Package ‘insurancerating’

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Type Package
Title Analytic Insurance Rating Techniques
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BugReports https://github.com/mharinga/insurancerating/issues

Description Methods for insurance rating. It helps actuaries to implement GLMs within all relevant steps needed to construct
a risk premium from raw data. It provides a data driven strategy for the construction of insurance tariff classes.
This strategy is based on the work by Antonio and Valdez (2012) <doi:10.1007/s10182-011-0152-7>. It also provides recipes
on how to easily perform one-way, or univariate, analyses on an insurance portfolio. In addition it adds functionality
to include reference categories in the levels of the coefficients in the output of a generalized linear regression analysis.

License GPL (>= 2)
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https://mharinga.github.io/insurancerating/

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add_prediction .......................................................... 3
autoplot.bootstrap_rmse ........................................... 3
autoplot.check_residuals .......................................... 4
autoplot.construct_tariff_classes ............................... 5
autoplot.fitgam ....................................................... 6
autoplot.restricted .................................................. 8
autoplot.riskfactor ................................................... 8
autoplot.smooth ...................................................... 10
autoplot.truncated_dist ........................................... 10
autoplot.univariate ................................................ 11
biggest_reference ................................................... 13
bootstrap_rmse ....................................................... 14
check_overdispersion .............................................. 15
check_residuals ........................................................ 16
construct_model_points ............................................ 17
construct_tariff_classes .......................................... 19
fisher .................................................................. 21
fit_gam .................................................................. 22
fit_truncated_dist .................................................... 23
histbin .................................................................. 25
model_data .............................................................. 26
model_performance ................................................... 27
MTPL .............................................................. 28
MTPL2 .......................................................... 29
period_to_months ....................................................... 29
rating_factors .......................................................... 30
rating_factors1 ........................................................ 32
reduce .................................................................. 33
refit_glm ................................................................. 34
restrict_coef ............................................................. 35
rgammat ................................................................. 36
rlnorm ................................................................. 37
rmse .................................................................... 38
rows_per_date ........................................................... 39
smooth_coef .............................................................. 40
summary.reduce ....................................................... 42
univariate ................................................................. 43
update_glm .............................................................. 44

Index ................................................................. 45
**add_prediction**

**Add predictions to a data frame**

**Description**

Add model predictions and confidence bounds to a data frame.

**Usage**

```r
add_prediction(data, ..., var = NULL, conf_int = FALSE, alpha = 0.1)
```

**Arguments**

- `data` a data frame of new data.
- `...` one or more objects of class `glm`.
- `var` the name of the output column(s), defaults to NULL.
- `conf_int` determines whether confidence intervals will be shown. Defaults to `conf_int = FALSE`.
- `alpha` a real number between 0 and 1. Controls the confidence level of the interval estimates (defaults to 0.10, representing 90 percent confidence interval).

**Value**

data.frame

**Examples**

```r
mod1 <- glm(nclaims ~ age_policyholder, data = MTPL,
            offset = log(exposure), family = poisson())
add_prediction(MTPL, mod1)
# Include confidence bounds
add_prediction(MTPL, mod1, conf_int = TRUE)
```

---

**autoplot.bootstrap_rmse**

Automatically create a ggplot for objects obtained from `bootstrap_rmse()`

**Description**

Takes an object produced by `bootstrap_rmse()`, and plots the simulated RMSE.
Usage

```r
## S3 method for class 'bootstrap_rmse'
autoplot(object, fill = NULL, color = NULL, ...)
```

Arguments

- `object`: bootstrap_rmse object produced by `bootstrap_rmse()`
- `fill`: color to fill histogram (default is "steelblue")
- `color`: color to plot line colors of histogram
- `...`: other plotting parameters to affect the plot

Value

- a ggplot object

Author(s)

Martin Haringa

---

autoplot.check_residuals

 Automatically create a ggplot for objects obtained from check_residuals()

Description

Takes an object produced by `check_residuals()`, and produces a uniform quantile-quantile plot.

Usage

```r
## S3 method for class 'check_residuals'
autoplot(object, show_message = TRUE, ...)
```

Arguments

- `object`: check_residuals object produced by `check_residuals()`
- `show_message`: show output from test (defaults to TRUE)
- `...`: other plotting parameters to affect the plot

Value

- a ggplot object

Author(s)

Martin Haringa
**autoplot.constructtariffclasses**

Automatically create a ggplot for objects obtained from `construct_tariff_classes()`

---

**Description**

Takes an object produced by `construct_tariff_classes()`, and plots the fitted GAM. In addition the constructed tariff classes are shown.

**Usage**

```r
## S3 method for class 'constructtariffclasses'
autoplot(
  object,
  conf_int = FALSE,
  color_gam = "steelblue",
  show_observations = FALSE,
  color_splits = "grey50",
  size_points = 1,
  color_points = "black",
  rotate_labels = FALSE,
  remove_outliers = NULL,
  ...
)
```

**Arguments**

- `object`: `constructtariffclasses` object produced by `construct_tariff_classes`
- `conf_int`: determines whether 95 percent confidence intervals will be plotted. The default is `conf_int = FALSE`
- `color_gam`: a color can be specified either by name (e.g.: "red") or by hexadecimal code (e.g.: "#FF1234") (default is "steelblue")
- `show_observations`: add observed frequency/severity points for each level of the variable for which tariff classes are constructed
- `color_splits`: change the color of the splits in the graph ("grey50" is default)
- `size_points`: size for points (1 is default)
- `color_points`: change the color of the points in the graph ("black" is default)
- `rotate_labels`: rotate x-labels 45 degrees (this might be helpful for overlapping x-labels)
- `remove_outliers`: do not show observations above this number in the plot. This might be helpful for outliers.
- `...`: other plotting parameters to affect the plot
Value

a ggplot object

Author(s)

Martin Haringa

Examples

```r
## Not run:
library(ggplot2)
library(dplyr)
fit_gam(MTPL, nclaims = nclaims, x = age_policyholder,
exposure = exposure) %>%
construct_tariff_classes(.) %>%
autoplot(., show_observations = TRUE)
## End(Not run)
```

Description

Takes an object produced by `fit_gam()`, and plots the fitted GAM.

