

# Package ‘gratia’

February 7, 2026

**Version** 0.11.2

**Title** Graceful 'ggplot'-Based Graphics and Other Functions for GAMs  
Fitted Using 'mgcv'

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**Depends** R (>= 4.1.0)

**Imports** mgcv (>= 1.9-0), ggplot2 (>= 3.5.0), tibble (>= 3.0.0), dplyr  
(>= 1.2.0), tidyr, rlang, patchwork (>= 1.2.0), vctrs, grid,  
mvnfast, purrr (>= 1.1.0), stats, tools, grDevices, stringr,  
tidyselect (>= 1.2.0), lifecycle, pillar, cli, nlme,  
ggokabeito, withr, scales, mirai, tweedie (>= 2.3.5)

**Suggests** gamm4, lme4, testthat, vdiff, MASS, scam (>= 1.2-21),  
datasets, knitr, rmarkdown, forcats, GJRM, readr, glmmTMB,  
ggdist, distributional, hexbin, gamair, sf (>= 0.7-3), svglite  
(>= 2.0.0), curl, marginaleffects, carrier

**Description** Graceful 'ggplot'-based graphics and utility functions for working with generalized additive models (GAMs) fitted using the 'mgcv' package. Provides a reimplementa-  
tion of the plot() method for GAMs that 'mgcv' provides, as well as 'tidyverse' compatible repre-  
sentations of estimated smooths.

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**LazyData** true

**URL** <https://gavinsimpson.github.io/gratia/>

**BugReports** <https://github.com/gavinsimpson/gratia/issues>

**RoxygenNote** 7.3.3

**Encoding** UTF-8

**VignetteBuilder** knitr

**Config/testthat/edition** 3

**Config/Needs/website** rmarkdown, ggdist

**Language** en-GB

**NeedsCompilation** no

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**Repository** CRAN

**Date/Publication** 2026-02-07 06:10:36 UTC

## Contents

add_confint	5
add_constant	5
add_fitted	6
add_fitted.gam	7
add_fitted_samples	8
add_partial_residuals	9
add_residuals	10
add_residuals.gam	10
add_sizer	11
appraise	12
assemble	14
assemble.gam	15
basis	19
basis_size	22
bird_move	23
boundary	23
check_user_select_smooths	24
coef.scam	25
compare_smooths	25
conditional_values	26
confint.fderiv	29
confint.gam	31
data_combos	33
data_sim	34
data_slice	36
derivatives	38
derivative_samples	40
difference_smooths	43
dispersion	45
draw	45
draw.basis	46
draw.compare_smooths	47
draw.conditional_values	48
draw.derivatives	49
draw.difference_smooth	51
draw.evaluated_parametric_term	52
draw.gam	54
draw.gamlss	58
draw.mgcv_smooth	59

draw.pairwise_concurvity . . . . .	61
draw.parametric_effects . . . . .	62
draw.penalty_df . . . . .	63
draw.rootogram . . . . .	65
draw.smooth_estimates . . . . .	66
draw.smooth_samples . . . . .	69
edf . . . . .	71
evaluate_parametric_term . . . . .	73
evaluate_smooth . . . . .	74
eval_smooth . . . . .	74
evenly . . . . .	78
factor_combos . . . . .	79
family.gam . . . . .	79
family_name . . . . .	80
family_type . . . . .	80
fitted_samples . . . . .	81
fitted_values . . . . .	84
fixef . . . . .	85
fixef.gam . . . . .	86
fix_offset . . . . .	87
gaussian_draws . . . . .	87
get_by_smooth . . . . .	89
get_smooth . . . . .	89
get_smooths_by_id . . . . .	90
gss_vocab . . . . .	90
gw_f0 . . . . .	91
has_theta . . . . .	92
is_by_smooth . . . . .	92
is_factor_term . . . . .	93
is_mgcv_family . . . . .	94
is_mgcv_smooth . . . . .	95
is_multivariate_y . . . . .	95
is_offset . . . . .	96
link . . . . .	96
load_mgcv . . . . .	99
lp_matrix . . . . .	99
mh_draws . . . . .	100
model_concurvity . . . . .	101
model_constant . . . . .	102
model_terms . . . . .	103
model_vars . . . . .	105
nb_theta . . . . .	106
null_deviance . . . . .	107
n_eta . . . . .	107
n_smooths . . . . .	108
observed_fitted_plot . . . . .	108
overview . . . . .	109
parametric_effects . . . . .	110

parametric_terms . . . . .	111
partial_derivatives . . . . .	112
partial_residuals . . . . .	115
penalty . . . . .	116
posterior_samples . . . . .	118
post_draws . . . . .	121
predicted_samples . . . . .	123
qq_plot . . . . .	125
quantile_residuals . . . . .	128
ref_level . . . . .	129
ref_sims . . . . .	129
rep_first_factor_value . . . . .	130
residuals_hist_plot . . . . .	130
residuals_linpred_plot . . . . .	131
response_derivatives . . . . .	132
rootogram . . . . .	135
rtw . . . . .	137
scale_fill_partial_effect . . . . .	137
seq_min_max_eps . . . . .	138
shift_values . . . . .	138
simulate.gam . . . . .	139
smallAges . . . . .	141
smooths . . . . .	141
smooth_coefs . . . . .	142
smooth_coef_indices . . . . .	143
smooth_data . . . . .	144
smooth_dim . . . . .	145
smooth_estimates . . . . .	146
smooth_label . . . . .	148
smooth_samples . . . . .	149
smooth_terms . . . . .	152
smooth_type . . . . .	152
spline_values . . . . .	154
term_names . . . . .	155
term_variables . . . . .	156
theta . . . . .	157
tidy_basis . . . . .	157
too_far . . . . .	159
too_far_to_na . . . . .	159
to_na . . . . .	160
transform_fun . . . . .	160
typical_values . . . . .	161
user_draws . . . . .	162
variance_comp . . . . .	163
vars_from_label . . . . .	163
which_smooths . . . . .	164
worm_plot . . . . .	165
zooplankton . . . . .	167

**Index****169**

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add_confint	<i>Add a confidence interval to an existing object</i>
-------------	--

---

**Description**

Add a confidence interval to an existing object

**Usage**

```
add_confint(object, coverage = 0.95, ...)

## S3 method for class 'smooth_estimates'
add_confint(object, coverage = 0.95, ...)

## S3 method for class 'parametric_effects'
add_confint(object, coverage = 0.95, ...)

## Default S3 method:
add_confint(object, coverage = 0.95, ...)
```

**Arguments**

object	a R object.
coverage	numeric; the coverage for the interval. Must be in the range $0 < \text{coverage} < 1$ .
...	arguments passed to other methods.

---

add_constant	<i>Add a constant to estimated values</i>
--------------	---

---

**Description**

Add a constant to estimated values

**Usage**

```
add_constant(object, constant = NULL, ...)

## S3 method for class 'smooth_estimates'
add_constant(object, constant = NULL, ...)

## S3 method for class 'smooth_samples'
add_constant(object, constant = NULL, ...)

## S3 method for class 'mgcv_smooth'
```

```

add_constant(object, constant = NULL, ...)

## S3 method for class 'parametric_effects'
add_constant(object, constant = NULL, ...)

## S3 method for class 'tbl_df'
add_constant(object, constant = NULL, column = NULL, ...)

## S3 method for class 'evaluated_parametric_term'
add_constant(object, constant = NULL, ...)

```

### Arguments

object	a object to add a constant to.
constant	the constant to add.
...	additional arguments passed to methods.
column	character; for the "tbl_df" method, which column to add the constant too.

### Value

Returns object but with the estimate shifted by the addition of the supplied constant.

### Author(s)

Gavin L. Simpson

---

add_fitted	<i>Add fitted values from a model to a data frame</i>
------------	---

---

### Description

Add fitted values from a model to a data frame

### Usage

```
add_fitted(data, model, value = ".value", ...)
```

### Arguments

data	a data frame containing values for the variables used to fit the model. Passed to <code>stats::predict()</code> as newdata.
model	a fitted model for which a <code>stats::predict()</code> method is available. S3 method dispatch is performed on the model argument.
value	character; the name of the variable in which model predictions will be stored.
...	additional arguments passed to methods.

**Value**

A data frame (tibble) formed from data and fitted values from model.

---

add_fitted.gam	<i>Add fitted values from a GAM to a data frame</i>
----------------	---

---

**Description**

Add fitted values from a GAM to a data frame

**Usage**

```
## S3 method for class 'gam'
add_fitted(data, model, value = ".fitted", type = "response", ...)
```

**Arguments**

data	a data frame containing values for the variables used to fit the model. Passed to <code>stats::predict()</code> as newdata.
model	a fitted model for which a <code>stats::predict()</code> method is available. S3 method dispatch is performed on the model argument.
value	character; the name of the variable in which model predictions will be stored.
type	character; the type of predictions to return. See <code>mgcv::predict.gam()</code> for options.
...	additional arguments passed to <code>mgcv::predict.gam()</code> .

**Value**

A data frame (tibble) formed from data and predictions from model.

**Examples**

```
load_mgcv()
df <- data_sim("eg1", seed = 1)
df <- df[, c("y", "x0", "x1", "x2", "x3")]
m <- gam(y ~ s(x0) + s(x1) + s(x2) + s(x3), data = df, method = "REML")

# add fitted values to our data
add_fitted(df, m)

# with type = "terms" or "iterms"
add_fitted(df, m, type = "terms")
```

---

add_fitted_samples	<i>Add posterior draws from a model to a data object</i>
--------------------	--

---

### Description

Adds draws from the posterior distribution of model to the data object using one of `fitted_samples()`, `predicted_samples()`, or `posterior_samples()`.

### Usage

```
add_fitted_samples(object, model, n = 1, seed = NULL, ...)

add_predicted_samples(object, model, n = 1, seed = NULL, ...)

add_posterior_samples(object, model, n = 1, seed = NULL, ...)

add_smooth_samples(object, model, n = 1, seed = NULL, select = NULL, ...)
```

### Arguments

object	a data frame or tibble to which the posterior draws will be added.
model	a fitted GAM (or GAM-like) object for which a posterior draw method exists.
n	integer; the number of posterior draws to add.
seed	numeric; a value to seed the random number generator.
...	arguments are passed to the posterior draw function, currently one of <code>fitted_samples()</code> , <code>predicted_samples()</code> , or <code>posterior_samples()</code> . <code>n</code> and <code>seed</code> are already specified here as arguments and are also passed on to the posterior sampling function.
select	character; select which smooth's posterior to draw from. The default, <code>NULL</code> , means the posteriors of all smooths in model will be sampled from individually. If supplied, a character vector of requested smooth terms.

### Examples

```
load_mgcv()

df <- data_sim("eg1", n = 400, seed = 42)

m <- gam(y ~ s(x0) + s(x1) + s(x2) + s(x3), data = df, method = "REML")

# add fitted samples (posterior draws of the expected value of the response)
# note that there are 800 rows in the output: 400 data by `n = 2` samples.
df |>
  add_fitted_samples(m, n = 2, seed = 84)

# add posterior draws from smooth s(x2)
df |>
```



```
add_smooth_samples(m, n = 2, seed = 2, select= "s(x2)")
```

---

add\_partial\_residuals *Add partial residuals*

---

## Description

Add partial residuals

## Usage

```
add_partial_residuals(data, model, ...)

## S3 method for class 'gam'
add_partial_residuals(data, model, select = NULL, partial_match = FALSE, ...)
```

## Arguments

data	a data frame containing values for the variables used to fit the model. Passed to <code>stats::residuals()</code> as newdata.
model	a fitted model for which a <code>stats::residuals()</code> method is available. S3 method dispatch is performed on the model argument.
...	arguments passed to other methods.
select	character, logical, or numeric; which smooths to plot. If NULL, the default, then all model smooths are drawn. Numeric select indexes the smooths in the order they are specified in the formula and stored in object. Character select matches the labels for smooths as shown for example in the output from <code>summary(object)</code> . Logical select operates as per numeric select in the order that smooths are stored.
partial_match	logical; should smooths be selected by partial matches with select? If TRUE, select can only be a single string to match against.

## Examples

```
load_mgcv()

df <- data_sim("eg1", seed = 1)
df <- df[, c("y", "x0", "x1", "x2", "x3")]
m <- gam(y ~ s(x0) + s(x1) + s(x2) + s(x3), data = df, method = "REML")

## add partial residuals
add_partial_residuals(df, m)

## add partial residuals for selected smooths
add_partial_residuals(df, m, select = "s(x0)")
```

---

add_residuals	<i>Add residuals from a model to a data frame</i>
---------------	---

---

**Description**

Add residuals from a model to a data frame

**Usage**

```
add_residuals(data, model, value = ".residual", ...)
```

**Arguments**

data	a data frame containing values for the variables used to fit the model. Passed to <code>stats::residuals()</code> as newdata.
model	a fitted model for which a <code>stats::residuals()</code> method is available. S3 method dispatch is performed on the model argument.
value	character; the name of the variable in which model residuals will be stored.
...	additional arguments passed to methods.

**Value**

A data frame (tibble) formed from data and residuals from model.

---

add_residuals.gam	<i>Add residuals from a GAM to a data frame</i>
-------------------	---

---

**Description**

Add residuals from a GAM to a data frame

**Usage**

```
## S3 method for class 'gam'
add_residuals(data, model, value = ".residual", type = "deviance", ...)
```

**Arguments**

data	a data frame containing values for the variables used to fit the model. Passed to <code>stats::predict()</code> as newdata.
model	a fitted model for which a <code>stats::predict()</code> method is available. S3 method dispatch is performed on the model argument.
value	character; the name of the variable in which model predictions will be stored.
type	character; the type of residuals to return. See <code>mgcv::residuals.gam()</code> for options.
...	additional arguments passed to <code>mgcv::residuals.gam()</code> .

**Value**

A data frame (tibble) formed from data and residuals from model.

**Examples**

```
load_mgcv()

df <- data_sim("eg1", seed = 1)
df <- df[, c("y", "x0", "x1", "x2", "x3")]
m <- gam(y ~ s(x0) + s(x1) + s(x2) + s(x3), data = df, method = "REML")

##
add_residuals(df, m)
```

---

add_sizer	<i>Add indicators of significant change after SiZeR</i>
-----------	---

---

**Description**

Add indicators of significant change after SiZeR

**Usage**

```
add_sizer(object, type = c("change", "sizer"), ...)

## S3 method for class 'derivatives'
add_sizer(object, type = c("change", "sizer"), ...)

## S3 method for class 'smooth_estimates'
add_sizer(object, type = c("change", "sizer"), derivatives = NULL, ...)
```

**Arguments**

object	an R object. Currently supported methods are for classes "derivatives".
type	character; "change" adds a single variable to object indicating where the credible interval on the derivative excludes 0. "sizer" adds two variables indicating whether the derivative is positive or negative.
...	arguments passed to other methods
derivatives	an object of class "derivatives", resulting from a call to <a href="#">derivatives()</a> .

**Examples**

```
load_mgcv()

df <- data_sim("eg1", n = 400, dist = "normal", scale = 2, seed = 42)
m <- gam(y ~ s(x0) + s(x1) + s(x2) + s(x3), data = df, method = "REML")

## first derivatives of all smooths using central finite differences
d <- derivatives(m, type = "central") |>
  add_sizer()

# default adds a .change column
names(d)
```

appraise

*Model diagnostic plots***Description**

Model diagnostic plots

**Usage**

```
appraise(model, ...)

## S3 method for class 'gam'
appraise(
  model,
  method = c("uniform", "simulate", "normal", "direct"),
  use_worm = FALSE,
  n_uniform = 10,
  n_simulate = 50,
  seed = NULL,
  type = c("deviance", "pearson", "response"),
  n_bins = c("sturges", "scott", "fd"),
  ncol = NULL,
  nrow = NULL,
  guides = "keep",
  level = 0.9,
  ci_col = "black",
  ci_alpha = 0.2,
  point_col = "grey20",
  point_alpha = 1,
  line_col = "red",
  ...
)

## S3 method for class 'lm'
appraise(model, ...)
```

**Arguments**

model	a fitted model. Currently models inheriting from class "gam", as well as classes "glm" and "lm" from calls to <a href="#">stats::glm</a> or <a href="#">stats::lm</a> are supported.
...	arguments passed to <a href="#">patchwork::wrap_plots()</a> .
method	character; method used to generate theoretical quantiles. The default is "uniform", which generates reference quantiles using random draws from a uniform distribution and the inverse cumulative distribution function (CDF) of the fitted values. The reference quantiles are averaged over n_uniform draws. "simulate" generates reference quantiles by simulating new response data from the model at the observed values of the covariates, which are then residualised to generate reference quantiles, using n_simulate simulated data sets. "normal" generates reference quantiles using the standard normal distribution. "uniform" is more computationally efficient, but "simulate" allows reference bands to be drawn on the QQ-plot. "normal" should be avoided but is used as a fall back if a random number generator ("simulate") or the inverse of the CDF ("uniform") are not available from the family used during model fitting. Note that method = "direct" is deprecated in favour of method = "uniform".
use_worm	logical; should a worm plot be drawn in place of the QQ plot?
n_uniform	numeric; number of times to randomize uniform quantiles in the direct computation method (method = "direct") for QQ plots.
n_simulate	numeric; number of data sets to simulate from the estimated model when using the simulation method (method = "simulate") for QQ plots.
seed	numeric; the random number seed to use for method = "simulate" and method = "uniform".
type	character; type of residuals to use. Only "deviance", "response", and "pearson" residuals are allowed.
n_bins	character or numeric; either the number of bins or a string indicating how to calculate the number of bins.
ncol, nrow	numeric; the numbers of rows and columns over which to spread the plots.
guides	character; one of "keep" (the default), "collect", or "auto". Passed to <a href="#">patchwork::plot_layout()</a>
level	numeric; the coverage level for QQ plot reference intervals. Must be strictly $0 < \text{level} < 1$ . Only used with method = "simulate".
ci_alpha, ci_col	colour and transparency used to draw the QQ plot reference interval when method = "simulate".
point_col, point_alpha	colour and transparency used to draw points in the plots. See <a href="#">graphics::par()</a> section <b>Color Specification</b> . This is passed to the individual plotting functions, and therefore affects the points of all plots.
line_col	colour specification for the 1:1 line in the QQ plot and the reference line in the residuals vs linear predictor plot.

**Note**

The wording used in `mgcv::qq.gam()` uses *direct* in reference to the simulated residuals method (`method = "simulated"`). To avoid confusion, `method = "direct"` is deprecated in favour of `method = "uniform"`.

**See Also**

The plots are produced by functions `qq_plot()`, `residuals_linpred_plot()`, `residuals_hist_plot()`, and `observed_fitted_plot()`.

**Examples**

```
load_mgcv()
## simulate some data...
dat <- data_sim("eg1", n = 400, dist = "normal", scale = 2, seed = 2)
mod <- gam(y ~ s(x0) + s(x1) + s(x2) + s(x3), data = dat)
## run some basic model checks
appraise(mod, point_col = "steelblue", point_alpha = 0.4)

## To change the theme for all panels use the & operator, for example to
## change the ggplot theme for all panels
library("ggplot2")
if (packageVersion("ggplot2") <= "3.5.2") {
  # Throws warning with ggplot rc 4.0.0 and patchwork 1.3.1 - will be fixed
  # in patchwork 1.3.2 - so temporarily skipping during ggplot release
  # process
  appraise(mod, seed = 42,
    point_col = "steelblue", point_alpha = 0.4,
    line_col = "black"
  ) & theme_minimal()
}
```

---

assemble

---

*Prepare plots via ggplot2 and assembles them as a list*


---

**Description**

Generic function for assembling plot objects created from R objects, using the ggplot2 package.

**Usage**

```
assemble(object, ...)
```

**Arguments**

<code>object</code>	and R object to plot.
<code>...</code>	arguments passed to other methods.

**Value**

A list of `ggplot2::ggplot()` objects.

**Author(s)**

Gavin L. Simpson

---

assemble.gam

---

*Plot estimated smooths from a fitted GAM*


---

**Description**

Plots estimated smooths from a fitted GAM model in a similar way to `mgcv::plot.gam()` but instead of using base graphics, `ggplot2::ggplot()` is used instead.

**Usage**

```
## S3 method for class 'gam'
assemble(
  object,
  data = NULL,
  select = NULL,
  parametric = FALSE,
  terms = NULL,
  residuals = FALSE,
  scales = c("free", "fixed"),
  ci_level = 0.95,
  n = 100,
  n_3d = 16,
  n_4d = 4,
  unconditional = FALSE,
  overall_uncertainty = TRUE,
  constant = NULL,
  fun = NULL,
  dist = 0.1,
  rug = TRUE,
  distinct_rug = TRUE,
  contour = TRUE,
  grouped_by = FALSE,
  ci_alpha = 0.2,
  ci_col = "black",
  smooth_col = "black",
  resid_col = "steelblue3",
  contour_col = "black",
  n_contour = NULL,
  partial_match = FALSE,
  discrete_colour = NULL,
```

```

discrete_fill = NULL,
continuous_colour = NULL,
continuous_fill = NULL,
position = "identity",
angle = NULL,
ncol = NULL,
nrow = NULL,
guides = "keep",
widths = NULL,
heights = NULL,
crs = NULL,
default_crs = NULL,
lims_method = "cross",
wrap = TRUE,
caption = TRUE,
envir = environment(formula(object)),
...
)

```

## Arguments

object	a fitted GAM, the result of a call to <code>mgcv::gam()</code> .
data	an optional data frame that is used to supply the data at which the smooths will be evaluated and plotted. This is usually not needed, but is an option if you need fine control over exactly what data are used for plotting.
select	character, logical, or numeric; which smooths to plot. If NULL, the default, then all model smooths are drawn. Numeric select indexes the smooths in the order they are specified in the formula and stored in object. Character select matches the labels for smooths as shown for example in the output from <code>summary(object)</code> . Logical select operates as per numeric select in the order that smooths are stored.
parametric	logical; plot parametric terms also? Note that select is used for selecting which smooths to plot. The terms argument is used to select which parametric effects are plotted. The default, as with <code>mgcv::plot.gam()</code> , is to not draw parametric effects.
terms	character; which model parametric terms should be drawn? The Default of NULL will plot all parametric terms that can be drawn.
residuals	logical; should partial residuals for a smooth be drawn? Ignored for anything but a simple univariate smooth.
scales	character; should all univariate smooths be plotted with the same y-axis scale? If scales = "free", the default, each univariate smooth has its own y-axis scale. If scales = "fixed", a common y axis scale is used for all univariate smooths. Currently does not affect the y-axis scale of plots of the parametric terms.
ci_level	numeric between 0 and 1; the coverage of credible interval.
n	numeric; the number of points over the range of the covariate at which to evaluate the smooth.



n_3d	numeric; the number of new observations to generate for the third dimension of a 3D smooth.
n_4d	numeric; the number of new observations to generate for the dimensions higher than 2 (!) of a $k$ D smooth ( $k \geq 4$ ). For example, if the smooth is a 4D smooth, each of dimensions 3 and 4 will get n_4d new observations.
unconditional	logical; should confidence intervals include the uncertainty due to smoothness selection? If TRUE, the corrected Bayesian covariance matrix will be used.
overall_uncertainty	logical; should the uncertainty in the model constant term be included in the standard error of the evaluate values of the smooth?
constant	numeric; a constant to add to the estimated values of the smooth. constant, if supplied, will be added to the estimated value before the confidence band is computed.
fun	function; a function that will be applied to the estimated values and confidence interval before plotting. Can be a function or the name of a function. Function fun will be applied after adding any constant, if provided.
dist	numeric; if greater than 0, this is used to determine when a location is too far from data to be plotted when plotting 2-D smooths. The data are scaled into the unit square before deciding what to exclude, and dist is a distance within the unit square. See <code>mgcv::exclude.too.far()</code> for further details.
rug	logical; draw a rug plot at the bottom of each plot for 1-D smooths or plot locations of data for higher dimensions.
distinct_rug	logical; should the data for the rug plots be reduced to the distinct values?
contour	logical; should contours be draw on the plot using <code>ggplot2::geom_contour()</code> .
grouped_by	logical; should factor by smooths be drawn as one panel per level of the factor (FALSE, the default), or should the individual smooths be combined into a single panel containing all levels (TRUE)?
ci_alpha	numeric; alpha transparency for confidence or simultaneous interval.
ci_col	colour specification for the confidence/credible intervals band. Affects the fill of the interval.
smooth_col	colour specification for the smooth line.
resid_col	colour specification for the partial residuals.
contour_col	colour specification for contour lines.
n_contour	numeric; the number of contour bins. Will result in $n\_contour - 1$ contour lines being drawn. See <code>ggplot2::geom_contour()</code> .
partial_match	logical; should smooths be selected by partial matches with select? If TRUE, select can only be a single string to match against.
discrete_colour	a suitable colour scale to be used when plotting discrete variables.
discrete_fill	a suitable fill scale to be used when plotting discrete variables.
continuous_colour	a suitable colour scale to be used when plotting continuous variables.

<code>continuous_fill</code>	a suitable fill scale to be used when plotting continuous variables.
<code>position</code>	Position adjustment, either as a string, or the result of a call to a position adjustment function.
<code>angle</code>	numeric; the angle at which the x axis tick labels are to be drawn passed to the <code>angle</code> argument of <code>ggplot2::guide_axis()</code> .
<code>ncol, nrow</code>	numeric; the numbers of rows and columns over which to spread the plots
<code>guides</code>	character; one of "keep" (the default), "collect", or "auto". Passed to <code>patchwork::plot_layout()</code>
<code>widths, heights</code>	The relative widths and heights of each column and row in the grid. Will get repeated to match the dimensions of the grid. If there is more than 1 plot and <code>widths = NULL</code> , the value of <code>widths</code> will be set internally to <code>widths = 1</code> to accommodate plots of smooths that use a fixed aspect ratio.
<code>crs</code>	the coordinate reference system (CRS) to use for the plot. All data will be projected into this CRS. See <code>ggplot2::coord_sf()</code> for details.
<code>default_crs</code>	the coordinate reference system (CRS) to use for the non-sf layers in the plot. If left at the default <code>NULL</code> , the CRS used is 4326 (WGS84), which is appropriate for spline-on-the-sphere smooths, which are parameterized in terms of latitude and longitude as coordinates. See <code>ggplot2::coord_sf()</code> for more details.
<code>lims_method</code>	character; affects how the axis limits are determined. See <code>ggplot2::coord_sf()</code> . Be careful; in testing of some examples, changing this to "orthogonal" for example with the chlorophyll-a example from Simon Wood's GAM book quickly used up all the RAM in my test system and the OS killed R. This could be incorrect usage on my part; right now the grid of points at which SOS smooths are evaluated (if not supplied by the user) can produce invalid coordinates for the corners of tiles as the grid is generated for tile centres without respect to the spacing of those tiles.
<code>wrap</code>	logical; wrap plots as a patchwork? If <code>FALSE</code> , a list of ggplot objects is returned, 1 per term plotted.
<code>caption</code>	logical; show the smooth type in the caption of each plot?
<code>envir</code>	an environment to look up the data within.
<code>...</code>	Arguments to other methods; not used.

**Value**

A list of `ggplot2::ggplot()` objects.

**Note**

Internally, plots of each smooth are created using `ggplot2::ggplot()` and composed into a single plot using `patchwork::wrap_plots()`. As a result, it is not possible to use `+` to add to the plots in the way one might typically work with `ggplot()` plots. Instead, use the `&` operator; see the examples.

**Author(s)**

Gavin L. Simpson

## Examples

```
load_mgcv()

# simulate some data
df1 <- data_sim("eg1", n = 400, dist = "normal", scale = 2, seed = 2)
# fit GAM
m1 <- gam(y ~ s(x0) + s(x1) + s(x2) + s(x3), data = df1, method = "REML")

# assemble plots of all smooths
assemble(m1)

# can be passed to patchwork::wrap_plots()
suppressPackageStartupMessages(library("patchwork"))
assemble(m1) |> wrap_plots(ncol = 2, nrow = 2)
```

---

basis

*Basis expansions for smooths*


---

## Description

Basis expansions from a definition of a smoother using the syntax of *mgcv*'s smooths via `mgcv::s()`., `mgcv::te()`, `mgcv::ti()`, and `mgcv::t2()`, or directly from a fitted GAM(M).

## Usage

```
basis(object, ...)
```

## S3 method for class 'gam'

```
basis(
  object,
  select = NULL,
  term = deprecated(),
  data = NULL,
  n = 100,
  n_2d = 50,
  n_3d = 16,
  n_4d = 4,
  partial_match = FALSE,
  ...
)
```

## S3 method for class 'scam'

```
basis(
  object,
  select = NULL,
  term = deprecated(),
  data = NULL,
```

```

    n = 100,
    n_2d = 50,
    n_3d = 16,
    n_4d = 4,
    partial_match = FALSE,
    ...
)

## S3 method for class 'gamm'
basis(
  object,
  select = NULL,
  term = deprecated(),
  data = NULL,
  n = 100,
  n_2d = 50,
  n_3d = 16,
  n_4d = 4,
  partial_match = FALSE,
  ...
)

## S3 method for class 'gamm4'
basis(
  object,
  select = NULL,
  term = deprecated(),
  data = NULL,
  n = 100,
  n_2d = 50,
  n_3d = 16,
  n_4d = 4,
  partial_match = FALSE,
  ...
)

## Default S3 method:
basis(
  object,
  data,
  knots = NULL,
  constraints = FALSE,
  at = NULL,
  diagonalize = FALSE,
  coefficients = NULL,
  ...
)

```

**Arguments**

object	a smooth specification, the result of a call to one of <code>mgcv::s()</code> , <code>mgcv::te()</code> , <code>mgcv::ti()</code> , or <code>mgcv::t2()</code> , or a fitted GAM(M) model.
...	other arguments passed to <code>mgcv::smoothCon()</code> .
select	character; select smooths in a fitted model
term	<b>[Deprecated]</b> This argument has been renamed select
data	a data frame containing the variables used in smooth.
n	numeric; the number of points over the range of the covariate at which to evaluate the smooth.
n_2d	numeric; the number of new observations for each dimension of a bivariate smooth. Not currently used; n is used for both dimensions.
n_3d	numeric; the number of new observations to generate for the third dimension of a 3D smooth.
n_4d	numeric; the number of new observations to generate for the dimensions higher than 2 (!) of a $k$ D smooth ( $k \geq 4$ ). For example, if the smooth is a 4D smooth, each of dimensions 3 and 4 will get <code>n_4d</code> new observations.
partial_match	logical; in the case of character select, should select match partially against smooths? If <code>partial_match = TRUE</code> , select must only be a single string, a character vector of length 1.
knots	a list or data frame with named components containing knots locations. Names must match the covariates for which the basis is required. See <code>mgcv::smoothCon()</code> .
constraints	logical; should identifiability constraints be applied to the smooth basis. See argument <code>absorb.cons</code> in <code>mgcv::smoothCon()</code> .
at	a data frame containing values of the smooth covariate(s) at which the basis should be evaluated.
diagonalize	logical; if TRUE, reparameterises the smooth such that the associated penalty is an identity matrix. This has the effect of turning the last diagonal elements of the penalty to zero, which highlights the penalty null space.
coefficients	numeric; vector of values for the coefficients of the basis functions.

**Value**

A tibble.

