Package: regplot (via r-universe)

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Type Package

Title Enhanced Regression Nomogram Plot

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Description A function to plot a regression nomogram of regression objects. Covariate distributions are superimposed on nomogram scales and the plot can be animated to allow on-the-fly changes to distribution representation and to enable outcome calculation.

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Imports vioplot, sm, beanplot, survival, graphics, stats, lme4

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Contents

`regplot` *Plots a regression nomogram showing covariate distribution*

Description

`regplot` plots enhanced regression nomograms. Covariate distributions are superimposed on nomogram scales and the plot can be animated to allow on-the-fly changes to distribution representation and to enable interactive outcome calculation.

Usage

```
regplot(
  reg,
  plots = c("density", "boxes"),
  center = TRUE,
  observation = NULL,
  title = NULL,
  points = FALSE,
  failtime = NULL,
  prfail = NULL,
  baseS = NULL,
  odds = FALSE,
  nsamp = 10000,
  showP = TRUE,
  rank = NULL,
  subticks = FALSE,
  interval = NULL,
  clickable = FALSE,
  ...
)
```

Arguments

`reg`	An R regression object from a regression command (see Details, for allowed regressions)
`plots`	Specifies type of covariate plot. Default `plots=c("density","boxes")` specifies density plots for numeric covariates and boxes for factors (see Details for other options).
`center`	If `TRUE` the mean values of continuous variables and reference categories of factors are aligned vertically. Otherwise continuous distributions are vertically aligned at zero together with reference categories of factors.
`observation`	To superimpose an observation, shown in (default) red. If `TRUE` superimposes an observation that is first row of the data used to build `reg`. Otherwise it may be a specified as any row of `reg` data or as a dataframe conforming to the structure of the regression data. `FALSE` omits any superposition.

`title`	A string title for the plot. If omitted the regression object name and class are output.
`points`	If `FALSE` the regression scores of each βx contribution are shown. Otherwise contributions are represented by a 0-100 "points" scale.
`failtime`	For survival models only, otherwise ignored. Used to specify cutoff times for risk probabilities or for quantiles of survival time. For the former `failtime=c(5,10)`, for example, specifies two probability scales for survival to 5 and 10 time units while `failtime=c("50%","10%")` specifies scales for `50%` and `10%` quantiles. If `failtime` is omitted or `NULL`, a probability scale for a cutoff that is the median of the time variable is adopted. .
`prfail`	For survival models, otherwise ignored. If `TRUE` the probability scale is of failure before `failtime`, otherwise after `failtime`.
`baseS`	For `coxph` and `cph` regressions only. If non-null, it specifies the baseline survival probability, for a non-centered model, corresponding to value(s) of `failtime`. If `NULL` the baseline probability is established from the regression object `reg`. Specifying `baseS` can be used coerce alternative baselines.
`odds`	For probability outcomes, the nomogram scale is of odds rather than probability.
`nsamp`	The size of a random sub-sample of data to plot covariate distributions (as plotting huge data may be slow and graphical precision, beyond a certain point, unnecessary).
`showP`	Whether P-value asterisk codes are to be displayed. For factors, the code for the most highly significant level is shown.
`rank`	Positions the nomogram scales by importance, top down. Two options: `rank="range"` is by the range of the βx's, and `rank="sd"` is by the standard deviation of the βx's. If `NULL` nomogram scales are arranged by order of main effects in the formula, and with interactions at top of the page.
`subticks`	Puts minor tick marks on axes, where possible.
`interval`	Draws `95%` confidence and prediction intervals. Values `"confidence"`, or `"prediction"`, place intervals on a calculated outcome for a specified `observation` (if `observation` is non `NULL`). A value `"coefficients"` draws confidence intervals on βx for some values of x.
`clickable`	`TRUE` if the graphic is active for on-the-fly mouse input (see Details).
`...`	Additional graphics control parameters for font sizes, colours, layout (see Details).