Usage

```r
## S3 method for class 'fitgam'
autoplot(
  object,
  conf_int = FALSE,
  color_gam = "steelblue",
  show_observations = FALSE,
  x_stepsize = NULL,
  size_points = 1,
  color_points = "black",
  rotate_labels = FALSE,
  remove_outliers = NULL,
  ...
)
```
autoplot.fitgam

Arguments

object: fitgam object produced by fit_gam()

conf_int: determines whether 95 percent confidence intervals will be plotted. The default is conf_int = FALSE.

color_gam: a color can be specified either by name (e.g.: "red") or by hexadecimal code (e.g.: "#FF1234") (default is "steelblue")

show_observations: add observed frequency/ severity points for each level of the variable for which tariff classes are constructed

x_stepsize: set step size for labels horizontal axis

size_points: size for points (1 is default)

color_points: change the color of the points in the graph ("black" is default)

rotate_labels: rotate x-labels 45 degrees (this might be helpful for overlapping x-labels)

remove_outliers: do not show observations above this number in the plot. This might be helpful for outliers.

... other plotting parameters to affect the plot

Value

a ggplot object

Author(s)

Martin Haringa

Examples

## Not run:
library(ggplot2)
library(dplyr)
fit_gam(MTPL, nclaims = nclaims, x = age_policyholder, 
  exposure = exposure) %>%
  autoplot(., show_observations = TRUE)

## End(Not run)
**autoplot.restricted**  
*Automatically create a ggplot for objects obtained from restrict_coef()*

**Description**  

[Experimental] Takes an object produced by restrict_coef(), and produces a line plot with a comparison between the restricted coefficients and estimated coefficients obtained from the model.

**Usage**  

```r  
## S3 method for class 'restricted'
autoplot(object, ...)
```

**Arguments**  

- `object`: object produced by `restrict_coef()`
- `...`: other plotting parameters to affect the plot

**Value**  

Object of class `ggplot2`

**Author(s)**  

Martin Haringa

**Examples**  

```r  
freq <- glm(nclaims ~ bm + zip, weights = power, family = poisson(),
            data = MTPL)
zip_df <- data.frame(zip = c(0,1,2,3), zip_rst = c(0.8, 0.9, 1, 1.2))
freq %>%
  restrict_coef(., zip_df) %>%
  autoplot()
```

**autoplot.riskfactor**  
*Automatically create a ggplot for objects obtained from rating_factors()*

**Description**  

Takes an object produced by `univariate()`, and plots the available input.
## autoplot.riskfactor

### Usage

```r
## S3 method for class 'riskfactor'
autoplot(
  object,
  risk_factors = NULL,
  ncol = 1,
  labels = TRUE,
  dec.mark = ",",
  ylab = "rate",
  fill = NULL,
  color = NULL,
  linetype = FALSE,
  ...)
```

### Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>object</td>
<td>riskfactor object produced by rating_factors()</td>
</tr>
<tr>
<td>risk_factors</td>
<td>character vector to define which factors are included. Defaults to all risk factors.</td>
</tr>
<tr>
<td>ncol</td>
<td>number of columns in output (default is 1)</td>
</tr>
<tr>
<td>labels</td>
<td>show labels with the exposure (default is TRUE)</td>
</tr>
<tr>
<td>dec.mark</td>
<td>control the format of the decimal point, as well as the mark between intervals before the decimal point, choose either &quot;,&quot; (default) or &quot;.&quot;</td>
</tr>
<tr>
<td>ylab</td>
<td>modify label for the y-axis</td>
</tr>
<tr>
<td>fill</td>
<td>color to fill histogram</td>
</tr>
<tr>
<td>color</td>
<td>color to plot line colors of histogram (default is &quot;skyblue&quot;)</td>
</tr>
<tr>
<td>linetype</td>
<td>use different linetypes (default is FALSE)</td>
</tr>
<tr>
<td>...</td>
<td>other plotting parameters to affect the plot</td>
</tr>
</tbody>
</table>

### Value

a ggplot2 object

### Author(s)

Martin Haringa

### Examples

```r
library(dplyr)
df <- MTPL2 %>%
  mutate(across(c(area), as.factor)) %>%
  mutate(across(c(area), ~biggest_reference(., exposure)))
mod1 <- glm(nclaims ~ area + premium, offset = log(exposure),
family = poisson(), data = df)
mod2 <- glm(nclaims ~ area, offset = log(exposure), family = poisson(),
...)
```
autoplot.truncated_dist

```r
data = df
x <- rating_factors(mod1, mod2, model_data = df, exposure = exposure)
autoplot(x)
```

### autoplot.smooth

Automatically create a ggplot for objects obtained from `smooth_coef()`

**Description**

[Experimental] Takes an object produced by `smooth_coef()`, and produces a plot with a comparison between the smoothed coefficients and estimated coefficients obtained from the model.

**Usage**

```r
## S3 method for class 'smooth'
autoplot(object, ...)
```

**Arguments**

- `object`: object produced by `smooth_coef()`
- `...`: other plotting parameters to affect the plot

**Value**

Object of class `ggplot2`

**Author(s)**

Martin Haringa

### autoplot.truncated_dist

Automatically create a ggplot for objects obtained from `fit_truncated_dist()`

**Description**

Takes an object produced by `fit_truncated_dist()`, and plots the available input.
Usage

```r
## S3 method for class 'truncated_dist'
autoplot(
  object,
  geom_ecdf = c("point", "step"),
  xlab = NULL,
  ylab = NULL,
  ylim = c(0, 1),
  xlim = NULL,
  print_title = TRUE,
  print_dig = 2,
  print_trunc = 2,
  ...
)
```

Arguments

- `object` object univariate object produced by `fit_truncated_dist()`
- `geom_ecdf` the geometric object to use display the data (point or step)
- `xlab` the title of the x axis
- `ylab` the title of the y axis
- `ylim` two numeric values, specifying the lower limit and the upper limit of the scale
- `xlim` two numeric values, specifying the left limit and the right limit of the scale
- `print_title` show title (default to TRUE)
- `print_dig` number of digits for parameters in title (default 2)
- `print_trunc` number of digits for truncation values to print
- `...` other plotting parameters to affect the plot

Value

a ggplot2 object

Author(s)

Martin Haringa

Description

Takes an object produced by `univariate()`, and plots the available input.
Usage

```r
## S3 method for class 'univariate'
autoplot(
  object,
  show_plots = 1:9,
  ncol = 1,
  background = TRUE,
  labels = TRUE,
  sort = FALSE,
  sort_manual = NULL,
  dec.mark = ",",
  color = "dodgerblue",
  color_bg = "lightskyblue",
  label_width = 10,
  coord_flip = FALSE,
  show_total = FALSE,
  total_color = NULL,
  total_name = NULL,
  ...
)
```

