Package 'rpst'

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Type Package

Title Recursive Partitioning Survival Trees

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Description An implementation of Recursive Partitioning Survival Trees via a node-splitting rule that builds decision tree models that reflected within-node and within-treatment responses. The algorithm aims to find the maximal difference in survival time among different treatments.

License GPL-3

Depends R (>= 2.0.0)

Imports plotrix, survival

NeedsCompilation no

Repository CRAN

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R topics documented:

gen.data *Generate simulated data*

Description

Generate survival data for simulations.

Usage

```
gen.data(n=100, p=10, c = 4, beta = NULL)
```

Arguments

n	The number of observations.
p	The number of predictors of interest.
c	The censoring paramter to control the censoring rate. Default is 4.
beta	The coefficient values in the underlying regression model.

Value

A list with the following components: data, beta.

data	The simulated dataset.
beta	The coefficients.

Author(s)

Yewei Li

References

Zhang, H., Legro, R. S., Zhang, J., Zhang, L., Chen, X., Huang, H., ... & Eisenberg, E. (2010). Decision trees for identifying predictors of treatment effectiveness in clinical trials and its application to ovulation in a study of women with polycystic ovary syndrome.. Human Reproduction, 25(10), 2612-2621.

See Also

rpst, predict.rpst, plot.rpst.

Examples

```
#require(survival)
data <- gen.data(n = 20, p = 5, c = 2)
tree <- rpst(data$data, minsize = 2)
print.rpst(tree)
```

plot.rpst *Produces a tree plot of a "rpst" object*

Description

Produces a tree plot of a "rpst" object.

Usage

```
   ## S3 method for class 'rpst'
plot(x, xlength = 1, ylength = 3, xshift = 0.5 , ysegment = 6,...)
```

Arguments

x	a "rpst" project.
xlength	xlength of the plot.
ylength	ylength of the plot.
xshift	xshift of the plot.
ysegment	ysegment of the plot.
...	additional summary arguments.

Author(s)

Yewei Li

References

Zhang, H., Legro, R. S., Zhang, J., Zhang, L., Chen, X., Huang, H., ... & Eisenberg, E. (2010). De-cision trees for identifying predictors of treatment effectiveness in clinical trials and its application to ovulation in a study of women with polycystic ovary syndrome.. Human Reproduction, 25(10), 2612-2621.

See Also

rpst, print.rpst, predict.rpst.

Examples

```
#require(survival)
data <- gen.data(n = 20, p = 5, c = 2)
tree <- rpst(data$data, minsize = 2)
print.rpst(tree)

plot.rpst(tree)
```

---

predict.rpst *Make predictions from a "rpst" object*

Description

Similar to other predict methods, which returns predictions from a fitted "rpst" object.

Usage

```
## S3 method for class 'rpst'
predict(object, newdata,...)
```

Arguments

object	Output from the rpst function.
newdata	New data used for prediction.
...	additional summary arguments.

Value

predict.rpst returns a dataframe that contain a new column "class", which contains the class labels of each sample.

Author(s)

Yewei Li

References

Zhang, H., Legro, R. S., Zhang, J., Zhang, L., Chen, X., Huang, H., ... & Eisenberg, E. (2010). Decision trees for identifying predictors of treatment effectiveness in clinical trials and its application to ovulation in a study of women with polycystic ovary syndrome.. Human Reproduction, 25(10), 2612-2621.

See Also

print.rpst, predict.rpst, plot.rpst.

Examples

```
#require(survival)
##not run##
#data <- gen.data(n = 100, p = 10, c = 2)
#tree <- rpst(data$data, minsize = 2)
#class = predict.rpst(tree,data$data)$class

data <- gen.data(n = 20, p = 5, c = 2)
tree <- rpst(data$data, minsize = 2)
class = predict.rpst(tree,data$data)$class
```

---

print.rpst   *Print out a "rpst" object*

Description

Print node and node information details of `"rpst"`.

Usage

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

Arguments

x   a `"rpst"` project.

...   additional summary arguments.

Author(s)

Yewei Li

See Also

[rpst](), [predict.rpst](), [plot.rpst]().

Examples

```
#require(survival)
data <- gen.data(n = 20, p = 5, c = 2)
tree <- rpst(data$data, minsize = 2)
print.rpst(tree)
```

---

rpst   *Recursive Partitioning Survival Trees*

Description

Build recursive partitioning survival trees via a node-splitting rule that builds decision tree models that reflected within-node and within-treatment responses.

Usage

```
rpst(data, datapath, maxlay = 12, minsize = 5)
```

Arguments

`data`	Input dataframe, it should be set in the particular way showed in detail.
`datapath`	The file path of the input dataframe.
`maxlay`	The maximum layer of the survival tree.
`minsize`	The minimum sample size in the each leaf node of the survival tree.

Details

The input dataframe should be set in the following way: (i) The variable names are specified in the first line in the data file. (ii) The variable types are specified in the second line in the data file. The variable types can include treatment (1), survival time and censor status (2), ordered (3), binary (4), nominal (5), and unwanted (6) variables.

For potential predictors, they are categorized in three types, including ordered, binary, and nominal ones.

Specifically, ordered covariates include continuous and ordinal data types, binary covariates must have only two factors (they are typically coded as 0 and 1), and nominal covariates must have more than two factors. The number in the parenthesis represents each variable type.

Author(s)

Yewei Li

References

Zhang, H., Legro, R. S., Zhang, J., Zhang, L., Chen, X., Huang, H., ... & Eisenberg, E. (2010). Decision trees for identifying predictors of treatment effectiveness in clinical trials and its application to ovulation in a study of women with polycystic ovary syndrome.. Human Reproduction, 25(10), 2612-2621.

See Also

print.rpst, predict.rpst, plot.rpst.

Examples

```
#require(survival)
data <- gen.data(n = 20, p = 5, c = 2)
tree <- rpst(data$data, minsize = 2)
print.rpst(tree)
```

---

rpst.km   *Produces KM-curve plot of a "rpst" object*

Description

Produces a KM-curve plot of a "rpst" object.

Usage

```
rpst.km(object, newdata, ...)
```

Arguments

object	a "rpst" project.
newdata	New data used for prediction and plot.
...	additional summary arguments.

Author(s)

Yewei Li

References

Zhang, H., Legro, R. S., Zhang, J., Zhang, L., Chen, X., Huang, H., ... & Eisenberg, E. (2010). Decision trees for identifying predictors of treatment effectiveness in clinical trials and its application to ovulation in a study of women with polycystic ovary syndrome.. Human Reproduction, 25(10), 2612-2621.

See Also

rpst, print.rpst, predict.rpst.

Examples

```
#require(survival)
data <- gen.data(n = 20, p = 5, c = 2)
tree <- rpst(data$data, minsize = 2)
print.rpst(tree)

rpst.km(tree,data$data)

##not run##
#data <- gen.data(n = 100, p = 10, c = 2)
#tree <- rpst(data$data, minsize = 2)
#print.rpst(tree)

#rpst.km(tree,data$data)
```

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