**Author(s)**

Gavin L. Simpson

**Examples**

```
load_mgcv()

df <- data_sim("eg4", n = 400, seed = 42)

bf <- basis(s(x0), data = df)
```

```
bf <- basis(s(x2, by = fac, bs = "bs"), data = df, constraints = TRUE)
```

---

**basis\_size**
*Extract basis dimension of a smooth*


---

### Description

Extract basis dimension of a smooth

### Usage

```
basis_size(object, ...)

## S3 method for class 'mgcv.smooth'
basis_size(object, ...)

## S3 method for class 'gam'
basis_size(object, ...)

## S3 method for class 'gamm'
basis_size(object, ...)
```

### Arguments

<code>object</code>	A fitted GAM(M). Currently <code>mgcv::gam()</code> (and anything that inherits from the "gam" class, e.g. <code>mgcv::bam()</code> ) and <code>mgcv::gamm()</code> are supported.
<code>...</code>	Arguments passed to other methods.

### Examples

```
load_mgcv()

df <- data_sim("eg1", n = 200, seed = 1)
m <- bam(y ~ s(x0) + s(x1) + s(x2) + s(x3), data = df)

basis_size(m)
```

bird\_move

*Simulated bird migration data***Description**

Data generated from a hypothetical study of bird movement along a migration corridor, sampled throughout the year. This dataset consists of simulated sample records of numbers of observed locations of 100 tagged individuals each from six species of bird, at ten locations along a latitudinal gradient, with one observation taken every four weeks. Counts were simulated randomly for each species in each location and week by creating a species-specific migration curve that gave the probability of finding an individual of a given species in a given location, then simulated the distribution of individuals across sites using a multinomial distribution, and subsampling that using a binomial distribution to simulation observation error (i.e. not every bird present at a location would be detected). The data set (bird\_move) consists of the variables count, latitude, week and species.

**Format**

A data frame

**Source**

Pedersen EJ, Miller DL, Simpson GL, Ross N. 2018. Hierarchical generalized additive models: an introduction with mgcv. *PeerJ Preprints* 6:e27320v1 [doi:10.7287/peerj.preprints.27320v1](https://doi.org/10.7287/peerj.preprints.27320v1).

boundary

*Extract the boundary of a soap film smooth***Description**

**[Experimental]**

**Usage**

```
boundary(x, ...)

## S3 method for class 'soap.film'
boundary(x, ...)

## S3 method for class 'gam'
boundary(x, select, ...)
```

**Arguments**

x	an R object. Currently only objects that inherit from classes "soap.film" and "gam".
...	arguments passed to other methods.
select	character; the label of the soap film smooth from which to extract the boundary.

**Value**

A list of lists or data frames specifying the loops that define the boundary of the soap film smooth.

**See Also**

[mgcv::soap](#)

---

check\_user\_select\_smooths

*Select smooths based on user's choices*

---

**Description**

Given a vector indexing the smooths of a GAM, returns a logical vector selecting the requested smooths.

**Usage**

```
check_user_select_smooths(
  smooths,
  select = NULL,
  partial_match = FALSE,
  model_name = NULL
)
```

**Arguments**

smooths	character; a vector of smooth labels.
select	numeric, logical, or character vector of selected smooths.
partial_match	logical; in the case of character select, should select match partially against smooths? If partial_match = TRUE, select must only be a single string, a character vector of length 1.
model_name	character; a model name that will be used in error messages.

**Value**

A logical vector the same length as `length(smooths)` indicating which smooths have been selected.

**Author(s)**

Gavin L. Simpson



---

coef.scam	<i>Extract coefficients from a fitted scam model.</i>
-----------	---

---

### Description

Extract coefficients from a fitted scam model.

### Usage

```
## S3 method for class 'scam'
coef(object, parametrized = TRUE, ...)
```

### Arguments

object	a model object fitted by scam()
parametrized	logical; extract parametrized coefficients, which respect the linear inequality constraints of the model.
...	other arguments.

---

compare_smooths	<i>Compare smooths across models</i>
-----------------	--------------------------------------

---

### Description

Compare smooths across models

### Usage

```
compare_smooths(
  model,
  ...,
  select = NULL,
  smooths = deprecated(),
  n = 100,
  data = NULL,
  unconditional = FALSE,
  overall_uncertainty = TRUE,
  partial_match = FALSE
)
```

**Arguments**

model	Primary model for comparison.
...	Additional models to compare smooths against those of model.
select	character; select which smooths to compare. The default (NULL) means all smooths in model will be compared. Numeric select indexes the smooths in the order they are specified in the formula and stored in model. Character select matches the labels for smooths as shown for example in the output from <code>summary(object)</code> . Logical select operates as per numeric select in the order that smooths are stored.
smooths	<b>[Deprecated]</b> Use select instead.
n	numeric; the number of points over the range of the covariate at which to evaluate the smooth.
data	a data frame of covariate values at which to evaluate the smooth.
unconditional	logical; should confidence intervals include the uncertainty due to smoothness selection? If TRUE, the corrected Bayesian covariance matrix will be used.
overall_uncertainty	logical; should the uncertainty in the model constant term be included in the standard error of the evaluate values of the smooth?
partial_match	logical; should smooths be selected by partial matches with select? If TRUE, select can only be a single string to match against.

**Examples**

```
load_mgcv()
dat <- data_sim("eg1", seed = 2)

## models to compare smooths across - artificially create differences
m1 <- gam(y ~ s(x0, k = 5) + s(x1, k = 5) + s(x2, k = 5) + s(x3, k = 5),
  data = dat, method = "REML"
)
m2 <- gam(y ~ s(x0, bs = "ts") + s(x1, bs = "ts") + s(x2, bs = "ts") +
  s(x3, bs = "ts"), data = dat, method = "REML")

## build comparisons
comp <- compare_smooths(m1, m2)
comp
## notice that the result is a nested tibble

draw(comp)
```

## Description

Generate predicted values from a GAM, conditional upon supplied values of covariates. `conditional_values()` is modelled after `marginaleffects::plot_predictions()`, but with an intentionally simpler, more restrictive functionality. The intended use case is for quickly visualizing predicted values from a fitted GAM on the response scale. For more complex model predictions, you are strongly encouraged to use `marginaleffects::plot_predictions()`.

## Usage

```
conditional_values(
  model,
  condition = NULL,
  data = NULL,
  scale = c("response", "link", "linear_predictor"),
  ...
)

## S3 method for class 'gam'
conditional_values(
  model,
  condition = NULL,
  data = NULL,
  scale = c("response", "link", "linear_predictor"),
  n_vals = 100,
  ci_level = 0.95,
  ...
)
```

## Arguments

<code>model</code>	a fitted GAM object.
<code>condition</code>	either a character vector or a list supplying the names of covariates, and possibly their values, to condition up. The order of the values determines how these are plotted via the <code>draw.conditional_values()</code> method; the first element is mapped to the <i>x</i> channel, the second element to the <i>colour</i> channel, the third to <code>ggplot2::facet_wrap()</code> <b>if no fourth element is present</b> , if present, the fourth element is mapped to the rows and the third element is mapped to the columns of <code>ggplot2::facet_grid()</code> .
<code>data</code>	data frame of values at which to predict. If supplied overrides values supplied through <code>condition</code> .
<code>scale</code>	character; which scale should predictions be returned on?
<code>...</code>	arguments passed to <code>fitted_values()</code> .
<code>n_vals</code>	numeric; number of values to generate for numeric variables named in <code>condition</code> .
<code>ci_level</code>	numeric; a number on interval (0,1) giving the coverage for credible intervals.

## Value

A data frame (tibble) of class "conditional\_values".

**Author(s)**

Gavin L. Simpson

**Examples**

```

load_mgcv()
df <- data_sim("eg1", seed = 2)
m1 <- gam(y ~ s(x0) + s(x1) + s(x2) + s(x3), data = df, method = "REML")

# predictions conditional on values evenly spaced over x2, all other
# variables in model are held at representative values
cv <- conditional_values(
  m1,
  condition = "x2"
)
# plot
cv |> draw()

# as above but condition on `x1` also. When plotted, `x1` is mapped to the
# colour channel, noting that it has been summarised using fivenum()
cv <- conditional_values(
  m1,
  condition = c("x2", "x1")
)
# plot
cv |> draw()

# can pass `condition` a list, allowing for greater flexibility
# For example, here we condition on all four variables in the model,
# summarising:
# * `x1` at its five number summary,
# * `x0` at its quartiles
# * `x3` at its mean and mean +/- sd
cv <- conditional_values(
  m1,
  condition = list("x2", x1 = "fivenum", x0 = "quartile", x3 = "threenum")
)
# plot
cv |> draw()

# some model terms can be exclude from the conditional predictions using the
# `exclude` mechanism of `predict.gam`. Here we exclude the effects of
# `s(x0)` and `s(x3)` from the conditional predictions. This, in effect,
# treats these smooths as having **0** effect on the conditional predictions
# of the response, even though the two smooths conditioned on (`s(x2)` and
# `s(x1)`) were estimated given the two excluded smooths were in the model
cv <- conditional_values(
  m1,
  condition = list("x2", x1 = "minmax"),
  exclude = c("s(x0)", "s(x3)")
)
# plot

```

```

cv |> draw()

# categorical conditions are also handled
df <- data_sim("eg4", seed = 2)
m2 <- gam(y ~ fac + s(x2, by = fac) + s(x0), data = df, method = "REML")
cv <- conditional_values(
  m2,
  condition = list("fac", x2 = "fivenum")
)
# plot - we see a discrete x axis
cv |> draw()

# in this example we condition on `x2` and `fac` %in% c(2,3)`
cv <- conditional_values(
  m2,
  condition = list("x2", fac = 2:3)
)
# plot - smooths of `x2` for `fac == 2` and `fac == 3`
cv |> draw()

```

---

confint.fderiv	<i>Point-wise and simultaneous confidence intervals for derivatives of smooths</i>
----------------	--

---

## Description

Calculates point-wise confidence or simultaneous intervals for the first derivatives of smooth terms in a fitted GAM.

## Usage

```

## S3 method for class 'fderiv'
confint(
  object,
  parm,
  level = 0.95,
  type = c("confidence", "simultaneous"),
  nsim = 10000,
  ncores = 1L,
  ...
)

```

## Arguments

object	an object of class "fderiv" containing the estimated derivatives.
parm	which parameters (smooth terms) are to be given intervals as a vector of terms. If missing, all parameters are considered.
level	numeric, $0 < \text{level} < 1$ ; the confidence level of the point-wise or simultaneous interval. The default is 0.95 for a 95% interval.

type	character; the type of interval to compute. One of "confidence" for point-wise intervals, or "simultaneous" for simultaneous intervals.
nsim	integer; the number of simulations used in computing the simultaneous intervals.
ncores	number of cores for generating random variables from a multivariate normal distribution. Passed to <code>mvnfast::rmvn()</code> . Parallelization will take place only if OpenMP is supported (but appears to work on Windows with current R).
...	additional arguments for methods

### Value

a data frame with components:

1. term; factor indicating to which term each row relates,
2. lower; lower limit of the confidence or simultaneous interval,
3. est; estimated derivative
4. upper; upper limit of the confidence or simultaneous interval.

### Author(s)

Gavin L. Simpson

### Examples

```
load_mgcv()

dat <- data_sim("eg1", n = 1000, dist = "normal", scale = 2, seed = 2)
mod <- gam(y ~ s(x0) + s(x1) + s(x2) + s(x3), data = dat, method = "REML")

# new data to evaluate the derivatives at, say over the middle 50% of range
# of each covariate
middle <- function(x, n = 25, coverage = 0.5) {
  v <- (1 - coverage) / 2
  q <- quantile(x, prob = c(0 + v, 1 - v), type = 8)
  seq(q[1], q[2], length = n)
}
new_data <- sapply(dat[c("x0", "x1", "x2", "x3")], middle)
new_data <- data.frame(new_data)
## first derivatives of all smooths...
fd <- fderiv(mod, newdata = new_data)

## point-wise interval
ci <- confint(fd, type = "confidence")
ci

## simultaneous interval for smooth term of x2

x2_sint <- confint(fd,
  parm = "x2", type = "simultaneous",
  nsim = 10000, ncores = 2
)
```

x2\_sint

---

 confint.gam

---

*Point-wise and simultaneous confidence intervals for smooths*


---

**Description**

Calculates point-wise confidence or simultaneous intervals for the smooth terms of a fitted GAM.

**Usage**

```
## S3 method for class 'gam'
confint(
  object,
  parm,
  level = 0.95,
  data = newdata,
  n = 100,
  type = c("confidence", "simultaneous"),
  nsim = 10000,
  shift = FALSE,
  transform = FALSE,
  unconditional = FALSE,
  ncores = 1,
  partial_match = FALSE,
  ...,
  newdata = NULL
)

## S3 method for class 'gamm'
confint(object, ...)

## S3 method for class 'list'
confint(object, ...)
```

**Arguments**

object	an object of class "gam" or "gamm".
parm	which parameters (smooth terms) are to be given intervals as a vector of terms. If missing, all parameters are considered, although this is not currently implemented.
level	numeric, $0 < \text{level} < 1$ ; the confidence level of the point-wise or simultaneous interval. The default is 0.95 for a 95% interval.

data	data frame; new values of the covariates used in the model fit. The selected smooth(s) will be evaluated at the supplied values.
n	numeric; the number of points to evaluate smooths at.
type	character; the type of interval to compute. One of "confidence" for point-wise intervals, or "simultaneous" for simultaneous intervals.
nsim	integer; the number of simulations used in computing the simultaneous intervals.
shift	logical; should the constant term be add to the smooth?
transform	logical; should the smooth be evaluated on a transformed scale? For generalised models, this involves applying the inverse of the link function used to fit the model. Alternatively, the name of, or an actual, function can be supplied to transform the smooth and it's confidence interval.
unconditional	logical; if TRUE (and freq == FALSE) then the Bayesian smoothing parameter uncertainty corrected covariance matrix is returned, if available.
ncores	number of cores for generating random variables from a multivariate normal distribution. Passed to <code>mvnfast::rmvn()</code> . Parallelization will take place only if OpenMP is supported (but appears to work on Windows with current R).
partial_match	logical; should matching parm use a partial match or an exact match? Can only be used if <code>length(parm)</code> is 1.
...	additional arguments for methods
newdata	DEPRECATED! data frame; containing new values of the covariates used in the model fit. The selected smooth(s) will be evaluated at the supplied values.

## Value

a tibble with components:

1. `.smooth`; character indicating to which term each row relates,
2. `.type`; the type of smooth,
3. `.by` the name of the by variable if a by smooth, NA otherwise,
4. one or more vectors of values at which the smooth was evaluated, named as per the variables in the smooth,
5. zero or more variables containing values of the by variable,
6. `.estimate`; estimated value of the smooth,
7. `.se`; standard error of the estimated value of the smooth,
8. `.crit`; critical value for the  $100 * level\%$  confidence interval.
9. `.lower_ci`; lower limit of the confidence or simultaneous interval,
10. `.upper_ci`; upper limit of the confidence or simultaneous interval,

## Author(s)

Gavin L. Simpson



**Examples**

```
load_mgcv()

dat <- data_sim("eg1", n = 1000, dist = "normal", scale = 2, seed = 2)
mod <- gam(y ~ s(x0) + s(x1) + s(x2) + s(x3), data = dat, method = "REML")

# new data to evaluate the smooths at, say over the middle 50% of range
# of each covariate
middle <- function(x, n = 50, coverage = 0.5) {
  v <- (1 - coverage) / 2
  q <- quantile(x, prob = c(0 + v, 1 - v), type = 8)
  seq(q[1], q[2], length = n)
}
new_data <- sapply(dat[c("x0", "x1", "x2", "x3")], middle)
new_data <- data.frame(new_data)

## point-wise interval for smooth of x2
ci <- confint(mod, parm = "s(x2)", type = "confidence", data = new_data)
ci
```

---

data_combos	<i>All combinations of factor levels plus typical values of continuous variables</i>
-------------	--

---

**Description**

All combinations of factor levels plus typical values of continuous variables

**Usage**

```
data_combos(object, ...)

## S3 method for class 'gam'
data_combos(
  object,
  vars = everything(),
  complete = TRUE,
  envir = environment(formula(object)),
  data = NULL,
  ...
)
```

**Arguments**

object	a fitted model object.
...	arguments passed to methods.
vars	terms to include or exclude from the returned object. Uses tidyselect principles.

complete	logical; should all combinations of factor levels be returned? If FALSE, only those combinations of levels observed in the model are retained.
envir	the environment within which to recreate the data used to fit object.
data	an optional data frame of data used to fit the model if reconstruction of the data from the model doesn't work.

---

data_sim	<i>Simulate example data for fitting GAMs</i>
----------	---

---

## Description

A tidy reimplementation of the functions implemented in `mgcv::gamSim()` that can be used to fit GAMs. An new feature is that the sampling distribution can be applied to all the example types.

## Usage

```
data_sim(
  model = "eg1",
  n = 400,
  scale = NULL,
  theta = 3,
  power = 1.5,
  dist = c("normal", "poisson", "binary", "negbin", "tweedie", "gamma", "ocat",
    "ordered categorical"),
  n_cat = 4,
  cuts = c(-1, 0, 5),
  seed = NULL,
  gfam_families = c("binary", "tweedie", "normal")
)
```

## Arguments

model	character; either "egX" where X is an integer 1:7, or the name of a model. See Details for possible options.
n	numeric; the number of observations to simulate.
scale	numeric; the level of noise to use.
theta	numeric; the dispersion parameter $\theta$ to use. The default is entirely arbitrary, chosen only to provide simulated data that exhibits extra dispersion beyond that assumed by under a Poisson.
power	numeric; the Tweedie power parameter.
dist	character; a sampling distribution for the response variable. "ordered categorical" is a synonym of "ocat".
n_cat	integer; the number of categories for categorical response. Currently only used for distr %in% c("ocat", "ordered categorical").

cuts	numeric; vector of cut points on the latent variable, excluding the end points $-\text{Inf}$ and $\text{Inf}$ . Must be one fewer than the number of categories: $\text{length}(\text{cuts}) == n_{\text{cat}} - 1$ .
seed	numeric; the seed for the random number generator. Passed to <code>base::set.seed()</code> .
gfam_families	character; a vector of distributions to use in generating data with grouped families for use with <code>family = gfam()</code> . The allowed distributions as as per <code>dist</code> .

## Details

`data_sim()` can simulate data from several underlying models of known true functions. The available options currently are:

- "eg1": a four term additive true model. This is the classic Gu & Wahba four univariate term test model. See [gw\\_functions](#) for more details of the underlying four functions.
- "eg2": a bivariate smooth true model.
- "eg3": an example containing a continuous by smooth (varying coefficient) true model. The model is  $\hat{y}_i = f_2(x_{1i})x_{2i}$  where the function  $f_2()$  is  $f_2(x) = 0.2 * x^{11} * (10 * (1 - x))^6 + 10 * (10 * x)^3 * (1 - x)^{10}$ .
- "eg4": a factor by smooth true model. The true model contains a factor with 3 levels, where the response for the  $n$ th level follows the  $n$ th Gu & Wahba function (for  $n \in 1, 2, 3$ ).
- "eg5": an additive plus factor true model. The response is a linear combination of the Gu & Wahba functions 2, 3, 4 (the latter is a null function) plus a factor term with four levels.
- "eg6": an additive plus random effect term true model.
- "eg7": a version of the model in "eg1", but where the covariates are correlated.
- "gwf2": a model where the response is Gu & Wahba's  $f_2(x_i)$  plus noise.
- "lwf6": a model where the response is Luo & Wahba's "example 6" function  $\sin(2(4x - 2)) + 2\exp(-256(x - 0.5)^2)$  plus noise.
- "gfam": simulates data for use with GAMs with `family = gfam(families)`. See example in [mgcv::gfam\(\)](#). If this model is specified then `dist` is ignored and `gfam_families` is used to specify which distributions are included in the simulated data. Can be a vector of any of the families allowed by `dist`. For "ocat" %in% `gfam_families` (or "ordered categorical"), 4 classes are assumed, which can't be changed. Link functions used are "identity" for "normal", "logit" for "binary", "ocat", and "ordered categorical", and "exp" elsewhere.

The random component providing noise or sampling variation can follow one of the distributions, specified via argument `dist`

- "normal": Gaussian,
- "poisson": Poisson,
- "binary": Bernoulli,
- "negbin": Negative binomial,
- "tweedie": Tweedie,
- "gamma": gamma, and
- "ordered categorical": ordered categorical

Other arguments provide the parameters for the distribution.

## References

- Gu, C., Wahba, G., (1993). Smoothing Spline ANOVA with Component-Wise Bayesian "Confidence Intervals." *J. Comput. Graph. Stat.* **2**, 97–117.
- Luo, Z., Wahba, G., (1997). Hybrid adaptive splines. *J. Am. Stat. Assoc.* **92**, 107–116.

## Examples

```
data_sim("eg1", n = 100, seed = 1)

# an ordered categorical response
data_sim("eg1", n = 100, dist = "ocat", n_cat = 4, cuts = c(-1, 0, 5))
```

---

data_slice	<i>Prepare a data slice through model covariates</i>
------------	--

---

## Description

Prepare a data slice through model covariates

## Usage

```
data_slice(object, ...)

## Default S3 method:
data_slice(object, ...)

## S3 method for class 'data.frame'
data_slice(object, ..., .observed_only = FALSE)

## S3 method for class 'gam'
data_slice(object, ..., data = NULL, envir = NULL, .observed_only = FALSE)

## S3 method for class 'gamm'
data_slice(object, ...)

## S3 method for class 'list'
data_slice(object, ...)

## S3 method for class 'scam'
data_slice(object, ...)
```

## Arguments

object	an R model object.
...	<dynamic-dots> User supplied variables defining the data slice. Arguments passed via ... need to be <i>named</i> .

<code>.observed_only</code>	logical or character; should the data slice be trimmed to those combinations of the variables specified that are observed in object. If TRUE, the observed combinations of variables mentioned in <code>...</code> are matched against those in object and filtered to return only those combinations. If FALSE, no filtering is done. If <code>.observed_only</code> is a character vector, on those variables named in the vector are used to in the comparison with the combinations in object.
<code>data</code>	an alternative data frame of values containing all the variables needed to fit the model. If NULL, the default, the data used to fit the model will be recovered using <code>model.frame</code> . User-supplied expressions passed in <code>...</code> will be evaluated in data.
<code>envir</code>	the environment within which to recreate the data used to fit object.

## Details

A data slice is the data set that results where one (or more covariates) is varied systematically over some or all of its (their) range or at a specified subset of values of interest, while any remaining covariates in the model are held at fixed, representative values. This is known as a *reference grid* in package **emmeans** and a *data grid* in the **marginaleffects** package.

For GAMs, any covariates not specified via `...` will take representative values determined from the data used to fit the model as follows:

- for numeric covariates, the value in the fitting data that is closest to the median value is used,
- for factor covariates, the modal (most frequently observed) level is used, or the first level (sorted as per the vector returned by `base::levels()` if several levels are observed the same number of times.

These values are already computed when calling `gam()` or `bam()` for example and can be found in the `var.summary` component of the fitted model. Function `typical_values()` will extract these values for you if you are interested.

Convenience functions `evenly()`, `ref_level()`, and `level()` are provided to help users specify data slices. `ref_level()`, and `level()` also ensure that factor covariates have the correct levels, as needed by `mgcv::predict.gam()` for example.

For an extended discussion of `data_slice()` and further examples, see `vignette("data-slices", package = "gratia")`.

## See Also

The convenience functions `evenly()`, `ref_level()`, and `level()`. `typical_values()` for extracting the representative values used for covariates in the model but not named in the slice.

## Examples

```
load_mgcv()

# simulate some Gaussian data
df <- data_sim("eg1", n = 50, seed = 2)

# fit a GAM with 1 smooth and 1 linear term
m <- gam(y ~ s(x2, k = 7) + x1, data = df, method = "REML")
```

```
# Want to predict over f(x2) while holding `x1` at some value.
# Default will use the observation closest to the median for unspecified
# variables.
ds <- data_slice(m, x2 = evenly(x2, n = 50))
ds

# for full control, specify the values you want
ds <- data_slice(m, x2 = evenly(x2, n = 50), x1 = 0.3)

# or provide an expression (function call) which will be evaluated in the
# data frame passed to `data` or `model.frame(object)`
ds <- data_slice(m, x2 = evenly(x2, n = 50), x1 = mean(x1))
```

---

derivatives

*Derivatives of estimated smooths via finite differences*


---

## Description

Derivatives of estimated smooths via finite differences

## Usage

```
derivatives(object, ...)

## Default S3 method:
derivatives(object, ...)

## S3 method for class 'gamm'
derivatives(object, ...)

## S3 method for class 'gam'
derivatives(
  object,
  select = NULL,
  term = deprecated(),
  data = newdata,
  order = 1L,
  type = c("forward", "backward", "central"),
  n = 100,
  eps = 1e-07,
  interval = c("confidence", "simultaneous"),
  n_sim = 10000,
  level = 0.95,
  unconditional = FALSE,
  frequentist = FALSE,
  offset = NULL,
  ncores = 1,
```

```

    partial_match = FALSE,
    ...,
    newdata = NULL
  )

```

### Arguments

<code>object</code>	an R object to compute derivatives for.
<code>...</code>	arguments passed to other methods.
<code>select</code>	character; select which smooth's posterior to draw from. The default (NULL) means the posteriors of all smooths in <code>model</code> will be sampled from. If supplied, a character vector of requested terms. Can be a partial match to a smooth term; see argument <code>partial_match</code> below.
<code>term</code>	<b>[Deprecated]</b> Use <code>select</code> instead.
<code>data</code>	a data frame containing the values of the model covariates at which to evaluate the first derivatives of the smooths.
<code>order</code>	numeric; the order of derivative.
<code>type</code>	character; the type of finite difference used. One of "forward", "backward", or "central".
<code>n</code>	numeric; the number of points to evaluate the derivative at.
<code>eps</code>	numeric; the finite difference.
<code>interval</code>	character; the type of interval to compute. One of "confidence" for point-wise intervals, or "simultaneous" for simultaneous intervals.
<code>n_sim</code>	integer; the number of simulations used in computing the simultaneous intervals.
<code>level</code>	numeric; $0 < \text{level} < 1$ ; the confidence level of the point-wise or simultaneous interval. The default is 0.95 for a 95% interval.
<code>unconditional</code>	logical; use smoothness selection-corrected Bayesian covariance matrix?
<code>frequentist</code>	logical; use the frequentist covariance matrix?
<code>offset</code>	numeric; a value to use for any offset term
<code>ncores</code>	number of cores for generating random variables from a multivariate normal distribution. Passed to <code>mvnfast::rmvn()</code> . Parallelization will take place only if OpenMP is supported (but appears to work on Windows with current R).
<code>partial_match</code>	logical; should smooths be selected by partial matches with <code>term</code> ? If TRUE, <code>term</code> can only be a single string to match against.
<code>newdata</code>	Deprecated: use <code>data</code> instead.

### Value

A tibble, currently with the following variables:

- `.smooth`: the smooth each row refers to,
- `.by`: the name of any factor by variable involved in the smooth,
- `.fs`: the name of any random factor variable involved in the smooth,

- `.derivative`: the estimated derivative,
- `.se`: the standard error of the estimated derivative,
- `.crit`: the critical value such that  $\text{derivative} \pm (\text{crit} * \text{se})$  gives the upper and lower bounds of the requested confidence or simultaneous interval (given level),
- `.lower_ci`: the lower bound of the confidence or simultaneous interval,
- `.upper_ci`: the upper bound of the confidence or simultaneous interval.
- plus one or more columns of data containing the values of covariates at which the derivative was evaluated.

### Note

`derivatives()` will ignore any random effect smooths it encounters in object.

### Author(s)

Gavin L. Simpson

### Examples

```
load_mgcv()

dat <- data_sim("eg1", n = 400, dist = "normal", scale = 2, seed = 42)
mod <- gam(y ~ s(x0) + s(x1) + s(x2) + s(x3), data = dat, method = "REML")

## first derivatives of all smooths using central finite differences
derivatives(mod, type = "central")

## derivatives for a selected smooth
derivatives(mod, type = "central", select = "s(x1)")
## or via a partial match
derivatives(mod, type = "central", select = "x1", partial_match = TRUE)
```

---

derivative_samples	<i>Posterior expectations of derivatives from an estimated model</i>
--------------------	--

---

### Description

Posterior expectations of derivatives from an estimated model

### Usage

```
derivative_samples(object, ...)

## Default S3 method:
derivative_samples(object, ...)
```



```

## S3 method for class 'gamm'
derivative_samples(object, ...)

## S3 method for class 'gam'
derivative_samples(
  object,
  focal = NULL,
  data = NULL,
  order = 1L,
  type = c("forward", "backward", "central"),
  scale = c("response", "linear_predictor"),
  method = c("gaussian", "mh", "inla", "user"),
  n = 100,
  eps = 1e-07,
  n_sim = 10000,
  level = lifecycle::deprecated(),
  seed = NULL,
  envir = environment(formula(object)),
  draws = NULL,
  mvn_method = c("mvnfast", "mgcv"),
  ...
)

## S3 method for class 'scam'
derivative_samples(
  object,
  focal = NULL,
  data = NULL,
  order = 1L,
  type = c("forward", "backward", "central"),
  scale = c("response", "linear_predictor"),
  method = c("gaussian", "mh", "inla", "user"),
  n = 100,
  eps = 1e-07,
  n_sim = 10000,
  seed = NULL,
  envir = environment(formula(object)),
  draws = NULL,
  mvn_method = c("mvnfast", "mgcv"),
  ...
)

```

### Arguments

<code>object</code>	an R object to compute derivatives for
<code>...</code>	arguments passed to other methods and on to <code>fitted_samples()</code>
<code>focal</code>	character; name of the focal variable. The response derivative of the response with respect to this variable will be returned. All other variables involved in the

	model will be held at constant values. This can be missing if supplying data, in which case, the focal variable will be identified as the one variable that is not constant.
data	a data frame containing the values of the model covariates at which to evaluate the first derivatives of the smooths. If supplied, all but one variable must be held at a constant value.
order	numeric; the order of derivative.
type	character; the type of finite difference used. One of "forward", "backward", or "central".
scale	character; should the derivative be estimated on the response or the linear predictor (link) scale? One of "response" (the default), or "linear predictor".
method	character; which method should be used to draw samples from the posterior distribution. "gaussian" uses a Gaussian (Laplace) approximation to the posterior. "mh" uses a Metropolis Hastings sample that alternates t proposals with proposals based on a shrunk version of the posterior covariance matrix. "inla" uses a variant of Integrated Nested Laplace Approximation due to Wood (2019), (currently not implemented). "user" allows for user-supplied posterior draws (currently not implemented).
n	numeric; the number of points to evaluate the derivative at (if data is not supplied).
eps	numeric; the finite difference.
n_sim	integer; the number of simulations used in computing the simultaneous intervals.
level	<b>[Deprecated]</b>
seed	numeric; a random seed for the simulations.
envir	the environment within which to recreate the data used to fit object.
draws	matrix; user supplied posterior draws to be used when method = "user".
mvn_method	character; one of "mvnfast" or "mgcv". The default is uses mvnfast::rmvn(), which can be considerably faster at generate large numbers of MVN random values than mgcv::rmvn(), but which might not work for some marginal fits, such as those where the covariance matrix is close to singular.