Arguments

- **object**: univariate object produced by `univariate()`
- **show_plots**: numeric vector of plots to be shown (default is c(1,2,3,4,5,6,7,8,9)), there are nine available plots:
  - 1. frequency (i.e. number of claims / exposure)
  - 2. average severity (i.e. severity / number of claims)
  - 3. risk premium (i.e. severity / exposure)
  - 4. loss ratio (i.e. severity / premium)
  - 5. average premium (i.e. premium / exposure)
  - 6. exposure
  - 7. severity
  - 8. nclaims
  - 9. premium
- **ncol**: number of columns in output (default is 1)
- **background**: show exposure as a background histogram (default is TRUE)
- **labels**: show labels with the exposure (default is TRUE)
- **sort**: sort (or order) risk factor into descending order by exposure (default is FALSE)
- **sort_manual**: sort (or order) risk factor into own ordering; should be a character vector (default is NULL)
- **dec.mark**: decimal mark; defaults to ","
- **color**: change the color of the points and line ("dodgerblue" is default)
- **color_bg**: change the color of the histogram ("#f8e6b1" is default)
biggest_reference

- **label_width**: width of labels on the x-axis (10 is default)
- **coord_flip**: flip cartesian coordinates so that horizontal becomes vertical, and vertical, horizontal (default is FALSE)
- **show_total**: show line for total if by is used in univariate (default is FALSE)
- **total_color**: change the color for the total line ("black" is default)
- **total_name**: add legend name for the total line (e.g. "total")
- **...**: other plotting parameters to affect the plot

**Value**

a ggplot2 object

**Author(s)**

Marc Haine, Martin Haringa

**Examples**

```r
library(ggplot2)
x <- univariate(MTPL2, x = area, severity = amount, nclaims = nclaims, exposure = exposure)
autoplot(x)
autoplot(x, show_plots = c(6,1), background = FALSE, sort = TRUE)

# Group by `zip`
xzip <- univariate(MTPL, x = bm, severity = amount, nclaims = nclaims, exposure = exposure, by = zip)
autoplot(xzip, show_plots = 1:2)
```

**Description**

This function specifies the first level of a factor to the level with the largest exposure. Levels of factors are sorted using an alphabetic ordering. If the factor is used in a regression context, then the first level will be the reference. For insurance applications it is common to specify the reference level to the level with the largest exposure.

**Usage**

```r
biggest_reference(x, weight)
```

**Arguments**

- **x**: an unordered factor
- **weight**: a vector containing weights (e.g. exposure). Should be numeric.
Value

a factor of the same length as x

Author(s)

Martin Haringa

References


Examples

```r
## Not run:
library(dplyr)
df <- chickwts %>%
mutate(across(where(is.character), as.factor)) %>%
mutate(across(where(is.factor), ~biggest_reference(.x, weight)))
## End(Not run)
```

---

**bootstrap_rmse**  
*Bootstrapped RMSE*

**Description**

Generate n bootstrap replicates to compute n root mean squared errors.

**Usage**

```r
bootstrap_rmse(
  model,
  data,
  n = 50,
  frac = 1,
  show_progress = TRUE,
  rmse_model = NULL
)
```

**Arguments**

- **model** a model object
- **data** data used to fit model object
- **n** number of bootstrap replicates (defaults to 50)
- **frac** fraction used in training set if cross-validation is applied (defaults to 1)
- **show_progress** show progress bar (defaults to TRUE)
- **rmse_model** numeric RMSE to show as vertical dashed line in autoplot() (defaults to NULL)
check_overdispersion

Details

To test the predictive ability of the fitted model it might be helpful to determine the variation in the computed RMSE. The variation is calculated by computing the root mean squared errors from \(n\) generated bootstrap replicates. More precisely, for each iteration a sample with replacement is taken from the data set and the model is refitted using this sample. Then, the root mean squared error is calculated.

Value

A list with components

- \texttt{rmse\_bs} numerical vector with \(n\) root mean squared errors
- \texttt{rmse\_mod} root mean squared error for fitted (i.e. original) model

Author(s)

Martin Haringa

Examples

```r
## Not run:
mod1 <- glm(nclaims ~ age_policyholder, data = MTPL,
            offset = log(exposure), family = poisson())
# Use all records in MTPL
x <- bootstrap_rmse(mod1, MTPL, n = 80, show_progress = FALSE)
print(x)
autoplot(x)

# Use 80\% of records to test whether predictive ability depends on which 80\% is used. This might for example be useful in case portfolio contains large claim sizes
x_frac <- bootstrap_rmse(mod1, MTPL, n = 50, frac = .8,
                         show_progress = FALSE)
autoplot(x_frac) # Variation is quite small for Poisson GLM

## End(Not run)
```

---

check_overdispersion  Check overdispersion of Poisson GLM

Description

Check Poisson GLM for overdispersion.

Usage

```r
check_overdispersion(object)
```
check_residuals

Arguments

object: a fitted model of class glm and family Poisson

Details

A dispersion ratio larger than one indicates overdispersion, this occurs when the observed variance is higher than the variance of the theoretical model. If the dispersion ratio is close to one, a Poisson model fits well to the data. A p-value < .05 indicates overdispersion. Overdispersion > 2 probably means there is a larger problem with the data: check (again) for outliers, obvious lack of fit. Adopted from performance::check_overdispersion().

Value

A list with dispersion ratio, chi-squared statistic, and p-value.

Author(s)

Martin Haringa

References

• Bolker B et al. (2017): GLMM FAQ.

Examples

x <- glm(nclaims ~ area, offset = log(exposure), family = poisson(), data = MTPL2)
check_overdispersion(x)

check_residuals

Description

Detect overall deviations from the expected distribution.

Usage

check_residuals(object, n_simulations = 30)

Arguments

object: a model object
n_simulations: number of simulations (defaults to 30)
Details

Misspecifications in GLMs cannot reliably be diagnosed with standard residual plots, and GLMs are thus often not as thoroughly checked as LMs. One reason why GLMs residuals are harder to interpret is that the expected distribution of the data changes with the fitted values. As a result, standard residual plots, when interpreted in the same way as for linear models, seem to show all kind of problems, such as non-normality, heteroscedasticity, even if the model is correctly specified. check_residuals() aims at solving these problems by creating readily interpretable residuals for GLMs that are standardized to values between 0 and 1, and that can be interpreted as intuitively as residuals for the linear model. This is achieved by a simulation-based approach, similar to the Bayesian p-value or the parametric bootstrap, that transforms the residuals to a standardized scale. This explanation is adopted from DHARMa::simulateResiduals().

Value

Invisibly returns the p-value of the test statistics. A p-value < 0.05 indicates a significant deviation from expected distribution.

