

Package ‘plotRCS’

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Type Package

Title Plot Restricted Cubic Splines Curves

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Description Simple drawing of restricted cubic spline (RCS) curves through 'ggplot2' package from a logistic regression model or a Cox proportional hazards regression model. This method was described by Harrell FE (2015) <[doi:10.1007/978-3-319-19425-7](https://doi.org/10.1007/978-3-319-19425-7)>.

License GPL (>= 3)

Depends R (>= 3.6.0)

Encoding UTF-8

LazyData true

Imports ggplot2, rms

RoxygenNote 7.2.3

URL <https://github.com/KunHuo/plotRCS>

NeedsCompilation no

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Repository CRAN

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cancer	<i>Liver cancer data</i>
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Description

Survival in patients with liver cancer from the the Surveillance, Epidemiology, and End Results (SEER) dataset.

Usage

```
data(cancer)
```

Format

An object of class `data.frame` with 903 rows and 8 columns.

Examples

```
data(cancer)
head(cancer)
```

knot	<i>Location of knots for RCS</i>
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Description

Location of knots from Harrell (2015), Regression Modeling Strategies.

Usage

```
knot(k = 3)
```

Arguments

`k` number of knots, must be strictly between 3 and 7.

Details

Harrell (2015) states that for many datasets, $k = 4$ offers an adequate fit of the model and is a good compromise between flexibility and loss of precision caused by overfitting a small sample". If the sample size is small, three knots should be used in order to have enough observations in between the knots to be able to fit each polynomial. If the sample size is large and if there is reason to believe that the relationship being studied changes quickly, more than five knots can be used.

Value

a numeric vector.

References

Harrell FE (2015). Regression models for continuous y and case study in ordinal regression. In: Harrell FE, ed. Regression Modeling Strategies. New York: Springer.

Examples

```
# Location of 3 knots
knot(3)

# Location of 7 knots
knot(7)
```

rcsplot

Plot restricted cubic splines curves

Description

Drawing of restricted cubic spline (RCS) curves from a logistic regression model or a Cox proportional hazards regression model.

Usage

```
rcsplot(
  data,
  outcome = NULL,
  time = NULL,
  exposure = NULL,
  covariates = NULL,
  positive = NULL,
  group = NULL,
  knots = c(0.05, 0.35, 0.65, 0.95),
  knots.line = FALSE,
  ref.value = "k1",
  ref.line = TRUE,
  conf.int = TRUE,
  conf.level = 0.95,
  conf.type = c("shape", "line"),
  pvalue = TRUE,
  pvalue.digits = 3,
  pvalue.position = c(0.02, 0.98),
  pvalue.label.overall = "P for overall",
  pvalue.label.nonlinear = "P for nonlinear",
  fontsize = 12,
  fontfamily = "serif",
  linesize = 0.25,
  linecolor = "#0072B5FF",
  alpha = 0.1,
```

```

    xbreaks = NULL,
    ybreaks = NULL,
    xlab = "",
    ylab = "",
    explain = TRUE,
    ...
)

```

Arguments

<code>data</code>	a data frame contain the columns of outcome, time, exposure, covariates, and group.
<code>outcome</code>	the name of outcome variable in the data.
<code>time</code>	the name of time variable in the data, for Cox regressions.
<code>exposure</code>	the name of exposure variable in the data.
<code>covariates</code>	the names of covariate variables in the data.
<code>positive</code>	in which positive of outcome variable to make the comparison. By default, positive is automatically defined. If outcome is a factor variable, then positive is defined as the highest level. If outcome is a numerical variable, then positive is defined as the largest value.
<code>group</code>	the name of group variable in the data.
<code>knots</code>	location of knots, detail see knot function.
<code>knots.line</code>	logical indicating whether or not to show the vertical lines for the knots, default FALSE.
<code>ref.value</code>	reference value for the RCS curve, 'min' means using the minimum value of exposure as a reference, 'median' uses the median, 'mean' uses the mean, 'k1' uses the first knot. 'k2' uses the second knot, 'k3' uses the third 'knot', and so on. In addition, you can directly set the numerical vector as the reference value.
<code>ref.line</code>	logical indicating whether or not to show the reference line, default TRUE.
<code>conf.int</code>	logical indicating whether or not to draw confidence interval. Defaults to TRUE.
<code>conf.level</code>	the confidence level to use for the confidence interval if <code>conf.int = TRUE</code> . Must be strictly greater than 0 and less than 1. Defaults to 0.95, which corresponds to a 95 percent confidence interval.
<code>conf.type</code>	confidence interval type of 'shape' (default) or 'line'.
<code>pvalue</code>	logical indicating whether or not to show P values, include P for overall association and P for nonlinear, default TRUE.
<code>pvalue.digits</code>	digits for P values, default 3.
<code>pvalue.position</code>	position for P value, numeric vector of length two (x-axis and y-axis).
<code>pvalue.label.overall</code>	label for P value of overall.
<code>pvalue.label.nonlinear</code>	label for P value of nonlinear.

fontsize	font size, default 12.
fontfamily	font family, default 'serif' (Times New Roman).
linesize	line size, default 0.25.
linecolor	line color, default '#0072B5FF'.
alpha	alpha for the shape of confidence interval, default 0.1.
xbreaks	breaks of x-axis.
ybreaks	breaks of y-axis.
xlab	label of x-axis.
ylab	label of y-axis.
explain	logical indicating whether or not to explain the figure, default TRUE.
...	further arguments.

Value

A ggplot2 object with class 'rcsplot' containing the attributes of 'title' and 'note'.

See Also

[rcs](#), [knot](#)

Examples

```
# View data
head(cancer)

# RCS curves for a logistic regression model
rcsplot(data = cancer,
        outcome = "status",
        exposure = "age",
        covariates = c("sex", "race", "size", "metastasis"))

# RCS curves for a Cox regression model
rcsplot(data = cancer,
        outcome = "status",
        time = "time",
        exposure = "age",
        covariates = c("sex", "race", "size", "metastasis"))

# Unadjusted covariates
rcsplot(data = cancer,
        outcome = "status",
        time = "time",
        exposure = "age")

# By group
rcsplot(data = cancer,
        outcome = "status",
        time = "time",
```

```
    exposure = "age",
    covariates = c("sex", "race", "size", "metastasis"),
    group = "sex")

# Set 5 knots from 'kont' function
rcsplot(data = cancer,
        outcome = "status",
        time = "time",
        exposure = "age",
        covariates = c("sex", "race", "size", "metastasis"),
        knots = knot(5))

# Set the second knot as the reference value
rcsplot(data = cancer,
        outcome = "status",
        time = "time",
        exposure = "age",
        covariates = c("sex", "race", "size", "metastasis"),
        knots = knot(5),
        ref.value = "k2")
```

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