

# Package ‘qbrms’

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**Title** Quick Bayesian Regression Models Using 'INLA' with 'brms' Syntax

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**Description** Provides a 'brms'-like interface for fitting Bayesian regression models using 'INLA' (Integrated Nested Laplace Approximations) and 'TMB' (Template Model Builder). The package offers faster model fitting while maintaining familiar 'brms' syntax and output formats. Supports fixed and mixed effects models, multiple probability distributions, conditional effects plots, and posterior predictive checks with summary methods compatible with 'brms'. 'TMB' integration provides fast ordinal regression capabilities. Implements methods adapted from 'emmeans' for marginal means estimation and 'bayestestR' for Bayesian inference assessment. Methods are based on Rue et al. (2009) <doi:10.1111/j.1467-9868.2008.00700.x>, Kristensen et al. (2016) <doi:10.18637/jss.v070.i05>, Lenth (2016) <doi:10.18637/jss.v069.i01>, Bürkner (2017) <doi:10.18637/jss.v080.i01>, Makowski et al. (2019) <doi:10.21105/joss.01541>, and Kruschke (2014, ISBN:9780124058880).

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---

qbrms-package

*qbrms: Quick Bayesian Regression Models using INLA*

---

### Description

The qbrms package provides a brms-like interface for fitting Bayesian regression models using INLA (Integrated Nested Laplace Approximations). It offers faster model fitting while maintaining familiar brms syntax and output formats.

### Details

The main function is `qbrms` which fits Bayesian models using INLA with brms-like syntax. The package supports:

- Fixed and mixed effects models
- Multiple probability distributions
- Conditional effects plots
- Posterior predictive checks
- Summary methods compatible with brms
- Interactive model building with `model_builder`
- RStudio add-in for point-and-click model specification

### Author(s)

Tony Myers

### See Also

Useful links:

- <https://github.com/Tony-Myers/qbrms>
- Report bugs at <https://github.com/Tony-Myers/qbrms/issues>

---

asymmetric\_laplace

*Asymmetric Laplace for Quantile Regression*

---

### Description

Asymmetric Laplace for Quantile Regression

### Usage

```
asymmetric_laplace()
```

### Value

An object of class "family" representing the Asymmetric Laplace distribution.

---

`bayesfactor`*Bayesian Hypothesis Testing (very simple approximations)*

---

### Description

Compute a crude Bayes factor for a point, interval, or comparison hypothesis using approximate posterior draws recovered from a `qbrms_fit`. This is deliberately simple and intended for exploratory use.

### Usage

```
bayesfactor(  
  object,  
  hypothesis,  
  prior = NULL,  
  null = 0,  
  direction = "two-sided",  
  rope = NULL,  
  nsim = 4000,  
  verbose = TRUE  
)
```

### Arguments

<code>object</code>	A <code>qbrms_fit</code> object.
<code>hypothesis</code>	Character string, for example "Intercept > 0", "b_x = 0", or "b_x > 0.2".
<code>prior</code>	Optional prior information (unused here, kept for API compatibility).
<code>null</code>	Numeric null value for point tests (default 0).
<code>direction</code>	One of "two-sided", "greater", "less" (kept for API compatibility).
<code>rope</code>	Optional numeric length-2 vector <code>c(lower, upper)</code> to define a ROPE for point tests.
<code>nsim</code>	Number of posterior draws to simulate from the fitted summary.
<code>verbose</code>	Logical; print progress information.

### Value

An object of class `qbrms_bayesfactor`.

**Description**

Compute Bayesian R-squared values for qbrms regression models following the method of Gelman et al. (2019). This corrected version properly handles mixed-effects models to match brms output exactly.

**Usage**

```
bayes_R2(
  object,
  summary = TRUE,
  robust = FALSE,
  probs = c(0.025, 0.975),
  ndraws = 1000,
  newdata = NULL,
  verbose = TRUE
)
```

**Arguments**

object	A qbrms_fit object.
summary	Logical; if TRUE (default), return summary statistics. If FALSE, return the posterior draws.
robust	Logical; if TRUE, use robust summary statistics.
probs	Numeric vector of quantiles for summary (default: c(0.025, 0.975)).
ndraws	Number of posterior draws to use (default: 1000).
newdata	Optional data frame for predictions. If NULL, uses the original data.
verbose	Logical; print progress information.

**Details**

This implementation handles mixed-effects models by:

1. Using INLA's fitted values that include random effects when available
2. Correctly sampling random effects from their posterior distributions
3. Properly accounting for the variance decomposition in mixed models

**Value**

If `summary = TRUE`, a matrix with summary statistics. If `summary = FALSE`, a vector of R-squared values from posterior draws.

---

Beta	<i>Beta Family Constructor (Capital B)</i>
------	--

---

**Description**

Beta distribution family for response variables in (0,1)

**Usage**

```
Beta(link = "logit", link.phi = "log")
```

```
Beta(link = "logit", link.phi = "log")
```

**Arguments**

link            Link function for the mean parameter (default: "logit")

link.phi        Link function for precision parameter (default: "log")

**Value**

A family object of class "family".

A family object for use with qbrms()

**Examples**

```
## Not run:  
# Beta regression for proportions  
fit <- qbrms(proportion ~ predictor, data = data, family = Beta())  
  
## End(Not run)
```

---

beta_binomial	<i>Beta Binomial Family for Overdispersed Binary Data</i>
---------------	---

---

**Description**

Beta Binomial Family for Overdispersed Binary Data

**Usage**

```
beta_binomial(link = "logit")
```

**Arguments**

link            Link function for probability parameter (default: "logit")

**Value**

A family object of class "family".