Author(s)

Martin Haringa

References


Gelman, A. & Hill, J. Data analysis using regression and multilevel/hierarchical models Cambridge University Press, 2006


Examples

```r
## Not run:
m1 <- glm(nclaims ~ area, offset = log(exposure), family = poisson(),
data = MTPL2)
check_residuals(m1, n_simulations = 50) %>% autoplot()

## End(Not run)
```

Construct model points from Generalized Linear Model

---
construct_model_points

Description

[Experimental] construct_model_points() is used to construct model points from generalized linear models, and must be preceded by model_data(). construct_model_points() can also be used in combination with a data.frame.

Usage

construct_model_points(
  x,
  exposure = NULL,
  exposure_by = NULL,
  agg_cols = NULL,
  drop_na = FALSE
)

Arguments

x Object of class model_data or of class data.frame
exposure column with exposure
exposure_by split column exposure by (e.g. year)
agg_cols list of columns to aggregate (sum) by, e.g. number of claims
drop_na drop na values (default to FALSE)

Value
data.frame

Author(s)

Martin Haringa

Examples

## Not run:
# With data.frame
library(dplyr)
mtcars %>%
  select(cyl, vs) %>%
  construct_model_points()

mtcars %>
  select(cyl, vs, disp) %>%
  construct_model_points(exposure = disp)

mtcars %>
  select(cyl, vs, disp, gear) %>
  construct_model_points(exposure = disp, exposure_by = gear)

mtcars %>
construct_tariff_classes

Construct insurance tariff classes

Description

Constructs insurance tariff classes to fitgam objects produced by fit_gam. The goal is to bin the continuous risk factors such that categorical risk factors result which capture the effect of the covariate on the response in an accurate way, while being easy to use in a generalized linear model (GLM).

Usage

construct_tariff_classes(
  object,
  alpha = 0,
  niterations = 10000,
  ntrees = 200,
  seed = 1
)

select(cyl, vs, disp, gear, mpg) %>%
construct_model_points(exposure = disp, exposure_by = gear,
  agg_cols = list(mpg))

# With glm
library(datasets)
data1 <- warpbreaks %>%
  mutate(jaar = c(rep(2000, 10), rep(2010, 44))) %>%
  mutate(nclaims = 1)
pmodel <- glm(breaks ~ wool + tension, data1, offset = log(nclaims),
  family = poisson(link = "log"))
model_data(pmodel) %>%
  construct_model_points()
model_data(pmodel) %>%
  construct_model_points(exposure = breaks, agg_cols = list(nclaims))
model_data(pmodel) %>%
  construct_model_points(exposure = breaks, exposure_by = jaar,
    agg_cols = list(nclaims)) %>%
  add_prediction(., pmodel)

## End(Not run)
construct_tariff_classes

Arguments

- **object**: fitgam object produced by `fit_gam`
- **alpha**: complexity parameter. The complexity parameter (alpha) is used to control the number of tariff classes. Higher values for alpha render less tariff classes. (alpha = 0 is default).
- **niterations**: in case the run does not converge, it terminates after a specified number of iterations defined by `niterations`.
- **ntrees**: the number of trees in the population.
- **seed**: an numeric seed to initialize the random number generator (for reproducibility).

Details

Evolutionary trees are used as a technique to bin the fitgam object produced by `fit_gam` into risk homogeneous categories. This method is based on the work by Henckaerts et al. (2018). See Grubinger et al. (2014) for more details on the various parameters that control aspects of the evtree fit.

Value

A list of class `constructtariffclasses` with components

- **prediction**: data frame with predicted values
- **x**: name of continuous risk factor for which tariff classes are constructed
- **model**: either 'frequency', 'severity' or 'burning'
- **data**: data frame with predicted values and observed values
- **x_obs**: observations for continuous risk factor
- **splits**: vector with boundaries of the constructed tariff classes
- **tariff_classes**: values in vector x coded according to which constructed tariff class they fall

Author(s)

Martin Haringa

References


Examples

```r
## Not run:
library(dplyr)
fit_gam(MTPL, nclaims = nclaims, x = age_policyholder,
exposure = exposure) %>%
  construct_tariff_classes(.)

## End(Not run)
```

### fisher

Fisher's natural breaks classification

**Description**

The function provides an interface to finding class intervals for continuous numerical variables, for example for choosing colours for plotting maps.

**Usage**

`fisher(vec, n = 7, diglab = 2)`

**Arguments**

- `vec` a continuous numerical variable
- `n` number of classes required (n = 7 is default)
- `diglab` number of digits (n = 2 is default)

**Details**

The "fisher" style uses the algorithm proposed by W. D. Fisher (1958) and discussed by Slocum et al. (2005) as the Fisher-Jenks algorithm. This function is adopted from the classInt package.

**Value**

Vector with clustering

**Author(s)**

Martin Haringa

**References**

Bivand, R. (2018). classInt: Choose Univariate Class Intervals. R package version 0.2-3. [https://CRAN.R-project.org/package=classInt](https://CRAN.R-project.org/package=classInt)

fit_gam

**Description**

Fits a generalized additive model (GAM) to continuous risk factors in one of the following three types of models: the number of reported claims (claim frequency), the severity of reported claims (claim severity) or the burning cost (i.e. risk premium or pure premium).

**Usage**

```r
fit_gam(
  data,  # data.frame of an insurance portfolio
  nclaims,  # column in data with number of claims
  x,  # column in data with continuous risk factor
  exposure,  # column in data with exposure
  amount = NULL,  # column in data with claim amount
  pure_premium = NULL,  # column in data with pure premium
  model = "frequency",  # choose either 'frequency', 'severity' or 'burning' (model = 'frequency' is default). See details section.
  round_x = NULL)
```

**Arguments**

- **data**: data.frame of an insurance portfolio
- **nclaims**: column in data with number of claims
- **x**: column in data with continuous risk factor
- **exposure**: column in data with exposure
- **amount**: column in data with claim amount
- **pure_premium**: column in data with pure premium
- **model**: choose either 'frequency', 'severity' or 'burning' (model = 'frequency' is default). See details section.
- **round_x**: round elements in column x to multiple of round_x. This gives a speed enhancement for data containing many levels for x.

**Details**

The 'frequency' specification uses a Poisson GAM for fitting the number of claims. The logarithm of the exposure is included as an offset, such that the expected number of claims is proportional to the exposure.

The 'severity' specification uses a lognormal GAM for fitting the average cost of a claim. The average cost of a claim is defined as the ratio of the claim amount and the number of claims. The number of claims is included as a weight.

The 'burning' specification uses a lognormal GAM for fitting the pure premium of a claim. The pure premium is obtained by multiplying the estimated frequency and the estimated severity of
claims. The word burning cost is used here as equivalent of risk premium and pure premium. Note that the functionality for fitting a GAM for pure premium is still experimental (in the early stages of development).

