

# Package ‘regplot’

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**Type** Package  
**Title** Enhanced Regression Nomogram Plot  
**Version** 1.1  
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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.  
**License** GPL-2  
**Imports** vioplot, sm, beanplot, survival, graphics, stats, lme4  
**RoxygenNote** 7.0.2  
**NeedsCompilation** no  
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## Contents

regplot . . . . .	1
<b>Index</b>	<b>5</b>

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regplot	<i>Plots a regression nomogram showing covariate distribution</i>
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## 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**

<code>reg</code>	An R regression object from a regression command (see Details, for allowed regressions)
<code>plots</code>	Specifies type of covariate plot. Default <code>plots=c("density", "boxes")</code> specifies density plots for numeric covariates and boxes for factors (see Details for other options).
<code>center</code>	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.
<code>observation</code>	To superimpose an observation, shown in (default) red. If TRUE superimposes an observation that is first row of the data used to build <code>reg</code> . Otherwise it may be specified as any row of <code>reg</code> data or as a dataframe conforming to the structure of the regression data. FALSE omits any superposition.
<code>title</code>	A string title for the plot. If omitted the regression object name and class are output.
<code>points</code>	If FALSE the regression scores of each $\beta x$ contribution are shown. Otherwise contributions are represented by a 0-100 "points" scale.
<code>failtime</code>	For survival models only, otherwise ignored. Used to specify cutoff times for risk probabilities or for quantiles of survival time. For the former <code>failtime=c(5,10)</code> , for example, specifies two probability scales for survival to 5 and 10 time units while <code>failtime=c("50%", "10%")</code> specifies scales for 50% and 10% quantiles. If <code>failtime</code> is omitted or NULL, a probability scale for a cutoff that is the median of the time variable is adopted. .
<code>prfail</code>	For survival models, otherwise ignored. If TRUE the probability scale is of failure before <code>failtime</code> , otherwise after <code>failtime</code> .

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 to 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 $\beta x$ 's, and rank="sd" is by the standard deviation of the $\beta x$ '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 $\beta x$ 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 an 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

regplot, [1](#)