---

beta_prior	<i>Specify Beta Prior Distribution</i>
------------	--

---

**Description**

Specify Beta Prior Distribution

**Usage**

```
beta_prior(alpha = 1, beta = 1)
```

**Arguments**

alpha	First shape parameter
beta	Second shape parameter

**Value**

A prior distribution object

---

beta_variants	<i>Alternative Beta Parameterizations</i>
---------------	---

---

**Description**

Alternative Beta Parameterizations

**Usage**

```
beta0(link = "logit")
```

```
beta1(link = "logit")
```

```
logitbeta(link = "logit")
```

**Arguments**

link	Link function (default: "logit")
------	----------------------------------

**Value**

A family object of class "family".

---

**bf** *Create a Bayesian Formula*


---

**Description**

Function to set up a model formula for use in qbrms, allowing specification of distributional parameters (e.g., sigma) in addition to the mean structure.

**Usage**

```
bf(formula, ..., flist = NULL, family = NULL, nl = FALSE)
```

**Arguments**

formula	Main model formula (for the mean/location parameter).
...	Additional formulas for distributional parameters (e.g., sigma ~ x).
flist	Optional list of formulas (for internal use).
family	Same as in qbrms() (optional here).
nl	Logical; indicating if the model is non-linear (not yet fully supported).

**Details**

This function mimics the brms::bf() syntax to allow users familiar with brms to define distributional models.

Supported distributional parameters depend on the family:

- gaussian: sigma (residual standard deviation)
- student\_t: sigma, nu (degrees of freedom)
- lognormal: sigma (shape parameter)
- beta: phi (precision)
- simplex: phi (precision)

**Value**

An object of class brmsformula (and qbrmsformula) containing the parsed formulas.

**Examples**

```
## Not run:
# Standard model
f1 <- bf(y ~ x)

# Distributional model (heteroscedasticity)
# Sigma varies by group
f2 <- bf(y ~ x, sigma ~ group)

## End(Not run)
```

---

binomial	<i>Binomial Family</i>
----------	------------------------

---

**Description**

Binomial Family

**Usage**

```
binomial()
```

**Value**

An object of class "family" representing the Binomial distribution.

---

c.qbrms_prior_spec	<i>Combine Multiple Prior Specifications</i>
--------------------	--

---

**Description**

Combine Multiple Prior Specifications

**Usage**

```
## S3 method for class 'qbrms_prior_spec'  
c(...)
```

**Arguments**

... Prior specification objects created by prior()

**Value**

A combined prior object

---

cauchy	<i>Specify Cauchy Prior Distribution</i>
--------	--

---

**Description**

Specify Cauchy Prior Distribution

**Usage**

```
cauchy(location = 0, scale = 1)
```

**Arguments**

location	Location parameter (default 0)
scale	Scale parameter (default 1)

**Value**

A prior distribution object

---

check_convergence	<i>Quick model diagnostics</i>
-------------------	--------------------------------

---

**Description**

Quick model diagnostics

**Usage**

```
check_convergence(object)
```

**Arguments**

object	A qbrms_fit object.
--------	---------------------

**Value**

Invisible TRUE if successful.

---

circular_normal	<i>Circular Normal Family for Directional Data</i>
-----------------	--

---

**Description**

Circular Normal Family for Directional Data

**Usage**

```
circular_normal(link = "tan_half", link.kappa = "log")
```

```
von_mises(link = "tan_half", link.kappa = "log")
```

**Arguments**

link            Link function for mean direction

link.kappa    Link function for concentration

**Value**

A family object of class "family".

---

coef.qbrms_fit	<i>Extract Coefficients from qbrms Models</i>
----------------	---

---

**Description**

Extract Coefficients from qbrms Models

**Usage**

```
## S3 method for class 'qbrms_fit'
```

```
coef(object, ...)
```

**Arguments**

object            A qbrms\_fit object

...                Additional arguments (unused)

**Value**

Named vector of coefficients

---

 coef.qbrms\_multinomial\_fit

*Coefficients for multinomial qbrms fits*


---

### Description

Extract a concatenated vector of coefficients from a `qbrms_multinomial_fit`, combining the per-category binary submodels if present.

### Usage

```
## S3 method for class 'qbrms_multinomial_fit'
coef(object, ...)
```

### Arguments

<code>object</code>	A <code>qbrms_multinomial_fit</code> .
<code>...</code>	Unused.

### Value

A named numeric vector of coefficients. If coefficient information is not available, a minimal intercept-only vector is returned.

---

 coef.tmb\_ordinal\_qbrms\_fit

*Coefficients Method for TMB Ordinal Fits*


---

### Description

Coefficients Method for TMB Ordinal Fits

### Usage

```
## S3 method for class 'tmb_ordinal_qbrms_fit'
coef(object, ...)
```

### Arguments

<code>object</code>	A <code>tmb_ordinal_qbrms_fit</code> object
<code>...</code>	Additional arguments

### Value

Named vector of coefficients

---

compare_models	<i>Compare qbrms models</i>
----------------	-----------------------------

---

**Description**

Compares multiple fitted models using information criteria and simple predictive metrics. Preference order for criterion = "auto" is: LOO (from CPO) > WAIC > DIC. When information criteria are unavailable it falls back to predictive metrics (RMSE/MAE).