**Value**

A list with components

- `prediction` data frame with predicted values
- `x` name of continuous risk factor
- `model` either 'frequency', 'severity' or 'burning'
- `data` data frame with predicted values and observed values
- `x_obs` observations for continuous risk factor

**Author(s)**

Martin Haringa

**References**


**Examples**

```r
fit_gam(MTPL, nclaims = nclaims, x = age_policyholder, exposure = exposure)
```

---

*fit_truncated_dist*  
*Fit a distribution to truncated severity (loss) data*

**Description**

[Experimental] Estimate the original distribution from truncated data. Truncated data arise frequently in insurance studies. It is common that only claims above a certain threshold are known.
Usage

fit_truncated_dist(
  y,
  dist = c("gamma", "lognormal"),
  left = NULL,
  right = NULL,
  start = NULL,
  print_initial = TRUE
)

Arguments

y vector with observations of losses
dist distribution for severity ("gamma" or "lognormal"). Defaults to "gamma".
left numeric. Observations below this threshold are not present in the sample.
right numeric. Observations above this threshold are not present in the sample. Defaults to Inf.
start list of starting parameters for the algorithm.
print_initial print attempts for initial parameters.

Value

fitdist returns an object of class "fitdist"

Author(s)

Martin Haringa

Examples

## Not run:
# Original observations for severity
set.seed(1)
e <- rgamma(1000, scale = 148099.5, shape = 0.4887023)
# Truncated data (only claims above 30.000 euros)
threshold <- 30000
f <- e[e > threshold]
library(dplyr)
library(ggplot2)
data.frame(value = c(e, f),
  variable = rep(c("Original data", "Only claims above 30.000 euros"),
  c(length(e), length(f)))) %>%
  filter(value < 5e5) %>%
  mutate(value = value / 1000) %>%
  ggplot(aes(x = value)) +
  geom_histogram(colour = "white") +
  facet_wrap(~variable, ncol = 1) +
histbin

```r
labs(y = "Number of observations",
     x = "Severity (x 1000 EUR)"
)

# scale = 156259.7 and shape = 0.4588. Close to parameters of original
# distribution!
x <- fit_truncated_dist(f, left = threshold, dist = "gamma")

# Print cdf
autoplot(x)

# CDF with modifications
autoplot(x, print_dig = 5, xlab = "loss", ylab = "cdf", ylim = c(.9, 1))

est_scale <- x$estimate[1]
est_shape <- x$estimate[2]

# Generate data from truncated distribution (between 30k en 20 mln)
rg <- rgammat(10, scale = est_scale, shape = est_shape, lower = 3e4,
              upper = 20e6)

# Calculate quantiles
quantile(rg, probs = c(.5, .9, .99, .995))

## End(Not run)
```

**histbin**

Create a histogram with outlier bins

**Description**

Visualize the distribution of a single continuous variable by dividing the x axis into bins and counting the number of observations in each bin. Data points that are considered outliers can be binned together. This might be helpful to display numerical data over a very wide range of values in a compact way.

**Usage**

```r
histbin(
  data,
  x,
  left = NULL,
  right = NULL,
  line = FALSE,
  bins = 30,
  fill = NULL,
  color = NULL,
  fill_outliers = "#a7d1a7"
)
```
model_data

Arguments

data data.frame
x variable name in data.frame data that should be mapped
left numeric indicating the floor of the range
right numeric indicating the ceiling of the range
line show density line (default is FALSE)
bins numeric to indicate number of bins
fill color used to fill bars
color color for bar lines
fill_outliers color used to fill outlier bars

Details

Wrapper function around ggplot2::geom_histogram(). The method is based on suggestions from https://edwinth.github.io/blog/outlier-bin/.

Value

a ggplot2 object

Examples

histbin(MTPL2, premium)
histbin(MTPL2, premium, left = 30, right = 120, bins = 30)

model_data

Get model data

Description

[Experimental] model_data() is used to get data from glm, and must be preceded by update_glm() or glm().

Usage

model_data(x)

Arguments

x Object of class refitsmooth, refitrestricted or glm

Value

data.frame
**model_performance**

**Author(s)**

Martin Haringa

---

**model_performance** *Performance of fitted GLMs*

**Description**

Compute indices of model performance for (one or more) GLMs.

**Usage**

```r
model_performance(...)
```

**Arguments**

...  

One or more objects of class `glm`.

**Details**

The following indices are computed:

- **AIC** Akaike’s Information Criterion, see `stats::AIC()`
- **BIC** Bayesian Information Criterion, see `stats::BIC()`
- **RMSE** Root mean squared error, `rmse()`

Adopted from `performance::model_performance()`.

**Value**

data frame

**Author(s)**

Martin Haringa

**Examples**

```r
m1 <- glm(nclaims ~ area, offset = log(exposure), family = poisson(),
          data = MTPL2)
m2 <- glm(nclaims ~ area, offset = log(exposure), family = poisson(),
          data = MTPL2)
model_performance(m1, m2)
```
MTPL

*Characteristics of 30,000 policyholders in a Motor Third Party Liability (MTPL) portfolio.*

**Description**

A dataset containing the age, number of claims, exposure, claim amount, power, bm, and region of 30,000 policyholders.

**Usage**

**MTPL**

**Format**

A data frame with 30,000 rows and 7 variables:

- **age_policyholder** age of policyholder, in years.
- **nclaims** number of claims.
- **exposure** exposure, for example, if a vehicle is insured as of July 1 for a certain year, then during that year, this would represent an exposure of 0.5 to the insurance company.
- **amount** claim amount in Euros.
- **power** engine power of vehicle (in kilowatts).
- **bm** level occupied in the 23-level (0-22) bonus-malus scale (the higher the level occupied, the worse the claim history).
- **zip** region indicator (0-3).

**Author(s)**

Martin Haringa

**Source**

The data is derived from the portfolio of a large Dutch motor insurance company.
MTPL2

Characteristics of 3,000 policyholders in a Motor Third Party Liability (MTPL) portfolio.

Description

A dataset containing the area, number of claims, exposure, claim amount, exposure, and premium of 3,000 policyholders

Usage

MTPL2

Format

A data frame with 3,000 rows and 6 variables:

customer_id  customer id
area  region where customer lives (0-3)
nclaims  number of claims
amount  claim amount (severity)
exposure  exposure
premium  earned premium

Author(s)

Martin Haringa

Source

The data is derived from the portfolio of a large Dutch motor insurance company.

period_to_months  Split period to months

Description

The function splits rows with a time period longer than one month to multiple rows with a time period of exactly one month each. Values in numeric columns (e.g. exposure or premium) are divided over the months proportionately.

Usage

period_to_months(df, begin, end, ...)