## Value

A tibble, currently with the following variables:

- `.derivative`: the estimated partial derivative,
- additional columns containing the covariate values at which the derivative was evaluated.

## Author(s)

Gavin L. Simpson

## Examples

```
load_mgcv()
df <- data_sim("eg1", dist = "negbin", scale = 0.25, seed = 42)

# fit the GAM (note: for execution time reasons using bam())
m <- bam(y ~ s(x0) + s(x1) + s(x2) + s(x3),
  data = df, family = nb(), method = "FREML")

# data slice through data along x2 - all other covariates will be set to
# typical values (value closest to median)
ds <- data_slice(m, x2 = evenly(x2, n = 200))

# samples from posterior of derivatives
fd_samp <- derivative_samples(m,
  data = ds, type = "central",
  focal = "x2", eps = 0.01, seed = 21, n_sim = 100
)

# plot the first 20 posterior draws
if (requireNamespace("ggplot2") && requireNamespace("dplyr")) {
  library("ggplot2")
  fd_samp |>
    dplyr::filter(.draw <= 20) |>
    ggplot(aes(x = x2, y = .derivative, group = .draw)) +
    geom_line(alpha = 0.5)
}
```

---

difference_smooths	<i>Differences of factor smooth interactions</i>
--------------------	--

---

## Description

Estimates pairwise differences (comparisons) between factor smooth interactions (smooths with a factor by argument) for pairs of groups defined by the factor. The group means can be optionally included in the difference.

## Usage

```
difference_smooths(model, ...)

## S3 method for class 'gam'
difference_smooths(
  model,
  select = NULL,
  smooth = deprecated(),
  n = 100,
  ci_level = 0.95,
  data = NULL,
```

```

    group_means = FALSE,
    partial_match = TRUE,
    unconditional = FALSE,
    frequentist = FALSE,
    ...
  )

```

## Arguments

<code>model</code>	A fitted model.
<code>...</code>	arguments passed to other methods. Not currently used.
<code>select</code>	character, logical, or numeric; which smooths to compare. If <code>NULL</code> , the default, then all model smooths are factor-smooth interactions are compared. Numeric <code>select</code> indexes the smooths in the order they are specified in the formula and stored in object. Character <code>select</code> matches the labels for smooths as shown for example in the output from <code>summary(object)</code> . Logical <code>select</code> operates as per numeric <code>select</code> in the order that smooths are stored. Careful selection is needed because it is not allowed to compare smooths of different covariates or of different factor-by variables.  For character <code>select</code> , specific named smooths can be provided, in which case, the exact names of the smooths (as given by <code>smooths()</code> , for example, can be specified, and <code>partial_match</code> must be set to <code>FALSE</code> .
<code>smooth</code>	<b>[Deprecated]</b> Use <code>select</code> instead.
<code>n</code>	numeric; the number of points at which to evaluate the difference between pairs of smooths.
<code>ci_level</code>	numeric between 0 and 1; the coverage of credible interval.
<code>data</code>	data frame of locations at which to evaluate the difference between smooths.
<code>group_means</code>	logical; should the group means be included in the difference?
<code>partial_match</code>	logical; should smooth match partially against smooths? If <code>partial_match = TRUE</code> , <code>smooth</code> must only be a single string, a character vector of length 1. Unlike similar functions, the default here is <code>TRUE</code> because the intention is that users will be matching against factor-by smooth labels.
<code>unconditional</code>	logical; account for smoothness selection in the model?
<code>frequentist</code>	logical; use the frequentist covariance matrix?

## Examples

```

load_mgcv()

df <- data_sim("eg4", seed = 42)
m <- gam(y ~ fac + s(x2, by = fac) + s(x0), data = df, method = "REML")

sm_dif <- difference_smooths(m, select = "s(x2)")
sm_dif

draw(sm_dif)

```

```
# include the groups means for `fac` in the difference
sm_dif2 <- difference_smooths(m, select = "s(x2)", group_means = TRUE)
draw(sm_dif2)

# compare specific smooths
sm_dif3 <- difference_smooths(m,
  select = c("s(x2):fac1", "s(x2):fac2"), partial_match = FALSE
)
```

---

dispersion	<i>Dispersion parameter for fitted model</i>
------------	--

---

**Description****[Experimental]****Usage**

```
dispersion(model, ...)

## S3 method for class 'gam'
dispersion(model, ...)

## S3 method for class 'glm'
dispersion(model, ...)
```

**Arguments**

model	a fitted model.
...	arguments passed to other methods.

---

draw	<i>Generic plotting via ggplot2</i>
------	-------------------------------------

---

**Description**

Generic plotting via ggplot2

**Usage**

```
draw(object, ...)
```

**Arguments**

object	and R object to plot.
...	arguments passed to other methods.

**Details**

Generic function for plotting of R objects that uses the ggplot2 package.

**Value**

A `ggplot2::ggplot()` object.

**Author(s)**

Gavin L. Simpson

---

draw.basis

*Plot basis functions*


---

**Description**

Plots basis functions using ggplot2

**Usage**

```
## S3 method for class 'basis'
draw(
  object,
  legend = FALSE,
  labeller = NULL,
  ylab = NULL,
  title = NULL,
  subtitle = NULL,
  caption = NULL,
  ncol = NULL,
  nrow = NULL,
  angle = NULL,
  guides = "keep",
  contour = FALSE,
  n_contour = 10,
  contour_col = "black",
  ...
)
```

**Arguments**

object	an object, the result of a call to <code>basis()</code> .
legend	logical; should a legend by drawn to indicate basis functions?
labeller	a labeller function with which to label facets. The default is to use <code>ggplot2::label_both()</code> .
ylab	character or expression; the label for the y axis. If not supplied, a suitable label will be generated from object.

title	character or expression; the title for the plot. See <a href="#">ggplot2::labs()</a> .
subtitle	character or expression; the subtitle for the plot. See <a href="#">ggplot2::labs()</a> .
caption	character or expression; the plot caption. See <a href="#">ggplot2::labs()</a> .
ncol, nrow	numeric; the numbers of rows and columns over which to spread the plots
angle	numeric; the angle at which the x axis tick labels are to be drawn passed to the angle argument of <a href="#">ggplot2::guide_axis()</a> .
guides	character; one of "keep" (the default), "collect", or "auto". Passed to <a href="#">patchwork::plot_layout()</a>
contour	logical; should contours be draw on the plot using <a href="#">ggplot2::geom_contour()</a> .
n_contour	numeric; the number of contour bins. Will result in n_contour - 1 contour lines being drawn. See <a href="#">ggplot2::geom_contour()</a> .
contour_col	colour specification for contour lines.
...	arguments passed to other methods. Not used by this method.

**Value**

A patchwork object.

**Author(s)**

Gavin L. Simpson

**Examples**

```
load_mgcv()
df <- data_sim("eg1", n = 400, seed = 42)
m <- gam(y ~ s(x0) + s(x1) + s(x2) + s(x3), data = df, method = "REML")

bf <- basis(m)
draw(bf)

bf <- basis(m, "s(x2)")
draw(bf)
```

---

draw.compare\_smooths    *Plot comparisons of smooths*

---

**Description**

Plot comparisons of smooths

**Usage**

```
## S3 method for class 'compare_smooths'
draw(object, ncol = NULL, nrow = NULL, guides = "collect", ...)
```

**Arguments**

object	of class "compare_smooths", the result of a call to <a href="#">compare_smooths()</a> .
ncol, nrow	numeric; the numbers of rows and columns over which to spread the plots
guides	character; one of "keep" (the default), "collect", or "auto". Passed to <a href="#">patchwork::plot_layout()</a>
...	additional arguments passed to <a href="#">patchwork::wrap_plots()</a> .

---

draw.conditional\_values

*Plot conditional predictions*


---

**Description**

Plot conditional predictions

**Usage**

```
## S3 method for class 'conditional_values'
draw(
  object,
  facet_scales = "fixed",
  discrete_colour = NULL,
  discrete_fill = NULL,
  xlab = NULL,
  ylab = NULL,
  ...
)
```

**Arguments**

object	an object of class "conditional_values", the result of a call to <a href="#">conditional_values()</a> .
facet_scales	character; should facets have the same axis scales across facets? See <a href="#">ggplot2::facet_wrap()</a> for details. Options are: "fixed" (default), "free_x", "free_y", and "free".
discrete_colour	a suitable colour scale to be used when plotting discrete variables.
discrete_fill	a suitable fill scale to be used when plotting discrete variables.
xlab	character; label for the x axis of the plot.
ylab	character; label for the y axis of the plot.
...	additional arguments passed to <a href="#">patchwork::wrap_plots()</a> .



---

draw.derivatives	<i>Plot derivatives of smooths</i>
------------------	------------------------------------

---

## Description

Plot derivatives of smooths

## Usage

```
## S3 method for class 'derivatives'
draw(
  object,
  select = NULL,
  scales = c("free", "fixed"),
  add_change = FALSE,
  change_type = c("change", "size"),
  alpha = 0.2,
  change_col = "black",
  decrease_col = "#56B4E9",
  increase_col = "#E69F00",
  lwd_change = 1.5,
  ncol = NULL,
  nrow = NULL,
  guides = "keep",
  angle = NULL,
  differentiate_factor_smooths = TRUE,
  ...
)

## S3 method for class 'partial_derivatives'
draw(
  object,
  select = NULL,
  scales = c("free", "fixed"),
  alpha = 0.2,
  ncol = NULL,
  nrow = NULL,
  guides = "keep",
  angle = NULL,
  ...
)
```

## Arguments

object	a fitted GAM, the result of a call to <code>mgcv::gam()</code> .
select	character, logical, or numeric; which smooths to plot. If NULL, the default, then all model smooths are drawn. Numeric select indexes the smooths in

	the order they are specified in the formula and stored in object. Character select matches the labels for smooths as shown for example in the output from <code>summary(object)</code> . Logical select operates as per numeric select in the order that smooths are stored.
scales	character; should all univariate smooths be plotted with the same y-axis scale? If <code>scales = "free"</code> , the default, each univariate smooth has its own y-axis scale. If <code>scales = "fixed"</code> , a common y axis scale is used for all univariate smooths. Currently does not affect the y-axis scale of plots of the parametric terms.
add_change	logical; should the periods of significant change be highlighted on the plot?
change_type	character; the type of change to indicate. If <code>"change"</code> , no differentiation is made between periods of significant increase or decrease. If <code>"sizer"</code> , the periods of increase and decrease are differentiated in the resulting plot.
alpha	numeric; alpha transparency for confidence or simultaneous interval.
change_col, decrease_col, increase_col	colour specifications to use for indicating periods of change. <code>col_change</code> is used when <code>change_type = "change"</code> , while <code>col_decrease</code> and <code>col_increase</code> are used when <code>'change_type = "sizer"'</code> .
lwd_change	numeric; the linewidth to use for the change indicators.
ncol, nrow	numeric; the numbers of rows and columns over which to spread the plots
guides	character; one of <code>"keep"</code> (the default), <code>"collect"</code> , or <code>"auto"</code> . Passed to <code>patchwork::plot_layout()</code>
angle	numeric; the angle at which the x axis tick labels are to be drawn passed to the angle argument of <code>ggplot2::guide_axis()</code> .
differentiate_factor_smooths	logical; should colour be used to differentiate the levels of the factors involved in random factor smooths ( <code>bs = "fs"</code> ) or constrained factor smooths ( <code>bs = "sz"</code> )? If TRUE, the factor(s) are used to define groups and mapped to the colour aesthetic.
...	additional arguments passed to <code>patchwork::wrap_plots()</code> .

## Examples

```
load_mgcv()
dat <- data_sim("eg1", n = 800, dist = "normal", scale = 2, seed = 42)
mod <- gam(y ~ s(x0) + s(x1) + s(x2) + s(x3), data = dat, method = "REML")

## first derivative of all smooths
df <- derivatives(mod, type = "central")
draw(df)
## fixed axis scales
draw(df, scales = "fixed")
```

---

draw.difference\_smooth

*Plot differences of smooths*


---

## Description

Plot differences of smooths

## Usage

```
## S3 method for class 'difference_smooth'
draw(
  object,
  select = NULL,
  rug = FALSE,
  ref_line = FALSE,
  contour = FALSE,
  contour_col = "black",
  n_contour = NULL,
  ci_alpha = 0.2,
  ci_col = "black",
  smooth_col = "black",
  line_col = "red",
  scales = c("free", "fixed"),
  ncol = NULL,
  nrow = NULL,
  guides = "keep",
  xlab = NULL,
  ylab = NULL,
  title = NULL,
  subtitle = NULL,
  caption = NULL,
  angle = NULL,
  ...
)
```

## Arguments

object	a fitted GAM, the result of a call to <code>mgcv::gam()</code> .
select	character, logical, or numeric; which smooths to plot. If NULL, the default, then all model smooths are drawn. Numeric select indexes the smooths in the order they are specified in the formula and stored in object. Character select matches the labels for smooths as shown for example in the output from <code>summary(object)</code> . Logical select operates as per numeric select in the order that smooths are stored.
rug	logical;

ref_line	logical;
contour	logical; should contour lines be added to smooth surfaces?
contour_col	colour specification for contour lines.
n_contour	numeric; the number of contour bins. Will result in $n\_contour - 1$ contour lines being drawn. See <a href="#">ggplot2::geom_contour()</a> .
ci_alpha	numeric; alpha transparency for confidence or simultaneous interval.
ci_col	colour specification for the confidence/credible intervals band. Affects the fill of the interval.
smooth_col	colour specification for the the smooth or difference line.
line_col	colour specification for drawing reference lines
scales	character; should all univariate smooths be plotted with the same y-axis scale? If scales = "free", the default, each univariate smooth has its own y-axis scale. If scales = "fixed", a common y axis scale is used for all univariate smooths. Currently does not affect the y-axis scale of plots of the parametric terms.
ncol, nrow	numeric; the numbers of rows and columns over which to spread the plots
guides	character; one of "keep" (the default), "collect", or "auto". Passed to <a href="#">patchwork::plot_layout()</a>
xlab, ylab, title, subtitle, caption	character; labels with which to annotate plots
angle	numeric; the angle at which the x axis tick labels are to be drawn passed to the angle argument of <a href="#">ggplot2::guide_axis()</a> .
...	additional arguments passed to <a href="#">patchwork::wrap_plots()</a> .

### Examples

```
load_mgcv()
# simulate some data; a factor smooth example
df <- data_sim("eg4", seed = 42)
# fit GAM
m <- gam(y ~ fac + s(x2, by = fac) + s(x0), data = df, method = "REML")

# calculate the differences between pairs of smooths the f_j(x2) term
diffs <- difference_smooths(m, select = "s(x2)")
draw(diffs)
```

---

```
draw.evaluated_parametric_term
```

*Plot estimated parametric effects*

---

### Description

#### [Deprecated]

Plots estimated univariate and bivariate smooths using [ggplot2](#).

**Usage**

```
## S3 method for class 'evaluated_parametric_term'
draw(
  object,
  ci_level = 0.95,
  constant = NULL,
  fun = NULL,
  xlab,
  ylab,
  title = NULL,
  subtitle = NULL,
  caption = NULL,
  rug = TRUE,
  position = "identity",
  response_range = NULL,
  ...
)
```

**Arguments**

object	an object, the result of a call to <a href="#">evaluate_parametric_term()</a> .
ci_level	numeric between 0 and 1; the coverage of credible interval.
constant	numeric; a constant to add to the estimated values of the smooth. constant, if supplied, will be added to the estimated value before the confidence band is computed.
fun	function; a function that will be applied to the estimated values and confidence interval before plotting. Can be a function or the name of a function. Function fun will be applied after adding any constant, if provided.
xlab	character or expression; the label for the x axis. If not supplied, a suitable label will be generated from object.
ylab	character or expression; the label for the y axis. If not supplied, a suitable label will be generated from object.
title	character or expression; the title for the plot. See <a href="#">ggplot2::labs()</a> .
subtitle	character or expression; the subtitle for the plot. See <a href="#">ggplot2::labs()</a> .
caption	character or expression; the plot caption. See <a href="#">ggplot2::labs()</a> .
rug	For <a href="#">evaluate_parametric_terms()</a> , a logical to indicate if a rug plot should be drawn.
position	Position adjustment, either as a string, or the result of a call to a position adjustment function.
response_range	numeric; a vector of two values giving the range of response data for the guide. Used to fix plots to a common scale/range. Ignored if show is set to "se".
...	arguments passed to other methods.

**Value**

A [ggplot2::ggplot\(\)](#) object.

**Author(s)**

Gavin L. Simpson

---

draw.gam*Plot estimated smooths from a fitted GAM*

---

**Description**

Plots estimated smooths from a fitted GAM model in a similar way to `mgcv::plot.gam()` but instead of using base graphics, `ggplot2::ggplot()` is used instead.

**Usage**

```
## S3 method for class 'gam'
draw(
  object,
  data = NULL,
  select = NULL,
  parametric = FALSE,
  terms = NULL,
  residuals = FALSE,
  scales = c("free", "fixed"),
  ci_level = 0.95,
  n = 100,
  n_3d = 16,
  n_4d = 4,
  unconditional = FALSE,
  overall_uncertainty = TRUE,
  constant = NULL,
  fun = NULL,
  dist = 0.1,
  rug = TRUE,
  distinct_rug = TRUE,
  contour = TRUE,
  grouped_by = FALSE,
  ci_alpha = 0.2,
  ci_col = "black",
  smooth_col = "black",
  resid_col = "steelblue3",
  contour_col = "black",
  n_contour = NULL,
  partial_match = FALSE,
  discrete_colour = NULL,
  discrete_fill = NULL,
  continuous_colour = NULL,
  continuous_fill = NULL,
```

```

    position = "identity",
    angle = NULL,
    ncol = NULL,
    nrow = NULL,
    guides = "keep",
    widths = NULL,
    heights = NULL,
    crs = NULL,
    default_crs = NULL,
    lims_method = "cross",
    wrap = TRUE,
    caption = TRUE,
    envir = environment(formula(object)),
    ...
  )

```

### Arguments

object	a fitted GAM, the result of a call to <code>mgcv::gam()</code> .
data	an optional data frame that is used to supply the data at which the smooths will be evaluated and plotted. This is usually not needed, but is an option if you need fine control over exactly what data are used for plotting.
select	character, logical, or numeric; which smooths to plot. If NULL, the default, then all model smooths are drawn. Numeric select indexes the smooths in the order they are specified in the formula and stored in object. Character select matches the labels for smooths as shown for example in the output from <code>summary(object)</code> . Logical select operates as per numeric select in the order that smooths are stored.
parametric	logical; plot parametric terms also? Note that select is used for selecting which smooths to plot. The terms argument is used to select which parametric effects are plotted. The default, as with <code>mgcv::plot.gam()</code> , is to not draw parametric effects.
terms	character; which model parametric terms should be drawn? The Default of NULL will plot all parametric terms that can be drawn.
residuals	logical; should partial residuals for a smooth be drawn? Ignored for anything but a simple univariate smooth.
scales	character; should all univariate smooths be plotted with the same y-axis scale? If <code>scales = "free"</code> , the default, each univariate smooth has its own y-axis scale. If <code>scales = "fixed"</code> , a common y axis scale is used for all univariate smooths. Currently does not affect the y-axis scale of plots of the parametric terms.
ci_level	numeric between 0 and 1; the coverage of credible interval.
n	numeric; the number of points over the range of the covariate at which to evaluate the smooth.
n_3d	numeric; the number of new observations to generate for the third dimension of a 3D smooth.

n_4d	numeric; the number of new observations to generate for the dimensions higher than 2 (!) of a $k$ D smooth ( $k \geq 4$ ). For example, if the smooth is a 4D smooth, each of dimensions 3 and 4 will get n_4d new observations.
unconditional	logical; should confidence intervals include the uncertainty due to smoothness selection? If TRUE, the corrected Bayesian covariance matrix will be used.
overall_uncertainty	logical; should the uncertainty in the model constant term be included in the standard error of the evaluate values of the smooth?
constant	numeric; a constant to add to the estimated values of the smooth. constant, if supplied, will be added to the estimated value before the confidence band is computed.
fun	function; a function that will be applied to the estimated values and confidence interval before plotting. Can be a function or the name of a function. Function fun will be applied after adding any constant, if provided.
dist	numeric; if greater than 0, this is used to determine when a location is too far from data to be plotted when plotting 2-D smooths. The data are scaled into the unit square before deciding what to exclude, and dist is a distance within the unit square. See <code>mgcv::exclude.too.far()</code> for further details.
rug	logical; draw a rug plot at the bottom of each plot for 1-D smooths or plot locations of data for higher dimensions.
distinct_rug	logical; should the data for the rug plots be reduced to the distinct values?
contour	logical; should contours be draw on the plot using <code>ggplot2::geom_contour()</code> .
grouped_by	logical; should factor by smooths be drawn as one panel per level of the factor (FALSE, the default), or should the individual smooths be combined into a single panel containing all levels (TRUE)?
ci_alpha	numeric; alpha transparency for confidence or simultaneous interval.
ci_col	colour specification for the confidence/credible intervals band. Affects the fill of the interval.
smooth_col	colour specification for the smooth line.
resid_col	colour specification for the partial residuals.
contour_col	colour specification for contour lines.
n_contour	numeric; the number of contour bins. Will result in n_contour - 1 contour lines being drawn. See <code>ggplot2::geom_contour()</code> .
partial_match	logical; should smooths be selected by partial matches with select? If TRUE, select can only be a single string to match against.
discrete_colour	a suitable colour scale to be used when plotting discrete variables.
discrete_fill	a suitable fill scale to be used when plotting discrete variables.
continuous_colour	a suitable colour scale to be used when plotting continuous variables.
continuous_fill	a suitable fill scale to be used when plotting continuous variables.



position	Position adjustment, either as a string, or the result of a call to a position adjustment function.
angle	numeric; the angle at which the x axis tick labels are to be drawn passed to the angle argument of <code>ggplot2::guide_axis()</code> .
ncol, nrow	numeric; the numbers of rows and columns over which to spread the plots
guides	character; one of "keep" (the default), "collect", or "auto". Passed to <code>patchwork::plot_layout()</code>
widths, heights	The relative widths and heights of each column and row in the grid. Will get repeated to match the dimensions of the grid. If there is more than 1 plot and widths = NULL, the value of widths will be set internally to widths = 1 to accommodate plots of smooths that use a fixed aspect ratio.
crs	the coordinate reference system (CRS) to use for the plot. All data will be projected into this CRS. See <code>ggplot2::coord_sf()</code> for details.
default_crs	the coordinate reference system (CRS) to use for the non-sf layers in the plot. If left at the default NULL, the CRS used is 4326 (WGS84), which is appropriate for spline-on-the-sphere smooths, which are parameterized in terms of latitude and longitude as coordinates. See <code>ggplot2::coord_sf()</code> for more details.
lims_method	character; affects how the axis limits are determined. See <code>ggplot2::coord_sf()</code> . Be careful; in testing of some examples, changing this to "orthogonal" for example with the chlorophyll-a example from Simon Wood's GAM book quickly used up all the RAM in my test system and the OS killed R. This could be incorrect usage on my part; right now the grid of points at which SOS smooths are evaluated (if not supplied by the user) can produce invalid coordinates for the corners of tiles as the grid is generated for tile centres without respect to the spacing of those tiles.
wrap	logical; wrap plots as a patchwork? If FALSE, a list of ggplot objects is returned, 1 per term plotted.
caption	logical; show the smooth type in the caption of each plot?
envir	an environment to look up the data within.
...	additional arguments passed to <code>patchwork::wrap_plots()</code> .

**Value**

The object returned is created by `patchwork::wrap_plots()`.

**Note**

Internally, plots of each smooth are created using `ggplot2::ggplot()` and composed into a single plot using `patchwork::wrap_plots()`. As a result, it is not possible to use + to add to the plots in the way one might typically work with `ggplot()` plots. Instead, use the & operator; see the examples.

**Author(s)**

Gavin L. Simpson

## Examples

```
load_mgcv()

# simulate some data
df1 <- data_sim("eg1", n = 400, dist = "normal", scale = 2, seed = 2)
# fit GAM
m1 <- gam(y ~ s(x0) + s(x1) + s(x2) + s(x3), data = df1, method = "REML")

# plot all smooths
draw(m1)

# can add partial residuals
draw(m1, residuals = TRUE)

df2 <- data_sim("eg2", n = 1000, dist = "normal", scale = 1, seed = 2)
m2 <- gam(y ~ s(x, z, k = 40), data = df2, method = "REML")
draw(m2, contour = FALSE, n = 50)

# See https://gavinsimpson.github.io/gratia/articles/custom-plotting.html
# for more examples and for details on how to modify the theme of all the
# plots produced by draw(). To modify all panels, for example to change the
# theme, use the & operator
```

---

draw.gamlss

---

*Plot smooths of a GAMLSS model estimated by GJRM::gamlss*


---

## Description

Provides a `draw()` method for GAMLSS (distributional GAMs) fitted by `GJRM::gamlss()`.

## Usage

```
## S3 method for class 'gamlss'
draw(
  object,
  scales = c("free", "fixed"),
  ncol = NULL,
  nrow = NULL,
  guides = "keep",
  widths = NULL,
  heights = NULL,
  ...
)
```

## Arguments

`object` a model, fitted by `GJRM::gamlss()`

scales	character; should all univariate smooths be plotted with the same y-axis scale? If scales = "free", the default, each univariate smooth has its own y-axis scale. If scales = "fixed", a common y axis scale is used for all univariate smooths. Currently does not affect the y-axis scale of plots of the parametric terms.
ncol, nrow	numeric; the numbers of rows and columns over which to spread the plots
guides	character; one of "keep" (the default), "collect", or "auto". Passed to <code>patchwork::plot_layout()</code>
widths, heights	The relative widths and heights of each column and row in the grid. Will get repeated to match the dimensions of the grid. If there is more than 1 plot and widths = NULL, the value of widths will be set internally to widths = 1 to accommodate plots of smooths that use a fixed aspect ratio.
...	arguments passed to <code>draw.gam()</code>

**Note**

Plots of smooths are not labelled with the linear predictor to which they belong.

**Examples**

```
if (suppressPackageStartupMessages(require("GJRM", quietly = TRUE))) {
  # follow example from ?GJRM:gamlss
  load_mgcv()
  suppressPackageStartupMessages(library("GJRM"))
  set.seed(0)
  n <- 100
  x1 <- round(runif(n))
  x2 <- runif(n)
  x3 <- runif(n)
  f1 <- function(x) cos(pi * 2 * x) + sin(pi * x)
  y1 <- -1.55 + 2 * x1 + f1(x2) + rnorm(n)
  dataSim <- data.frame(y1, x1, x2, x3)

  eq_mu <- y1 ~ x1 + s(x2)
  eq_s <- ~ s(x3, k = 6)
  fl <- list(eq_mu, eq_s)
  m <- gamlss(fl, data = dataSim)

  draw(m)
}
```

---

draw.mgcv\_smooth

---

*Plot basis functions*


---

**Description**

Plots basis functions using ggplot2

**Usage**

```
## S3 method for class 'mgcv_smooth'
draw(
  object,
  legend = FALSE,
  use_facets = TRUE,
  labeller = NULL,
  xlab,
  ylab,
  title = NULL,
  subtitle = NULL,
  caption = NULL,
  angle = NULL,
  ...
)
```

**Arguments**

object	an object, the result of a call to <a href="#">basis()</a> .
legend	logical; should a legend by drawn to indicate basis functions?
use_facets	logical; for factor by smooths, use facets to show the basis functions for each level of the factor? If FALSE, a separate ggplot object will be created for each level and combined using <a href="#">patchwork::wrap_plots()</a> . <b>Currently ignored.</b>
labeller	a labeller function with which to label facets. The default is to use <a href="#">ggplot2::label_both()</a> .
xlab	character or expression; the label for the x axis. If not supplied, a suitable label will be generated from object.
ylab	character or expression; the label for the y axis. If not supplied, a suitable label will be generated from object.
title	character or expression; the title for the plot. See <a href="#">ggplot2::labs()</a> .
subtitle	character or expression; the subtitle for the plot. See <a href="#">ggplot2::labs()</a> .
caption	character or expression; the plot caption. See <a href="#">ggplot2::labs()</a> .
angle	numeric; the angle at which the x axis tick labels are to be drawn passed to the angle argument of <a href="#">ggplot2::guide_axis()</a> .
...	arguments passed to other methods. Not used by this method.

**Value**

A [ggplot2::ggplot\(\)](#) object.