**Usage**

```
compare_models(
  ...,
  criterion = c("auto", "loo", "waic", "dic", "all"),
  compare_predictions = TRUE,
  weights = TRUE
)
```

**Arguments**

...	Two or more fitted model objects (qbrms_fit or qbrmO_fit)
criterion	One of "auto", "loo", "waic", "dic", "all"
compare_predictions	Logical; if TRUE, include RMSE/MAE comparison
weights	Logical; if TRUE, compute weights when a single criterion is used

**Value**

An object of class "qbrms\_comparison".

---

compare_significance	<i>Compare Significance Across Multiple Models</i>
----------------------	--

---

**Description**

Compare the probability of practical significance for parameters across multiple qbrms models.

**Usage**

```
compare_significance(
  ...,
  parameters = NULL,
  threshold = "default",
  model_names = NULL
)
```

**Arguments**

...	qbrms_fit objects to compare
parameters	Character vector of parameters to compare
threshold	Threshold specification (same as p_significance)
model_names	Character vector of model names

**Value**

Data frame with comparison results

---

conditional\_effects    *Conditional effects (generic)*

---

**Description**

Compute one-dimensional conditional effects / marginal fitted values as a predictor varies while other covariates are held fixed (typically at means / modes). Methods should return an object that `plot()` can visualise.

**Usage**

```
conditional_effects(object, ...)
```

**Arguments**

object	A model object.
...	Passed to methods.

**Value**

An object of class "qbrms\_conditional\_effects" containing conditional effect estimates. The structure is method-dependent.

---

 conditional\_effects.qbrms\_fit

*Conditional effects for qbrms Gaussian models*


---

## Description

Conditional effects for qbrms Gaussian models

## Usage

```
## S3 method for class 'qbrms_fit'
conditional_effects(
  object,
  effects = NULL,
  spaghetti = FALSE,
  ndraws = 200L,
  n_points = 100L,
  at = list(),
  seed = NULL,
  prob = 0.95,
  ...
)
```

## Arguments

object	A qbrms fit object (Gaussian).
effects	Character vector: names of predictors to vary. Supports simple two-way interactions "num:fac" or "fac:num" where one is numeric and the other factor.
spaghetti	Logical; if TRUE draw per-draw "spaghetti" lines. If FALSE, draw a mean line with a credible-interval ribbon.
ndraws	Number of joint coefficient draws for uncertainty (default 200).
n_points	Size of the x-grid across the observed range (default 100).
at	Optional named list of covariate values to hold constant.
seed	Optional integer seed for reproducibility.
prob	Interval probability for ribbons (default 0.95).
...	Ignored.

## Value

An object of class "qbrms\_conditional\_effects" containing a list with one element per effect. Each element is a data frame with columns for the predictor values, point estimates (estimate\_\_), and credible interval bounds (lower\_\_, upper\_\_).

---

conditional\_effects.tmb\_ordinal\_qbrms\_fit  
*Conditional Effects for TMB Ordinal Models*

---

## Description

Conditional Effects for TMB Ordinal Models

## Usage

```
## S3 method for class 'tmb_ordinal_qbrms_fit'
conditional_effects(
  object,
  effects = NULL,
  prob = 0.95,
  ndraws = 100,
  spaghetti = FALSE,
  n_points = 100,
  plot = TRUE,
  at = list(),
  seed = NULL,
  conditions = NULL,
  categorical = TRUE,
  resolution = NULL,
  ...
)
```

## Arguments

object	A tmb_ordinal_qbrms_fit object
effects	Character vector of effect names (defaults to auto-detected)
prob	Confidence level
ndraws	Number of draws
spaghetti	Logical
n_points	Number of points for continuous predictors
plot	Logical, whether to return plots
at	Named list of conditioning values
seed	Random seed
conditions	Ordinal-specific conditions (for backwards compatibility)
categorical	Whether to show categorical plot (for backwards compatibility)
resolution	Grid resolution (for backwards compatibility)
...	Additional arguments

**Value**

List of conditional effects

---

conditional\_effects\_slices

*Discrete-slice conditional effects (brms-style) for qbrms*

---

**Description**

Build point/interval summaries at a few values of a numeric moderator, plotted against the factor on the x-axis.

**Usage**

```
conditional_effects_slices(
  object,
  effects,
  slices = NULL,
  nslices = 3L,
  prob = 0.95,
  ndraws = 200L,
  at = list(),
  seed = NULL,
  ...
)
```

**Arguments**

object	A qbrms_fit object.
effects	Character vector specifying effects to plot. If NULL, all numeric predictors are used.
slices	Named list of variables and values at which to slice the data.
nslices	Number of slices to use for each slicing variable.
prob	Probability mass to include in uncertainty intervals (default 0.95).
ndraws	Number of posterior draws to use for predictions.
at	Named list of values at which to fix other predictors.
seed	Random seed for reproducibility.
...	Additional arguments passed to prediction functions.

**Value**

An object of class "qbrms\_conditional\_effects" containing a list with one element per effect. Each element is a data frame with columns for the predictor values, estimates, and credible intervals.

---

`convert_family_to_inla`*Convert Family Object to INLA-Compatible Specification*

---

**Description**

Enhanced family conversion supporting all standard and additional families with automatic routing to specialised implementations when enabled.

**Usage**

```
convert_family_to_inla(family, quantile = 0.5, allow_ordinal_routing = FALSE)
```

**Arguments**

<code>family</code>	A family object, character string, or list specifying the response distribution
<code>quantile</code>	Numeric value between 0 and 1 for quantile regression
<code>allow_ordinal_routing</code>	Logical; if TRUE, enables routing for ordinal families

**Value**

Character string, list, or routing object specifying family/routing info

---

`create_dummy_data`*Create Dummy Data for Testing*

---

**Description**

Create dummy data that preserves structure for testing purposes.