Arguments

df    data.frame
begin    column in df with begin dates
end    column in df with end dates
...    numeric columns in df to split

Details

In insurance portfolios it is common that rows relate to periods longer than one month. This is for example problematic in case exposures per month are desired.

Since insurance premiums are constant over the months, and do not depend on the number of days per month, the function assumes that each month has the same number of days (i.e. 30).

Value

data.frame with same columns as in df, and one extra column called id

Author(s)

Martin Haringa

Examples

library(lubridate)
portfolio <- data.frame(
    begin1 = ymd(c("2014-01-01", "2014-01-01")),
    end = ymd(c("2014-03-14", "2014-05-10")),
    termination = ymd(c("2014-03-14", "2014-05-10")),
    exposure = c(0.2025, 0.3583),
    premium = c(125, 150))
period_to_months(portfolio, begin1, end, premium, exposure)

rating_factors    Include reference group in regression output

Description

Extract coefficients in terms of the original levels of the coefficients rather than the coded variables.
Usage

```r
rating_factors(
  ..., model_data = NULL,
  exposure = NULL,
  exponentiate = TRUE,
  signif_stars = TRUE,
  round_exposure = 0
)
```

Arguments

- `...`: glm object(s) produced by `glm()`
- `model_data`: data.frame used to create glm object(s), this should only be specified in case the exposure is desired in the output, default value is NULL
- `exposure`: column in `model_data` with exposure, default value is NULL
- `exponentiate`: logical indicating whether or not to exponentiate the coefficient estimates. Defaults to TRUE.
- `signif_stars`: show significance stars for p-values (defaults to TRUE)
- `round_exposure`: number of digits for exposure (defaults to 0)

Details

A fitted linear model has coefficients for the contrasts of the factor terms, usually one less in number than the number of levels. This function re-expresses the coefficients in the original coding. This function is adopted from `dummy.coef()`. Our adoption prints a data.frame as output.

Value

data.frame

Author(s)

Martin Haringa

Examples

```r
library(dplyr)
df <- MTPL2 %>%
  mutate(across(c(area), as.factor)) %>%
  mutate(across(c(area), ~biggest_reference(.[, exposure])))

mod1 <- glm(nclaims ~ area + premium, offset = log(exposure),
  family = poisson(), data = df)
mod2 <- glm(nclaims ~ area, offset = log(exposure), family = poisson(),
  data = df)

rating_factors(mod1, mod2, model_data = df, exposure = exposure)
```
Include reference group in regression output

Description

Extract coefficients in terms of the original levels of the coefficients rather than the coded variables. Use rating_factors() to compare the output obtained from two or more glm objects.

Usage

```r
rating_factors1(
  model,
  model_data = NULL,  # data.frame used to create glm object, this should only be specified in case the exposure is desired in the output, default value is NULL
  exposure = NULL,  # the name of the exposure column in model_data, default value is NULL
  colname = "estimate",  # the name of the output column, default value is "estimate"
  exponentiate = TRUE,  # logical indicating whether or not to exponentiate the coefficient estimates. Defaults to TRUE.
  round_exposure = 0  # number of digits for exposure (default to 0)
)
```

Arguments

- `model`: a single glm object produced by glm()
- `model_data`: data.frame used to create glm object, this should only be specified in case the exposure is desired in the output, default value is NULL
- `exposure`: the name of the exposure column in `model_data`, default value is NULL
- `colname`: the name of the output column, default value is "estimate"
- `exponentiate`: logical indicating whether or not to exponentiate the coefficient estimates. Defaults to TRUE.
- `round_exposure`: number of digits for exposure (default to 0)

Author(s)

Martin Haringa

Examples

```r
MTPL2a <- MTPL2
MTPL2a$area <- as.factor(MTPL2a$area)
x <- glm(nclaims ~ area, offset = log(exposure), family = poisson(), data = MTPL2a)
rating_factors1(x)
```
reduce

Reduce portfolio by merging redundant date ranges

Description

Transform all the date ranges together as a set to produce a new set of date ranges. Ranges separated by a gap of at least `min.gapwidth` days are not merged.

Usage

```r
reduce(df, begin, end, ..., agg_cols = NULL, agg = "sum", min.gapwidth = 5)
```

Arguments

- `df` data.frame
- `begin` name of column in `df` with begin dates
- `end` name of column in `df` with end dates
- `...` names of columns in `df` used to group date ranges by
- `agg_cols` list with columns in `df` to aggregate by (defaults to NULL)
- `agg` aggregation type (defaults to "sum")
- `min.gapwidth` ranges separated by a gap of at least `min.gapwidth` days are not merged. Defaults to 5.

Details

This function is adopted from IRanges::reduce().

Value

An object of class "reduce". The function summary is used to obtain and print a summary of the results. An object of class "reduce" is a list usually containing at least the following elements:

- `df` data frame with reduced time periods
- `begin` name of column in `df` with begin dates
- `end` name of column in `df` with end dates
- `cols` names of columns in `df` used to group date ranges by

Author(s)

Martin Haringa
Examples

```r
portfolio <- structure(list(policy_nr = c("12345", "12345", "12345", "12345",
"12345", "12345", "12345", "12345", "12345", "12345", "12345", "12345"),
productgroup = c("fire", "fire", "fire", "fire", "fire", "fire",
"fire", "fire", "fire", "fire"), product = c("contents", "contents",
"contents", "contents", "contents", "contents", "contents",
"contents", "contents", "contents"),
begin_dat = structure(c(16709, 16740, 16801, 17410, 17440, 17805, 17897,
17956, 17987, 18017, 18262), class = "Date"),
end_dat = structure(c(16739, 16800, 16831, 17439, 17531, 17896, 17955,
17986, 18016, 18261, 18292), class = "Date"),
premium = c(89L, 58L, 83L, 73L, 69L, 94L, 91L, 97L, 57L, 65L, 55L)),
row.names = c(NA, -11L), class = "data.frame")

# Merge periods
pt1 <- reduce(portfolio, begin = begin_dat, end = end_dat, policy_nr,
productgroup, product, min.gapwidth = 5)

# Aggregate per period
summary(pt1, period = "days", policy_nr, productgroup, product)

# Merge periods and sum premium per period
pt2 <- reduce(portfolio, begin = begin_dat, end = end_dat, policy_nr,
productgroup, product, agg_cols = list(premium), min.gapwidth = 5)

# Create summary with aggregation per week
summary(pt2, period = "weeks", policy_nr, productgroup, product)
```

---

**refit_glm**

*Refitting Generalized Linear Models*

**Description**

[Experimental] `refit_glm()` is used to refit generalized linear models, and must be preceded by `restrict_coef()`.

