

# Package ‘insurancerating’

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**Type** Package

**Title** Analytic Insurance Rating Techniques

**Version** 0.6.2

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**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)

**URL** <https://github.com/mharinga/insurancerating>,  
<https://mharinga.github.io/insurancerating/>

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## R topics documented:

add_prediction	2
autoplot.bootstrap_rmse	3
autoplot.check_residuals	4
autoplot.constructtariffclasses	4
autoplot.fitgam	6
autoplot.riskfactor	7
autoplot.univariate	8
biggest_reference	10
bootstrap_rmse	11
check_overdispersion	12
check_residuals	13
construct_tariff_classes	14
fisher	16
fit_gam	17
model_performance	19
MTPL	20
MTPL2	21
period_to_months	21
rating_factors	22
rating_factors1	23
reduce	24
rmse	26
summary.reduce	27
univariate	28
<b>Index</b>	<b>30</b>

---

add_prediction	<i>Add predictions to a data frame</i>
----------------	--

---

### Description

Add model predictions and confidence bounds to a data frame.

### Usage

```
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 <code>glm</code> .
var	the name of the output column(s), defaults to <code>NULL</code>
conf_int	determines whether confidence intervals will be shown. Defaults to <code>conf_int = FALSE</code> .
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**

```
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**

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

**Arguments**

object	bootstrap_rmse object produced by <code>bootstrap_rmse()</code>
...	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**

```
## 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**

```
## 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**

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

## End(Not run)

```

---

autoplot.fitgam	<i>Automatically create a ggplot for objects obtained from fit_gam()</i>
-----------------	--

---

### Description

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

### Usage

```

## 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,
  ...
)

```

### Arguments

<code>object</code>	fitgam object produced by <code>fit_gam()</code>
<code>conf_int</code>	determines whether 95% confidence intervals will be plotted. The default is <code>conf_int = FALSE</code>
<code>color_gam</code>	a color can be specified either by name (e.g.: "red") or by hexadecimal code (e.g. : "#FF1234") (default is "steelblue")
<code>show_observations</code>	add observed frequency/severity points for each level of the variable for which tariff classes are constructed
<code>x_stepsize</code>	set step size for labels horizontal axis
<code>size_points</code>	size for points (1 is default)
<code>color_points</code>	change the color of the points in the graph ("black" is default)
<code>rotate_labels</code>	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.riskfactor    *Automatically create a ggplot for objects obtained from rating\_factors()*

---

**Description**

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

**Usage**

```
## S3 method for class 'riskfactor'
autoplot(
  object,
  risk_factors = NULL,
  ncol = 1,
  labels = TRUE,
  dec.mark = ",",
  ylab = "rate",
  color_bg = "#E7B800",
  linetype = FALSE,
  ...
)
```

**Arguments**

object	riskfactor object produced by <code>rating_factors()</code>
risk_factors	character vector to define which factors are included. Defaults to all risk factors.
ncol	number of columns in output (default is 1)
labels	show labels with the exposure (default is TRUE)
dec.mark	control the format of the decimal point, as well as the mark between intervals before the decimal point, choose either "," (default) or "."
ylab	modify label for the y-axis
color_bg	change the color of the histogram ("E7B800" is default)
linetype	use different linetypes (default is FALSE)
...	other plotting parameters to affect the plot

**Value**

a ggplot2 object

**Examples**

```
library(dplyr)
df <- MTPL2 %>%
  mutate_at(vars(area), as.factor) %>%
  mutate_at(vars(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)

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

---

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

---

**Description**

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

**Usage**

```
## 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 = "#E7B800",
label_width = 10,
coord_flip = FALSE,
...
)

```

### 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: <ul style="list-style-type: none"> <li>• 1. frequency (i.e. number of claims / exposure)</li> <li>• 2. average severity (i.e. severity / number of claims)</li> <li>• 3. risk premium (i.e. severity / exposure)</li> <li>• 4. loss ratio (i.e. severity / premium)</li> <li>• 5. average premium (i.e. premium / exposure)</li> <li>• 6. exposure</li> <li>• 7. severity</li> <li>• 8. nclaims</li> <li>• 9. premium</li> </ul>
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	control the format of the decimal point, as well as the mark between intervals before the decimal point, choose either "," (default) or "."
color	change the color of the points and line ("dodgerblue" is default)
color_bg	change the color of the histogram ("#E7B800" is default)
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)
...	other plotting parameters to affect the plot