**Usage**

```
create_dummy_data(  
  formula,  
  data,  
  n_dummy = 10,  
  family_name = "gaussian",  
  verbose = FALSE  
)
```

**Arguments**

formula	Model formula.
data	Original data frame.
n_dummy	Number of dummy observations to create.
family_name	The name of the model family (e.g., "gaussian").
verbose	Logical, whether to print messages.

**Value**

Data frame with dummy structure.

---

create\_prior\_object    *Create Prior-Only Object for pp\_check*

---

**Description**

Construct a small qbrms\_prior\_only object that contains simulated data and prior draws, suitable for passing to pp\_check().

**Usage**

```
create_prior_object(
  formula,
  family = gaussian(),
  prior = NULL,
  n_obs = 100,
  predictor_values = NULL,
  verbose = TRUE
)
```

**Arguments**

formula	Model formula.
family	Model family (default gaussian()).
prior	Prior specifications (default NULL uses defaults).
n_obs	Number of observations to simulate (default 100).
predictor_values	Named list of fixed predictor values (default NULL).
verbose	Logical; print progress messages (default TRUE).

**Value**

An object of class qbrms\_prior\_only.

---

cumulative	<i>Cumulative Family for Ordinal Regression</i>
------------	---

---

**Description**

Cumulative Family for Ordinal Regression

**Usage**

```
cumulative(link = "logit")
```

**Arguments**

link            Link function (default: "logit").

**Value**

An object of class "family" representing the Cumulative distribution for ordinal models.

---

default_priors	<i>Default Priors for qbrms Models</i>
----------------	--

---

**Description**

Default Priors for qbrms Models

**Usage**

```
default_priors()
```

**Value**

A default prior list

---

`density_plot`*Density Plot for qbrms Models*

---

## Description

Create density plots of posterior distributions with optional prior and observed-data overlays. Returns a ggplot2 object that can be modified with standard ggplot2 syntax.

## Usage

```
density_plot(  
  object,  
  parameter = NULL,  
  show_prior = FALSE,  
  show_data = FALSE,  
  ndraws = 100,  
  prior_ndraws = 100,  
  alpha_levels = list(posterior = 0.8, prior = 0.6, data = 1),  
  colours = list(posterior = "#1F78B4", prior = "#E31A1C", data = "#000000"),  
  seed = NULL,  
  verbose = TRUE  
)
```

## Arguments

<code>object</code>	A <code>qbrms_fit</code> object.
<code>parameter</code>	Parameter name to plot. If <code>NULL</code> , plots the response distribution.
<code>show_prior</code>	Logical; if <code>TRUE</code> , overlay the prior density.
<code>show_data</code>	Logical; if <code>TRUE</code> , overlay the observed data density.
<code>ndraws</code>	Number of posterior draws to use (default 100).
<code>prior_ndraws</code>	Number of prior draws to use (default 100).
<code>alpha_levels</code>	Named list controlling transparency for layers.
<code>colours</code>	Named list of colours for layers.
<code>seed</code>	Optional random seed.
<code>verbose</code>	Logical; print progress messages.

## Value

A ggplot2 object.

---

 diagnose\_binomial\_mixed

*Diagnose Binomial Mixed Effects Models*


---

### Description

Diagnose potential issues in binomial mixed effects models before fitting

### Usage

```
diagnose_binomial_mixed(formula, data, verbose = TRUE)
```

### Arguments

formula	Model formula with mixed effects
data	Data frame containing variables
verbose	Logical; print diagnostic information (default: TRUE)

### Value

List with diagnostic information

---

 diagnose\_model

*Automated Model Diagnostics and Recommendations*


---

### Description

Comprehensive automated diagnostics for qbrms models with actionable recommendations for model improvement.

### Usage

```
diagnose_model(model, checks = "all", verbose = TRUE)
```

### Arguments

model	A fitted qbrms model object
checks	Character vector specifying which checks to perform. Options: "all" (default), "convergence", "fit", "residuals", "posterior", "influential"
verbose	Logical; if TRUE, prints detailed diagnostic information (default: TRUE)

## Details

This function performs comprehensive model diagnostics including:

- Convergence checks (for MCMC-based inference)
- Goodness-of-fit assessment
- Residual analysis
- Posterior predictive checks
- Influential observation detection
- Prior-posterior overlap assessment

Each check produces a pass/warning/fail status with specific recommendations for addressing any issues detected.

## Value

An object of class "qbrms\_diagnostics" containing:

- `summary`: Overall assessment (pass/warning/fail)
- `checks`: Detailed results for each diagnostic check
- `recommendations`: Specific suggestions for improvement
- `plots`: List of diagnostic plots

## Examples

```
## Not run:  
# Fit a model  
fit <- qbrms(mpg ~ hp + wt, data = mtcars, family = gaussian())  
  
# Run diagnostics  
diag <- diagnose_model(fit)  
  
# View summary  
print(diag)  
  
# View specific recommendations  
diag$recommendations  
  
# Create diagnostic plots  
plot(diag)  
  
## End(Not run)
```

---

drop_random_effects	<i>Drop Random Effects from Formula</i>
---------------------	---

---

**Description**

Remove random effects terms from a model formula.

**Usage**

```
drop_random_effects(formula)
```

**Arguments**

formula            A model formula that may contain random effects.

**Value**

Formula with random effects terms removed.

---

emmeans	<i>Estimated marginal means (compatibility wrapper)</i>
---------	---

---

**Description**

This wrapper lets you call `emmeans()` on a `qbrms_fit` without attaching the external **emmeans** package. For non-`qbrms_fit` objects, it forwards to **emmeans** if that package is installed.

