survival\_tree

*Build a Survival Tree (Data Supplied as a Dataframe)*

---

## Description

The function `survival_tree` build a survival tree given the survival outcomes and predictors of numeric and factor variables.

**Usage**

```

survival_tree(
  survival_outcome,
  numeric_predictor,
  factor_predictor,
  weights = NULL,
  data,
  significance = 0.05,
  min_weights = 50,
  missing = "omit",
  test_type = "univariate",
  cut_type = 0
)

```

**Arguments**

- survival\_outcome** a Surv object of right-censored outcomes. In `Surv(time,event)`, `time[i]` is the survival time of the *i*th sample. `event[i]` is the survival event of the *i*th sample.
- numeric\_predictor** a formula specifying the numeric predictors. As in `~x1+x2+x3`, the three numeric variables `x1`, `x2`, and `x3` are included as numeric predictors. `x1[i]`, `x2[i]`, and `x3[i]` are the predictors of the *i*th sample.
- factor\_predictor** a formula specifying the numeric predictors. As in `~z1+z2+z3`, the three character variables `z1`, `z2`, and `z3` are included as factor predictors. `z1[i]`, `z2[i]`, and `z3[i]` are the predictors of the *i*th sample.
- weights** sample weights, a numeric vector. `weights[i]` is the weight of the *i*th sample.
- data** the dataframe that stores the outcome and predictor variables. Variables in the global environment will be used if `data` is missing.
- significance** significance threshold, a numeric value. Stop the splitting algorithm when no splits give a p-value smaller than `significance`.
- min\_weights** minimum weight threshold, a numeric value. The weights in a node are greater than `min_weights`.
- missing** a character value that specifies the handling of missing data. If `missing=="omit"`, samples with missing values in the splitting variables will be discarded. If `missing=="majority"`, samples with missing values in the splitting variables will be assigned to the majority node. If `missing=="weighted"`, samples with missing values in the splitting variables will be weighted by the weights of branch nodes.
- test\_type** a character value that specifies the type of statistical tests. If `test_type=="univariate"`, then it performs a log-rank test without p-value adjustments. If `test_type` is in `p.adjust.methods`, i.e., one of `holm`, `hochberg`, `hommel`, `bonferroni`, `BH`, `BY`, or `fdr`, then the p-values will be adjusted using the corresponding method.



cut\_type an integer value that specifies how to cut between two numeric values. If cut\_type==0, then cut at the ends. If cut\_type==1, then cut from the middle. If cut\_type==2, then cut randomly between the two values.

### Details

Build a Survival Tree (Data Supplied as a Dataframe)

### Value

A list containing the information of the survival tree fit.

### Examples

```
library(survival)
a_survival_tree<-
  survival_tree(
    survival_outcome=Surv(time,status==2)~1,
    numeric_predictor=~age+ph.ecog+ph.karno+pat.karno+meal.cal,
    factor_predictor=~as.factor(sex),
    data=lung)
```

---

survival\_tree\_matrix *Build a Survival Tree (Data Supplied as Matrices)*

---

### Description

The function `survival_tree_matrix` build a survival tree given the survival outcomes and predictors of numeric and factor variables.

### Usage

```
survival_tree_matrix(
  time,
  event,
  matrix_numeric,
  matrix_factor,
  weights = rep(1, length(time)),
  significance = 0.05,
  min_weights = 50,
  missing = "omit",
  test_type = "univariate",
  cut_type = 0
)
```

**Arguments**

<code>time</code>	survival times, a numeric vector. <code>time[i]</code> is the survival time of the <i>i</i> th sample.
<code>event</code>	survival events, a logical vector. <code>event[i]</code> is the survival event of the <i>i</i> th sample.
<code>matrix_numeric</code>	numeric predictors, a numeric matrix. <code>matrix_numeric[i, j]</code> is the <i>j</i> th numeric predictor of the <i>i</i> th sample.
<code>matrix_factor</code>	factor predictors, a character matrix. <code>matrix_factor[i, j]</code> is the <i>j</i> th predictor of the <i>i</i> th sample.
<code>weights</code>	sample weights, a numeric vector. <code>weights[i]</code> is the weight of the <i>i</i> th sample.
<code>significance</code>	significance threshold, a numeric value. Stop the splitting algorithm when no splits give a p-value smaller than <code>significance</code> .
<code>min_weights</code>	minimum weight threshold, a numeric value. The weights in a node are greater than <code>min_weights</code> .
<code>missing</code>	a character value that specifies the handling of missing data. If <code>missing=="omit"</code> , samples with missing values in the splitting variables will be discarded. If <code>missing=="majority"</code> , samples with missing values in the splitting variables will be assigned to the majority node. If <code>missing=="weighted"</code> , samples with missing values in the splitting variables will be weighted by the weights of branch nodes.
<code>test_type</code>	a character value that specifies the type of statistical tests. If <code>test_type=="univariate"</code> , then it performs a log-rank test without p-value adjustments. If <code>test_type</code> is in <code>p.adjust.methods</code> , i.e., one of <code>holm</code> , <code>hochberg</code> , <code>hommel</code> , <code>bonferroni</code> , <code>BH</code> , <code>BY</code> , or <code>fdr</code> , then the p-values will be adjusted using the corresponding method.
<code>cut_type</code>	an integer value that specifies how to cut between two numeric values. If <code>cut_type==0</code> , then cut at the ends. If <code>cut_type==1</code> , then cut from the middle. If <code>cut_type==2</code> , then cut randomly between the two values.

**Details**

Build a Survival Tree (Data Supplied as Matrices)

**Value**

A list containing the information of the survival tree fit.

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