**Usage**

`refit_glm(x)`

**Arguments**

- `x` Object of class restricted or of class smooth

**Value**

Object of class GLM
**restrict_coef**

**Author(s)**

Martin Haringa

---

**restrict_coef**

*Restrict coefficients in the model*

**Description**

*Experimental* Add restrictions, like a bonus-malus structure, on the risk factors used in the model. *restrict_coef()* must always be followed by *update_glm()*.

**Usage**

`restrict_coef(model, restrictions)`

**Arguments**

- **model**: object of class glm/restricted
- **restrictions**: data.frame with two columns containing restricted data. The first column, with the name of the risk factor as column name, must contain the levels of the risk factor. The second column must contain the restricted coefficients.

**Details**

Although restrictions could be applied either to the frequency or the severity model, it is more appropriate to impose the restrictions on the premium model. This can be achieved by calculating the pure premium for each record (i.e. expected number of claims times the expected claim amount), then fitting an "unrestricted" Gamma GLM to the pure premium, and then imposing the restrictions in a final "restricted" Gamma GLM.

**Value**

Object of class restricted.

**Author(s)**

Martin Haringa

**See Also**

*update_glm()* for refitting the restricted model, and *autoplot.restricted()*.

Other *update_glm*: *smooth_coef()*
Examples

```r
## Not run:
# Add restrictions to risk factors for region (zip) -------------------------

# Fit frequency and severity model
library(dplyr)
freq <- glm(nclaims ~ bm + zip, offset = log(exposure), family = poisson(),
    data = MTPL)
sev <- glm(amount ~ bm + zip, weights = nclaims,
    family = Gamma(link = "log"),
    data = MTPL %>% filter(amount > 0))

# Add predictions for freq and sev to data, and calculate premium
premium_df <- MTPL %>%
    add_prediction(freq, sev) %>%
    mutate(premium = pred_nclaims_freq * pred_amount_sev)

# Restrictions on risk factors for region (zip)
zip_df <- data.frame(zip = c(0,1,2,3, zip_rst = c(0.8, 0.9, 1, 1.2))

# Fit unrestricted model
burn <- glm(premium ~ bm + zip, weights = exposure,
    family = Gamma(link = "log"), data = premium_df)

# Fit restricted model
burn_rst <- burn %>%
    restrict_coef(., zip_df) %>%
    update_glm()

# Show rating factors
rating_factors(burn_rst)

## End(Not run)
```

rgammat

Generate data from truncated gamma distribution

Description

Random generation for the truncated Gamma distribution with parameters shape and scale.

Usage

```r
rgammat(n, scale = scale, shape = shape, lower, upper)
```

Arguments

- `n`: number of observations
scale  scale parameter
shape  shape parameter
lower  numeric. Observations below this threshold are not present in the sample.
upper  numeric. Observations above this threshold are not present in the sample.

Value
The length of the result is determined by \( n \).

Author(s)
Martin Haringa

---

### Value
The length of the result is determined by \( n \).

### Author(s)
Martin Haringa

---

### Description
Random generation for the truncated log normal distribution whose logarithm has mean equal to \( \text{meanlog} \) and standard deviation equal to \( \text{sdlog} \).

### Usage
\[
\text{rlnormt}(n, \text{meanlog}, \text{sdlog}, \text{lower}, \text{upper})
\]

### Arguments
- \( n \) number of observations
- \( \text{meanlog} \) mean of the distribution on the log scale
- \( \text{sdlog} \) standard deviation of the distribution on the log scale
- \( \text{lower} \) numeric. Observations below this threshold are not present in the sample.
- \( \text{upper} \) numeric. Observations above this threshold are not present in the sample.

### Value
The length of the result is determined by \( n \).

### Author(s)
Martin Haringa
Description

Compute root mean squared error.

Usage

`rmse(object, data)`

Arguments

- `object`: fitted model
- `data`: data.frame (defaults to NULL)

Details

The RMSE is the square root of the average of squared differences between prediction and actual observation and indicates the absolute fit of the model to the data. It can be interpreted as the standard deviation of the unexplained variance, and is in the same units as the response variable. Lower values indicate better model fit.

Value

numeric value

Author(s)

Martin Haringa

Examples

```r
x <- glm(nclaims ~ area, offset = log(exposure), family = poisson(),
        data = MTPL2)
rmse(x, MTPL2)
```
rows_per_date  

*Find active rows per date*

**Description**

Fast overlap joins. Usually, `df` is a very large data.table (e.g. insurance portfolio) with small interval ranges, and `dates` is much smaller with (e.g.) claim dates.

**Usage**

```r
rows_per_date(
  df,
  dates,
  df_begin,
  df_end,
  dates_date,
  ..., 
  nomatch = NULL,
  mult = "all"
)
```

**Arguments**

- `df`  
  data.frame with portfolio (df should include time period)
- `dates`  
  data.frame with dates to join
- `df_begin`  
  column name with begin dates of time period in df
- `df_end`  
  column name with end dates of time period in df
- `dates_date`  
  column name with dates in dates
- `...`  
  additional column names in dates to join by
- `nomatch`  
  When a row (with interval say, `[a,b]`) in x has no match in y, nomatch=NA means NA is returned for y’s non-by:y columns for that row of x. nomatch=NULL (default) means no rows will be returned for that row of x.
- `mult`  
  When multiple rows in y match to the row in x, mult controls which values are returned - "all" (default), "first" or "last".

**Value**

returned class is equal to class of `df`

**Author(s)**

Martin Haringa
Examples

```r
library(lubridate)
portfolio <- data.frame(
  begin1 = ymd(c("2014-01-01", "2014-01-01")),
  end = ymd(c("2014-03-14", "2014-05-10")),
  termination = ymd(c("2014-03-14", "2014-05-10")),
  exposure = c(0.2025, 0.3583),
  premium = c(125, 150),
  car_type = c("BMW", "TESLA"))

# Find active rows on different dates
dates0 <- data.frame(active_date = seq(ymd("2014-01-01"), ymd("2014-05-01"),
  by = "months"))
rows_per_date(portfolio, dates0, df_begin = begin1, df_end = end,
  dates_date = active_date)

# With extra identifiers (merge claim date with time interval in portfolio)
claim_dates <- data.frame(claim_date = ymd("2014-01-01"),
  car_type = c("BMW", "VOLVO"))

### Only rows are returned that can be matched
rows_per_date(portfolio, claim_dates, df_begin = begin1,
  df_end = end, dates_date = claim_date, car_type)

### When row cannot be matched, NA is returned for that row
rows_per_date(portfolio, claim_dates, df_begin = begin1,
  df_end = end, dates_date = claim_date, car_type, nomatch = NA)
```

---

**smooth_coef**  
*Smooth coefficients in the model*

**Description**

[Experimental] Apply smoothing on the risk factors used in the model. smooth_coef() must always be followed by update_glm().