**Usage**

```
emmeans(object, specs, ...)
```

**Arguments**

object            A model object; if it is a `qbrms_fit` we dispatch to `qbrms_emmeans()`.  
 specs            Term(s) for which to compute estimated marginal means. For `qbrms_fit`, this is passed to `qbrms_emmeans()` unchanged.  
 ...              Additional arguments forwarded either to `qbrms_emmeans()` or to `emmeans::emmeans()` as appropriate.

**Value**

A data frame for `qbrms_fit`; otherwise whatever `emmeans::emmeans()` returns.

---

exponential	<i>Exponential Distribution (Prior or Family)</i>
-------------	---

---

**Description**

Exponential Distribution (Prior or Family)

**Usage**

```
exponential(rate_or_link = "log", link = NULL, ...)
```

```
prior_exponential(rate_or_link = 1)
```

**Arguments**

rate\_or\_link    Rate parameter (numeric) or link function (character).

link            Optional link function (if acting as family).

...             Additional arguments.

**Value**

A family object or prior object depending on inputs.

---

export_model	<i>Export Model Specification</i>
--------------	-----------------------------------

---

**Description**

Export model specifications to various formats for sharing, documentation, or reproduction.

**Usage**

```
export_model(  
  model,  
  file,  
  format = c("R", "markdown", "text", "json"),  
  include_data = TRUE,  
  include_diagnostics = FALSE  
)
```

**Arguments**

model	A fitted qbrms model object or qbrms_model_spec object
file	Character string specifying output file path
format	Character string specifying export format: "R" (R script), "markdown" (Rmd document), "text" (plain text), or "json" (JSON format)
include_data	Logical; if TRUE, includes data summary in export (default: TRUE)
include_diagnostics	Logical; if TRUE and model is fitted, includes diagnostic information (default: FALSE)

**Details**

This function facilitates model sharing and documentation by exporting:

- Model formula and family specification
- Prior specifications (if any)
- Data summary and structure
- Model fitting code
- Results summary (for fitted models)
- Diagnostic information (if requested)

The exported content can be used to:

- Share analyses with collaborators
- Document modelling decisions
- Create reproducible research reports
- Archive model specifications

**Value**

Invisibly returns the export content as a character string

**Examples**

```
## Not run:
# Export model specification
spec <- model_builder(data = mtcars, response = "mpg")
export_model(spec, "my_model_spec.R", format = "R")

# Export fitted model
fit <- qbrms(mpg ~ hp + wt, data = mtcars, family = gaussian())
export_model(fit, "my_model.Rmd", format = "markdown",
             include_diagnostics = TRUE)

# Export as JSON
export_model(spec, "my_model.json", format = "json")

## End(Not run)
```

---

`family_info`*Get Family Documentation*

---

**Description**

Get Family Documentation

**Usage**

```
family_info(family_name)
```

**Arguments**

`family_name`      Name of the family

**Value**

Character string with family information

---

`family_supports_quantile`*Check if Family Supports Quantile Regression*

---

**Description**

Determine whether a given family supports quantile regression.

**Usage**

```
family_supports_quantile(family_obj)
```

**Arguments**

`family_obj`      Family object or name.

**Value**

Logical indicating whether the family supports quantile regression.

---

fitted.qbrms\_fit      *Extract fitted values from qbrms models*

---

### Description

Extract fitted values from qbrms models

### Usage

```
## S3 method for class 'qbrms_fit'
fitted(object, ...)
```

### Arguments

object            A qbrms\_fit object  
 ...              Additional arguments (currently unused)

### Value

Numeric vector of fitted values

### Examples

```
## Not run:
fit <- qbrms(mpg ~ hp, data = mtcars, family = gaussian())
fitted_values <- fitted(fit)

## End(Not run)
```

---

fitted.tmb\_ordinal\_qbrms\_fit  
*Fitted Values Method for TMB Ordinal Fits*

---

### Description

Fitted Values Method for TMB Ordinal Fits

### Usage

```
## S3 method for class 'tmb_ordinal_qbrms_fit'
fitted(object, ...)
```

### Arguments

object            A tmb\_ordinal\_qbrms\_fit object  
 ...              Additional arguments

**Value**

Fitted values

---

gamma	<i>Gamma Distribution (Prior or Family)</i>
-------	---

---

**Description**

Gamma Distribution (Prior or Family)

**Usage**

```
gamma(shape_or_link = "log", rate = 1, link = NULL, ...)
```

```
gamma_prior(shape_or_link = 2, rate = 1)
```

**Arguments**

shape_or_link	Shape parameter (numeric) or link function (character).
rate	Rate parameter.
link	Optional link function (if acting as family).
...	Additional arguments.

**Value**

A family object or prior object depending on inputs.

---

Gamma_family	<i>Gamma family (GLM-style)</i>
--------------	---------------------------------

---

**Description**

Gamma family constructor to avoid conflict with base::gamma.

**Usage**

```
Gamma(link = "log")
```

**Arguments**

link	Link function (default: "log")
------	--------------------------------

**Value**

A family object of class "family".

---

gaussian	<i>Gaussian Family</i>
----------	------------------------

---

**Description**

Gaussian Family

**Usage**

```
gaussian()
```

**Value**

An object of class "family" representing the Gaussian distribution.

---

gen_student_t	<i>Generalized t Family</i>
---------------	-----------------------------

---

**Description**

Generalized t Family

**Usage**

```
gen_student_t(link = "identity", link.sigma = "log", link.nu = "log")
```

**Arguments**

link	Link function for location
link.sigma	Link function for scale
link.nu	Link function for degrees of freedom

**Value**

A family object of class "family".