**Author(s)**

Gavin L. Simpson

**Examples**

```
load_mgcv()
df <- data_sim("eg4", n = 400, seed = 42)

bf <- basis(s(x0), data = df)
draw(bf)

bf <- basis(s(x2, by = fac, bs = "bs"), data = df)
draw(bf)
```

---

```
draw.pairwise_concurvity
      Plot concurvity measures
```

---

**Description**

Plot concurvity measures

**Usage**

```
## S3 method for class 'pairwise_concurvity'
draw(
  object,
  title = "Smooth-wise concurvity",
  subtitle = NULL,
  caption = NULL,
  x_lab = "Term",
  y_lab = "With",
  fill_lab = "Concurvity",
  continuous_colour = NULL,
  ...
)

## S3 method for class 'overall_concurvity'
draw(
  object,
  title = "Overall concurvity",
  subtitle = NULL,
  caption = NULL,
  y_lab = "Concurvity",
  x_lab = NULL,
  bar_col = "steelblue",
  bar_fill = "steelblue",
  ...
)
```

**Arguments**

object	An object inheriting from class "concurvity", usually the result of a call to <code>model_concurvity()</code> or its abbreviated form <code>concrvity()</code> .
title	character; the plot title.
subtitle	character; the plot subtitle.
caption	character; the plot caption
x_lab	character; the label for the x axis.
y_lab	character; the label for the y axis.
fill_lab	character; the label to use for the fill guide.
continuous_colour	function; continuous colour (fill) scale to use.
...	arguments passed to other methods.
bar_col	colour specification for the bar colour.
bar_fill	colour specification for the bar fill

---

draw.parametric\_effects

*Plot estimated effects for model parametric terms*


---

**Description**

Plot estimated effects for model parametric terms

**Usage**

```
## S3 method for class 'parametric_effects'
draw(
  object,
  scales = c("free", "fixed"),
  ci_level = 0.95,
  ci_col = "black",
  ci_alpha = 0.2,
  line_col = "black",
  constant = NULL,
  fun = NULL,
  rug = TRUE,
  position = "identity",
  angle = NULL,
  ...,
  ncol = NULL,
  nrow = NULL,
  guides = "keep"
)
```

**Arguments**

object	a fitted GAM, the result of a call to <code>mgcv::gam()</code> .
scales	character; should all univariate smooths be plotted with the same y-axis scale? If <code>scales = "free"</code> , the default, each univariate smooth has its own y-axis scale. If <code>scales = "fixed"</code> , a common y axis scale is used for all univariate smooths. Currently does not affect the y-axis scale of plots of the parametric terms.
ci_level	numeric between 0 and 1; the coverage of credible interval.
ci_col	colour specification for the confidence/credible intervals band. Affects the fill of the interval.
ci_alpha	numeric; alpha transparency for confidence or simultaneous interval.
line_col	colour specification used for regression lines of linear continuous terms.
constant	numeric; a constant to add to the estimated values of the smooth. <code>constant</code> , if supplied, will be added to the estimated value before the confidence band is computed.
fun	function; a function that will be applied to the estimated values and confidence interval before plotting. Can be a function or the name of a function. Function <code>fun</code> will be applied after adding any constant, if provided.
rug	logical; draw a rug plot at the bottom of each plot for 1-D smooths or plot locations of data for higher dimensions.
position	Position adjustment, either as a string, or the result of a call to a position adjustment function.
angle	numeric; the angle at which the x axis tick labels are to be drawn passed to the <code>angle</code> argument of <code>ggplot2::guide_axis()</code> .
...	additional arguments passed to <code>patchwork::wrap_plots()</code> .
ncol, nrow	numeric; the numbers of rows and columns over which to spread the plots
guides	character; one of "keep" (the default), "collect", or "auto". Passed to <code>patchwork::plot_layout()</code>

---

<code>draw.penalty_df</code>	<i>Display penalty matrices of smooths using ggplot</i>
------------------------------	---

---

**Description**

Displays the penalty matrices of smooths as a heatmap using ggplot

**Usage**

```
## S3 method for class 'penalty_df'
draw(
  object,
  normalize = FALSE,
  as_matrix = TRUE,
  continuous_fill = NULL,
```

```

xlab = NULL,
ylab = NULL,
title = NULL,
subtitle = NULL,
caption = NULL,
ncol = NULL,
nrow = NULL,
guides = "keep",
...
)

```

## Arguments

<code>object</code>	a fitted GAM, the result of a call to <code>mgcv::gam()</code> .
<code>normalize</code>	logical; normalize the penalty to the range -1, 1?
<code>as_matrix</code>	logical; how should the plotted penalty matrix be oriented? If TRUE row 1, column 1 of the penalty matrix is drawn in the upper left, whereas, if FALSE it is drawn in the lower left of the plot.
<code>continuous_fill</code>	a suitable fill scale to be used when plotting continuous variables.
<code>xlab</code>	character or expression; the label for the x axis. If not supplied, no axis label will be drawn. May be a vector, one per penalty.
<code>ylab</code>	character or expression; the label for the y axis. If not supplied, no axis label will be drawn. May be a vector, one per penalty.
<code>title</code>	character or expression; the title for the plot. See <code>ggplot2::labs()</code> . May be a vector, one per penalty.
<code>subtitle</code>	character or expression; the subtitle for the plot. See <code>ggplot2::labs()</code> . May be a vector, one per penalty.
<code>caption</code>	character or expression; the plot caption. See <code>ggplot2::labs()</code> . May be a vector, one per penalty.
<code>ncol, nrow</code>	numeric; the numbers of rows and columns over which to spread the plots.
<code>guides</code>	character; one of "keep" (the default), "collect", or "auto". Passed to <code>patchwork::plot_layout()</code>
<code>...</code>	additional arguments passed to <code>patchwork::wrap_plots()</code> .

## Examples

```

load_mgcv()
dat <- data_sim("eg4", n = 400, seed = 42)
m <- gam(y ~ s(x0) + s(x1, bs = "cr") + s(x2, bs = "bs", by = fac),
  data = dat, method = "REML"
)

## produce a multi-panel plot of all penalties
draw(penalty(m))

# for a specific smooth
draw(penalty(m, select = "s(x2):fac1"))

```



---

draw.rootogram	<i>Draw a rootogram</i>
----------------	-------------------------

---

## Description

A rootogram is a model diagnostic tool that assesses the goodness of fit of a statistical model. The observed values of the response are compared with those expected from the fitted model. For discrete, count responses, the frequency of each count (0, 1, 2, etc) in the observed data and expected from the conditional distribution of the response implied by the model are compared. For continuous variables, the observed and expected frequencies are obtained by grouping the data into bins. The rootogram is drawn using `ggplot2::ggplot()` graphics. The design closely follows Kleiber & Zeileis (2016).

## Usage

```
## S3 method for class 'rootogram'
draw(
  object,
  type = c("hanging", "standing", "suspended"),
  sqrt = TRUE,
  ref_line = TRUE,
  warn_limits = TRUE,
  fitted_colour = "steelblue",
  bar_colour = NA,
  bar_fill = "grey",
  ref_line_colour = "black",
  warn_line_colour = "black",
  ylab = NULL,
  xlab = NULL,
  ...
)
```

## Arguments

<code>object</code>	and R object to plot.
<code>type</code>	character; the type of rootogram to draw.
<code>sqrt</code>	logical; show the observed and fitted frequencies
<code>ref_line</code>	logical; draw a reference line at zero?
<code>warn_limits</code>	logical; draw Tukey's warning limit lines at +/- 1?
<code>fitted_colour</code> , <code>bar_colour</code> , <code>bar_fill</code> , <code>ref_line_colour</code> , <code>warn_line_colour</code>	colours used to draw the respective element of the rootogram.
<code>xlab</code> , <code>ylab</code>	character; labels for the x and y axis of the rootogram. May be missing (NULL), in which case suitable labels will be used. '
<code>...</code>	arguments passed to other methods.

**Value**

A 'ggplot' object.

**References**

Kleiber, C., Zeileis, A., (2016) Visualizing Count Data Regressions Using Rootograms. *Am. Stat.* **70**, 296–303. doi:[10.1080/00031305.2016.1173590](https://doi.org/10.1080/00031305.2016.1173590)

**See Also**

[rootogram\(\)](#) to compute the data for the rootogram.

**Examples**

```
load_mgcv()
df <- data_sim("eg1", n = 1000, dist = "poisson", scale = 0.1, seed = 6)

# A poisson example
m <- gam(y ~ s(x0, bs = "cr") + s(x1, bs = "cr") + s(x2, bs = "cr") +
  s(x3, bs = "cr"), family = poisson(), data = df, method = "REML")
rg <- rootogram(m)

# plot the rootogram
draw(rg)

# change the type of rootogram
draw(rg, type = "suspended")
```

---

`draw.smooth_estimates` *Plot the result of a call to smooth\_estimates()*

---

**Description**

Plot the result of a call to `smooth_estimates()`

**Usage**

```
## S3 method for class 'smooth_estimates'
draw(
  object,
  constant = NULL,
  fun = NULL,
  contour = TRUE,
  grouped_by = FALSE,
  contour_col = "black",
  n_contour = NULL,
  ci_alpha = 0.2,
  ci_col = "black",
```

```

smooth_col = "black",
resid_col = "steelblue3",
decrease_col = "#56B4E9",
increase_col = "#E69F00",
change_lwd = 1.75,
partial_match = FALSE,
discrete_colour = NULL,
discrete_fill = NULL,
continuous_colour = NULL,
continuous_fill = NULL,
angle = NULL,
ylim = NULL,
crs = NULL,
default_crs = NULL,
lims_method = "cross",
caption = TRUE,
...
)

```

## Arguments

object	a fitted GAM, the result of a call to <code>mgcv::gam()</code> .
constant	numeric; a constant to add to the estimated values of the smooth. constant, if supplied, will be added to the estimated value before the confidence band is computed.
fun	function; a function that will be applied to the estimated values and confidence interval before plotting. Can be a function or the name of a function. Function fun will be applied after adding any constant, if provided.
contour	logical; should contours be draw on the plot using <code>ggplot2::geom_contour()</code> .
grouped_by	logical; should factor by smooths be drawn as one panel per level of the factor (FALSE, the default), or should the individual smooths be combined into a single panel containing all levels (TRUE)?
contour_col	colour specification for contour lines.
n_contour	numeric; the number of contour bins. Will result in <code>n_contour - 1</code> contour lines being drawn. See <code>ggplot2::geom_contour()</code> .
ci_alpha	numeric; alpha transparency for confidence or simultaneous interval.
ci_col	colour specification for the confidence/credible intervals band. Affects the fill of the interval.
smooth_col	colour specification for the smooth line.
resid_col	colour specification for the partial residuals.
decrease_col, increase_col	colour specifications to use for indicating periods of change. <code>col_change</code> is used when <code>change_type = "change"</code> , while <code>col_decrease</code> and <code>col_increase</code> are used when <code>change_type = "sizer"</code> .
change_lwd	numeric; the value to set the linewidth to in <code>ggplot2::geom_line()</code> , used to represent the periods of change.

<code>partial_match</code>	logical; should smooths be selected by partial matches with <code>select</code> ? If TRUE, <code>select</code> can only be a single string to match against.
<code>discrete_colour</code>	a suitable colour scale to be used when plotting discrete variables.
<code>discrete_fill</code>	a suitable fill scale to be used when plotting discrete variables.
<code>continuous_colour</code>	a suitable colour scale to be used when plotting continuous variables.
<code>continuous_fill</code>	a suitable fill scale to be used when plotting continuous variables.
<code>angle</code>	numeric; the angle at which the x axis tick labels are to be drawn passed to the <code>angle</code> argument of <code>ggplot2::guide_axis()</code> .
<code>ylim</code>	numeric; vector of y axis limits to use all <i>all</i> panels drawn.
<code>crs</code>	the coordinate reference system (CRS) to use for the plot. All data will be projected into this CRS. See <code>ggplot2::coord_sf()</code> for details.
<code>default_crs</code>	the coordinate reference system (CRS) to use for the non-sf layers in the plot. If left at the default NULL, the CRS used is 4326 (WGS84), which is appropriate for spline-on-the-sphere smooths, which are parameterized in terms of latitude and longitude as coordinates. See <code>ggplot2::coord_sf()</code> for more details.
<code>lims_method</code>	character; affects how the axis limits are determined. See <code>ggplot2::coord_sf()</code> . Be careful; in testing of some examples, changing this to "orthogonal" for example with the chlorophyll-a example from Simon Wood's GAM book quickly used up all the RAM in my test system and the OS killed R. This could be incorrect usage on my part; right now the grid of points at which SOS smooths are evaluated (if not supplied by the user) can produce invalid coordinates for the corners of tiles as the grid is generated for tile centres without respect to the spacing of those tiles.
<code>caption</code>	logical; show the smooth type in the caption of each plot?
<code>...</code>	additional arguments passed to <code>patchwork::wrap_plots()</code> .

## Examples

```
load_mgcv()
# example data
df <- data_sim("eg1", seed = 21)
# fit GAM
m <- gam(y ~ s(x0) + s(x1) + s(x2) + s(x3), data = df, method = "REML")
# plot all of the estimated smooths
sm <- smooth_estimates(m)
draw(sm)
# evaluate smooth of `x2`
sm <- smooth_estimates(m, select = "s(x2)")
# plot it
draw(sm)

# customising some plot elements
draw(sm, ci_col = "steelblue", smooth_col = "forestgreen", ci_alpha = 0.3)
```

```
# Add a constant to the plotted smooth
draw(sm, constant = coef(m)[1])

# Adding change indicators to smooths based on derivatives of the smooth
d <- derivatives(m, n = 100) # n to match smooth_estimates()

smooth_estimates(m) |>
  add_sizer(derivatives = d, type = "sizer") |>
  draw()
```

---

draw.smooth_samples	<i>Plot posterior smooths</i>
---------------------	-------------------------------

---

## Description

Plot posterior smooths

## Usage

```
## S3 method for class 'smooth_samples'
draw(
  object,
  select = NULL,
  n_samples = NULL,
  seed = NULL,
  xlab = NULL,
  ylab = NULL,
  title = NULL,
  subtitle = NULL,
  caption = NULL,
  alpha = 1,
  colour = "black",
  contour = FALSE,
  contour_col = "black",
  n_contour = NULL,
  scales = c("free", "fixed"),
  rug = TRUE,
  partial_match = FALSE,
  angle = NULL,
  ncol = NULL,
  nrow = NULL,
  guides = "keep",
  ...
)
```

**Arguments**

object	a fitted GAM, the result of a call to <code>mgcv::gam()</code> .
select	character, logical, or numeric; which smooths to plot. If NULL, the default, then all model smooths are drawn. Numeric select indexes the smooths in the order they are specified in the formula and stored in object. Character select matches the labels for smooths as shown for example in the output from <code>summary(object)</code> . Logical select operates as per numeric select in the order that smooths are stored.
n_samples	numeric; if not NULL, sample n_samples from the posterior draws for plotting.
seed	numeric; random seed to be used to if sampling draws.
xlab	character or expression; the label for the x axis. If not supplied, a suitable label will be generated from object.
ylab	character or expression; the label for the y axis. If not supplied, a suitable label will be generated from object.
title	character or expression; the title for the plot. See <code>ggplot2::labs()</code> .
subtitle	character or expression; the subtitle for the plot. See <code>ggplot2::labs()</code> .
caption	character or expression; the plot caption. See <code>ggplot2::labs()</code> .
alpha	numeric; alpha transparency for confidence or simultaneous interval.
colour	The colour to use to draw the posterior smooths. Passed to <code>ggplot2::geom_line()</code> as argument colour.
contour	logical; should contour lines be added to smooth surfaces?
contour_col	colour specification for contour lines.
n_contour	numeric; the number of contour bins. Will result in n_contour - 1 contour lines being drawn. See <code>ggplot2::geom_contour()</code> .
scales	character; should all univariate smooths be plotted with the same y-axis scale? If scales = "free", the default, each univariate smooth has its own y-axis scale. If scales = "fixed", a common y axis scale is used for all univariate smooths. Currently does not affect the y-axis scale of plots of the parametric terms.
rug	logical; draw a rug plot at the bottom of each plot for 1-D smooths or plot locations of data for higher dimensions.
partial_match	logical; should smooths be selected by partial matches with select? If TRUE, select can only be a single string to match against.
angle	numeric; the angle at which the x axis tick labels are to be drawn passed to the angle argument of <code>ggplot2::guide_axis()</code> .
ncol, nrow	numeric; the numbers of rows and columns over which to spread the plots
guides	character; one of "keep" (the default), "collect", or "auto". Passed to <code>patchwork::plot_layout()</code>
...	arguments to be passed to <code>patchwork::wrap_plots()</code> .

**Author(s)**

Gavin L. Simpson

## Examples

```
load_mgcv()
dat1 <- data_sim("eg1", n = 400, dist = "normal", scale = 1, seed = 1)
## a single smooth GAM
m1 <- gam(y ~ s(x0) + s(x1) + s(x2) + s(x3), data = dat1, method = "REML")
## posterior smooths from m1
sm1 <- smooth_samples(m1, n = 15, seed = 23478)
## plot
draw(sm1, alpha = 0.7)
## plot only 5 randomly sampled draws
draw(sm1, n_samples = 5, alpha = 0.7)

## A factor-by smooth example
dat2 <- data_sim("eg4", n = 400, dist = "normal", scale = 1, seed = 1)
## a multi-smooth GAM with a factor-by smooth
m2 <- gam(y ~ fac + s(x2, by = fac) + s(x0), data = dat2, method = "REML")
## posterior smooths from m1
sm2 <- smooth_samples(m2, n = 15, seed = 23478)
## plot, this time selecting only the factor-by smooth
draw(sm2, select = "s(x2)", partial_match = TRUE, alpha = 0.7)

## A 2D smooth example
dat3 <- data_sim("eg2", n = 400, dist = "normal", scale = 1, seed = 1)
## fit a 2D smooth
m3 <- gam(y ~ te(x, z), data = dat3, method = "REML")
## get samples
sm3 <- smooth_samples(m3, n = 10)
## plot just 6 of the draws, with contour line overlays
draw(sm3, n_samples = 6, contour = TRUE, seed = 42)
```

---

edf

*Effective degrees of freedom for smooths and GAMs*


---

## Description

Extracts the effective degrees of freedom (EDF) for model smooth terms or overall EDF for fitted GAMs

## Usage

```
edf(object, ...)
```

```
## S3 method for class 'gam'
edf(
  object,
  select = NULL,
  smooth = deprecated(),
```

```

    type = c("default", "unconditional", "alternative"),
    partial_match = FALSE,
    ...
)

model_edf(object, ..., type = c("default", "unconditional", "alternative"))

```

## Arguments

<code>object</code>	a fitted model from which to extract smooth-specific EDFs.
<code>...</code>	arguments passed to methods.
<code>select</code>	character, logical, or numeric; which smooths EDF to extract. If <code>NULL</code> , the default, EDFs for all smooths will be returned. Numeric <code>select</code> indexes the smooths in the order they are specified in the formula and stored in <code>object</code> . Character <code>select</code> matches the labels for smooths as shown for example in the output from <code>summary(object)</code> . Logical <code>select</code> operates as per numeric <code>select</code> in the order that smooths are stored.
<code>smooth</code>	<b>[Deprecated]</b> Use <code>select</code> instead.
<code>type</code>	character: which type of EDF to return. "default" returns the standard EDF; "unconditional" selects the EDF corrected for smoothness parameter selection, if available; "alternative" returns the alternative formulation for EDF from Wood (2017, pp. 252)
<code>partial_match</code>	logical; should smooths be selected by partial matches with <code>select</code> ? If <code>TRUE</code> , <code>select</code> can only be a single string to match against.

## Details

Multiple formulations for the effective degrees of freedom are available. The additional uncertainty due to selection of smoothness parameters can be taken into account when computing the EDF of smooths. This form of the EDF is available with `type = "unconditional"`.

Wood (2017; pp. 252) describes an alternative EDF for the model

$$\text{EDF} = 2\text{tr}(\mathbf{F}) - \text{tr}(\mathbf{F}\mathbf{F}),$$

where `tr` is the matrix trace and  $\mathbf{F}$  is a matrix mapping unpenalised coefficient estimates to the penalized coefficient estimates. The trace of  $\mathbf{F}$  is effectively the average shrinkage of the coefficients multiplied by the number of coefficients (Wood, 2017). Smooth-specific EDFs then are obtained by summing up the relevant elements of  $\text{diag}(2\mathbf{F} - \mathbf{F}\mathbf{F})$ .

## Examples

```

load_mgcv()

df <- data_sim("eg1", n = 400, seed = 42)
m <- gam(y ~ s(x0) + s(x1) + s(x2) + s(x3), data = df, method = "REML")

# extract the EDFs for all smooths
edf(m)

```



```

# or selected smooths
edf(m, select = c("s(x0)", "s(x2)"))

# accounting for smoothness parameter uncertainty
edf(m, type = "unconditional")

# over EDF of the model, including the intercept
model_edf(m)

# can get model EDF for multiple models
m2 <- gam(y ~ s(x0) + s(x1) + s(x3), data = df, method = "REML")
model_edf(m, m2)

```

---

```
evaluate_parametric_term
```

*Evaluate parametric model terms*

---

## Description

**[Deprecated]** Returns values of parametric model terms at values of factor terms and over a grid of covariate values for linear parametric terms. This function is now deprecated in favour of [parametric\\_effects\(\)](#).

## Usage

```

evaluate_parametric_term(object, ...)

## S3 method for class 'gam'
evaluate_parametric_term(object, term, unconditional = FALSE, ...)

```

## Arguments

object	an object of class "gam" or "gamm".
...	arguments passed to other methods.
term	character; which parametric term whose effects are evaluated
unconditional	logical; should confidence intervals include the uncertainty due to smoothness selection? If TRUE, the corrected Bayesian covariance matrix will be used.

---

evaluate_smooth	<i>Evaluate a smooth</i>
-----------------	--------------------------

---

### Description

**[Deprecated]** Evaluate a smooth at a grid of evenly spaced value over the range of the covariate associated with the smooth. Alternatively, a set of points at which the smooth should be evaluated can be supplied.

### Usage

```
evaluate_smooth(object, ...)
```

### Arguments

object	an object of class "gam" or "gamm".
...	arguments passed to other methods.

### Details

**[Deprecated]** `evaluate_smooth()` is deprecated in favour of `smooth_estimates()`, which provides a cleaner way to evaluate a smooth over a range of covariate values. `smooth_estimates()` can handle a much wider range of models than `evaluate_smooth()` is capable of and `smooth_estimates()` is much easier to extend to handle new smooth types.

Most code that uses `evaluate_smooth()` should work simply by changing the function call to `smooth_estimates()`. However, there are some differences:

- the `newdata` argument becomes `data`

### Value

A data frame, which is of class "evaluated\_1d\_smooth" or "evaluated\_2d\_smooth", which inherit from classes "evaluated\_smooth" and "data.frame".

---

eval_smooth	<i>S3 methods to evaluate individual smooths</i>
-------------	--

---

### Description

S3 methods to evaluate individual smooths

**Usage**

```
eval_smooth(smooth, ...)  
  
## S3 method for class 'mgcv.smooth'  
eval_smooth(  
  smooth,  
  model,  
  n = 100,  
  n_3d = NULL,  
  n_4d = NULL,  
  data = NULL,  
  unconditional = FALSE,  
  overall_uncertainty = TRUE,  
  dist = NULL,  
  ...  
)  
  
## S3 method for class 'soap.film'  
eval_smooth(  
  smooth,  
  model,  
  n = 100,  
  n_3d = NULL,  
  n_4d = NULL,  
  data = NULL,  
  unconditional = FALSE,  
  overall_uncertainty = TRUE,  
  clip = TRUE,  
  ...  
)  
  
## S3 method for class 'scam_smooth'  
eval_smooth(  
  smooth,  
  model,  
  n = 100,  
  n_3d = NULL,  
  n_4d = NULL,  
  data = NULL,  
  unconditional = FALSE,  
  overall_uncertainty = TRUE,  
  dist = NULL,  
  ...  
)  
  
## S3 method for class 'fs.interaction'  
eval_smooth(  
  smooth,
```

```
    model,
    n = 100,
    data = NULL,
    unconditional = FALSE,
    overall_uncertainty = TRUE,
    ...
)

## S3 method for class 'sz.interaction'
eval_smooth(
  smooth,
  model,
  n = 100,
  data = NULL,
  unconditional = FALSE,
  overall_uncertainty = TRUE,
  ...
)

## S3 method for class 'random.effect'
eval_smooth(
  smooth,
  model,
  n = 100,
  data = NULL,
  unconditional = FALSE,
  overall_uncertainty = TRUE,
  ...
)

## S3 method for class 'mrf.smooth'
eval_smooth(
  smooth,
  model,
  n = 100,
  data = NULL,
  unconditional = FALSE,
  overall_uncertainty = TRUE,
  ...
)

## S3 method for class 't2.smooth'
eval_smooth(
  smooth,
  model,
  n = 100,
  n_3d = NULL,
  n_4d = NULL,
```

```

    data = NULL,
    unconditional = FALSE,
    overall_uncertainty = TRUE,
    dist = NULL,
    ...
)

## S3 method for class 'tensor.smooth'
eval_smooth(
  smooth,
  model,
  n = 100,
  n_3d = NULL,
  n_4d = NULL,
  data = NULL,
  unconditional = FALSE,
  overall_uncertainty = TRUE,
  dist = NULL,
  ...
)
```

## Arguments

<code>smooth</code>	currently an object that inherits from class <code>mgcv.smooth</code> .
<code>...</code>	arguments passed to other methods
<code>model</code>	a fitted model; currently only <code>mgcv::gam()</code> and <code>mgcv::bam()</code> models are supported.
<code>n</code>	numeric; the number of points over the range of the covariate at which to evaluate the smooth.
<code>n_3d, n_4d</code>	numeric; the number of points over the range of last covariate in a 3D or 4D smooth. The default is <code>NULL</code> which achieves the standard behaviour of using <code>n</code> points over the range of all covariate, resulting in $n^d$ evaluation points, where <code>d</code> is the dimension of the smooth. For $d > 2$ this can result in very many evaluation points and slow performance. For smooths of $d > 4$ , the value of <code>n_4d</code> will be used for all dimensions $> 4$ , unless this is <code>NULL</code> , in which case the default behaviour (using <code>n</code> for all dimensions) will be observed.
<code>data</code>	an optional data frame of values to evaluate smooth at.
<code>unconditional</code>	logical; should confidence intervals include the uncertainty due to smoothness selection? If <code>TRUE</code> , the corrected Bayesian covariance matrix will be used.
<code>overall_uncertainty</code>	logical; should the uncertainty in the model constant term be included in the standard error of the evaluate values of the smooth?
<code>dist</code>	numeric; if greater than 0, this is used to determine when a location is too far from data to be plotted when plotting 2-D smooths. The data are scaled into the unit square before deciding what to exclude, and <code>dist</code> is a distance within the unit square. See <code>mgcv::exclude.too.far()</code> for further details.

clip	logical; should evaluation points be clipped to the boundary of a soap film smooth? The default is FALSE, which will return NA for any point that is deemed to lie outside the boundary of the soap film.
------	---

---

evenly	<i>Create a sequence of evenly-spaced values</i>
--------	--

---

## Description

For a continuous vector `x`, `evenly` and `seq_min_max()` create a sequence of `n` evenly-spaced values over the range `lower – upper`. By default, `lower` is defined as `min(x)` and `upper` as `max(x)`, excluding NAs. For a factor `x`, the function returns `levels(x)`.

## Usage

```
evenly(x, n = 100, by = NULL, lower = NULL, upper = NULL)
```

```
seq_min_max(x, n, by = NULL, lower = NULL, upper = NULL)
```

## Arguments

<code>x</code>	numeric; vector over which evenly-spaced values are returned
<code>n</code>	numeric; the number of evenly-spaced values to return. A default of 100 is used for convenience as that what is typically used when evaluating a smooth.
<code>by</code>	numeric; the increment of the sequence. If specified, argument <code>n</code> is ignored and the sequence returned will be from <code>min(x)</code> to <code>max(x)</code> in increments of <code>by</code> .
<code>lower</code>	numeric; the lower bound of the interval.
<code>upper</code>	numeric; the upper bound of the interval.

## Value

A numeric vector of length `n`.

## See Also

See [base::seq\(\)](#) for details of the behaviour of `evenly()` when using `by`.

## Examples

```
x <- rnorm(10)
n <- 10L

# 10 values evenly over the range of `x`
evenly(x, n = n)

# evenly spaced values, incrementing by 0.2
evenly(x, by = 0.2)
```

```
# evenly spaced values, incrementing by 0.2, starting at -2
evenly(x, by = 0.2, lower = -2)
```

---

factor_combos	<i>All combinations of factor levels</i>
---------------	--

---

## Description

All combinations of factor levels

## Usage

```
factor_combos(object, ...)

## S3 method for class 'gam'
factor_combos(object, vars = everything(), complete = TRUE, ...)
```

## Arguments

object	a fitted model object.
...	arguments passed to methods.
vars	terms to include or exclude from the returned object. Uses tidyselect principles.
complete	logical; should all combinations of factor levels be returned? If FALSE, only those combinations of levels observed in the model are retained.

---

family.gam	<i>Extract family objects from models</i>
------------	---

---

## Description

Provides a `stats::family()` method for a range of GAM objects.

## Usage

```
## S3 method for class 'gam'
family(object, ...)

## S3 method for class 'gamm'
family(object, ...)

## S3 method for class 'bam'
family(object, ...)

## S3 method for class 'list'
family(object, ...)
```

Arguments

object            a fitted model. Models fitted by `mgcv::gam()`, `mgcv::bam()`, `mgcv::gamm()`,  
and `gamm4::gamm4()` are currently supported.  
...               arguments passed to other methods.

---

family_name	<i>Name of family used to fit model</i>
-------------	---

---

Description

Extracts the name of the family used to fit the supplied model.

Usage

```
family_name(object, ...)
```

Arguments

object            an R object.  
...               arguments passed to other methods.

Value

A character vector containing the family name.

---

family_type	<i>Extracts the type of family in a consistent way</i>
-------------	--

---

Description

Extracts the type of family in a consistent way

Usage

```
family_type(object, ...)

## S3 method for class 'family'
family_type(object, ...)

## Default S3 method:
family_type(object, ...)
```

Arguments

object            an R object. Currently `family()` objects and anything with a `family()` method.  
...               arguments passed to other methods.



---

fitted_samples	<i>Draw fitted values from the posterior distribution</i>
----------------	---

---

### Description

Expectations (fitted values) of the response drawn from the posterior distribution of fitted model using a Gaussian approximation to the posterior or a simple Metropolis Hastings sampler.

### Usage

```
fitted_samples(model, ...)

## S3 method for class 'gam'
fitted_samples(
  model,
  n = 1,
  data = newdata,
  seed = NULL,
  scale = c("response", "linear_predictor"),
  method = c("gaussian", "mh", "inla", "user"),
  n_cores = 1,
  burnin = 1000,
  thin = 1,
  t_df = 40,
  rw_scale = 0.25,
  freq = FALSE,
  unconditional = FALSE,
  draws = NULL,
  mvn_method = c("mvnfast", "mgcv"),
  ...,
  newdata = NULL,
  ncores = NULL
)

## S3 method for class 'scam'
fitted_samples(
  model,
  n = 1,
  data = NULL,
  seed = NULL,
  scale = c("response", "linear_predictor"),
  method = c("gaussian", "mh", "inla", "user"),
  n_cores = 1,
  burnin = 1000,
  thin = 1,
  t_df = 40,
  rw_scale = 0.25,
```

```

    freq = FALSE,
    unconditional = FALSE,
    draws = NULL,
    mvn_method = c("mvnfast", "mgcv"),
    ...
)

```

## Arguments

model	a fitted model of the supported types
...	arguments passed to other methods. For <code>fitted_samples()</code> , these are passed on to <code>mgcv::predict.gam()</code> . For <code>posterior_samples()</code> these are passed on to <code>fitted_samples()</code> . For <code>predicted_samples()</code> these are passed on to the relevant <code>simulate()</code> method.
n	numeric; the number of posterior samples to return.
data	data frame; new observations at which the posterior draws from the model should be evaluated. If not supplied, the data used to fit the model will be used for data, if available in model.
seed	numeric; a random seed for the simulations.
scale	character; what scale should the fitted values be returned on? "linear predictor" is a synonym for "link" if you prefer that terminology.
method	character; which method should be used to draw samples from the posterior distribution. "gaussian" uses a Gaussian (Laplace) approximation to the posterior. "mh" uses a Metropolis Hastings sampler that alternates t proposals with proposals based on a shrunken version of the posterior covariance matrix. "inla" uses a variant of Integrated Nested Laplace Approximation due to Wood (2019), (currently not implemented). "user" allows for user-supplied posterior draws (currently not implemented).
n_cores	number of cores for generating random variables from a multivariate normal distribution. Passed to <code>mvnfast::rmvn()</code> . Parallelization will take place only if OpenMP is supported (but appears to work on Windows with current R).
burnin	numeric; number of samples to discard as the burnin draws. Only used with <code>method = "mh"</code> .
thin	numeric; the number of samples to skip when taking n draws. Results in <code>thin * n</code> draws from the posterior being taken. Only used with <code>method = "mh"</code> .
t_df	numeric; degrees of freedom for t distribution proposals. Only used with <code>method = "mh"</code> .
rw_scale	numeric; Factor by which to scale posterior covariance matrix when generating random walk proposals. Negative or non finite to skip the random walk step. Only used with <code>method = "mh"</code> .
freq	logical; TRUE to use the frequentist covariance matrix of the parameter estimators, FALSE to use the Bayesian posterior covariance matrix of the parameters.
unconditional	logical; if TRUE (and <code>freq == FALSE</code> ) then the Bayesian smoothing parameter uncertainty corrected covariance matrix is used, if available.
draws	matrix; user supplied posterior draws to be used when <code>method = "user"</code> .

mvn_method	character; one of "mvnfast" or "mgcv". The default is uses <code>mvnfast::rmvn()</code> , which can be considerably faster at generate large numbers of MVN random values than <code>mgcv::rmvn()</code> , but which might not work for some marginal fits, such as those where the covariance matrix is close to singular.
newdata	Deprecated: use data instead.
ncores	Deprecated; use <code>n_cores</code> instead. The number of cores for generating random variables from a multivariate normal distribution. Passed to <code>mvnfast::rmvn()</code> . Parallelization will take place only if OpenMP is supported (but appears to work on Windows with current R).

