Package: rmsMD (via r-universe)

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Type Package

Title Output Results from 'rms' Models for Medical Journals

Version 1.0.1

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Description Provides streamlined functions for summarising and visualising regression models fitted with the 'rms' package, in the preferred format for medical journals. The 'modelsummary_rms()' function produces concise summaries for linear, logistic, and Cox regression models, including automatic handling of models containing restricted cubic spline (RCS) terms. The resulting summary dataframe can be easily converted into publication-ready documents using the 'flextable' and 'officer' packages. The 'ggrmsMD()' function creates clear and customizable plots ('ggplot2' objects) to visualise RCS terms.

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Encoding UTF-8

LazyData true

URL https://rmsmd.github.io/rmsMD/

BugReports https://github.com/rmsMD/rmsMD/issues/

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.3

Imports rms, ggplot2, rlang, cowplot

Suggests knitr, rmarkdown, devtools, officer, flextable, dplyr, testthat (>= 3.0.0), vdiffr, Hmisc

VignetteBuilder knitr

Config/testthat/edition 3

Config/pak/sysreqs cmake make libicu-dev libuv1-dev

Repository https://rmsmd.r-universe.dev

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ggrmsMD *Create plots for RCS variables from an* rms *model*

Description

The ggrmsMD function processes the output from models fitted using the rms package and produces one or more ggplot2 objects visualising restricted cubic splines (RCS). The function detects RCS terms in the model and plots them all, with a suitable y-axis selected based on the model type. This outputs a list of plots, or a multi-panel figure using the combined argument. As outputs are ggplot objects they can easily be further customised by the user.

Usage

```
ggrmsMD(
  modelfit,
  data,
  noeffline = TRUE,
  shade_inferior = "none",
  combined = TRUE,
  ylab = NULL,
  xlabs = NULL,
  titles = NULL,
  ylim = NULL,
  log_y = FALSE,
  log_y_breaks = NULL,
  xlims = NULL,
  log_x_vars = NULL,
  log_x_breaks = NULL,
  lrm_prob = FALSE,
  var = NULL,
  np = 400,
  ...
)
```

Arguments

modelfit	A model object from ols, lrm, or cph (from the rms package).
data	The dataset used to fit the model.
noeffline	Logical. If TRUE (default), adds a horizontal dashed line at 1 for odds/hazard ratio plots.
shade_inferior	Character. Options are "none" (default), "higher", or "lower". Applies red/green shading above or below 1 on the y-axis to indicate worse/better outcomes.
combined	Logical. If TRUE, returns a single multi-panel plot using cowplot::plot_grid().
ylab	Optional character. Override the default y-axis label.
xlabs	A named list of x-axis labels for each variable. E.g., list(age = "Age (years)", bmi = "BMI (kg/m²")
titles	A named list of plot titles for each variable.
ylim	Numeric vector (length 2). y-axis limits applied to all plots. E.g., c(0.5, 2).
log_y	Logical. If TRUE, y-axis is log10-transformed.
log_y_breaks	Optional numeric vector specifying y-axis tick marks when log_y = TRUE. E.g., c(0.25, 0.5, 1, 2, 4).
xlims	A named list of x-axis limits per variable. E.g., list(age = c(20, 80)).
log_x_vars	Character vector. Names of variables for which x-axis should be log10-transformed.
log_x_breaks	A named list specifying x-axis tick marks for variables with log10-transformed x-axis.
lrm_prob	Logical. If TRUE and model is lrm, plots predicted probabilities instead of odds ratios.
var	Character vector. Optional. Variables to plot. If NULL (default), all RCS variables in the model will be plotted.
np	Integer. Number of points used to predict spline curves. Default is 400. Consider increasing when using log-transformed x-axes.
...	Additional arguments passed to cowplot::plot_grid() when combined = TRUE.

Value

A ggplot object (if one variable is plotted), a list of ggplot objects (if multiple variables), or a single combined cowplot plot if combined = TRUE.

Examples

```
# For details examples and plots please see the provided vignettes
```

`modelsummary_rms` *Create model summary for rms models*

Description

The `modelsummary_rms` function processes the output from models fitted using the `rms` package and generates a summarized dataframe of the results. This summary is tailored for publication in medical journals, presenting effect estimates, confidence intervals, and p-values.

Usage

```
modelsummary_rms(
  modelfit,
  combine_ci = TRUE,
  round_dp_coef = 3,
  round_dp_p = 3,
  rcs_overallp = TRUE,
  hide_rcs_coef = TRUE,
  exp_coef = NULL,
  fullmodel = FALSE,
  MI_lrt = FALSE
)
```

Arguments

`modelfit`	The output from an rms model.
`combine_ci`	If `TRUE`, combines the effect estimates and 95% confidence intervals into a single column. Default is `TRUE`.
`round_dp_coef`	Specifies the number of decimal places to display for the effect estimates. Default is `3`.
`round_dp_p`	Specifies the number of decimal places to display for P values. Default is `3`.
`rcs_overallp`	If `TRUE`, provides an overall P value for Restricted Cubic Spline (RCS) terms, sourced from `anova(modelfit)`. Automatically selects appropriate test (LR, F or Wald)
`hide_rcs_coef`	If `TRUE`, hides the individual coefficients for Restricted Cubic Spline (RCS) variables.
`exp_coef`	If `TRUE`, outputs the exponentiated coefficients (`exp(coef)`) as the effect estimates. Applicable only for model types other than `ols`, `lrm`, or `cph`. If `NULL`, no exponentiation is performed. Default is `NULL`.
`fullmodel`	If `TRUE`, includes all intermediate steps in the summary, allowing users to verify and compare with standard model outputs.
`MI_lrt`	If `TRUE` then overall p-values for RCS terms from models with multiple imputed data from `fit.mult.impute` will represent likelihood ratio chi-square tests from `rms::processMI()`, rather than Wald tests.

Value

Returns a dataframe of results. This can easily be outputted to word using packages such as flextable and officer.

Examples

```
# For detailed examples please see the provided vignettes
```

`simulated_rmsMD_data` *Simulated Data for the Vignette*

Description

Generates a synthetic dataset for testing and demonstration purposes in the `rmsMD` package.

Usage

```
simulated_rmsMD_data(type = c("complete_case", "missing_for_MI"))
```

Arguments

`type`	Character string; either `"complete_case"` (no missing data) or `"missing_for_MI"` (introduces 10% missing data in each predictor).

Value

A data frame with simulated variables: `age`, `bmi`, `sex`, `smoking`, `majorcomplication`, `lengthstay`, `time`, and `event`.

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