---

get\_default\_prior      *Get Default Prior for Parameter Class*

---

**Description**

Get Default Prior for Parameter Class

**Usage**

```
get_default_prior(class)
```

**Arguments**

class                  Parameter class

**Value**

A default prior for that class

---

gev                      *Generalized Extreme Value Family*

---

**Description**

Generalized Extreme Value Family

**Usage**

```
gev(link = "identity", link.sigma = "log", link.xi = "identity")
```

```
gumbel(link = "identity", link.sigma = "log")
```

**Arguments**

link                    Link function for location

link.sigma            Link function for scale

link.xi                Link function for shape

**Value**

A family object of class "family".

---

hdi	<i>Highest Density Interval (HDI)</i>
-----	---------------------------------------

---

**Description**

Compute highest density intervals for parameters based on simulated posterior draws from a `qbrms_fit`.

**Usage**

```
hdi(object, parameters = NULL, prob = 0.95, nsim = 4000)
```

**Arguments**

object	A <code>qbrms_fit</code> .
parameters	Optional character vector; default uses all fixed effects.
prob	Probability mass for the interval (default 0.95).
nsim	Number of draws to simulate.

**Value**

A data frame of class `qbrms_hdi`.

---

hurdle_families	<i>Hurdle Families for Two-Part Models</i>
-----------------	--

---

**Description**

Hurdle Families for Two-Part Models

**Usage**

```
hurdle_poisson(link = "log", link.hu = "logit")
```

```
hurdle_negbinomial(link = "log", link.hu = "logit")
```

**Arguments**

link	Link function for count component
link.hu	Link function for hurdle component

**Value**

A family object of class "family".

---

iid	<i>IID Random Effects</i>
-----	---------------------------

---

**Description**

IID Random Effects

**Usage**

```
iid(scale.model = "log", diagonal = 1e-06)
```

**Arguments**

scale.model	Scaling model for precision
diagonal	Diagonal precision matrix structure

**Value**

A family object of class "family".

---

import_model	<i>Import Model Specification from JSON</i>
--------------	---

---

**Description**

Import a previously exported model specification from JSON format.

**Usage**

```
import_model(file)
```

**Arguments**

file	Character string specifying JSON file path
------	--

**Value**

A list containing the model specification components

**Examples**

```
## Not run:
# Import model
spec <- import_model("my_model.json")

# Recreate model
fit <- qbrms(
  formula = as.formula(spec$model$formula),
  data = my_data,
  family = get(spec$model$family)()
)

## End(Not run)
```

---

kfold_cv	<i>K-fold cross-validation for qbrms models (ordinal and standard families)</i>
----------	---

---

**Description**

Performs K-fold cross-validation either from a fitted model or from formula + data. For **ordinal (cumulative/ordinal)** families, you can choose the re-fit engine used inside CV: TMB (qbrm0) or a robust fallback using MASS: :polr that avoids TMB compilation in each fold. Your original fitted model is unchanged.

**Usage**

```
kfold_cv(
  object,
  data = NULL,
  family = gaussian(),
  K = 10,
  folds = NULL,
  seed = NULL,
  stratify = TRUE,
  parallel = FALSE,
  workers = NULL,
  keep_fits = FALSE,
  engine = c("auto", "tmb", "polr"),
  verbose = TRUE,
  ...
)
```

**Arguments**

**object** Either a fitted qbrms/qbrmO object **or** a formula.

data	Required only if object is a formula. Ignored if object is a fit.
family	Optional family override (used if object is a formula; fits use their own).
K	Number of folds (default 10).
folds	Optional integer vector of length nrow(data) giving fold IDs.
seed	Optional seed for stratified folds.
stratify	Logical; stratify on response if factor/ordered (default TRUE).
parallel	Logical; use future.apply if available (default FALSE).
workers	Optional workers when parallel and no plan is set.
keep_fits	Logical; keep per-fold fits (default FALSE).
engine	Ordinal CV engine: "auto" (default), "tmb", or "polr". Only used for <b>ordinal</b> families during CV refits. "auto" uses getOption("qbrms.kfold.ordinal_engine", "polr").
verbose	Logical; brief progress (default TRUE).
...	Passed to qbrms() when refitting folds (non-ordinal or engine="tmb").

**Value**

An object of class qbrms\_kfold with ELPD, pointwise elpd, SE, etc.

---

laplace	<i>Laplace (Double Exponential) Family</i>
---------	--

---

**Description**

Laplace (Double Exponential) Family

**Usage**

```
laplace(link = "identity", link.sigma = "log")
```

```
double_exponential(link = "identity", link.sigma = "log")
```

**Arguments**

link	Link function for location
link.sigma	Link function for scale

**Value**

A family object of class "family".

---

```
list_extended_families
```

*List Available Extended Families*

---

### Description

List Available Extended Families

### Usage

```
list_extended_families()
```

### Value

Data frame with family names, categories, and brief descriptions

---

```
lognormal
```

*Lognormal Family Constructor*

---

### Description

Lognormal distribution family for positive continuous responses

### Usage

```
lognormal(meanlog_or_link = "identity", sdlog = 1, link = NULL, ...)
```

```
lognormal(meanlog_or_link = "identity", sdlog = 1, link = NULL, ...)
```

```
lognormal_prior(meanlog_or_link = 0, sdlog = 1)
```

### Arguments

meanlog_or_link	Mean on log scale (numeric) or link function (character).
sdlog	SD on log scale (numeric).
link	Optional link function (if acting as family).
...	Additional arguments.