## Value

A tibble (data frame) with 3 columns containing the posterior predicted values in long format. The columns are

- row (integer) the row of data that each posterior draw relates to,
- draw (integer) an index, in range 1:n, indicating which draw each row relates to,
- response (numeric) the predicted response for the indicated row of data.

## Note

Models with offset terms supplied via the `offset` argument to `mgcv::gam()` etc. are ignored by `mgcv::predict.gam()`. As such, this kind of offset term is also ignored by `posterior_samples()`. Offset terms that are included in the model formula supplied to `mgcv::gam()` etc are not ignored and the posterior samples produced will reflect those offset term values. This has the side effect of requiring any new data values provided to `posterior_samples()` via the `data` argument must include the offset variable.

## Author(s)

Gavin L. Simpson

## References

Wood, S.N., (2020). Simplified integrated nested Laplace approximation. *Biometrika* **107**, 223–230. doi:[10.1093/biomet/asz044](https://doi.org/10.1093/biomet/asz044)

## Examples

```
load_mgcv()

dat <- data_sim("eg1", n = 1000, dist = "normal", scale = 2, seed = 2)
m1 <- gam(y ~ s(x0) + s(x1) + s(x2) + s(x3), data = dat, method = "REML")

fs <- fitted_samples(m1, n = 5, seed = 42)

fs

# can generate own set of draws and use them
```

```
drws <- generate_draws(m1, n = 2, seed = 24)
fs2 <- fitted_samples(m1, method = "user", draws = drws)

fs2
```

---

fitted_values	<i>Generate fitted values from a estimated GAM</i>
---------------	--

---

## Description

Generate fitted values from a estimated GAM

## Usage

```
fitted_values(object, ...)

## S3 method for class 'gam'
fitted_values(
  object,
  data = NULL,
  scale = c("response", "link", "linear predictor"),
  ci_level = 0.95,
  ...
)

## S3 method for class 'gamm'
fitted_values(object, ...)

## S3 method for class 'scam'
fitted_values(object, ...)
```

## Arguments

object	a fitted model. Currently only models fitted by <code>mgcv::gam()</code> and <code>mgcv::bam()</code> are supported.
...	arguments passed to <code>mgcv::predict.gam()</code> . Note that <code>type</code> , <code>newdata</code> , and <code>se.fit</code> are already used and passed on to <code>mgcv::predict.gam()</code> .
data	optional data frame of covariate values for which fitted values are to be returned.
scale	character; what scale should the fitted values be returned on? "linear predictor" is a synonym for "link" if you prefer that terminology.
ci_level	numeric; a value between 0 and 1 indicating the coverage of the credible interval.

Value

A tibble (data frame) whose first *m* columns contain either the data used to fit the model (if data was NULL), or the variables supplied to data. Four further columns are added:

- fitted: the fitted values on the specified scale,
- se: the standard error of the fitted values (always on the *link* scale),
- lower, upper: the limits of the credible interval on the fitted values, on the specified scale.

Models fitted with certain families will include additional variables

- mgcv::ocat() models: when scale = "repsonse", the returned object will contain a row column and a category column, which indicate to which row of the data each row of the returned object belongs. Additionally, there will be nrow(data) \* n\_categories rows in the returned object; each row is the predicted probability for a single category of the response.

Note

For most families, regardless of the scale on which the fitted values are returned, the se component of the returned object is on the *link* (*linear predictor*) scale, not the response scale. An exception is the mgcv::ocat() family, for which the se is on the response scale if scale = "response".

Examples

```
load_mgcv()

sim_df <- data_sim("eg1", n = 400, dist = "normal", scale = 2, seed = 2)
m <- gam(y ~ s(x0) + s(x1) + s(x2) + s(x3), data = sim_df, method = "REML")
fv <- fitted_values(m)
fv
```

---

fixef	<i>Extract fixed effects estimates</i>
-------	--

---

Description

Extract fixed effects estimates

Arguments

- |        |                                   |
|--------|-----------------------------------|
| object | a fitted GAM                      |
| ...    | arguments passed to other methods |

---

fixef.gam

---

*Extract fixed effects estimates from a fitted GAM*


---

## Description

Extract fixed effects estimates from a fitted GAM

## Usage

```
## S3 method for class 'gam'
fixef(object, ...)

## S3 method for class 'gamm'
fixef(object, ...)

## S3 method for class 'lm'
fixef(object, ...)

## S3 method for class 'glm'
fixef(object, ...)

fixed_effects(object, ...)

## Default S3 method:
fixed_effects(object, ...)
```

## Arguments

object	a fitted GAM
...	arguments passed to other methods

## Examples

```
load_mgcv()

# run example if lme4 is available
if (require("lme4")) {
  data(sleepstudy, package = "lme4")
  m <- gam(
    Reaction ~ Days + s(Subject, bs = "re") +
    s(Days, Subject, bs = "re"),
    data = sleepstudy, method = "REML"
  )
  fixef(m)
}
```

---

fix\_offset

*Fix the names of a data frame containing an offset variable.*


---

### Description

Identifies which variable, if any, is the model offset, and fixed the name such that `offset(foo(var))` is converted to `var`, and possibly sets the values of that variable to `offset_val`.

### Usage

```
fix_offset(model, newdata, offset_val = NULL)
```

### Arguments

<code>model</code>	a fitted GAM.
<code>newdata</code>	data frame; new values at which to predict at.
<code>offset_val</code>	numeric, optional; if provided, then the offset variable in <code>newdata</code> is set to this constant value before returning <code>newdata</code>

### Value

The original `newdata` is returned with fixed names and possibly modified offset variable.

### Author(s)

Gavin L. Simpson

### Examples

```
load_mgcv()
df <- data_sim("eg1", n = 400, dist = "normal", seed = 2)
m <- gam(y ~ s(x0) + s(x1) + offset(x2), data = df, method = "REML")
names(model.frame(m))
names(fix_offset(m, model.frame(m), offset_val = 1L))
```

---

gaussian\_draws

*Posterior samples using a simple Metropolis Hastings sampler*


---

### Description

Posterior samples using a simple Metropolis Hastings sampler

**Usage**

```

gaussian_draws(model, ...)

## S3 method for class 'gam'
gaussian_draws(
  model,
  n,
  n_cores = 1L,
  index = NULL,
  frequentist = FALSE,
  unconditional = FALSE,
  mvn_method = "mvnfast",
  ...
)

## S3 method for class 'scam'
gaussian_draws(
  model,
  n,
  n_cores = 1L,
  index = NULL,
  frequentist = FALSE,
  parametrized = TRUE,
  mvn_method = "mvnfast",
  ...
)

```

**Arguments**

<code>model</code>	a fitted R model. Currently only models fitted by <code>mgcv::gam()</code> or <code>mgcv::bam()</code> , or return an object that <i>inherits</i> from such objects are supported. Here, "inherits" is used in a loose fashion; models fitted by <code>scam::scam()</code> are support even though those models don't strictly inherit from class "gam" as far as <code>inherits()</code> is concerned.
<code>...</code>	arguments passed to methods.
<code>n</code>	numeric; the number of posterior draws to take.
<code>n_cores</code>	integer; number of CPU cores to use when generating multivariate normal distributed random values. Only used if <code>mvn_method = "mvnfast"</code> <b>and</b> <code>method = "gaussian"</code> .
<code>index</code>	numeric; vector of indices of coefficients to use. Can be used to subset the mean vector and covariance matrix extracted from <code>model</code> .
<code>frequentist</code>	logical; if TRUE, the frequentist covariance matrix of the parameter estimates is used. If FALSE, the Bayesian posterior covariance matrix of the parameters is used. See <code>mgcv::vcov.gam()</code> .
<code>unconditional</code>	logical; if TRUE the Bayesian smoothing parameter uncertainty corrected covariance matrix is used, <i>if available</i> for <code>model</code> . See <code>mgcv::vcov.gam()</code> .



mvn_method	character; one of "mvnfast" or "mgcv". The default is uses mvnfast::rmvn(), which can be considerably faster at generate large numbers of MVN random values than mgcv::rmvn(), but which might not work for some marginal fits, such as those where the covariance matrix is close to singular.
parametrized	logical; use parametrized coefficients and covariance matrix, which respect the linear inequality constraints of the model. Only for scam::scam() model fits.

---

get_by_smooth	<i>Extract an factor-by smooth by name</i>
---------------	--

---

**Description**

Extract an factor-by smooth by name

**Usage**

```
get_by_smooth(object, term, level)
```

**Arguments**

object	a fitted GAM model object.
term	character; the name of a smooth term to extract.
level	character; which level of the factor to extract the smooth for.

**Value**

A single smooth object, or a list of smooths if several match the named term.

---

get_smooth	<i>Extract an mgcv smooth by name</i>
------------	---------------------------------------

---

**Description**

Extract an mgcv smooth by name

**Usage**

```
get_smooth(object, term)
```

**Arguments**

object	a fitted GAM model object.
term	character; the name of a smooth term to extract

**Value**

A single smooth object, or a list of smooths if several match the named term.

---

get_smooths_by_id	<i>Extract an mgcv smooth given its position in the model object</i>
-------------------	--

---

### Description

Extract an mgcv smooth given its position in the model object

### Usage

```
get_smooths_by_id(object, id)

## S3 method for class 'gam'
get_smooths_by_id(object, id)

## S3 method for class 'scam'
get_smooths_by_id(object, id)

## S3 method for class 'gamm'
get_smooths_by_id(object, id)

## S3 method for class 'gamm4'
get_smooths_by_id(object, id)

## S3 method for class 'list'
get_smooths_by_id(object, id)
```

### Arguments

object	a fitted GAM model object.
id	numeric; the position of the smooth in the model object.

---

gss_vocab	<i>Data from the General Social Survey (GSS) from the National Opinion Research Center of the University of Chicago</i>
-----------	---

---

### Description

A subset of the data from the `carData::GSSvocab` dataset from the `carData` package, containing observations from 2016 only.

**Format**

A data frame with 1858 rows and 3 variables:

- vocab: numeric; the number of words out of 10 correct on a vocabulary test.
- nativeBorn: factor; Was the respondent born in the US? A factor with levels no and yes.
- ageGroup: factor; grouped age of the respondent with levels 18-29 30-39, 40-49, 50-59, and 60+.

---

gw\_f0

*Gu and Wahba test functions*


---

**Description**

Gu and Wahba test functions

**Usage**

```
gw_f0(x, ...)
```

```
gw_f1(x, ...)
```

```
gw_f2(x, ...)
```

```
gw_f3(x, ...)
```

**Arguments**

x                      numeric; vector of points to evaluate the function at, on interval (0,1)

...                    arguments passed to other methods, ignored.

**Examples**

```
x <- seq(0, 1, length = 6)
gw_f0(x)
gw_f1(x)
gw_f2(x)
gw_f3(x) # should be constant 0
```

---

has_theta	<i>Are additional parameters available for a GAM?</i>
-----------	---

---

### Description

Are additional parameters available for a GAM?

### Usage

```
has_theta(object)
```

### Arguments

object	an R object, either a <code>family()</code> object or an object whose class has a <code>family()</code> method.
--------	---

### Value

A logical; TRUE if additional parameters available, FALSE otherwise.

### Examples

```
load_mgcv()
df <- data_sim("eg1", dist = "poisson", seed = 42, scale = 1 / 5)
m <- gam(y ~ s(x0) + s(x1) + s(x2) + s(x3),
  data = df, method = "REML",
  family = nb()
)
has_theta(m)
p <- theta(m)
```

---

is_by_smooth	<i>Tests for by variable smooths</i>
--------------	--------------------------------------

---

### Description

Functions to check if a smooth is a by-variable one and to test of the type of by-variable smooth is a factor-smooth or a continuous-smooth interaction.

**Usage**

```
is_by_smooth(smooth)

is_factor_by_smooth(smooth)

is_continuous_by_smooth(smooth)

by_variable(smooth)

by_level(smooth)
```

**Arguments**

smooth                    an object of class "mgcv.smooth"

**Value**

A logical vector.

**Author(s)**

Gavin L. Simpson

---

is_factor_term	<i>Is a model term a factor (categorical)?</i>
----------------	--

---

**Description**

Given the name (a term label) of a term in a model, identify if the term is a factor term or numeric. This is useful when considering interactions, where terms like fac1:fac2 or num1:fac1 may be requested by the user. Only for terms of the type fac1:fac2 will this function return TRUE.

**Usage**

```
is_factor_term(object, term, ...)

## S3 method for class 'terms'
is_factor_term(object, term, ...)

## S3 method for class 'gam'
is_factor_term(object, term, ...)

## S3 method for class 'bam'
is_factor_term(object, term, ...)

## S3 method for class 'gamm'
is_factor_term(object, term, ...)
```

```
## S3 method for class 'list'
is_factor_term(object, term, ...)
```

### Arguments

object	an R object on which method dispatch is performed
term	character; the name of a model term, in the sense of <code>attr(terms(object), "term.labels")</code> . Currently not checked to see if the term exists in the model.
...	arguments passed to other methods.

### Value

A logical: TRUE if and only if all variables involved in the term are factors, otherwise FALSE.

---

is_mgcv_family	<i>Is an object one of mgcv's family objects?</i>
----------------	---

---

### Description

Checks to determine if object is a family object of one of the three or so types that *mgcv* produces.

### Usage

```
is_mgcv_family(object)
```

### Arguments

object	the object to test.
--------	---------------------

### Value

A logical vector of length 1, indicating if object is one of *mgcv*'s (TRUE), or otherwise (FALSE).

---

is_mgcv_smooth	<i>Check if objects are smooths or are a particular type of smooth</i>
----------------	--

---

**Description**

Check if objects are smooths or are a particular type of smooth

**Usage**

```
is_mgcv_smooth(smooth)

stop_if_not_mgcv_smooth(smooth)

check_is_mgcv_smooth(smooth)

is_mrf_smooth(smooth)
```

**Arguments**

smooth                    an R object, typically a list

**Details**

Check if a smooth inherits from class "mgcv.smooth". stop\_if\_not\_mgcv\_smooth() is a wrapper around is\_mgcv\_smooth(), useful when programming for checking if the supplied object is one of mgcv's smooths, and throwing a consistent error if not. check\_is\_mgcv\_smooth() is similar to stop\_if\_not\_mgcv\_smooth() but returns the result of is\_mgcv\_smooth() invisibly.

---

is_multivariate_y	<i>Is a model multivariate?</i>
-------------------	---------------------------------

---

**Description**

Determines whether a fitted model (GAM) is truly multivariate or not.

**Usage**

```
is_multivariate_y(model)
```

**Arguments**

model                    a fitted model object; currently only for "gam" objects

**Value**

A logical vector of length 1, indicating if model is multivariate (TRUE), or otherwise (FALSE).

---

is_offset	<i>Is a model term an offset?</i>
-----------	-----------------------------------

---

**Description**

Given a character vector of model terms, checks to see which, if any, is the model offset.

**Usage**

```
is_offset(terms)
```

**Arguments**

terms	character vector of model terms.
-------	----------------------------------

**Value**

A logical vector of the same length as terms.

**Author(s)**

Gavin L. Simpson

**Examples**

```
load_mgcv()
df <- data_sim("eg1", n = 400, dist = "normal")
m <- gam(y ~ s(x0) + s(x1) + offset(x0), data = df, method = "REML")
nm <- names(model.frame(m))
nm
is_offset(nm)
```

---

link	<i>Extract link and inverse link functions from models</i>
------	--

---

**Description**

Returns the link or its inverse from an estimated model, and provides a simple way to extract these functions from complex models with multiple links, such as location scale models.



**Usage**

```
link(object, ...)

## S3 method for class 'family'
link(object, parameter = NULL, which_eta = NULL, ...)

## S3 method for class 'gam'
link(object, parameter = NULL, which_eta = NULL, ...)

## S3 method for class 'bam'
link(object, parameter = NULL, which_eta = NULL, ...)

## S3 method for class 'gamm'
link(object, ...)

## S3 method for class 'glm'
link(object, ...)

## S3 method for class 'list'
link(object, ...)

inv_link(object, ...)

## S3 method for class 'family'
inv_link(object, parameter = NULL, which_eta = NULL, ...)

## S3 method for class 'gam'
inv_link(object, parameter = NULL, which_eta = NULL, ...)

## S3 method for class 'bam'
inv_link(object, parameter = NULL, which_eta = NULL, ...)

## S3 method for class 'gamm'
inv_link(object, ...)

## S3 method for class 'list'
inv_link(object, ...)

## S3 method for class 'glm'
inv_link(object, ...)

extract_link(family, ...)

## S3 method for class 'family'
extract_link(family, inverse = FALSE, ...)

## S3 method for class 'general.family'
extract_link(family, parameter, inverse = FALSE, which_eta = NULL, ...)
```

**Arguments**

object	a family object or a fitted model from which to extract the family object. Models fitted by <code>stats::glm()</code> , <code>mgcv::gam()</code> , <code>mgcv::bam()</code> , <code>mgcv::gamm()</code> , and <code>gamm4::gamm4()</code> are currently supported.
...	arguments passed to other methods.
parameter	character; which parameter of the distribution. Usually "location" but "scale" and "shape" may be provided for location scale models. Other options include "mu" as a synonym for "location", "sigma" for the scale parameter in <code>mgcv::gaulss()</code> , "pi" for the zero-inflation term in <code>mgcv::ziplss()</code> , "power" for the <code>mgcv::twlss()</code> power parameter, "xi", the shape parameter for <code>mgcv::gevlss()</code> , "epsilon" or "skewness" for the skewness and "delta" or "kurtosis" for the kurtosis parameter for <code>mgcv::shash()</code> , or "phi" for the scale parameter of <code>mgcv::gammals()</code> & <code>mgcv::twlss()</code> .
which_eta	numeric; the linear predictor to extract for families <code>mgcv::mvn()</code> and <code>mgcv::multinom()</code> .
family	a family object, the result of a call to <code>family()</code> .
inverse	logical; return the inverse of the link function?

**Author(s)**

Gavin L. Simpson

**Examples**

```
load_mgcv()

link(gaussian())
link(nb())

inv_link(nb())

dat <- data_sim("eg1", seed = 4234)
mod <- gam(list(y ~ s(x0) + s(x1) + s(x2) + s(x3), ~1),
  data = dat,
  family = gaulss
)

link(mod, parameter = "scale")
inv_link(mod, parameter = "scale")

## Works with `family` objects too
link(shash(), parameter = "skewness")
```

---

load_mgcv	<i>Load mgcv quietly</i>
-----------	--------------------------

---

### Description

Simple function that loads the *mgcv* package whilst suppressing the startup messages that it prints to the console.

### Usage

```
load_mgcv()
```

### Value

Returns a logical vectors invisibly, indicating whether the package was loaded or not.

---

lp_matrix	<i>Return the linear prediction matrix of a fitted GAM</i>
-----------	--

---

### Description

lp\_matrix() is a wrapper to predict(..., type = "lpmatrix") for returning the linear predictor matrix for the model training data (when data = NULL), or user-specified data values supplied via data.

### Usage

```
lp_matrix(model, ...)

## S3 method for class 'gam'
lp_matrix(model, data = NULL, ...)
```

### Arguments

model	a fitted model
...	arguments passed to other methods and predict methods including <code>mgcv::predict.gam()</code> and <code>mgcv::predict.bam()</code>
data	a data frame of values at which to return the linear prediction matrix.

### Details

The linear prediction matrix  $\mathbf{X}_p$  is a matrix that maps values of parameters  $\hat{\beta}_p$  to values on the linear predictor of the model  $\hat{\eta}_p = \mathbf{X}_p \hat{\beta}_p$ .  $\mathbf{X}_p$  is the model matrix where spline covariates have been replaced by the values of the basis functions evaluated at the respective covariates. Parametric covariates are also included.

**Value**

The linear prediction matrix is returned as a matrix. The object returned is of class "lp\_matrix", which inherits from classes "matrix" and "array". The special class allows the printing of the matrix to be controlled, which we do by printing the matrix as a tibble.

**Examples**

```
load_mgcv()

df <- data_sim("eg1", seed = 1)
m <- gam(y ~ s(x0) + s(x1) + s(x2) + s(x3), data = df)

# linear prediction matrix for observed data
xp <- lp_matrix(m)
## IGNORE_RDIFF_BEGIN
xp
## IGNORE_RDIFF_END

# the object `xp` *is* a matrix
class(xp)
# but we print like a tibble to avoid spamming the R console

# linear predictor matrix for new data set
ds <- data_slice(m, x2 = evenly(x2))
xp <- lp_matrix(m, data = ds)
## IGNORE_RDIFF_BEGIN
xp
## IGNORE_RDIFF_END
```

mh\_draws

---

*Posterior samples using a Gaussian approximation to the posterior distribution*

---

**Description**

Posterior samples using a Gaussian approximation to the posterior distribution

**Usage**

```
mh_draws(model, ...)

## S3 method for class 'gam'
mh_draws(
  model,
  n,
  burnin = 1000,
  thin = 1,
  t_df = 40,
```

```

    rw_scale = 0.25,
    index = NULL,
    ...
  )

```

### Arguments

<code>model</code>	a fitted R model. Currently only models fitted by <code>mgcv::gam()</code> or <code>mgcv::bam()</code> , or return an object that <i>inherits</i> from such objects are supported. Here, "inherits" is used in a loose fashion; models fitted by <code>scam::scam()</code> are support even though those models don't strictly inherit from class "gam" as far as <code>inherits()</code> is concerned.
<code>...</code>	arguments passed to methods.
<code>n</code>	numeric; the number of posterior draws to take.
<code>burnin</code>	numeric; the length of any initial burn in period to discard. See <code>mgcv::gam.mh()</code> .
<code>thin</code>	numeric; retain only thin samples. See <code>mgcv::gam.mh()</code> .
<code>t_df</code>	numeric; degrees of freedom for static multivariate <i>t</i> proposal. See <code>mgcv::gam.mh()</code> .
<code>rw_scale</code>	numeric; factor by which to scale posterior covariance matrix when generating random walk proposals. See <code>mgcv::gam.mh()</code> .
<code>index</code>	numeric; vector of indices of coefficients to use. Can be used to subset the mean vector and covariance matrix extracted from <code>model</code> .

---

<code>model_concurvity</code>	<i>Concurvity of an estimated GAM</i>
-------------------------------	---------------------------------------

---

### Description

Concurvity of an estimated GAM

### Usage

```

model_concurvity(model, ...)

## S3 method for class 'gam'
model_concurvity(
  model,
  terms = everything(),
  type = c("all", "estimate", "observed", "worst"),
  pairwise = FALSE,
  ...
)

concrvity(
  model,
  terms = everything(),

```

```

  type = c("all", "estimate", "observed", "worst"),
  pairwise = FALSE,
  ...
)

```

### Arguments

model	a fitted GAM. Currently only objects of class "gam" are supported
...	arguments passed to other methods.
terms	currently ignored
type	character;
pairwise	logical; extract pairwise concurvity of model terms?

### Examples

```

## simulate data with concurvity...
library("tibble")
load_mgcv()
set.seed(8)
n <- 200
df <- tibble(
  t = sort(runif(n)),
  x = gw_f2(t) + rnorm(n) * 3,
  y = sin(4 * pi * t) + exp(x / 20) + rnorm(n) * 0.3
)

## fit model
m <- gam(y ~ s(t, k = 15) + s(x, k = 15), data = df, method = "REML")

## overall concurvity
o_conc <- concurvity(m)
draw(o_conc)

## pairwise concurvity
p_conc <- concurvity(m, pairwise = TRUE)
draw(p_conc)

```

---

model_constant	<i>Extract the model constant term</i>
----------------	--

---

### Description

**[Experimental]** Extracts the model constant term(s), the model intercept, from a fitted model object.

**Usage**

```

model_constant(model, ...)

## S3 method for class 'gam'
model_constant(model, lp = NULL, ...)

## S3 method for class 'gamlss'
model_constant(model, ...)

## S3 method for class 'glm'
model_constant(model, ...)

```

**Arguments**

model	a fitted model for which a <code>coef()</code> method exists.
...	arguments passed to other methods.
lp	numeric; which linear predictors to extract constant terms for.

**Examples**

```

load_mgcv()

# simulate a small example
df <- data_sim("eg1", seed = 42)

# fit the GAM
m <- gam(y ~ s(x0) + s(x1) + s(x2) + s(x3), data = df, method = "REML")

# extract the estimate of the constant term
model_constant(m)
# same as coef(m)[1L]
coef(m)[1L]

```

---

model\_terms

*Find the names of model terms*


---

**Description**

Returns the names of any terms in a model, without needing to call `summary()`. The list of model terms is especially useful when predicting from a `mgcv::gam()` model using the `exclude` or `terms` argument of `mgcv::predict.gam()` or `mgcv::predict.bam()`.

**Usage**

```

model_terms(object, ...)

## S3 method for class 'gam'
model_terms(object, ...)

## S3 method for class 'gamm'
model_terms(object, ...)

## S3 method for class 'gamm4'
model_terms(object, ...)

## S3 method for class 'lm'
model_terms(object, ...)

```

**Arguments**

<code>object</code>	a fitted model.
<code>...</code>	arguments to be passed to other methods; not currently used.

**Details**

From the point of view of *gratia*, models contain two types of term:

1. parametric terms, and
2. smooth terms.

If we consider the formula  $y \sim \text{fac} + s(x_2, \text{by} = \text{fac}) + s(x_0)$ , for a factor `fac` with three levels, there are seven terms in the model:

1. the model constant term, with name "(Intercept)",
2. the parametric factor term, with names
  - `fac2`,
  - `fac3`,
3. the univariate smooth of `x0`, named "`s(x0)`", and
4. the three factor-by smooths with names
  - "`s(x2):fac1`",
  - "`s(x2):fac2`", and
  - "`s(x2):fac3`".

`model_terms()` will return a vector of those names.

**Value**

A character vector of model terms.



**Examples**

```
load_mgcv()

# simulate data
df <- data_sim("eg4", n = 400, dist = "normal", scale = 2, seed = 1)

# fit model
m <- gam(y ~ fac + s(x2, by = fac) + s(x0),
  data = df, method = "REML")

# return the names of terms in this model
model_terms(m)
```

---

model_vars	<i>List the variables involved in a model fitted with a formula</i>
------------	---

---

**Description**

List the variables involved in a model fitted with a formula

**Usage**

```
model_vars(model, ...)

## S3 method for class 'gam'
model_vars(model, ...)

## Default S3 method:
model_vars(model, ...)

## S3 method for class 'bam'
model_vars(model, ...)

## S3 method for class 'gamm'
model_vars(model, ...)

## S3 method for class 'gamm4'
model_vars(model, ...)

## S3 method for class 'list'
model_vars(model, ...)
```

**Arguments**

model	a fitted model object with a \$pred.formula, \$terms component or a "terms" attribute
...	Arguments passed to other methods. Currently ignored.

**Examples**

```
load_mgcv()

# simulate some Gaussian data
df <- data_sim("eg1", n = 50, seed = 2)

# fit a GAM with 1 smooth and 1 linear term
m1 <- gam(y ~ s(x2, k = 7) + x1, data = df, method = "REML")
model_vars(m1)

# fit a lm with two linear terms
m2 <- lm(y ~ x2 + x1, data = df)
model_vars(m2)
```

---

nb_theta	<i>Negative binomial parameter theta</i>
----------	--

---

**Description**

Negative binomial parameter theta

**Usage**

```
nb_theta(model)

## S3 method for class 'gam'
nb_theta(model)
```

**Arguments**

model                      a fitted model.

**Value**

A numeric vector of length 1 containing the estimated value of theta.

**Methods (by class)**

- nb\_theta(gam): Method for class "gam"

**Examples**

```
load_mgcv()
df <- data_sim("eg1", n = 500, dist = "poisson", scale = 0.1, seed = 6)

m <- gam(y ~ s(x0, bs = "cr") + s(x1, bs = "cr") + s(x2, bs = "cr") +
  s(x3, bs = "cr"), family = nb, data = df, method = "REML")
## IGNORE_RDIFF_BEGIN
nb_theta(m)
## IGNORE_RDIFF_END
```

---

null_deviance	<i>Extract the null deviance of a fitted model</i>
---------------	--

---

**Description**

Extract the null deviance of a fitted model

**Usage**

```
null_deviance(model, ...)
```

```
## Default S3 method:  
null_deviance(model, ...)
```

**Arguments**

model	a fitted model
...	arguments passed to other methods

---

n_eta	<i>The Number of linear predictors in model</i>
-------	---

---

**Description**

**[Experimental]** Extracts the number of linear predictors from the fitted model.

**Usage**

```
n_eta(model, ...)
```

```
## S3 method for class 'gam'  
n_eta(model, ...)
```

**Arguments**

model	a fitted model. Currently, only models inheriting from class "gam" are supported.
...	arguments passed to methods.

**Value**

An integer vector of length 1 containing the number of linear predictors in the model.

---

n_smooths	<i>How many smooths in a fitted model</i>
-----------	---

---

**Description**

How many smooths in a fitted model

**Usage**

```
n_smooths(object)

## Default S3 method:
n_smooths(object)

## S3 method for class 'gam'
n_smooths(object)

## S3 method for class 'gamm'
n_smooths(object)

## S3 method for class 'bam'
n_smooths(object)
```

**Arguments**

object            a fitted GAM or related model. Typically the result of a call to `mgcv::gam()`, `mgcv::bam()`, or `mgcv::gamm()`.

---

observed_fitted_plot	<i>Plot of fitted against observed response values</i>
----------------------	--

---

**Description**

Plot of fitted against observed response values

**Usage**

```
observed_fitted_plot(
  model,
  ylab = NULL,
  xlab = NULL,
  title = NULL,
  subtitle = NULL,
  caption = NULL,
  point_col = "grey20",
  point_alpha = 1
)
```

**Arguments**

model	a fitted model. Currently only class "gam".
ylab	character or expression; the label for the y axis. If not supplied, a suitable label will be generated.
xlab	character or expression; the label for the x axis. If not supplied, a suitable label will be generated.
title	character or expression; the title for the plot. See <a href="#">ggplot2::labs()</a> .
subtitle	character or expression; the subtitle for the plot. See <a href="#">ggplot2::labs()</a> .
caption	character or expression; the plot caption. See <a href="#">ggplot2::labs()</a> .
point_col	colour used to draw points in the plots. See <a href="#">graphics::par()</a> section <b>Color Specification</b> . This is passed to the individual plotting functions, and therefore affects the points of all plots.
point_alpha	numeric; alpha transparency for points in plots.

overview

*Provides an overview of a model and the terms in that model***Description**

Provides an overview of a model and the terms in that model

**Usage**

```
overview(model, ...)

## S3 method for class 'gam'
overview(
  model,
  parametric = TRUE,
  random_effects = TRUE,
  dispersion = NULL,
  frequentist = FALSE,
  accuracy = 0.001,
  digits = 3,
  stars = FALSE,
  ...
)
```

**Arguments**

model	a fitted model object to overview.
...	arguments passed to other methods.
parametric	logical; include the model parametric terms in the overview?

random_effects	tests of fully penalized smooth terms (those with a zero-dimensional null space, e.g. random effects) are computationally expensive and for large data sets producing these p values can take a very long time. If random_effects = FALSE, the tests of the expensive terms will be skipped.
dispersion	numeric; a known value for the dispersion parameter. The default NULL implies that the estimated value or the default value (1 for the Poisson distribution for example) where this is specified is used instead.
frequentist	logical; by default the Bayesian estimated covariance matrix of the parameter estimates is used to calculate p values for parametric terms. If frequentist = FALSE, the frequentist covariance matrix of the parameter estimates is used.
accuracy	numeric; accuracy with which to report p values, with p values below this value displayed as "< accuracy".
digits	numeric; the number of significant digits to be used.
stars	logical; should significance stars be added to the output?