### Value

a ggplot2 object

## Examples

```
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)

MTPL2a <- MTPL2
MTPL2a$jaar <- sample(2015:2019, nrow(MTPL2a), replace = TRUE)
x1 <- univariate(MTPL2a, x = area, severity = amount, nclaims = nclaims,
exposure = exposure, by = jaar)
autoplot(x1, show_plots = 1:2)
```

---

biggest_reference	<i>Set reference group to the group with largest exposure</i>
-------------------	---

---

## 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

```
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

Kaas, Rob & Goovaerts, Marc & Dhaene, Jan & Denuit, Michel. (2008). Modern Actuarial Risk Theory: Using R. doi:10.1007/978-3-540-70998-5.

## Examples

```
## Not run:
library(dplyr)
df <- chickwts %>%
mutate_if(is.character, as.factor) %>%
mutate_if(is.factor, list(~biggest_reference(., weight)))

## End(Not run)
```

---

bootstrap_rmse	<i>Bootstrapped RMSE</i>
----------------	--------------------------

---

## Description

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

## Usage

```
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)

## 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

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

**Author(s)**

Martin Haringa

**Examples**

```
## 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**

```
check_overdispersion(object)
```

**Arguments**

object            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	<i>Check model residuals</i>
-----------------	------------------------------

---

**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 [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

Dunn, K. P., and Smyth, G. K. (1996). Randomized quantile residuals. *Journal of Computational and Graphical Statistics* 5, 1-10.

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

Hartig, F. (2020). DHARMA: Residual Diagnostics for Hierarchical (Multi-Level / Mixed) Regression Models. R package version 0.3.0. <https://CRAN.R-project.org/package=DHARMA>

## Examples

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

---

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
)
```

**Arguments**

<code>object</code>	fitgam object produced by <code>fit_gam</code>
<code>alpha</code>	complexity parameter. The complexity parameter ( <code>alpha</code> ) is used to control the number of tariff classes. Higher values for <code>alpha</code> render less tariff classes. ( <code>alpha = 0</code> is default).
<code>niterations</code>	in case the run does not converge, it terminates after a specified number of iterations defined by <code>niterations</code> .
<code>ntrees</code>	the number of trees in the population.
<code>seed</code>	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

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

**Author(s)**

Martin Haringa

**References**

Antonio, K. and Valdez, E. A. (2012). Statistical concepts of a priori and a posteriori risk classification in insurance. *Advances in Statistical Analysis*, 96(2):187–224. doi:10.1007/s10182-011-0152-7.

Grubinger, T., Zeileis, A., and Pfeiffer, K.-P. (2014). emtree: Evolutionary learning of globally optimal classification and regression trees in R. *Journal of Statistical Software*, 61(1):1–29. doi:10.18637/jss.v061.i01.

Henckaerts, R., Antonio, K., Clijsters, M. and Verbelen, R. (2018). A data driven binning strategy for the construction of insurance tariff classes. *Scandinavian Actuarial Journal*, 2018:8, 681-705. doi:10.1080/03461238.2018.1429300.

Wood, S.N. (2011). Fast stable restricted maximum likelihood and marginal likelihood estimation of semiparametric generalized linear models. *Journal of the Royal Statistical Society (B)* 73(1):3-36. doi:10.1111/j.1467-9868.2010.00749.x.

**Examples**

```
## 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>

Fisher, W. D. 1958 "On grouping for maximum homogeneity", Journal of the American Statistical Association, 53, pp. 789–798. doi: 10.1080/01621459.1958.10501479.

---

fit\_gam

*Generalized additive model*

---

**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**

```
fit_gam(  
  data,  
  nclaims,  
  x,  
  exposure,  
  amount = NULL,  
  pure_premium = NULL,  
  model = "frequency",  
  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.

**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**

Antonio, K. and Valdez, E. A. (2012). Statistical concepts of a priori and a posteriori risk classification in insurance. *Advances in Statistical Analysis*, 96(2):187–224. doi:10.1007/s10182-011-0152-7.

Grubinger, T., Zeileis, A., and Pfeiffer, K.-P. (2014). emtree: Evolutionary learning of globally optimal classification and regression trees in R. *Journal of Statistical Software*, 61(1):1–29. doi:10.18637/jss.v061.i01.

Henckaerts, R., Antonio, K., Clijsters, M. and Verbelen, R. (2018). A data driven binning strategy for the construction of insurance tariff classes. *Scandinavian Actuarial Journal*, 2018:8, 681-705. doi:10.1080/03461238.2018.1429300.

Wood, S.N. (2011). Fast stable restricted maximum likelihood and marginal likelihood estimation of semiparametric generalized linear models. *Journal of the Royal Statistical Society (B)* 73(1):3-36. doi:10.1111/j.1467-9868.2010.00749.x.