### Value

A family object for use with `qbrms()`

A family object or prior object depending on inputs.

**Examples**

```
## Not run:
# Lognormal regression
fit <- qbrms(response ~ predictor, data = data, family = lognormal())

## End(Not run)
```

---

loo_compare	<i>Compare models by LOO (default) or WAIC</i>
-------------	--

---

**Description**

Compare multiple fitted models and rank them by out-of-sample fit. If you pass qbrms/qbrmO fit objects, this uses the package's loo() / waic() wrappers under the hood. If you pass actual loo objects (from the **loo** package), it will delegate to loo::loo\_compare() automatically.

**Usage**

```
loo_compare(..., criterion = c("loo", "waic"), sort = TRUE)
```

**Arguments**

...	One or more fitted models (qbrms/qbrmO), or loo objects; you can also pass a single named list of models.
criterion	Character, "loo" (default) or "waic".
sort	Logical; if TRUE (default) the best model is first.

**Value**

A data.frame with model names, estimate on the ELPD scale (higher is better), standard error (if available), differences vs best, and ranks.

---

model_builder	<i>Interactive Model Builder for qbrms (console)</i>
---------------	--

---

**Description**

An interactive assistant that guides users through model specification by asking questions about their data, suggesting appropriate families, helping with prior selection, and building qbrms model code.

**Usage**

```
model_builder(data = NULL, response = NULL, predictors = NULL, quiet = FALSE)
```

**Arguments**

data	A data frame containing the variables to be modelled (optional). If not provided, the user will be prompted to specify it.
response	Character string specifying the response variable name (optional).
predictors	Character vector of predictor variable names (optional).
quiet	Logical; if TRUE, suppresses welcome messages (default: FALSE).

**Value**

An object with class "qbrms\_model\_spec" containing:

- formula: The model formula
- family: A list with name and the constructed family object
- prior: Prior specifications (if provided)
- data: The data frame
- data\_name: The symbol used for data in the emitted code
- model\_code: Character string with executable qbrms code
- response\_info: Summary information about the response

**Examples**

```
## Not run:
spec <- model_builder()
fit <- eval(parse(text = spec$model_code))

## End(Not run)
```

---

model\_lab\_addin

*qbrms Model Lab (RStudio Add-in)*

---

**Description**

Compare plausible families, run prior/posterior checks, plot conditional effects, compute diagnostics, and emit reproducible code. Does not load 'brms'.

**Usage**

```
model_lab_addin()
```

**Value**

This function is called for its side effects (launching a Shiny gadget in RStudio). It returns NULL invisibly.

---

model\_workflow\_addin    *Launch Guided Bayesian Workflow (RStudio Add-in)*

---

**Description**

A comprehensive, step-by-step assistant for Bayesian model building with qbrms.

**Usage**

```
model_workflow_addin()
```

**Value**

No return value. This function launches an interactive Shiny gadget for model building and code generation.

---

multinomial            *Multinomial Family*

---

**Description**

Multinomial Family

**Usage**

```
multinomial()
```

**Value**

An object of class "family" representing the Multinomial distribution.

---

negbinomial            *Negative Binomial Family (Alias)*

---

**Description**

Negative Binomial Family (Alias)

**Usage**

```
negbinomial()
```

**Value**

An object of class "family" representing the Negative Binomial distribution.

---

neg_binomial	<i>Negative Binomial Family</i>
--------------	---------------------------------

---

**Description**

Negative Binomial Family

**Usage**

```
neg_binomial()
```

**Value**

An object of class "family" representing the Negative Binomial distribution.

---

normal	<i>Specify Normal Prior Distribution</i>
--------	--

---

**Description**

Specify Normal Prior Distribution

**Usage**

```
normal(mean = 0, sd = 1)
```

**Arguments**

mean	Mean of the normal distribution (default 0)
sd	Standard deviation of the normal distribution (default 1)

**Value**

A prior distribution object

---

`plot.qbrms_conditional_effects`*Plot conditional effects for qbrms models*

---

### Description

Plot method for objects returned by [conditional\\_effects](#) and related helpers. For a single effect, this produces either a spaghetti plot of draws or a ribbon / slice plot of summary statistics. For multiple effects it can combine the plots using **patchwork** if available.

### Usage

```
## S3 method for class 'qbrms_conditional_effects'  
plot(x, ...)
```

### Arguments

`x` An object of class "qbrms\_conditional\_effects", typically the result of [conditional\\_effects](#) or [conditional\\_effects\\_slices](#).

`...` Currently ignored. Included for future extensions and method compatibility.

### Value

For a single effect, a ggplot2 object. For multiple effects, either

- a **patchwork** object combining the individual plots (if the **patchwork** package is installed), or
- a named list of ggplot2 objects otherwise.

---

`plot.qbrms_diagnostics`*Plot Method for Diagnostics*

---

### Description

Plot Method for Diagnostics

### Usage

```
## S3 method for class 'qbrms_diagnostics'  
plot(x, which = "all", ...)
```

**Arguments**

x	A qbrms_diagnostics object
which	Character vector specifying which plots to show
...	Additional arguments (unused)

**Value**

Invisibly returns the input object x.

---

plot.qbrms\_p\_significance

*Plot Method for Enhanced p\_significance*

---

**Description**

Create a visual plot of probability of practical significance results.

Create a visual plot of probability of practical significance results.