### Examples

```
load_mgcv()

df <- data_sim(n = 400, seed = 2)
m <- gam(y ~ x3 + s(x0) + s(x1, bs = "bs") + s(x2, bs = "ts"),
  data = df, method = "REML"
)
overview(m)
```

---

parametric_effects	<i>Estimated values for parametric model terms</i>
--------------------	--

---

### Description

Estimated values for parametric model terms

### Usage

```
parametric_effects(object, ...)

## S3 method for class 'gam'
parametric_effects(
  object,
  terms = NULL,
  data = NULL,
  unconditional = FALSE,
  unnest = TRUE,
  ci_level = 0.95,
  envir = environment(formula(object)),
```

```

    transform = FALSE,
    ...
)

```

### Arguments

object	a fitted model object.
...	arguments passed to other methods.
terms	character; which model parametric terms should be drawn? The Default of NULL will plot all parametric terms that can be drawn.
data	a optional data frame that may or may not be used? FIXME!
unconditional	logical; should confidence intervals include the uncertainty due to smoothness selection? If TRUE, the corrected Bayesian covariance matrix will be used.
unnest	logical; unnest the parametric effect objects?
ci_level	numeric; the coverage required for the confidence interval. Currently ignored.
envir	an environment to look up the data within.
transform	logical; if TRUE, the parametric effect will be plotted on its transformed scale which will result in the effect being a straight line. If FALSE, the effect will be plotted against the raw data (i.e. for $\log_{10}(x)$ , or $\text{poly}(z)$ , the x-axis of the plot will be x or z respectively.)

---

parametric_terms	<i>Names of any parametric terms in a GAM</i>
------------------	---

---

### Description

Names of any parametric terms in a GAM

### Usage

```

parametric_terms(model, ...)

## Default S3 method:
parametric_terms(model, ...)

## S3 method for class 'gam'
parametric_terms(model, ...)

```

### Arguments

model	a fitted model.
...	arguments passed to other methods.

---

partial_derivatives	<i>Partial derivatives of estimated multivariate smooths via finite differences</i>
---------------------	---

---

## Description

Partial derivatives of estimated multivariate smooths via finite differences

## Usage

```
partial_derivatives(object, ...)

## Default S3 method:
partial_derivatives(object, ...)

## S3 method for class 'gamm'
partial_derivatives(object, ...)

## S3 method for class 'gam'
partial_derivatives(
  object,
  select = NULL,
  term = deprecated(),
  focal = NULL,
  data = newdata,
  order = 1L,
  type = c("forward", "backward", "central"),
  n = 100,
  eps = 1e-07,
  interval = c("confidence", "simultaneous"),
  n_sim = 10000,
  level = 0.95,
  unconditional = FALSE,
  frequentist = FALSE,
  offset = NULL,
  ncores = 1,
  partial_match = FALSE,
  seed = NULL,
  ...,
  newdata = NULL
)
```

## Arguments

object	an R object to compute derivatives for.
...	arguments passed to other methods.



select	character; vector of one or more smooth terms for which derivatives are required. If missing, derivatives for all smooth terms will be returned. Can be a partial match to a smooth term; see argument partial_match below.
term	<b>[Deprecated]</b> Use select instead.
focal	character; name of the focal variable. The partial derivative of the estimated smooth with respect to this variable will be returned. All other variables involved in the smooth will be held at constant. This can be missing if supplying data, in which case, the focal variable will be identified as the one variable that is not constant.
data	a data frame containing the values of the model covariates at which to evaluate the first derivatives of the smooths. If supplied, all but one variable must be held at a constant value.
order	numeric; the order of derivative.
type	character; the type of finite difference used. One of "forward", "backward", or "central".
n	numeric; the number of points to evaluate the derivative at.
eps	numeric; the finite difference.
interval	character; the type of interval to compute. One of "confidence" for point-wise intervals, or "simultaneous" for simultaneous intervals.
n_sim	integer; the number of simulations used in computing the simultaneous intervals.
level	numeric; $0 < \text{level} < 1$ ; the confidence level of the point-wise or simultaneous interval. The default is 0.95 for a 95% interval.
unconditional	logical; use smoothness selection-corrected Bayesian covariance matrix?
frequentist	logical; use the frequentist covariance matrix?
offset	numeric; a value to use for any offset term
ncores	number of cores for generating random variables from a multivariate normal distribution. Passed to <code>mvnfast::rmvn()</code> . Parallelization will take place only if OpenMP is supported (but appears to work on Windows with current R).
partial_match	logical; should smooths be selected by partial matches with term? If TRUE, term can only be a single string to match against.
seed	numeric; RNG seed to use.
newdata	Deprecated: use data instead.

## Value

A tibble, currently with the following variables:

- `.smooth`: the smooth each row refers to,
- `.partial_deriv`: the estimated partial derivative,
- `.se`: the standard error of the estimated partial derivative,
- `.crit`: the critical value such that  $\text{derivative} \pm (\text{crit} * \text{se})$  gives the upper and lower bounds of the requested confidence or simultaneous interval (given level),
- `.lower_ci`: the lower bound of the confidence or simultaneous interval,
- `.upper_ci`: the upper bound of the confidence or simultaneous interval.

**Note**

partial\_derivatives() will ignore any random effect smooths it encounters in object.

**Author(s)**

Gavin L. Simpson

**Examples**

```
library("ggplot2")
library("patchwork")
load_mgcv()

df <- data_sim("eg2", n = 2000, dist = "normal", scale = 0.5, seed = 42)

# fit the GAM (note: for execution time reasons, k is set artificially low)
m <- gam(y ~ te(x, z, k = c(5, 5)), data = df, method = "REML")

# data slice through te(x,z) holding z == 0.4
ds <- data_slice(m, x = evenly(x, n = 100), z = 0.4)

# evaluate te(x,z) at values of x & z
sm <- smooth_estimates(m, select = "te(x,z)", data = ds) |>
  add_confint()

# partial derivatives
pd_x <- partial_derivatives(m, data = ds, type = "central", focal = "x")

# draw te(x,z)
p1 <- draw(m, rug = FALSE) &
  geom_hline(yintercept = 0.4, linewidth = 1)
p1

# draw te(x,z) along slice
cap <- expression(z == 0.4)
p2 <- sm |>
  ggplot(aes(x = x, y = .estimate)) +
  geom_ribbon(aes(ymin = .lower_ci, ymax = .upper_ci), alpha = 0.2) +
  geom_line() +
  labs(
    x = "x", y = "Partial effect", title = "te(x,z)",
    caption = cap
  )
p2

# draw partial derivs
p3 <- pd_x |>
  draw() +
  labs(caption = cap)
p3

# draw all three panels
```

```
p1 + p2 + p3 + plot_layout(ncol = 3)
```

---

partial_residuals	<i>Partial residuals</i>
-------------------	--------------------------

---

## Description

Partial residuals

## Usage

```
partial_residuals(object, ...)

## S3 method for class 'gam'
partial_residuals(object, select = NULL, partial_match = FALSE, ...)
```

## Arguments

object	an R object, typically a model. Currently only objects of class "gam" (or that inherit from that class) are supported.
...	arguments passed to other methods.
select	character, logical, or numeric; which smooths to plot. If NULL, the default, then all model smooths are drawn. Numeric select indexes the smooths in the order they are specified in the formula and stored in object. Character select matches the labels for smooths as shown for example in the output from <code>summary(object)</code> . Logical select operates as per numeric select in the order that smooths are stored.
partial_match	logical; should smooths be selected by partial matches with select? If TRUE, select can only be a single string to match against.

## Examples

```
## load mgcv
load_mgcv()

## example data - Gu & Wahba four term model
df <- data_sim("eg1", n = 400, seed = 42)
## fit the model
m <- gam(y ~ s(x0) + s(x1) + s(x2) + s(x3), data = df, method = "REML")

## extract partial residuals
partial_residuals(m)

## and for a select term
partial_residuals(m, select = "s(x2)")

## or with partial matching
```

```
partial_residuals(m, select = "x", partial_match = TRUE) # returns all
```

---

penalty

---

*Extract and tidy penalty matrices*


---

## Description

Extract and tidy penalty matrices

## Usage

```
penalty(object, ...)

## Default S3 method:
penalty(
  object,
  rescale = FALSE,
  data,
  knots = NULL,
  constraints = FALSE,
  diagonalize = FALSE,
  ...
)

## S3 method for class 'gam'
penalty(
  object,
  select = NULL,
  smooth = deprecated(),
  rescale = FALSE,
  partial_match = FALSE,
  ...
)

## S3 method for class 'mgcv.smooth'
penalty(object, rescale = FALSE, ...)

## S3 method for class 'tensor.smooth'
penalty(object, margins = FALSE, ...)

## S3 method for class 't2.smooth'
penalty(object, margins = FALSE, ...)

## S3 method for class 're.smooth.spec'
penalty(object, data, ...)
```

**Arguments**

object	a fitted GAM or a smooth.
...	additional arguments passed to methods.
rescale	logical; by default, <i>mgcv</i> will scale the penalty matrix for better performance in <code>mgcv::gam()</code> . If <code>rescale</code> is <code>TRUE</code> , this scaling will be undone to put the penalty matrix back on the original scale.
data	data frame; a data frame of values for terms mentioned in the smooth specification.
knots	a list or data frame with named components containing knots locations. Names must match the covariates for which the basis is required. See <code>mgcv::smoothCon()</code> .
constraints	logical; should identifiability constraints be applied to the smooth basis. See argument <code>absorb.cons</code> in <code>mgcv::smoothCon()</code> .
diagonalize	logical; if <code>TRUE</code> , reparameterises the smooth such that the associated penalty is an identity matrix. This has the effect of turning the last diagonal elements of the penalty to zero, which highlights the penalty null space.
select	character, logical, or numeric; which smooths to extract penalties for. If <code>NULL</code> , the default, then penalties for all model smooths are drawn. Numeric <code>select</code> indexes the smooths in the order they are specified in the formula and stored in object. Character <code>select</code> matches the labels for smooths as shown for example in the output from <code>summary(object)</code> . Logical <code>select</code> operates as per numeric <code>select</code> in the order that smooths are stored.
smooth	<b>[Deprecated]</b> Use <code>select</code> instead.
partial_match	logical; should smooths be selected by partial matches with <code>select</code> ? If <code>TRUE</code> , <code>select</code> can only be a single string to match against.
margins	logical; extract the penalty matrices for the tensor product or the marginal smooths of the tensor product?

**Value**

A 'tibble' (data frame) of class `penalty_df` inheriting from `tbl_df`, with the following components:

- `.smooth` - character; the label *mgcv* uses to refer to the smooth,
- `.type` - character; the type of smooth,
- `.penalty` - character; the label for the specific penalty. Some smooths have multiple penalty matrices, so the `penalty` component identifies the particular penalty matrix and uses the labelling that *mgcv* uses internally,
- `.row` - character; a label of the form `fn` where `n` is an integer for the `n`th basis function, referencing the columns of the penalty matrix,
- `.col` - character; a label of the form `fn` where `n` is an integer for the `n`th basis function, referencing the columns of the penalty matrix,
- `.value` - double; the value of the penalty matrix for the combination of `row` and `col`,

**Note**

The `print()` method uses `base::zapsmall()` to turn very small numbers into 0s for display purposes only; the underlying values of the penalty matrix or matrices are not changed.

For smooths that are subject to an eigendecomposition (e.g. the default thin plate regression splines, `bs = "tp"`), the signs of the eigenvectors are not defined and as such you can expect differences across systems in the penalties for such smooths that are system-, OS-, and CPU architecture-specific.

**Author(s)**

Gavin L. Simpson

**Examples**

```
load_mgcv()
dat <- data_sim("eg4", n = 400, seed = 42)
m <- gam(
  y ~ s(x0, bs = "cr") + s(x1, bs = "cr") +
    s(x2, by = fac, bs = "cr"),
  data = dat, method = "REML"
)

# penalties for all smooths
penalty(m)

# for a specific smooth
penalty(m, select = "s(x2):fac1")
```

---

posterior\_samples

*Draw samples from the posterior distribution of an estimated model*

---

**Description**

Draw samples from the posterior distribution of an estimated model

**Usage**

```
posterior_samples(model, ...)

## S3 method for class 'gam'
posterior_samples(
  model,
  n = 1,
  data = newdata,
  seed = NULL,
  method = c("gaussian", "mh", "inla", "user"),
```

```

    n_cores = 1,
    burnin = 1000,
    thin = 1,
    t_df = 40,
    rw_scale = 0.25,
    freq = FALSE,
    unconditional = FALSE,
    weights = NULL,
    draws = NULL,
    mvn_method = c("mvnfast", "mgcv"),
    ...,
    newdata = NULL,
    ncores = NULL
)

## S3 method for class 'scam'
posterior_samples(
  model,
  n = 1,
  data = NULL,
  seed = NULL,
  method = c("gaussian", "mh", "inla", "user"),
  n_cores = 1,
  burnin = 1000,
  thin = 1,
  t_df = 40,
  rw_scale = 0.25,
  freq = FALSE,
  unconditional = FALSE,
  weights = NULL,
  draws = NULL,
  mvn_method = c("mvnfast", "mgcv"),
  ...
)

```

## Arguments

<code>model</code>	a fitted model of the supported types
<code>...</code>	arguments passed to other methods. For <code>fitted_samples()</code> , these are passed on to <code>mgcv::predict.gam()</code> . For <code>posterior_samples()</code> these are passed on to <code>fitted_samples()</code> . For <code>predicted_samples()</code> these are passed on to the relevant <code>simulate()</code> method.
<code>n</code>	numeric; the number of posterior samples to return.
<code>data</code>	data frame; new observations at which the posterior draws from the model should be evaluated. If not supplied, the data used to fit the model will be used for data, if available in <code>model</code> .
<code>seed</code>	numeric; a random seed for the simulations.

method	character; which method should be used to draw samples from the posterior distribution. "gaussian" uses a Gaussian (Laplace) approximation to the posterior. "mh" uses a Metropolis Hastings sampler that alternates t proposals with proposals based on a shrunk version of the posterior covariance matrix. "inla" uses a variant of Integrated Nested Laplace Approximation due to Wood (2019), (currently not implemented). "user" allows for user-supplied posterior draws (currently not implemented).
n_cores	number of cores for generating random variables from a multivariate normal distribution. Passed to <code>mvnfast::rmvn()</code> . Parallelization will take place only if OpenMP is supported (but appears to work on Windows with current R).
burnin	numeric; number of samples to discard as the burnin draws. Only used with method = "mh".
thin	numeric; the number of samples to skip when taking n draws. Results in thin * n draws from the posterior being taken. Only used with method = "mh".
t_df	numeric; degrees of freedom for t distribution proposals. Only used with method = "mh".
rw_scale	numeric; Factor by which to scale posterior covariance matrix when generating random walk proposals. Negative or non finite to skip the random walk step. Only used with method = "mh".
freq	logical; TRUE to use the frequentist covariance matrix of the parameter estimators, FALSE to use the Bayesian posterior covariance matrix of the parameters.
unconditional	logical; if TRUE (and freq == FALSE) then the Bayesian smoothing parameter uncertainty corrected covariance matrix is used, if available.
weights	numeric; a vector of prior weights. If data is null then defaults to <code>object[["prior.weights"]]</code> , otherwise a vector of ones.
draws	matrix; user supplied posterior draws to be used when method = "user".
mvn_method	character; one of "mvnfast" or "mgcv". The default is uses <code>mvnfast::rmvn()</code> , which can be considerably faster at generate large numbers of MVN random values than <code>mgcv::rmvn()</code> , but which might not work for some marginal fits, such as those where the covariance matrix is close to singular.
newdata	Deprecated: use data instead.
ncores	Deprecated; use n_cores instead. The number of cores for generating random variables from a multivariate normal distribution. Passed to <code>mvnfast::rmvn()</code> . Parallelization will take place only if OpenMP is supported (but appears to work on Windows with current R).

## Value

A tibble (data frame) with 3 columns containing the posterior predicted values in long format. The columns are

- row (integer) the row of data that each posterior draw relates to,
- draw (integer) an index, in range 1:n, indicating which draw each row relates to,
- response (numeric) the predicted response for the indicated row of data.



**Note**

Models with offset terms supplied via the `offset` argument to `mgcv::gam()` etc. are ignored by `mgcv::predict.gam()`. As such, this kind of offset term is also ignored by `posterior_samples()`. Offset terms that are included in the model formula supplied to `mgcv::gam()` etc are not ignored and the posterior samples produced will reflect those offset term values. This has the side effect of requiring any new data values provided to `posterior_samples()` via the `data` argument must include the offset variable.

**Author(s)**

Gavin L. Simpson

**References**

Wood, S.N., (2020). Simplified integrated nested Laplace approximation. *Biometrika* **107**, 223–230. doi:[10.1093/biomet/asz044](https://doi.org/10.1093/biomet/asz044)

---

post_draws	<i>Low-level Functions to generate draws from the posterior distribution of model coefficients</i>
------------	--

---

**Description**

Low-level Functions to generate draws from the posterior distribution of model coefficients

Generate posterior draws from a fitted model

**Usage**

```
post_draws(model, ...)

## Default S3 method:
post_draws(
  model,
  n,
  method = c("gaussian", "mh", "inla", "user"),
  mu = NULL,
  sigma = NULL,
  n_cores = 1L,
  burnin = 1000,
  thin = 1,
  t_df = 40,
  rw_scale = 0.25,
  index = NULL,
  frequentist = FALSE,
  unconditional = FALSE,
  parametrized = TRUE,
```

```

    mvn_method = c("mvnfast", "mgcv"),
    draws = NULL,
    seed = NULL,
    ...
)

generate_draws(model, ...)

## S3 method for class 'gam'
generate_draws(
  model,
  n,
  method = c("gaussian", "mh", "inla"),
  mu = NULL,
  sigma = NULL,
  n_cores = 1L,
  burnin = 1000,
  thin = 1,
  t_df = 40,
  rw_scale = 0.25,
  index = NULL,
  frequentist = FALSE,
  unconditional = FALSE,
  mvn_method = c("mvnfast", "mgcv"),
  seed = NULL,
  ...
)

```

## Arguments

<code>model</code>	a fitted R model. Currently only models fitted by <code>mgcv::gam()</code> or <code>mgcv::bam()</code> , or return an object that <i>inherits</i> from such objects are supported. Here, "inherits" is used in a loose fashion; models fitted by <code>scam::scam()</code> are support even though those models don't strictly inherit from class "gam" as far as <code>inherits()</code> is concerned.
<code>...</code>	arguments passed to methods.
<code>n</code>	numeric; the number of posterior draws to take.
<code>method</code>	character; which algorithm to use to sample from the posterior. Currently implemented methods are: "gaussian" and "mh". "gaussian" calls <code>gaussian_draws()</code> which uses a Gaussian approximation to the posterior distribution. "mh" uses a simple Metropolis Hastings sampler which alternates static proposals based on a Gaussian approximation to the posterior, with random walk proposals. Note, setting <code>t_df</code> to a low value will result in heavier-tailed statistic proposals. See <code>mgcv::gam.mh()</code> for more details.
<code>mu</code>	numeric; user-supplied mean vector (vector of model coefficients). Currently ignored.
<code>sigma</code>	matrix; user-supplied covariance matrix for mu. Currently ignored.

n_cores	integer; number of CPU cores to use when generating multivariate normal distributed random values. Only used if mvn_method = "mvnfast" <b>and</b> method = "gaussian".
burnin	numeric; the length of any initial burn in period to discard. See mgcv::gam.mh().
thin	numeric; retain only thin samples. See mgcv::gam.mh().
t_df	numeric; degrees of freedom for static multivariate <i>t</i> proposal. See mgcv::gam.mh().
rw_scale	numeric; factor by which to scale posterior covariance matrix when generating random walk proposals. See mgcv::gam.mh().
index	numeric; vector of indices of coefficients to use. Can be used to subset the mean vector and covariance matrix extracted from model.
frequentist	logical; if TRUE, the frequentist covariance matrix of the parameter estimates is used. If FALSE, the Bayesian posterior covariance matrix of the parameters is used. See mgcv::vcov.gam().
unconditional	logical; if TRUE the Bayesian smoothing parameter uncertainty corrected covariance matrix is used, <i>if available</i> for model. See mgcv::vcov.gam().
parametrized	logical; use parametrized coefficients and covariance matrix, which respect the linear inequality constraints of the model. Only for scam::scam() model fits.
mvn_method	character; one of "mvnfast" or "mgcv". The default is uses mvnfast::rmvn(), which can be considerably faster at generate large numbers of MVN random values than mgcv::rmvn(), but which might not work for some marginal fits, such as those where the covariance matrix is close to singular.
draws	matrix; user supplied posterior draws to be used when method = "user".
seed	numeric; the random seed to use. If NULL, a random seed will be generated without affecting the current state of R's RNG.

---

predicted_samples	<i>Draw new response values from the conditional distribution of the response</i>
-------------------	---

---

## Description

Predicted values of the response (new response data) are drawn from the fitted model, created via simulate() (e.g. `simulate.gam()`) and returned in a tidy, long, format. These predicted values do not include the uncertainty in the estimated model; they are simply draws from the conditional distribution of the response.

## Usage

```
predicted_samples(model, ...)

## Default S3 method:
predicted_samples(model, ...)
```

```
## S3 method for class 'gam'
predicted_samples(
  model,
  n = 1,
  data = newdata,
  seed = NULL,
  weights = NULL,
  ...,
  newdata = NULL
)

## S3 method for class 'scam'
predicted_samples(model, n = 1, data = NULL, seed = NULL, weights = NULL, ...)
```

### Arguments

<code>model</code>	a fitted model of the supported types
<code>...</code>	arguments passed to other methods. For <code>fitted_samples()</code> , these are passed on to <code>mgcv::predict.gam()</code> . For <code>posterior_samples()</code> these are passed on to <code>fitted_samples()</code> . For <code>predicted_samples()</code> these are passed on to the relevant <code>simulate()</code> method.
<code>n</code>	numeric; the number of posterior samples to return.
<code>data</code>	data frame; new observations at which the posterior draws from the model should be evaluated. If not supplied, the data used to fit the model will be used for data, if available in model.
<code>seed</code>	numeric; a random seed for the simulations.
<code>weights</code>	numeric; a vector of prior weights. If data is null then defaults to <code>object[["prior.weights"]]</code> , otherwise a vector of ones.
<code>newdata</code>	Deprecated: use data instead.

### Value

A tibble (data frame) with 3 columns containing the posterior predicted values in long format. The columns are

- `row` (integer) the row of data that each posterior draw relates to,
- `draw` (integer) an index, in range `1:n`, indicating which draw each row relates to,
- `response` (numeric) the predicted response for the indicated row of data.

### Author(s)

Gavin L. Simpson

### Examples

```
load_mgcv()
```

```

dat <- data_sim("eg1", n = 1000, dist = "normal", scale = 2, seed = 2)
m <- gam(y ~ s(x0) + s(x1) + s(x2) + s(x3), data = dat, method = "REML")

predicted_samples(m, n = 5, seed = 42)

## Can pass arguments to predict.gam()

newd <- data.frame(
  x0 = runif(10), x1 = runif(10), x2 = runif(10),
  x3 = runif(10)
)

## Exclude s(x2)
predicted_samples(m, n = 5, newd, exclude = "s(x2)", seed = 25)

## Exclude s(x1)
predicted_samples(m, n = 5, newd, exclude = "s(x1)", seed = 25)

## Select which terms --- result should be the same as previous
## but note that we have to include any parametric terms, including the
## constant term
predicted_samples(m,
  n = 5, newd, seed = 25,
  terms = c("Intercept", "s(x0)", "s(x2)", "s(x3)")
)

```

---

qq\_plot

*Quantile-quantile plot of model residuals*


---

## Description

Quantile-quantile plots (QQ-plots) for GAMs using the reference quantiles of Augustin *et al* (2012).

## Usage

```

qq_plot(model, ...)

## Default S3 method:
qq_plot(model, ...)

## S3 method for class 'gam'
qq_plot(
  model,
  method = c("uniform", "simulate", "normal", "direct"),
  type = c("deviance", "response", "pearson"),
  n_uniform = 10,
  n_simulate = 50,
  seed = NULL,

```

```

    level = 0.9,
    ylab = NULL,
    xlab = NULL,
    title = NULL,
    subtitle = NULL,
    caption = NULL,
    ci_col = "black",
    ci_alpha = 0.2,
    point_col = "grey20",
    point_alpha = 1,
    line_col = "red",
    ...
)

## S3 method for class 'glm'
qq_plot(model, ...)

## S3 method for class 'lm'
qq_plot(model, ...)

```

### Arguments

model	a fitted model. Currently models inheriting from class "gam", as well as classes "glm" and "lm" from calls to <a href="#">stats::glm</a> or <a href="#">stats::lm</a> are supported.
...	arguments passed to other methods.
method	character; method used to generate theoretical quantiles. The default is "uniform", which generates reference quantiles using random draws from a uniform distribution and the inverse cumulative distribution function (CDF) of the fitted values. The reference quantiles are averaged over n_uniform draws. "simulate" generates reference quantiles by simulating new response data from the model at the observed values of the covariates, which are then residualised to generate reference quantiles, using n_simulate simulated data sets. "normal" generates reference quantiles using the standard normal distribution. "uniform" is more computationally efficient, but "simulate" allows reference bands to be drawn on the QQ-plot. "normal" should be avoided but is used as a fall back if a random number generator ("simulate") or the inverse of the CDF are not available from the family used during model fitting ("uniform"). Note that method = "direct" is deprecated in favour of method = "uniform".
type	character; type of residuals to use. Only "deviance", "response", and "pearson" residuals are allowed.
n_uniform	numeric; number of times to randomize uniform quantiles in the direct computation method (method = "uniform").
n_simulate	numeric; number of data sets to simulate from the estimated model when using the simulation method (method = "simulate").
seed	numeric; the random number seed to use for method = "simulate" and method = "uniform".

level	numeric; the coverage level for reference intervals. Must be strictly $0 < \text{level} < 1$ . Only used with <code>method = "simulate"</code> .
ylab	character or expression; the label for the y axis. If not supplied, a suitable label will be generated.
xlab	character or expression; the label for the x axis. If not supplied, a suitable label will be generated.
title	character or expression; the title for the plot. See <code>ggplot2::labs()</code> . May be a vector, one per penalty.
subtitle	character or expression; the subtitle for the plot. See <code>ggplot2::labs()</code> . May be a vector, one per penalty.
caption	character or expression; the plot caption. See <code>ggplot2::labs()</code> . May be a vector, one per penalty.
ci_col	fill colour for the reference interval when <code>method = "simulate"</code> .
ci_alpha	alpha transparency for the reference interval when <code>method = "simulate"</code> .
point_col	colour of points on the QQ plot.
point_alpha	alpha transparency of points on the QQ plot.
line_col	colour used to draw the reference line.

### Note

The wording used in `mgcv::qq.gam()` uses *direct* in reference to the simulated residuals method (`method = "simulated"`). To avoid confusion, `method = "direct"` is deprecated in favour of `method = "uniform"`.

### References

The underlying methodology used when `method` is `"simulate"` or `"uniform"` is described in Augustin *et al* (2012):

Augustin, N.H., Sauleau, E.-A., Wood, S.N., (2012) On quantile quantile plots for generalized linear models. *Computational Statistics and Data Analysis* **56**, 2404-2409 doi:[10.1016/j.csda.2012.01.026](https://doi.org/10.1016/j.csda.2012.01.026).

### See Also

[mgcv::qq.gam](#) for more details on the methods used.

### Examples

```
load_mgcv()
## simulate binomial data...
dat <- data_sim("eg1", n = 200, dist = "binary", scale = .33, seed = 0)
p <- binomial()$linkinv(dat$f) # binomial p
n <- sample(c(1, 3), 200, replace = TRUE) # binomial n
dat <- transform(dat, y = rbinom(n, n, p), n = n)
m <- gam(y / n ~ s(x0) + s(x1) + s(x2) + s(x3),
  family = binomial, data = dat, weights = n,
  method = "REML"
)
```

```
## Q-Q plot; default using direct randomization of uniform quantiles
qq_plot(m)

## Alternatively use simulate new data from the model, which
## allows construction of reference intervals for the Q-Q plot
qq_plot(m,
  method = "simulate",
  seed = 42,
  point_col = "steelblue",
  point_alpha = 0.4
)

## ... or use the usual normality assumption
qq_plot(m, method = "normal")
```

---

quantile_residuals	<i>Randomised residuals</i>
--------------------	-----------------------------

---

## Description

Randomised residuals

## Usage

```
quantile_residuals(model, type = c("pit", "quantile"), seed = NULL, ...)

## S3 method for class 'gam'
quantile_residuals(model, type = c("pit", "quantile"), seed = NULL, ...)

## S3 method for class 'glm'
quantile_residuals(model, type = c("pit", "quantile"), seed = NULL, ...)
```

## Arguments

model	a fitted model object.
type	character; which type of randomised residual to return
seed	integer; the random seed to use when generating randomised residuals. Can be missing, in which case the current state residuals are computed using the current state of the random number generator.
...	arguments passed to other methods.



---

ref_level	<i>Return the reference or specific level of a factor</i>
-----------	---

---

**Description**

Extracts the reference or a specific level the supplied factor, returning it as a factor with the same levels as the one supplied.

**Usage**

```
ref_level(fct)

level(fct, level)
```

**Arguments**

fct	factor; the factor from which the reference or specific level will be extracted.
level	character; the specific level to extract in the case of <code>level()</code> .

**Value**

A length 1 factor with the same levels as the supplied factor `fct`.

**Examples**

```
f <- factor(sample(letters[1:5], 100, replace = TRUE))

# the reference level
ref_level(f)

# a specific level
level(f, level = "b")

# note that the levels will always match the input factor
identical(levels(f), levels(ref_level(f)))
identical(levels(f), levels(level(f, "c")))
```

---

ref_sims	<i>Reference simulation data</i>
----------	----------------------------------

---

**Description**

A set of reference objects for testing `data_sim()`.

**Format**

A named list of simulated data sets created by `data_sim()`.

---

```
rep_first_factor_value
```

*Repeat the first level of a factor n times*

---

### Description

Function to repeat the first level of a factor n times and return this vector as a factor with the original levels intact

### Usage

```
rep_first_factor_value(f, n)
```

### Arguments

f	a factor
n	numeric; the number of times to repeat the first level of f

### Value

A factor of length n with the levels of f, but whose elements are all the first level of f.