Details

Creates a nomogram representation of a fitted regression. The regression object `reg` can be of different types from the `stats`, `survival` , `rms`, `MASS` and `lme4` libraries. Specifically models generated by the commands: `glm`, `Glm`, `lm`, `ols`, `lrm`,`survreg`, `psm`, `coxph`, `cph`, `glm.nb`, `polr` or mixed model regressions `lmer`, `glmer`, and `glmer.nb`. For `glm`, `Glm` and `glmer` the supported family/link pairings are: gaussian/identity, binomial/logit, quasibinomial/logit, poisson/log and quasipoisson/log. For ordinal regression, using `polr`, logit and probit models are supported. For `survreg` and `psm` the distribution may be lognormal, gaussian, weibull, exponential or loglogistic. For `glm.nb` (from package `MASS`) and `glmer.nb` only log-link is allowed.

The plot can be made active for mouse input if `clickable=TRUE` so allowing on-the-fly changes to distribution plot type (frequency boxes, bars, spikes, box plot, density, empirical cdf, violin and bean plots). These options are presented by a temporary heading menu bar. Individual plots may be selected. Also values of `observation` (if non-null) can be changed by clicking new values, effectively making `regplot` a interactive regression calculator.

The `plots` parameter specifies initial plot types. It is length 2. The first item specifies a plot type for non-factor variables as one of: `"no plot"`, `"density"`, `"boxes"`, `"spikes"`, `"ecdf"`, `"bars"`, `"boxplot"`, `"violin"` or `"bean"`. The second item, is for factors and is one of: `"no plot"`, `"boxes"`, `"bars"` or `"spikes"`.

The graphic shows a scale for all main effects in the regression formula. Interactions are shown by separate nomogram scales. Factor-by-factor interactions are considered as factors and displayed with factor combinations. Factor-by-numeric interactions are displayed for the scale of the numeric variable(s) and separate scale for each factor level. Numeric-by-numeric interactions are shown with respect to the interaction product scale.

For random effects models (`lmer` and `glmer`) an additional random effects scale is included.

If models are stratified, by a `strata()` (or `strat()` for `rms` models) in the model formula, the behaviour differs depending on the model class. For survival models each stratum has its own outcome scale, otherwise it is included as a term in the linear score with a its own nomogram scale.

If a model formula includes a function (e.g `log()` or a spline `rcs()`) a thumbnail plot of the shape of the transformation is placed on the right of the nomogram scale. It can be toggled on and off by clicking on it (if `clickable=TRUE`).

Additional `...` parameters may include items to control the look of the plot if users wish to change default settings: `dencol` colour fill of density plots and other representations of numeric data, `boxcol` fill of factor/logical frequency boxes, `obscol` colour of superimposed observation, `spkcol` colour of spikes. Also font sizes can be set: `cexscales` for font size of points and nomogram scales, `cexvars` for variable names, `cexcats` for category and variable values. To label scales immediately adjacent to the scale (not on the left) use `leftlabel=FALSE`. To draw dotted vertical lines to show more clearly score contributions to an observation use `droplines=TRUE`.

Value

If `points=TRUE`, an object is returned that is a list of dataframes, each frame giving points per covariate, and the last on the list a total points-to-outcome look-up table.

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Examples

```
## 1.  Simulation
n <-500
X <- cbind(rnorm(n, sd = 1),rnorm(n, sd = 0.5))
## make  outcome Y  with intercept 10 + random variation
Y <- 10 + X %*% c(0.2, 0.1) + rnorm(n, sd = 1)
D <- as.data.frame(cbind( Y,X)); colnames(D) <- c("Y","x1","x2")
model <- lm( Y ~ x1 + x2, data = D)
```

```
regplot(model, observation = D[1,], interval = "confidence")
## 2 Survival model for pbc data
library(survival)
data(pbc)
pbccox <-  coxph(formula = Surv(time,status==2) ~ age
                 + cut(bili,breaks=c(-Inf, 2, 4, Inf)) + sex
                 + copper +as.factor(stage),data=pbc)
regplot(pbccox,observation=pbc[1,], clickable=TRUE,
        points=TRUE, rank="sd",failtime = c(730,1825))
```

Index