**Usage**

```r
smooth_coef(model, x_cut, x_org, degree = NULL, breaks = NULL)
```

**Arguments**

- `model` : object of class glm/smooth
- `x_cut` : column name with breaks/cut
- `x_org` : column name where `x_cut` is based on
- `degree` : order of polynomial
- `breaks` : numerical vector with new clusters for `x`
Details

Although smoothing could be applied either to the frequency or the severity model, it is more appropriate to impose the smoothing on the premium model. This can be achieved by calculating the pure premium for each record (i.e. expected number of claims times the expected claim amount), then fitting an "unrestricted" Gamma GLM to the pure premium, and then imposing the restrictions in a final "restricted" Gamma GLM.

Value

Object of class smooth

Author(s)

Martin Haringa

See Also

update glm() for refitting the smoothed model, and autoplot.smooth().

Other update glm: restrict_coef()

Examples

## Not run:
library(insurancerating)
library(dplyr)

# Fit GAM for claim frequency
age_policyholder_frequency <- fit_gam(data = MTPL,
nclaims = nclaims,
x = age_policyholder,
exposure = exposure)

# Determine clusters
clusters_freq <- construct_tariff_classes(age_policyholder_frequency)

# Add clusters to MTPL portfolio
dat <- MTPL %>%
mutate(age_policyholder_freq_cat = clusters_freq$tariff_classes) %>%
mutate(across(where(is.character), as.factor)) %>%
mutate(across(where(is.factor), ~biggest_reference(., exposure)))

# Fit frequency and severity model
freq <- glm(nclaims ~ bm + age_policyholder_freq_cat, offset = log(exposure),
family = poisson(), data = dat)
sev <- glm(amount ~ bm + zip, weights = nclaims,
family = Gamma(link = "log"), data = dat %>% filter(amount > 0))

# Add predictions for freq and sev to data, and calculate premium
premium_df <- dat %>%
add_prediction(freq, sev) %>%
mutate(premium = pred_nclaims_freq * pred_amount_sev)
# Fit unrestricted model
burn_unrestricted <- glm(premium ~ zip + bm + age_policyholder_freq_cat, 
weights = exposure, 
family = Gamma(link = "log"), 
data = premium_df)

# Impose smoothing and create figure
burn_unrestricted %>%
  smooth_coef(x_cut = "age_policyholder_freq_cat", 
              x_org = "age_policyholder", 
              breaks = seq(18, 95, 5)) %>%
  autoplot()

# Impose smoothing and refit model
burn_restricted <- burn_unrestricted %>%
  smooth_coef(x_cut = "age_policyholder_freq_cat", 
              x_org = "age_policyholder", 
              breaks = seq(18, 95, 5)) %>%
  update_glm()

# Show new rating factors
rating_factors(burn_restricted)

## End(Not run)

summary.reduce

Automatically create a summary for objects obtained from reduce()

### Description
Takes an object produced by reduce(), and counts new and lost customers.

### Usage

```r
## S3 method for class 'reduce'
summary(object, ..., period = "days", name = "count")
```

### Arguments

- **object**: reduce object produced by reduce()
- **...**: names of columns to aggregate counts by
- **period**: a character string indicating the period to aggregate on. Four options are available: "quarters", "months", "weeks", and "days" (the default option)
- **name**: The name of the new column in the output. If omitted, it will default to count.

### Value

data.frame
Description

Univariate analysis for discrete risk factors in an insurance portfolio. The following summary statistics are calculated:

- frequency (i.e. number of claims / exposure)
- average severity (i.e. severity / number of claims)
- risk premium (i.e. severity / exposure)
- loss ratio (i.e. severity / premium)
- average premium (i.e. premium / exposure)

If input arguments are not specified, the summary statistics related to these arguments are ignored.

Usage

univariate(
  df, x, severity = NULL, nclaims = NULL, exposure = NULL, premium = NULL, by = NULL
)

Arguments

df data.frame with insurance portfolio
x column in df with risk factor
severity column in df with severity (default is NULL)
nclaims column in df with number of claims (default is NULL)
exposure column in df with exposure (default is NULL)
premium column in df with premium (default is NULL)
by list of column(s) in df to group by

Value

A data.frame

Author(s)

Martin Haringa
Examples

# Summarize by `area`
univariate(MTPL2, x = area, severity = amount, nclaims = nclaims,
       exposure = exposure, premium = premium)

# Summarize by `zip` and `bm`
univariate(MTPL, x = zip, severity = amount, nclaims = nclaims,
       exposure = exposure, by = bm)

# Summarize by `zip`, `bm` and `power`
univariate(MTPL, x = zip, severity = amount, nclaims = nclaims,
       exposure = exposure, by = list(bm, power))

update_glm  Refitting Generalized Linear Models

Description

[Experimental] update_glm() is used to refit generalized linear models, and must be preceded by restrict_coef().

Usage

update_glm(x)

Arguments

x             Object of class restricted or of class smooth

Value

Object of class GLM

Author(s)

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Index

* autoplot.restricted
  restrict_coef, 35
* autoplot.smooth
  smooth_coef, 40
* datasets
  MTPL, 28
  MTPL2, 29
* update_glm
  restrict_coef, 35
  smooth_coef, 40

add_prediction, 3
autoplot.bootstrap_rmse, 3
autoplot.check_residuals, 4
autoplot.construct_tariff_classes, 5
autoplot.fitgam, 6
autoplot.restricted, 8
autoplot.restricted(), 33
autoplot.riskfactor, 8
autoplot.smooth, 10
autoplot.smooth(), 41
autoplot.truncated_dist, 10
autoplot.univariate, 11

biggest_reference, 13
bootstrap_rmse, 14

check_overdispersion, 15
check_residuals, 16
construct_model_points, 17
construct_tariff_classes, 19

DHARMa::simulateResiduals(), 17

fisher, 21
fitGam, 22
fit_truncated_dist, 23

histbin, 25
model_data, 26

model_performance, 27
MTPL, 28
MTPL2, 29

period_to_months, 29
rating_factors, 30
rating_factors1, 32
reduce, 33
refit_glm, 34
restrict_coef, 35, 41
rgammat, 36
rlnormt, 37
rmse, 38
rmse(), 27
rows_per_date, 39

smooth_coef, 35, 40
stats::AIC(), 27
stats::BIC(), 27
summary.reduce, 42

univariate, 43
update_glm, 44
update_glm(), 35, 41