---

```
residuals_hist_plot
```

*Histogram of model residuals*

---

### Description

Histogram of model residuals

### Usage

```
residuals_hist_plot(
  model,
  type = c("deviance", "pearson", "response", "pit", "quantile"),
  n_bins = c("sturges", "scott", "fd"),
  ylab = NULL,
  xlab = NULL,
  title = NULL,
  subtitle = NULL,
  caption = NULL,
  seed = NULL
)
```

**Arguments**

model	a fitted model. Currently only class "gam".
type	character; type of residuals to use. One of "deviance", "response", "pearson", "pit", and "quantile" residuals are allowed. "pit" uses probability integral transform (PIT) residuals, which, if the model is correct should be approximately uniformly distributed, while "quantile" transforms the PIT residuals through application of the inverse CDF of the standard normal, and therefore the quantile residuals should be approximately normally distributed (mean = 0, sd = 1) if the model is correct. PIT and quantile residuals are not yet available for most families that can be handled by gam(), but most standard families are supported, e.g. those used by glm().
n_bins	character or numeric; either the number of bins or a string indicating how to calculate the number of bins.
ylab	character or expression; the label for the y axis. If not supplied, a suitable label will be generated.
xlab	character or expression; the label for the x axis. If not supplied, a suitable label will be generated.
title	character or expression; the title for the plot. See <a href="#">ggplot2::labs()</a> .
subtitle	character or expression; the subtitle for the plot. See <a href="#">ggplot2::labs()</a> .
caption	character or expression; the plot caption. See <a href="#">ggplot2::labs()</a> .
seed	integer; random seed to use for PIT or quantile residuals.

---

residuals\_linpred\_plot

*Plot of residuals versus linear predictor values*


---

**Description**

Plot of residuals versus linear predictor values

**Usage**

```
residuals_linpred_plot(
  model,
  type = c("deviance", "pearson", "response", "pit", "quantile"),
  ylab = NULL,
  xlab = NULL,
  title = NULL,
  subtitle = NULL,
  caption = NULL,
  point_col = "grey20",
  point_alpha = 1,
  line_col = "red",
  seed = NULL
)
```

**Arguments**

model	a fitted model. Currently only class "gam".
type	character; type of residuals to use. One of "deviance", "response", "pearson", "pit", and "quantile" residuals are allowed. "pit" uses probability integral transform (PIT) residuals, which, if the model is correct should be approximately uniformly distributed, while "quantile" transforms the PIT residuals through application of the inverse CDF of the standard normal, and therefore the quantile residuals should be approximately normally distributed (mean = 0, sd = 1) if the model is correct. PIT and quantile residuals are not yet available for most families that can be handled by gam(), but most standard families are supported, e.g. those used by glm().
ylab	character or expression; the label for the y axis. If not supplied, a suitable label will be generated.
xlab	character or expression; the label for the y axis. If not supplied, a suitable label will be generated.
title	character or expression; the title for the plot. See <a href="#">ggplot2::labs()</a> .
subtitle	character or expression; the subtitle for the plot. See <a href="#">ggplot2::labs()</a> .
caption	character or expression; the plot caption. See <a href="#">ggplot2::labs()</a> .
point_col	colour used to draw points in the plots. See <a href="#">graphics::par()</a> section <b>Color Specification</b> . This is passed to the individual plotting functions, and therefore affects the points of all plots.
point_alpha	numeric; alpha transparency for points in plots.
line_col	colour specification for 1:1 line.
seed	integer; random seed to use for PIT or quantile residuals.

---

response\_derivatives    *Derivatives on the response scale from an estimated GAM*

---

**Description**

Derivatives on the response scale from an estimated GAM

**Usage**

```
response_derivatives(object, ...)

## Default S3 method:
response_derivatives(object, ...)

## S3 method for class 'gamm'
response_derivatives(object, ...)

## S3 method for class 'gam'
```

```

response_derivatives(
  object,
  focal = NULL,
  data = NULL,
  order = 1L,
  type = c("forward", "backward", "central"),
  scale = c("response", "linear_predictor"),
  method = c("gaussian", "mh", "inla", "user"),
  n = 100,
  eps = 1e-07,
  n_sim = 10000,
  level = 0.95,
  seed = NULL,
  mvn_method = c("mvnfast", "mgcv"),
  ...
)

## S3 method for class 'scam'
response_derivatives(
  object,
  focal = NULL,
  data = NULL,
  order = 1L,
  type = c("forward", "backward", "central"),
  scale = c("response", "linear_predictor"),
  method = c("gaussian", "mh", "inla", "user"),
  n = 100,
  eps = 1e-07,
  n_sim = 10000,
  level = 0.95,
  seed = NULL,
  mvn_method = c("mvnfast", "mgcv"),
  ...
)

```

## Arguments

<code>object</code>	an R object to compute derivatives for.
<code>...</code>	arguments passed to other methods and on to <code>fitted_samples()</code>
<code>focal</code>	character; name of the focal variable. The response derivative of the response with respect to this variable will be returned. All other variables involved in the model will be held at constant values. This can be missing if supplying data, in which case, the focal variable will be identified as the one variable that is not constant.
<code>data</code>	a data frame containing the values of the model covariates at which to evaluate the first derivatives of the smooths. If supplied, all but one variable must be held at a constant value.
<code>order</code>	numeric; the order of derivative.

type	character; the type of finite difference used. One of "forward", "backward", or "central".
scale	character; should the derivative be estimated on the response or the linear predictor (link) scale? One of "response" (the default), or "linear predictor".
method	character; which method should be used to draw samples from the posterior distribution. "gaussian" uses a Gaussian (Laplace) approximation to the posterior. "mh" uses a Metropolis Hastings sample that alternates t proposals with proposals based on a shrunk version of the posterior covariance matrix. "inla" uses a variant of Integrated Nested Laplace Approximation due to Wood (2019), (currently not implemented). "user" allows for user-supplied posterior draws (currently not implemented).
n	numeric; the number of points to evaluate the derivative at (if data is not supplied).
eps	numeric; the finite difference.
n_sim	integer; the number of simulations used in computing the simultaneous intervals.
level	numeric; $0 < \text{level} < 1$ ; the coverage level of the credible interval. The default is 0.95 for a 95% interval.
seed	numeric; a random seed for the simulations.
mvn_method	character; one of "mvnfast" or "mgcv". The default is uses <code>mvnfast::rmvn()</code> , which can be considerably faster at generate large numbers of MVN random values than <code>mgcv::rmvn()</code> , but which might not work for some marginal fits, such as those where the covariance matrix is close to singular.

## Value

A tibble, currently with the following variables:

- `.row`: integer, indexing the row of data each row in the output represents
- `.focal`: the name of the variable for which the partial derivative was evaluated,
- `.derivative`: the estimated partial derivative,
- `.lower_ci`: the lower bound of the confidence or interval,
- `.upper_ci`: the upper bound of the confidence or interval,
- additional columns containing the covariate values at which the derivative was evaluated.

## Author(s)

Gavin L. Simpson

## Examples

```
library("ggplot2")
library("patchwork")
load_mgcv()

df <- data_sim("eg1", dist = "negbin", scale = 0.25, seed = 42)
```

```

# fit the GAM (note: for execution time reasons using bam())
m <- bam(y ~ s(x0) + s(x1) + s(x2) + s(x3),
  data = df, family = nb(), method = "fREML"
)

# data slice through data along x2 - all other covariates will be set to
# typical values (value closest to median)
ds <- data_slice(m, x2 = evenly(x2, n = 100))

# fitted values along x2
fv <- fitted_values(m, data = ds)

# response derivatives - ideally n_sim = >10000
y_d <- response_derivatives(m,
  data = ds, type = "central", focal = "x2",
  eps = 0.01, seed = 21, n_sim = 1000
)

# draw fitted values along x2
p1 <- fv |>
  ggplot(aes(x = x2, y = .fitted)) +
  geom_ribbon(aes(ymin = .lower_ci, ymax = .upper_ci, y = NULL),
    alpha = 0.2
  ) +
  geom_line() +
  labs(
    title = "Estimated count as a function of x2",
    y = "Estimated count"
  )

# draw response derivatives
p2 <- y_d |>
  ggplot(aes(x = x2, y = .derivative)) +
  geom_ribbon(aes(ymin = .lower_ci, ymax = .upper_ci), alpha = 0.2) +
  geom_line() +
  labs(
    title = "Estimated 1st derivative of estimated count",
    y = "First derivative"
  )

# draw both panels
p1 + p2 + plot_layout(nrow = 2)

```

## Description

A rootogram is a model diagnostic tool that assesses the goodness of fit of a statistical model. The observed values of the response are compared with those expected from the fitted model. For dis-

crete, count responses, the frequency of each count (0, 1, 2, etc) in the observed data and expected from the conditional distribution of the response implied by the model are compared. For continuous variables, the observed and expected frequencies are obtained by grouping the data into bins. The rootogram is drawn using `ggplot2::ggplot()` graphics. The design closely follows Kleiber & Zeileis (2016).

## Usage

```
rootogram(object, ...)

## S3 method for class 'gam'
rootogram(object, max_count = NULL, breaks = "Sturges", ...)
```

## Arguments

<code>object</code>	an R object
<code>...</code>	arguments passed to other methods
<code>max_count</code>	integer; the largest count to consider
<code>breaks</code>	for continuous responses, how to group the response. Can be anything that is acceptable as the breaks argument of <code>graphics::hist.default()</code>

## References

Kleiber, C., Zeileis, A., (2016) Visualizing Count Data Regressions Using Rootograms. *Am. Stat.* **70**, 296–303. doi:[10.1080/00031305.2016.1173590](https://doi.org/10.1080/00031305.2016.1173590)

## Examples

```
load_mgcv()

df <- data_sim("eg1", n = 1000, dist = "poisson", scale = 0.1, seed = 6)

# A poisson example
m <- gam(y ~ s(x0, bs = "cr") + s(x1, bs = "cr") + s(x2, bs = "cr") +
  s(x3, bs = "cr"), family = poisson(), data = df, method = "REML")
rg <- rootogram(m)
rg
draw(rg) # plot the rootogram

# A Gaussian example
df <- data_sim("eg1", dist = "normal", seed = 2)
m <- gam(y ~ s(x0) + s(x1) + s(x2) + s(x3), data = df, method = "REML")
draw(rootogram(m, breaks = "FD"), type = "suspended")
```



rtw

*Simulator for tweedie LSS models***Description**

Simulate random deviates from a Tweedie distribution with given parameters  $\mu$ ,  $p$ , and  $\phi$ . Works with vector values for all parameters, unlike the version on *mgcv*.

**Usage**

```
rtw(mu, p, phi)
```

**Arguments**

mu	numeric vector of mean values of Tweedie distribution.
p	numeric vector of values for the power parameter of the Tweedie distribution.
phi	numeric vector of values for the scale parameter $\phi$ of the Tweedie distribution.

---

```
scale_fill_partial_effect
```

*Default diverging red-blue colour palette for partial effects*

---

**Description**

Default diverging red-blue colour palette for partial effects

**Usage**

```
scale_fill_partial_effect(
  name = "Partial effect",
  ...,
  na.value = "grey50",
  guide = "colourbar",
  direction = -1
)
```

**Arguments**

name	The name of the scale. Used as the legend title. If NULL the legend title will be omitted.
...	arguments passed to <a href="#">ggplot2::continuous_scale()</a> .
na.value	Missing values will be replaced with this value (colour).
guide	A function used to create a guide or its name. See <a href="#">ggplot2::guides()</a> for more information.
direction	Sets the order of colours in the scale. If 1, the default, colours are as output by <a href="#">RColorBrewer::brewer.pal()</a> . If -1, the order of colours is reversed.

---

seq_min_max_eps	<i>Create a sequence of evenly-spaced values adjusted to accommodate a small adjustment</i>
-----------------	---

---

### Description

Creates a sequence of  $n$  evenly-spaced values over the range  $\min(x) - \max(x)$ , where the minimum and maximum are adjusted such that they are always contained within the range of  $x$  when  $x$  may be shifted forwards or backwards by an amount related to  $\text{eps}$ . This is particularly useful in computing derivatives via finite differences where without this adjustment we may be predicting for values outside the range of the data and hence the constraints of the penalty.

### Usage

```
seq_min_max_eps(x, n, order, type = c("forward", "backward", "central"), eps)
```

### Arguments

<code>x</code>	numeric; vector over which evenly-spaced values are returned
<code>n</code>	numeric; the number of evenly-spaced values to return
<code>order</code>	integer; the order of derivative. Either 1 or 2 for first or second order derivatives
<code>type</code>	character; the type of finite difference used. One of "forward", "backward", or "central"
<code>eps</code>	numeric; the finite difference

### Value

A numeric vector of length  $n$ .

---

shift_values	<i>Shift numeric values in a data frame by an amount eps</i>
--------------	--

---

### Description

Shift numeric values in a data frame by an amount  $\text{eps}$

### Usage

```
shift_values(df, h, i, FUN = `+`, focal = NULL)
```

**Arguments**

df	a data frame or tibble.
h	numeric; the amount to shift values in df by.
i	logical; a vector indexing columns of df that should not be included in the shift.
FUN	function; a function to apply the shift. Typically + or -.
focal	character; the focal variable when computing partial derivatives. This allows shifting only the focal variable by eps.

simulate.gam

*Simulate from the posterior distribution of a GAM***Description**

Simulations from the posterior distribution of a fitted GAM model involve computing predicted values for the observation data for which simulated data are required, then generating random draws from the probability distribution used when fitting the model.

**Usage**

```
## S3 method for class 'gam'
simulate(
  object,
  nsim = 1,
  seed = NULL,
  data = newdata,
  weights = NULL,
  ...,
  newdata = NULL
)

## S3 method for class 'gamm'
simulate(
  object,
  nsim = 1,
  seed = NULL,
  data = newdata,
  weights = NULL,
  ...,
  newdata = NULL
)

## S3 method for class 'scam'
simulate(
  object,
  nsim = 1,
```

```

    seed = NULL,
    data = newdata,
    weights = NULL,
    ...,
    newdata = NULL
  )

```

### Arguments

<code>object</code>	a fitted GAM, typically the result of a call to <code>mgcv::gam</code> or <code>mgcv::gamm</code> .
<code>nsim</code>	numeric; the number of posterior simulations to return.
<code>seed</code>	numeric; a random seed for the simulations.
<code>data</code>	data frame; new observations at which the posterior draws from the model should be evaluated. If not supplied, the data used to fit the model will be used for <code>newdata</code> , if available in <code>object</code> .
<code>weights</code>	numeric; a vector of prior weights. If <code>newdata</code> is null then defaults to <code>object[["prior.weights"]]</code> , otherwise a vector of ones.
<code>...</code>	arguments passed to methods. <code>simulate.gam()</code> and <code>simulate.scam()</code> pass ... on to <code>predict.gam()</code> . As such you can pass additional arguments such as <code>terms</code> , <code>exclude</code> , to select which model terms are included in the predictions. This may be useful, for example, for excluding the effects of random effect terms.
<code>newdata</code>	Deprecated. Use <code>data</code> instead.

### Details

For `simulate.gam()` to function, the family component of the fitted model must contain, or be updatable to contain, the required random number generator. See `mgcv::fix.family.rd()`.

### Value

(Currently) A data frame with `nsim` columns.

### Author(s)

Gavin L. Simpson

### Examples

```

load_mgcv()
dat <- data_sim("eg1", n = 400, dist = "normal", scale = 2, seed = 2)
m1 <- gam(y ~ s(x0) + s(x1) + s(x2) + s(x3), data = dat, method = "REML")

sims <- simulate(m1, nsim = 5, seed = 42)
head(sims)

```

---

smallAges	<i>Lead-210 age-depth measurements for Small Water</i>
-----------	--

---

**Description**

A dataset containing lead-210 based age depth measurements for the SMALL1 core from Small Water.

**Format**

A data frame with 12 rows and 7 variables.

**Details**

The variables are as follows:

- Depth
- Drymass
- Date
- Age
- Error
- SedAccRate
- SedPerCentChange

**Source**

Simpson, G.L. (Unpublished data).

---

smooths	<i>Names of smooths in a GAM</i>
---------	----------------------------------

---

**Description**

Names of smooths in a GAM

**Usage**

```
smooths(object)

## Default S3 method:
smooths(object)

## S3 method for class 'gamm'
smooths(object)

## S3 method for class 'gamm4'
smooths(object)
```

**Arguments**

object            a fitted GAM or related model. Typically the result of a call to `mgcv::gam()`, `mgcv::bam()`, or `mgcv::gamm()`.

---

smooth\_coefs

*Coefficients for a particular smooth*

---

**Description**

Returns a vector of model coefficients of the parametric terms that represent the supplied smooth.

**Usage**

```
smooth_coefs(object, ...)

## S3 method for class 'gam'
smooth_coefs(object, select, term = deprecated(), ...)

## S3 method for class 'bam'
smooth_coefs(object, select, term = deprecated(), ...)

## S3 method for class 'gamm'
smooth_coefs(object, select, term = deprecated(), ...)

## S3 method for class 'gamm4'
smooth_coefs(object, select, term = deprecated(), ...)

## S3 method for class 'list'
smooth_coefs(object, select, term = deprecated(), ...)

## S3 method for class 'mgcv.smooth'
smooth_coefs(object, model, ...)

## S3 method for class 'scam'
smooth_coefs(object, select, term = deprecated(), ...)
```

**Arguments**

object            a fitted GAM(M) object, or, for the "mgcv.smooth" method, an object that inherits from class `mgcv.smooth`.

...               arguments passed to other methods.

select            character; the label of the smooth whose coefficients will be returned.

term              **[Deprecated]** Use select instead.

model             a fitted GAM(M) object.

**Value**

A numeric vector of model coefficients.

**Author(s)**

Gavin L. Simpson

**See Also**

[smooth\\_coef\\_indices\(\)](#) for extracting the indices of the coefficients for a particular smooth.

**Examples**

```
load_mgcv()
df <- data_sim("eg1", seed = 2)
m <- gam(y ~ s(x0) + s(x1) + s(x2) + s(x3), data = df, method = "REML")

## IGNORE_RDIFF_BEGIN
smooth_coefs(m, select = "s(x2)")
## IGNORE_RDIFF_END
```

---

smooth_coef_indices	<i>Indices of the parametric terms for a particular smooth</i>
---------------------	--

---

**Description**

Returns a vector of indices of the parametric terms that represent the supplied smooth. Useful for extracting model coefficients and columns of their covariance matrix.

**Usage**

```
smooth_coef_indices(smooth)
```

**Arguments**

smooth                    an object that inherits from class `mgcv.smooth`

**Value**

A numeric vector of indices.

**Author(s)**

Gavin L. Simpson

**See Also**

[smooth\\_coefs\(\)](#) for extracting the coefficients for a particular smooth.

smooth\_data

Generate regular data over the covariates of a smooth

---

**Description**

Generate regular data over the covariates of a smooth

**Usage**

```
smooth_data(
  model,
  id,
  n = 100,
  n_2d = NULL,
  n_3d = NULL,
  n_4d = NULL,
  offset = NULL,
  include_all = FALSE,
  var_order = NULL
)
```

**Arguments**

model	a fitted model
id	the number ID of the smooth within model to process.
n	numeric; the number of new observations to generate.
n_2d	numeric; the number of new observations to generate for the second dimension of a 2D smooth. <i>Currently ignored.</i>
n_3d	numeric; the number of new observations to generate for the third dimension of a 3D smooth.
n_4d	numeric; the number of new observations to generate for the dimensions higher than 2 (!) of a $k$ D smooth ( $k \geq 4$ ). For example, if the smooth is a 4D smooth, each of dimensions 3 and 4 will get $n_{4d}$ new observations.
offset	numeric; value of the model offset to use.
include_all	logical; include all covariates involved in the smooth? if FALSE, only the covariates involved in the smooth will be included in the returned data frame. If TRUE, a representative value will be included for all other covariates in the model that aren't actually used in the smooth. This can be useful if you want to pass the returned data frame on to <code>mgcv::PredictMat()</code> .
var_order	character; the order in which the terms in the smooth should be processed. Only useful for tensor products with at least one 2d marginal smooth.



**Examples**

```
load_mgcv()
df <- data_sim("eg1", seed = 42)
m <- bam(y ~ s(x0) + s(x1) + s(x2) + s(x3), data = df)

# generate data over range of x1 for smooth s(x1)
smooth_data(m, id = 2)

# generate data over range of x1 for smooth s(x1), with typical value for
# other covariates in the model
smooth_data(m, id = 2, include_all = TRUE)
```

---

smooth_dim	<i>Dimension of a smooth</i>
------------	------------------------------

---

**Description**

Extracts the dimension of an estimated smooth.

**Usage**

```
smooth_dim(object)

## S3 method for class 'gam'
smooth_dim(object)

## S3 method for class 'gamm'
smooth_dim(object)

## S3 method for class 'mgcv.smooth'
smooth_dim(object)
```

**Arguments**

object                    an R object. See Details for list of supported objects.

**Details**

This is a generic function with methods for objects of class "gam", "gamm", and "mgcv.smooth".

**Value**

A numeric vector of dimensions for each smooth.

**Author(s)**

Gavin L. Simpson

smooth\_estimates

*Evaluate smooths at covariate values***Description**

Evaluate a smooth at a grid of evenly spaced value over the range of the covariate associated with the smooth. Alternatively, a set of points at which the smooth should be evaluated can be supplied. `smooth_estimates()` is a new implementation of `evaluate_smooth()`, and replaces that function, which has been removed from the package.

**Usage**

```
smooth_estimates(object, ...)

## S3 method for class 'gam'
smooth_estimates(
  object,
  select = NULL,
  smooth = deprecated(),
  n = 100,
  n_3d = 16,
  n_4d = 4,
  data = NULL,
  unconditional = FALSE,
  overall_uncertainty = TRUE,
  dist = NULL,
  unnest = TRUE,
  partial_match = FALSE,
  clip = FALSE,
  ...
)
```

**Arguments**

<code>object</code>	an object of class "gam" or "gamm".
<code>...</code>	arguments passed to other methods.
<code>select</code>	character; select which smooth's posterior to draw from. The default (NULL) means the posteriors of all smooths in <code>model</code> will be sampled from. If supplied, a character vector of requested terms.
<code>smooth</code>	<b>[Deprecated]</b> Use <code>select</code> instead.
<code>n</code>	numeric; the number of points over the range of the covariate at which to evaluate the smooth.
<code>n_3d, n_4d</code>	numeric; the number of points over the range of last covariate in a 3D or 4D smooth. The default is NULL which achieves the standard behaviour of using <code>n</code> points over the range of all covariate, resulting in $n^d$ evaluation points, where <code>d</code>

	is the dimension of the smooth. For $d > 2$ this can result in very many evaluation points and slow performance. For smooths of $d > 4$ , the value of <code>n_4d</code> will be used for all dimensions $> 4$ , unless this is <code>NULL</code> , in which case the default behaviour (using <code>n</code> for all dimensions) will be observed.
<code>data</code>	a data frame of covariate values at which to evaluate the smooth.
<code>unconditional</code>	logical; should confidence intervals include the uncertainty due to smoothness selection? If <code>TRUE</code> , the corrected Bayesian covariance matrix will be used.
<code>overall_uncertainty</code>	logical; should the uncertainty in the model constant term be included in the standard error of the evaluate values of the smooth?
<code>dist</code>	numeric; if greater than 0, this is used to determine when a location is too far from data to be plotted when plotting 2-D smooths. The data are scaled into the unit square before deciding what to exclude, and <code>dist</code> is a distance within the unit square. See <code>mgcv::exclude.too.far()</code> for further details.
<code>unnest</code>	logical; unnest the smooth objects?
<code>partial_match</code>	logical; in the case of character select, should select match partially against smooths? If <code>partial_match = TRUE</code> , select must only be a single string, a character vector of length 1.
<code>clip</code>	logical; should evaluation points be clipped to the boundary of a soap film smooth? The default is <code>FALSE</code> , which will return <code>NA</code> for any point that is deemed to lie outside the boundary of the soap film.

## Value

A data frame (tibble), which is of class "smooth\_estimates".

## Examples

```
load_mgcv()

dat <- data_sim("eg1", n = 400, dist = "normal", scale = 2, seed = 2)
m1 <- gam(y ~ s(x0) + s(x1) + s(x2) + s(x3), data = dat, method = "REML")

## evaluate all smooths
smooth_estimates(m1)

## or selected smooths
smooth_estimates(m1, select = c("s(x0)", "s(x1)"))

# parallel processing of smooths
if (requireNamespace("mirai") && requireNamespace("carrier")) {
  library("mirai")
  daemons(2) # only low for CRAN requirements
  smooth_estimates(m1)
}
```

smooth\_label

*Extract the label for a smooth used by 'mgcv'***Description**

The label 'mgcv' uses for smooths is useful in many contexts, including selecting smooths or labelling plots. `smooth_label()` extracts this label from an 'mgcv' smooth object, i.e. an object that inherits from class "mgcv.smooth". These would typically be found in the `$smooth` component of a GAM fitted by `mgcv::gam()` or `mgcv::bam()`, or related functions.

**Usage**

```
smooth_label(object, ...)

## S3 method for class 'gam'
smooth_label(object, id, ...)

## S3 method for class 'mgcv.smooth'
smooth_label(object, ...)
```

**Arguments**

<code>object</code>	an R object. Currently, methods for class "gam" and for mgcv smooth objects inheriting from class "mgcv.smooth" are supported.
<code>...</code>	arguments passed to other methods.
<code>id</code>	numeric; the indices of the smooths whose labels are to be extracted. If missing, labels for all smooths in the model are returned.

**Value**

A character vector.

**Examples**

```
load_mgcv()
df <- data_sim("gwf2", n = 100)
m <- gam(y ~ s(x), data = df, method = "REML")

# extract the smooth
sm <- get_smooths_by_id(m, id = 1)[[1]]

# extract the label
smooth_label(sm)

# or directly on the fitted GAM
smooth_label(m$smooth[[1]])

# or extract labels by index/position
smooth_label(m, id = 1)
```

smooth\_samples

*Posterior draws for individual smooths***Description**

Returns draws from the posterior distributions of smooth functions in a GAM. Useful, for example, for visualising the uncertainty in individual estimated functions.

**Usage**

```
smooth_samples(model, ...)

## S3 method for class 'gam'
smooth_samples(
  model,
  select = NULL,
  term = deprecated(),
  n = 1,
  data = newdata,
  method = c("gaussian", "mh", "inla", "user"),
  seed = NULL,
  freq = FALSE,
  unconditional = FALSE,
  n_cores = 1L,
  n_vals = 200,
  burnin = 1000,
  thin = 1,
  t_df = 40,
  rw_scale = 0.25,
  rng_per_smooth = FALSE,
  draws = NULL,
  partial_match = NULL,
  mvn_method = c("mvnfast", "mgcv"),
  ...,
  newdata = NULL,
  ncores = NULL
)
```

**Arguments**

<code>model</code>	a fitted model of the supported types
<code>...</code>	arguments passed to other methods. For <code>fitted_samples()</code> , these are passed on to <code>mgcv::predict.gam()</code> . For <code>posterior_samples()</code> these are passed on to <code>fitted_samples()</code> . For <code>predicted_samples()</code> these are passed on to the relevant <code>simulate()</code> method.

select	character; select which smooth's posterior to draw from. The default (NULL) means the posteriors of all smooths in model will be sampled from. If supplied, a character vector of requested terms.
term	<b>[Deprecated]</b> Use select instead.
n	numeric; the number of posterior samples to return.
data	data frame; new observations at which the posterior draws from the model should be evaluated. If not supplied, the data used to fit the model will be used for data, if available in model.
method	character; which method should be used to draw samples from the posterior distribution. "gaussian" uses a Gaussian (Laplace) approximation to the posterior. "mh" uses a Metropolis Hastings sampler that alternates t proposals with proposals based on a shrunk version of the posterior covariance matrix. "inla" uses a variant of Integrated Nested Laplace Approximation due to Wood (2019), (currently not implemented). "user" allows for user-supplied posterior draws (currently not implemented).
seed	numeric; a random seed for the simulations.
freq	logical; TRUE to use the frequentist covariance matrix of the parameter estimators, FALSE to use the Bayesian posterior covariance matrix of the parameters.
unconditional	logical; if TRUE (and freq == FALSE) then the Bayesian smoothing parameter uncertainty corrected covariance matrix is used, if available.
n_cores	number of cores for generating random variables from a multivariate normal distribution. Passed to <code>mvnfast::rmvn()</code> . Parallelization will take place only if OpenMP is supported (but appears to work on Windows with current R).
n_vals	numeric; how many locations to evaluate the smooth at if data not supplied
burnin	numeric; number of samples to discard as the burnin draws. Only used with method = "mh".
thin	numeric; the number of samples to skip when taking n draws. Results in thin * n draws from the posterior being taken. Only used with method = "mh".
t_df	numeric; degrees of freedom for t distribution proposals. Only used with method = "mh".
rw_scale	numeric; Factor by which to scale posterior covariance matrix when generating random walk proposals. Negative or non finite to skip the random walk step. Only used with method = "mh".
rng_per_smooth	logical; if TRUE, the behaviour of gratia version 0.8.1 or earlier is used, whereby a separate call the the random number generator (RNG) is performed for each smooth. If FALSE, a single call to the RNG is performed for all model parameters
draws	matrix; user supplied posterior draws to be used when method = "user".
partial_match	logical; should smooths be selected by partial matches with select? If TRUE, select can only be a single string to match against.
mvn_method	character; one of "mvnfast" or "mgcv". The default is uses <code>mvnfast::rmvn()</code> , which can be considerably faster at generate large numbers of MVN random values than <code>mgcv::rmvn()</code> , but which might not work for some marginal fits, such as those where the covariance matrix is close to singular.

newdata	Deprecated: use data instead.
ncores	Deprecated; use n_cores instead. The number of cores for generating random variables from a multivariate normal distribution. Passed to <code>mvnfast::rmvn()</code> . Parallelization will take place only if OpenMP is supported (but appears to work on Windows with current R).

## Value

A tibble with additional classes "smooth\_samples" and "posterior\_samples".

For the "gam" method, the columns currently returned (not in this order) are:

- `.smooth`; character vector. Indicates the smooth function for that particular draw,
- `.term`; character vector. Similar to `smooth`, but will contain the full label for the smooth, to differentiate factor-by smooths for example.
- `.by`; character vector. If the smooth involves a by term, the by variable will be named here, `NA_character_ otherwise`.
- `.row`; integer. A vector of values `seq_len(n_vals)`, repeated if `n > 1L`. Indexes the row in data for that particular draw.
- `.draw`; integer. A vector of integer values indexing the particular posterior draw that each row belongs to.
- `.value`; numeric. The value of smooth function for this posterior draw and covariate combination.
- `xxx`; numeric. A series of one or more columns containing data required for the smooth, named as per the variables involved in the respective smooth.
- Additional columns will be present in the case of factor by smooths, which will contain the level for the factor named in `by_variable` for that particular posterior draw.

## Warning

The set of variables returned and their order in the tibble is subject to change in future versions. Don't rely on position.