## Examples

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

---

model_performance	<i>Performance of fitted GLMs</i>
-------------------	-----------------------------------

---

## Description

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

## Usage

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

## Arguments

... One or more objects of class `glm`.

## Details

The following indices are computed:

- **AIC** Akaike's Information Criterion, see [AIC](#)
- **BIC** Bayesian Information Criterion, see [BIC](#)
- **RMSE** Root mean squared error, [rmse](#)

Adopted from `performance::model_performance()`.

## Value

data frame

## Author(s)

Martin Haringa

### Examples

```
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	<i>Ages of 32,731 policyholders in a Motor Third Party Liability (MTPL) portfolio.</i>
------	--

---

### Description

A dataset containing the age, number of claims, and exposure of almost 33,000 policyholders

### Usage

MTPL

### Format

A data frame with 32,731 rows and 4 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.

### Author(s)

Martin Haringa

### Source

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

---

MTPL2	<i>Characteristics of 3,000 policyholders in a Motor Third Party Liability (MTPL) portfolio.</i>
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**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  
**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.

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period_to_months	<i>Split period to months</i>
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**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**

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

**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 the coefficient estimates. Defaults to TRUE.
signif_stars	show significance stars for p-values (defaults to TRUE)

**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**

```
library(dplyr)
df <- MTPL2 %>%
  mutate_at(vars(area), as.factor) %>%
  mutate_at(vars(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)
```

---

rating\_factors1

*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**

```
rating_factors1(
  model,
  model_data = NULL,
  exposure = NULL,
  colname = "estimate",
  exponentiate = TRUE
)
```

**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 the coefficient estimates. Defaults to TRUE.

**Examples**

```
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*


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**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**

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

**Arguments**

df	data.frame
begin	name of column 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

### Examples

```
portfolio <- structure(list(policy_nr = c("12345", "12345", "12345", "12345",
"12345", "12345", "12345", "12345", "12345", "12345"),
productgroup = c("fire", "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
reduce(portfolio, begin = begin_dat, end = end_dat, policy_nr,
       productgroup, product, min.gapwidth = 5)

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

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rmse	<i>Root Mean Squared Error</i>
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### 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

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

---

summary.reduce	<i>Automatically create a summary for objects obtained from reduce()</i>
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---

**Description**

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

**Usage**

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

**Arguments**

object	reduce object produced by <code>reduce()</code>
period	a character string indicating the period to aggregate on. Four options are available: "quarters", "months", "weeks", and "days" (the default option)
...	names of columns to aggregate counts by

**Value**

data.frame

**Examples**

```
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", "fire"), product = c("contents",
"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")

pt1 <- reduce(portfolio, begin = begin_dat, end = end_dat, policy_nr,
productgroup, product, min.gapwidth = 5)
summary(pt1, period = "days", policy_nr, productgroup, product)

pt2 <- reduce(portfolio, begin = begin_dat, end = end_dat, policy_nr,
productgroup, product, agg_cols = list(premium), min.gapwidth = 5)
summary(pt2, period = "weeks", policy_nr, productgroup, product)
```

univariate

*Univariate analysis for discrete risk factors***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	column(s) in df to group by

**Value**

A list of class `univ_all` with components

df	data frame
xvar	name of column in df with risk factor

severity	name of column in df with severity
nclaims	name of column in df with number of claims
exposure	name of column in df with exposure
premium	name of column in df with premium

**Examples**

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

```
# The summary statistics related to premium are not calculated  
univariate(MTPL2, x = area, severity = amount, nclaims = nclaims, exposure = exposure)
```

# Index

## \*Topic **datasets**

MTPL, [20](#)

MTPL2, [21](#)

add\_prediction, [2](#)

AIC, [19](#)

autoplot.bootstrap\_rmse, [3](#)

autoplot.check\_residuals, [4](#)

autoplot.constructtariffclasses, [4](#)

autoplot.fitgam, [6](#)

autoplot.riskfactor, [7](#)

autoplot.univariate, [8](#)

BIC, [19](#)

biggest\_reference, [10](#)

bootstrap\_rmse, [11](#)

check\_overdispersion, [12](#)

check\_residuals, [13](#)

construct\_tariff\_classes, [14](#)

fisher, [16](#)

fit\_gam, [17](#)

model\_performance, [19](#)

MTPL, [20](#)

MTPL2, [21](#)

period\_to\_months, [21](#)

rating\_factors, [22](#)

rating\_factors1, [23](#)

reduce, [24](#)

rmse, [19](#), [26](#)

simulateResiduals, [14](#)

summary.reduce, [27](#)

univariate, [28](#)