## Author(s)

Gavin L. Simpson

## Examples

```
load_mgcv()

dat <- data_sim("eg1", n = 400, seed = 2)
m1 <- gam(y ~ s(x0) + s(x1) + s(x2) + s(x3), data = dat, method = "REML")

sms <- smooth_samples(m1, select = "s(x0)", n = 5, seed = 42)

sms
```

```
## A factor by example (with a spurious covariate x0)
dat <- data_sim("eg4", n = 1000, seed = 2)

## fit model...
m2 <- gam(y ~ fac + s(x2, by = fac) + s(x0), data = dat)
sms <- smooth_samples(m2, n = 5, seed = 42)
draw(sms)
```

---

smooth\_terms

*List the variables involved in smooths*


---

## Description

**[Experimental]**

## Usage

```
smooth_terms(object, ...)
```

## Arguments

object	an R object the result of a call to <code>mgcv::gam()</code> , <code>mgcv::bam()</code> , or <code>mgcv::gamm()</code> , or that inherits from classes "gam" or "mgcv.smooth", or "fs.interaction".
...	arguments passed to other methods. Currently unused.

---

smooth\_type

*Determine the type of smooth and return it in a human readable form*


---

## Description

Determine the type of smooth and return it in a human readable form

## Usage

```
smooth_type(smooth)

## Default S3 method:
smooth_type(smooth)

## S3 method for class 'tprs.smooth'
smooth_type(smooth)

## S3 method for class 'ts.smooth'
smooth_type(smooth)
```



```
## S3 method for class 'cr.smooth'
smooth_type(smooth)

## S3 method for class 'cs.smooth'
smooth_type(smooth)

## S3 method for class 'cyclic.smooth'
smooth_type(smooth)

## S3 method for class 'pspline.smooth'
smooth_type(smooth)

## S3 method for class 'cpspline.smooth'
smooth_type(smooth)

## S3 method for class 'Bspline.smooth'
smooth_type(smooth)

## S3 method for class 'duchon.spline'
smooth_type(smooth)

## S3 method for class 'fs.interaction'
smooth_type(smooth)

## S3 method for class 'sz.interaction'
smooth_type(smooth)

## S3 method for class 'gp.smooth'
smooth_type(smooth)

## S3 method for class 'mrf.smooth'
smooth_type(smooth)

## S3 method for class 'random.effect'
smooth_type(smooth)

## S3 method for class 'sw'
smooth_type(smooth)

## S3 method for class 'sf'
smooth_type(smooth)

## S3 method for class 'soap.film'
smooth_type(smooth)

## S3 method for class 't2.smooth'
smooth_type(smooth)
```

```
## S3 method for class 'sos.smooth'
smooth_type(smooth)

## S3 method for class 'tensor.smooth'
smooth_type(smooth)

## S3 method for class 'mpi.smooth'
smooth_type(smooth)

## S3 method for class 'mpd.smooth'
smooth_type(smooth)

## S3 method for class 'cx.smooth'
smooth_type(smooth)

## S3 method for class 'cv.smooth'
smooth_type(smooth)

## S3 method for class 'micx.smooth'
smooth_type(smooth)

## S3 method for class 'micv.smooth'
smooth_type(smooth)

## S3 method for class 'mdcx.smooth'
smooth_type(smooth)

## S3 method for class 'mdcv.smooth'
smooth_type(smooth)

## S3 method for class 'miso.smooth'
smooth_type(smooth)

## S3 method for class 'mifo.smooth'
smooth_type(smooth)
```

### Arguments

`smooth` an object inheriting from class `mgcv.smooth`.

---

`spline_values`

*Evaluate a spline at provided covariate values*

---

### Description

Evaluate a spline at provided covariate values

**Usage**

```
spline_values(
  smooth,
  data,
  model,
  unconditional,
  overall_uncertainty = TRUE,
  frequentist = FALSE
)
```

**Arguments**

smooth	currently an object that inherits from class <code>mgcv.smooth</code> .
data	a data frame of values to evaluate smooth at.
model	a fitted model; currently only <code>mgcv::gam()</code> and <code>mgcv::bam()</code> models are supported.
unconditional	logical; should confidence intervals include the uncertainty due to smoothness selection? If TRUE, the corrected Bayesian covariance matrix will be used.
overall_uncertainty	logical; should the uncertainty in the model constant term be included in the standard error of the evaluate values of the smooth?
frequentist	logical; use the frequentist covariance matrix?

---

term_names	<i>Extract names of all variables needed to fit a GAM or a smooth</i>
------------	---

---

**Description**

Extract names of all variables needed to fit a GAM or a smooth

**Usage**

```
term_names(object, ...)

## S3 method for class 'gam'
term_names(object, ...)

## S3 method for class 'mgcv.smooth'
term_names(object, ...)

## S3 method for class 'gamm'
term_names(object, ...)
```

**Arguments**

object	a fitted GAM object (inheriting from class "gam" or an <a href="#">mgcv::smooth.construct</a> smooth object, inheriting from class "mgcv.smooth").
...	arguments passed to other methods. Not currently used.

**Value**

A vector of variable names required for terms in the model

---

term_variables	<i>Names of variables involved in a specified model term</i>
----------------	--

---

**Description**

Given the name (a term label) of a term in a model, returns the names of the variables involved in the term.

**Usage**

```
term_variables(object, term, ...)

## S3 method for class 'terms'
term_variables(object, term, ...)

## S3 method for class 'gam'
term_variables(object, term, ...)

## S3 method for class 'bam'
term_variables(object, term, ...)
```

**Arguments**

object	an R object on which method dispatch is performed
term	character; the name of a model term, in the sense of <code>attr(terms(object), "term.labels")</code> . Currently not checked to see if the term exists in the model.
...	arguments passed to other methods.

**Value**

A character vector of variable names.

---

theta	<i>General extractor for additional parameters in mgcv models</i>
-------	---

---

### Description

General extractor for additional parameters in mgcv models

### Usage

```
theta(object, ...)

## S3 method for class 'gam'
theta(object, transform = TRUE, ...)

## S3 method for class 'family'
theta(object, transform = TRUE, ...)
```

### Arguments

object	a fitted model
...	arguments passed to other methods.
transform	logical; transform to the natural scale of the parameter

### Value

Returns a numeric vector of additional parameters

### Examples

```
load_mgcv()
df <- data_sim("eg1", dist = "poisson", seed = 42, scale = 1 / 5)
m <- gam(y ~ s(x0) + s(x1) + s(x2) + s(x3),
  data = df, method = "REML",
  family = nb()
)
p <- theta(m)
```

---

tidy_basis	<i>A tidy basis representation of a smooth object</i>
------------	---

---

### Description

Takes an object of class `mgcv.smooth` and returns a tidy representation of the basis.

**Usage**

```
tidy_basis(smooth, data = NULL, at = NULL, coefs = NULL, p_ident = NULL)
```

**Arguments**

smooth	a smooth object of or inheriting from class "mgcv.smooth". Typically, such objects are returned as part of a fitted GAM or GAMM in the \$smooth component of the model object or the \$gam\$smooth component if the model was fitted by <code>mgcv::gam()</code> or <code>gam4::gam4()</code> .
data	a data frame containing the variables used in smooth.
at	a data frame containing values of the smooth covariate(s) at which the basis should be evaluated.
coefs	numeric; an optional vector of coefficients for the smooth
p_ident	logical vector; only used for handling <code>scam::scam()</code> smooths.

**Value**

A tibble.

**Author(s)**

Gavin L. Simpson

**Examples**

```
load_mgcv()

df <- data_sim("eg1", n = 400, seed = 42)

# fit model
m <- gam(y ~ s(x0) + s(x1) + s(x2) + s(x3), data = df, method = "REML")

# tidy representation of a basis for a smooth definition
# extract the smooth
sm <- get_smooth(m, "s(x2)")
# get the tidy basis - need to pass where we want it to be evaluated
bf <- tidy_basis(sm, at = df)

# can weight the basis by the model coefficients for this smooth
bf <- tidy_basis(sm, at = df, coefs = smooth_coefs(sm, model = m))
```

---

too_far	<i>Exclude values that lie too far from the support of data</i>
---------	---

---

### Description

Identifies pairs of covariate values that lie too far from the original data. The function is currently a basic wrapper around `mgcv::exclude.too.far()`.

### Usage

```
too_far(x, y, ref_1, ref_2, dist = NULL)
```

### Arguments

<code>x, y</code>	numeric; vector of values of the covariates to compare with the observed data
<code>ref_1, ref_2</code>	numeric; vectors of covariate values that represent the reference against which <code>x1</code> and <code>x2</code> are compared
<code>dist</code>	if supplied, a numeric vector of length 1 representing the distance from the data beyond which an observation is excluded. For example, you want to exclude values that lie further from an observation than 10% of the range of the observed data, use <code>0.1</code> .

### Value

Returns a logical vector of the same length as `x1`.

---

too_far_to_na	<i>Set rows of data to NA if the lie too far from a reference set of values</i>
---------------	---

---

### Description

Set rows of data to NA if the lie too far from a reference set of values

### Usage

```
too_far_to_na(smooth, input, reference, cols, dist = NULL)
```

### Arguments

<code>smooth</code>	an mgcv smooth object
<code>input</code>	data frame containing the input observations and the columns to be set to NA
<code>reference</code>	data frame containing the reference values
<code>cols</code>	character vector of columns whose elements will be set to NA if the data lies too far from the reference set
<code>dist</code>	numeric, the distance from the reference set beyond which elements of input will be set to NA

---

to_na	<i>Sets the elements of vector to NA</i>
-------	--

---

**Description**

Given a vector `i` indexing the elements of `x`, sets the selected elements of `x` to NA.

**Usage**

```
to_na(x, i)
```

**Arguments**

<code>x</code>	vector of values
<code>i</code>	vector of values used to subset <code>x</code>

**Value**

Returns `x` with possibly some elements set to NA

---

transform_fun	<i>Transform estimated values and confidence intervals by applying a function</i>
---------------	---

---

**Description**

Transform estimated values and confidence intervals by applying a function

**Usage**

```
transform_fun(object, fun = NULL, ...)

## S3 method for class 'smooth_estimates'
transform_fun(object, fun = NULL, constant = NULL, ...)

## S3 method for class 'smooth_samples'
transform_fun(object, fun = NULL, constant = NULL, ...)

## S3 method for class 'mgcv_smooth'
transform_fun(object, fun = NULL, constant = NULL, ...)

## S3 method for class 'evaluated_parametric_term'
transform_fun(object, fun = NULL, constant = NULL, ...)

## S3 method for class 'parametric_effects'
```



```
transform_fun(object, fun = NULL, constant = NULL, ...)

## S3 method for class 'tbl_df'
transform_fun(object, fun = NULL, column = NULL, constant = NULL, ...)
```

### Arguments

object	an object to apply the transform function to.
fun	the function to apply.
...	additional arguments passed to methods.
constant	numeric; a constant to apply before transformation.
column	character; for the "tbl_df" method, which column to transform.

### Value

Returns object but with the estimate and upper and lower values of the confidence interval transformed via the function.

### Author(s)

Gavin L. Simpson

---

typical_values	<i>Typical values of model covariates</i>
----------------	---

---

### Description

Typical values of model covariates

### Usage

```
typical_values(object, ...)

## S3 method for class 'gam'
typical_values(
  object,
  vars = everything(),
  envir = environment(formula(object)),
  data = NULL,
  ...
)

## S3 method for class 'data.frame'
typical_values(object, vars = everything(), ...)
```

**Arguments**

object	a fitted GAM(M) model.
...	arguments passed to other methods.
vars	terms to include or exclude from the returned object. Uses tidyselect principles.
envir	the environment within which to recreate the data used to fit object.
data	an optional data frame of data used to fit the model if reconstruction of the data from the model doesn't work.

---

user_draws	<i>Handle user-supplied posterior draws</i>
------------	---

---

**Description**

Handle user-supplied posterior draws

**Usage**

```
user_draws(model, draws, ...)

## S3 method for class 'gam'
user_draws(model, draws, index = NULL, ...)
```

**Arguments**

model	a fitted R model. Currently only models fitted by <code>mgcv::gam()</code> or <code>mgcv::bam()</code> , or return an object that <i>inherits</i> from such objects are supported. Here, "inherits" is used in a loose fashion; models fitted by <code>scam::scam()</code> are support even though those models don't strictly inherit from class "gam" as far as <code>inherits()</code> is concerned.
draws	matrix; user supplied posterior draws to be used when <code>method = "user"</code> .
...	arguments passed to methods.
index	a vector to index (subset) the columns of draws.

**Details**

The supplied draws must be a matrix (currently), with 1 column per model coefficient, and 1 row per posterior draw. The "gam" method has argument `index`, which can be used to subset (select) coefficients (columns) of draws. `index` can be any valid way of selecting (indexing) columns of a matrix. `index` is useful if you have a set of posterior draws for the entire model (say from `mgcv::gam.mh()`) and you wish to use those draws for an individual smooth, via `smooth_samples()`.

---

variance_comp	<i>Variance components of smooths from smoothness estimates</i>
---------------	---

---

**Description**

A wrapper to `mgcv::gam.vcomp()` which returns the smoothing parameters expressed as variance components.

**Usage**

```
variance_comp(object, ...)

## S3 method for class 'gam'
variance_comp(object, rescale = TRUE, coverage = 0.95, ...)
```

**Arguments**

object	an R object. Currently only models fitted by <code>mgcv::gam()</code> or <code>mgcv::bam()</code> are supported.
...	arguments passed to other methods
rescale	logical; for numerical stability reasons the penalty matrices of smooths are rescaled before fitting. If <code>rescale = TRUE</code> , this rescaling is undone, resulting in variance components that are on their original scale. This is needed if comparing with other mixed model software, such as <code>lmer()</code> .
coverage	numeric; a value between 0 and 1 indicating the (approximate) coverage of the confidence interval that is returned.

**Details**

This function is a wrapper to `mgcv::gam.vcomp()` which performs three additional services

- it suppresses the annoying text output that `mgcv::gam.vcomp()` prints to the terminal,
- returns the variance of each smooth as well as the standard deviation, and
- returns the variance components as a tibble.

---

vars_from_label	<i>Returns names of variables from a smooth label</i>
-----------------	---

---

**Description**

Returns names of variables from a smooth label

**Usage**

```
vars_from_label(label)
```

**Arguments**

label                      character; a length 1 character vector containing the label of a smooth.

**Examples**

```
vars_from_label("s(x1)")
vars_from_label("t2(x1,x2,x3)")
```

---

which_smooths	<i>Identify a smooth term by its label</i>
---------------	--

---

**Description**

Identify a smooth term by its label

**Usage**

```
which_smooths(object, ...)

## Default S3 method:
which_smooths(object, ...)

## S3 method for class 'gam'
which_smooths(object, terms, ...)

## S3 method for class 'bam'
which_smooths(object, terms, ...)

## S3 method for class 'gamm'
which_smooths(object, terms, ...)
```

**Arguments**

object                    a fitted GAM.

...                        arguments passed to other methods.

terms                     character; one or more (partial) term labels with which to identify required smooths.

---

worm_plot	<i>Worm plot of model residuals</i>
-----------	-------------------------------------

---

## Description

Worm plot of model residuals

## Usage

```
worm_plot(model, ...)

## S3 method for class 'gam'
worm_plot(
  model,
  method = c("uniform", "simulate", "normal", "direct"),
  type = c("deviance", "response", "pearson"),
  n_uniform = 10,
  n_simulate = 50,
  level = 0.9,
  ylab = NULL,
  xlab = NULL,
  title = NULL,
  subtitle = NULL,
  caption = NULL,
  ci_col = "black",
  ci_alpha = 0.2,
  point_col = "grey20",
  point_alpha = 1,
  line_col = "red",
  ...
)

## S3 method for class 'glm'
worm_plot(model, ...)

## S3 method for class 'lm'
worm_plot(model, ...)
```

## Arguments

model	a fitted model. Currently models inheriting from class "gam", as well as classes "glm" and "lm" from calls to <a href="#">stats::glm</a> or <a href="#">stats::lm</a> are supported.
...	arguments passed to other methods.
method	character; method used to generate theoretical quantiles. The default is "uniform", which generates reference quantiles using random draws from a uniform distribution and the inverse cumulative distribution function (CDF) of the fitted values. The reference quantiles are averaged over n_uniform draws. "simulate"

generates reference quantiles by simulating new response data from the model at the observed values of the covariates, which are then residualised to generate reference quantiles, using `n_simulate` simulated data sets. "normal" generates reference quantiles using the standard normal distribution. "uniform" is more computationally efficient, but "simulate" allows reference bands to be drawn on the QQ-plot. "normal" should be avoided but is used as a fall back if a random number generator ("simulate") or the inverse of the CDF are not available from the family used during model fitting ("uniform").

Note that `method = "direct"` is deprecated in favour of `method = "uniform"`.

<code>type</code>	character; type of residuals to use. Only "deviance", "response", and "pearson" residuals are allowed.
<code>n_uniform</code>	numeric; number of times to randomize uniform quantiles in the direct computation method ( <code>method = "uniform"</code> ).
<code>n_simulate</code>	numeric; number of data sets to simulate from the estimated model when using the simulation method ( <code>method = "simulate"</code> ).
<code>level</code>	numeric; the coverage level for reference intervals. Must be strictly $0 < \text{level} < 1$ . Only used with <code>method = "simulate"</code> .
<code>ylab</code>	character or expression; the label for the y axis. If not supplied, a suitable label will be generated.
<code>xlab</code>	character or expression; the label for the y axis. If not supplied, a suitable label will be generated.
<code>title</code>	character or expression; the title for the plot. See <code>ggplot2::labs()</code> . May be a vector, one per penalty.
<code>subtitle</code>	character or expression; the subtitle for the plot. See <code>ggplot2::labs()</code> . May be a vector, one per penalty.
<code>caption</code>	character or expression; the plot caption. See <code>ggplot2::labs()</code> . May be a vector, one per penalty.
<code>ci_col</code>	fill colour for the reference interval when <code>method = "simulate"</code> .
<code>ci_alpha</code>	alpha transparency for the reference interval when <code>method = "simulate"</code> .
<code>point_col</code>	colour of points on the QQ plot.
<code>point_alpha</code>	alpha transparency of points on the QQ plot.
<code>line_col</code>	colour used to draw the reference line.

### Note

The wording used in `mgcv::qq.gam()` uses *direct* in reference to the simulated residuals method (`method = "simulated"`). To avoid confusion, `method = "direct"` is deprecated in favour of `method = "uniform"`.

### Examples

```
load_mgcv()
## simulate binomial data...
dat <- data_sim("eg1", n = 200, dist = "binary", scale = .33, seed = 0)
p <- binomial()$linkinv(dat$f) # binomial p
```

```

n <- sample(c(1, 3), 200, replace = TRUE) # binomial n
dat <- transform(dat, y = rbinom(n, n, p), n = n)
m <- gam(y / n ~ s(x0) + s(x1) + s(x2) + s(x3),
  family = binomial, data = dat, weights = n,
  method = "REML"
)

## Worm plot; default using direct randomization of uniform quantiles
## Note no reference bands are drawn with this method.
worm_plot(m)

## Alternatively use simulate new data from the model, which
## allows construction of reference intervals for the Q-Q plot
worm_plot(m,
  method = "simulate", point_col = "steelblue",
  point_alpha = 0.4
)

## ... or use the usual normality assumption
worm_plot(m, method = "normal")

```

---

zooplankton

*Madison lakes zooplankton data*


---

## Description

The Madison lake zooplankton data are from a long-term study in seasonal dynamics of zooplankton, collected by the Richard Lathrop. The data were collected from a chain of lakes in Wisconsin (Mendota, Monona, Kegonssa, and Waubesa) approximately bi-weekly from 1976 to 1994. They consist of samples of the zooplankton communities, taken from the deepest point of each lake via vertical tow. The data are provided by the Wisconsin Department of Natural Resources and their collection and processing are fully described in Lathrop (2000).

## Format

A data frame

## Details

Each record consists of counts of a given zooplankton taxon taken from a subsample from a single vertical net tow, which was then scaled to account for the relative volume of subsample versus the whole net sample and the area of the net tow and rounded to the nearest 1000 to give estimated population density per m2 for each taxon at each point in time in each sampled lake.

## Source

Pedersen EJ, Miller DL, Simpson GL, Ross N. 2018. Hierarchical generalized additive models: an introduction with mgcv. *PeerJ Preprints* 6:e27320v1 doi:10.7287/peerj.preprints.27320v1.

**References**

Lathrop RC. (2000). Madison Wisconsin Lakes Zooplankton 1976–1994. Environmental Data Initiative.



# Index

- \* **data**
  - bird\_move, [23](#)
  - gss\_vocab, [90](#)
  - ref\_sims, [129](#)
  - smallAges, [141](#)
  - zooplankton, [167](#)
- \* **draw methods**
  - draw.rootogram, [65](#)
- \* **utility**
  - boundary, [23](#)
  - n\_eta, [107](#)
- add\_confint, [5](#)
- add\_constant, [5](#)
- add\_fitted, [6](#)
- add\_fitted.gam, [7](#)
- add\_fitted\_samples, [8](#)
- add\_partial\_residuals, [9](#)
- add\_posterior\_samples
  - (add\_fitted\_samples), [8](#)
- add\_predicted\_samples
  - (add\_fitted\_samples), [8](#)
- add\_residuals, [10](#)
- add\_residuals.gam, [10](#)
- add\_sizer, [11](#)
- add\_smooth\_samples
  - (add\_fitted\_samples), [8](#)
- appraise, [12](#)
- assemble, [14](#)
- assemble.gam, [15](#)
- base::levels(), [37](#)
- base::seq(), [78](#)
- base::set.seed(), [35](#)
- base::zapsmall(), [118](#)
- basis, [19](#)
- basis(), [46](#), [60](#)
- basis\_size, [22](#)
- bird\_move, [23](#)
- boundary, [23](#)
- by\_level(is\_by\_smooth), [92](#)
- by\_variable(is\_by\_smooth), [92](#)
- check\_is\_mgcv\_smooth(is\_mgcv\_smooth), [95](#)
- check\_user\_select\_smooths, [24](#)
- coef.scam, [25](#)
- compare\_smooths, [25](#)
- compare\_smooths(), [48](#)
- concrvity(model\_concurvity), [101](#)
- concrvity(), [62](#)
- conditional\_values, [26](#)
- conditional\_values(), [27](#), [48](#)
- confint.fderiv, [29](#)
- confint.gam, [31](#)
- confint.gamm(confint.gam), [31](#)
- confint.list(confint.gam), [31](#)
- data\_combos, [33](#)
- data\_sim, [34](#)
- data\_sim(), [129](#)
- data\_slice, [36](#)
- data\_slice(), [37](#)
- derivative\_samples, [40](#)
- derivatives, [38](#)
- derivatives(), [11](#)
- difference\_smooths, [43](#)
- dispersion, [45](#)
- draw, [45](#)
- draw(), [58](#)
- draw.basis, [46](#)
- draw.compare\_smooths, [47](#)
- draw.conditional\_values, [48](#)
- draw.conditional\_values(), [27](#)
- draw.derivatives, [49](#)
- draw.difference\_smooth, [51](#)
- draw.evaluated\_parametric\_term, [52](#)
- draw.gam, [54](#)
- draw.gam(), [59](#)
- draw.gamlss, [58](#)

- draw.mgcv\_smooth, 59
- draw.overall\_concurvity
  - (draw.pairwise\_concurvity), 61
- draw.pairwise\_concurvity, 61
- draw.parametric\_effects, 62
- draw.partial\_derivatives
  - (draw.derivatives), 49
- draw.penalty\_df, 63
- draw.rootogram, 65
- draw.smooth\_estimates, 66
- draw.smooth\_samples, 69
- edf, 71
- eval\_smooth, 74
- evaluate\_parametric\_term, 73
- evaluate\_parametric\_term(), 53
- evaluate\_smooth, 74
- evenly, 78
- evenly(), 37
- extract\_link(link), 96
- factor\_combos, 79
- family(), 80, 92, 98
- family.bam(family.gam), 79
- family.gam, 79
- family.gamm(family.gam), 79
- family.list(family.gam), 79
- family\_name, 80
- family\_type, 80
- fitted\_samples, 81
- fitted\_samples(), 8
- fitted\_values, 84
- fitted\_values(), 27
- fix\_offset, 87
- fixed\_effects(fixef.gam), 86
- fixef, 85
- fixef.gam, 86
- fixef.gamm(fixef.gam), 86
- fixef.glm(fixef.gam), 86
- fixef.lm(fixef.gam), 86
- gamm4::gamm4(), 80, 98, 158
- gaussian\_draws, 87
- generate\_draws(post\_draws), 121
- get\_by\_smooth, 89
- get\_smooth, 89
- get\_smooths\_by\_id, 90
- ggplot2::continuous\_scale(), 137
- ggplot2::coord\_sf(), 18, 57, 68
- ggplot2::facet\_grid(), 27
- ggplot2::facet\_wrap(), 27, 48
- ggplot2::geom\_contour(), 17, 47, 52, 56, 67, 70
- ggplot2::geom\_line(), 67, 70
- ggplot2::ggplot(), 15, 18, 46, 53, 54, 57, 60, 65, 136
- ggplot2::guide\_axis(), 18, 47, 50, 52, 57, 60, 63, 68, 70
- ggplot2::guides(), 137
- ggplot2::label\_both(), 46, 60
- ggplot2::labs(), 47, 53, 60, 64, 70, 109, 127, 131, 132, 166
- GJRM::gamlss(), 58
- graphics::hist.default(), 136
- graphics::par(), 13, 109, 132
- gss\_vocab, 90
- gw\_f0, 91
- gw\_f1(gw\_f0), 91
- gw\_f2(gw\_f0), 91
- gw\_f3(gw\_f0), 91
- gw\_functions, 35
- gw\_functions(gw\_f0), 91
- has\_theta, 92
- inv\_link(link), 96
- is\_by\_smooth, 92
- is\_continuous\_by\_smooth(is\_by\_smooth), 92
- is\_factor\_by\_smooth(is\_by\_smooth), 92
- is\_factor\_term, 93
- is\_mgcv\_family, 94
- is\_mgcv\_smooth, 95
- is\_mrf\_smooth(is\_mgcv\_smooth), 95
- is\_multivariate\_y, 95
- is\_offset, 96
- level(ref\_level), 129
- level(), 37
- link, 96
- load\_mgcv, 99
- lp\_matrix, 99
- marginalEffects::plot\_predictions(), 27
- mgcv::bam(), 22, 77, 80, 84, 98, 108, 142, 148, 152, 155, 163
- mgcv::exclude\_too\_far(), 17, 56, 77, 147, 159

- `mgcv::fix.family.rd()`, 140
- `mgcv::gam`, 140
- `mgcv::gam()`, 16, 22, 49, 51, 55, 63, 64, 67, 70, 77, 80, 83, 84, 98, 103, 108, 121, 142, 148, 152, 155, 163
- `mgcv::gam.mh()`, 162
- `mgcv::gam.vcomp()`, 163
- `mgcv::gamm()`, 22, 80, 98, 108, 117, 140, 142, 152, 158
- `mgcv::gammals()`, 98
- `mgcv::gamSim()`, 34
- `mgcv::gauss()`, 98
- `mgcv::gevlss()`, 98
- `mgcv::gfam()`, 35
- `mgcv::multinom()`, 98
- `mgcv::mvn()`, 98
- `mgcv::plot.gam()`, 16, 55
- `mgcv::predict.bam()`, 99, 103
- `mgcv::predict.gam()`, 7, 37, 82–84, 99, 103, 119, 121, 124, 149
- `mgcv::PredictMat()`, 144
- `mgcv::qq.gam`, 127
- `mgcv::qq.gam()`, 14, 127, 166
- `mgcv::residuals.gam()`, 10
- `mgcv::s()`, 19, 21
- `mgcv::shash()`, 98
- `mgcv::smooth.construct`, 156
- `mgcv::smoothCon()`, 21, 117
- `mgcv::soap`, 24
- `mgcv::t2()`, 19, 21
- `mgcv::te()`, 19, 21
- `mgcv::ti()`, 19, 21
- `mgcv::twlss()`, 98
- `mgcv::ziplss()`, 98
- `mh_draws`, 100
- `model_concurvity`, 101
- `model_concurvity()`, 62
- `model_constant`, 102
- `model_edf (edf)`, 71
- `model_terms`, 103
- `model_vars`, 105
- `mvnfast::rmvn()`, 30, 32, 39, 82, 83, 113, 120, 150, 151
- `n_eta`, 107
- `n_smooths`, 108
- `nb_theta`, 106
- `null_deviance`, 107
- `observed_fitted_plot`, 108
- `observed_fitted_plot()`, 14
- `overview`, 109
- `parametric_effects`, 110
- `parametric_effects()`, 73
- `parametric_terms`, 111
- `partial_derivatives`, 112
- `partial_residuals`, 115
- `patchwork::plot_layout()`, 13, 18, 47, 48, 50, 52, 57, 59, 63, 64, 70
- `patchwork::wrap_plots()`, 13, 18, 48, 50, 52, 57, 60, 63, 64, 68, 70
- `penalty`, 116
- `post_draws`, 121
- `posterior_samples`, 118
- `posterior_samples()`, 8
- `predicted_samples`, 123
- `predicted_samples()`, 8
- `qq_plot`, 125
- `qq_plot()`, 14
- `quantile_residuals`, 128
- `RColorBrewer::brewer.pal()`, 137
- `ref_level`, 129
- `ref_level()`, 37
- `ref_sims`, 129
- `rep_first_factor_value`, 130
- `residuals_hist_plot`, 130
- `residuals_hist_plot()`, 14
- `residuals_linpred_plot`, 131
- `residuals_linpred_plot()`, 14
- `response_derivatives`, 132
- `rootogram`, 135
- `rootogram()`, 66
- `rtw`, 137
- `scale_fill_partial_effect`, 137
- `scam::scam()`, 158
- `seq_min_max (evenly)`, 78
- `seq_min_max_eps`, 138
- `shift_values`, 138
- `simulate.gam`, 139
- `simulate.gam()`, 123
- `simulate.gamm (simulate.gam)`, 139
- `simulate.scam (simulate.gam)`, 139
- `smallAges`, 141
- `smooth_coef_indices`, 143

`smooth_coef_indices()`, 143  
`smooth_coefs`, 142  
`smooth_coefs()`, 143  
`smooth_data`, 144  
`smooth_dim`, 145  
`smooth_estimates`, 146  
`smooth_estimates()`, 74  
`smooth_label`, 148  
`smooth_samples`, 149  
`smooth_samples()`, 162  
`smooth_terms`, 152  
`smooth_type`, 152  
`smooths`, 141  
`smooths()`, 44  
`spline_values`, 154  
`stats::family()`, 79  
`stats::glm`, 13, 126, 165  
`stats::glm()`, 98  
`stats::lm`, 13, 126, 165  
`stats::predict()`, 6, 7, 10  
`stats::residuals()`, 9, 10  
`stop_if_not_mgcv_smooth`  
    (`is_mgcv_smooth`), 95  
  
`term_names`, 155  
`term_variables`, 156  
`theta`, 157  
`tidy_basis`, 157  
`to_na`, 160  
`too_far`, 159  
`too_far_to_na`, 159  
`transform_fun`, 160  
`typical_values`, 161  
`typical_values()`, 37  
  
`user_draws`, 162  
  
`variance_comp`, 163  
`vars_from_label`, 163  
  
`which_smooths`, 164  
`worm_plot`, 165  
  
`zooplankton`, 167