**Usage**

```
## S3 method for class 'qbrms_p_significance'  
plot(x, ...)
```

```
## S3 method for class 'qbrms_p_significance'  
plot(x, ...)
```

**Arguments**

x	A qbrms_p_significance object from p_significance().
...	Additional arguments passed to ggplot2 functions.

**Value**

A ggplot2 object.

A ggplot2 object.

---

plot\_parameters      *Plot Parameters with Prior/Posterior Comparison*

---

### Description

Create density plots for multiple model parameters, optionally comparing posterior estimates with their priors. Returns a ggplot2 object with faceted parameter plots.

Create density plots for multiple model parameters, optionally comparing posterior estimates with their priors. Returns a ggplot2 object with faceted parameter plots.

### Usage

```
plot_parameters(  
  object,  
  pars = NULL,  
  show_prior = FALSE,  
  ndraws = 200,  
  prior_ndraws = 200,  
  ncol = 2,  
  alpha_levels = c(0.8, 0.5),  
  colours = c("#1F78B4", "#E31A1C"),  
  verbose = TRUE,  
  ...  
)
```

```
plot_parameters(  
  object,  
  pars = NULL,  
  show_prior = FALSE,  
  ndraws = 200,  
  prior_ndraws = 200,  
  ncol = 2,  
  alpha_levels = c(0.8, 0.5),  
  colours = c("#1F78B4", "#E31A1C"),  
  verbose = TRUE,  
  ...  
)
```

### Arguments

object	A qbrms_fit object.
pars	Optional character vector of parameter names to plot. If NULL, plots all fixed-effect parameters.
show_prior	Logical; if TRUE, overlay prior distributions.
ndraws	Number of posterior draws to use for plotting.

prior_ndraws	Number of prior draws to use if show_prior = TRUE.
ncol	Number of columns for faceting (default 2).
alpha_levels	Numeric vector of length 2 giving alpha levels for c(posterior, prior). Default c(0.8, 0.5).
colours	Character vector of length 2 giving colours for c(posterior, prior). Default c("#1F78B4", "#E31A1C").
verbose	Logical; print progress information.
...	Additional arguments (currently unused).

### Value

A ggplot2 object with faceted parameter density plots.

A ggplot2 object with faceted parameter density plots.

### Examples

```
## Not run:
fit <- qbrms(y ~ x1 + x2, data = my_data, sample_prior = "yes")

# Plot all parameters
plot_parameters(fit)

# Plot specific parameters with priors
plot_parameters(fit, pars = c("x1", "x2"), show_prior = TRUE)

# Customize appearance
plot_parameters(fit, show_prior = TRUE) +
  theme_bw() +
  labs(title = "My Parameter Estimates")

## End(Not run)

## Not run:
fit <- qbrms(y ~ x1 + x2, data = my_data, sample_prior = "yes")

# Plot all parameters
plot_parameters(fit)

# Plot specific parameters with priors
plot_parameters(fit, pars = c("x1", "x2"), show_prior = TRUE)

# Customize appearance
plot_parameters(fit, show_prior = TRUE) +
  theme_bw() +
  labs(title = "My Parameter Estimates")

## End(Not run)
```

---

poisson	<i>Poisson Family</i>
---------	-----------------------

---

**Description**

Poisson Family

**Usage**

```
poisson()
```

**Value**

An object of class "family" representing the Poisson distribution.

---

pp_check	<i>Posterior and prior predictive checks</i>
----------	--

---

**Description**

Create posterior or prior predictive diagnostic plots for fitted qbrms models.

**Usage**

```
pp_check(object, ...)  
  
## S3 method for class 'qbrms_fit'  
pp_check(  
  object,  
  type = "dens_overlay",  
  ndraws = 5000,  
  seed = NULL,  
  show_observed = FALSE,  
  ...  
)  
  
## S3 method for class 'qbrms_prior'  
pp_check(  
  object,  
  type = "dens_overlay",  
  ndraws = 5000,  
  seed = NULL,  
  show_observed = FALSE,  
  ...  
)
```

**Arguments**

object	A model object.
...	Additional arguments passed to methods.
type	Character string indicating the check type: one of "dens_overlay", "hist", "scatter", "scatter_avg".
ndraws	Integer number of draws to use.
seed	Optional RNG seed.
show_observed	Logical; show observed data where applicable.

---

pp\_check.tmb\_ordinal\_qbrms\_fit

*Posterior predictive checks for TMB ordinal models*

---

**Description**

Posterior predictive checks for TMB ordinal models

**Usage**

```
## S3 method for class 'tmb_ordinal_qbrms_fit'
pp_check(
  object,
  type = "bars",
  ndraws = 100,
  seed = NULL,
  newdata = NULL,
  prob = 0.9,
  ...
)
```

**Arguments**

object	A fitted TMB ordinal qbrms model object
type	Character; type of posterior predictive check
ndraws	Integer; number of posterior draws to use
seed	Random seed for reproducibility.
newdata	Optional data frame for predictions. If NULL, uses original data.
prob	Probability mass for credible intervals (default 0.95).
...	Additional arguments passed to methods.

**Value**

A ggplot object showing the posterior predictive check

---

```
print.qbrmb_fit      Print a qbrmb model fit
```

---

**Description**

Nicely formatted one-line summary plus key diagnostics for a qbrmb\_fit.

Prints a summary of a regularised binomial qbrms model.

**Usage**

```
## S3 method for class 'qbrmb_fit'
print(x, digits = 2, ...)
```

```
## S3 method for class 'qbrmb_fit'
print(x, digits = 2, ...)
```

**Arguments**

x	A qbrmb_fit object.
digits	Number of decimal places for output (default: 2).
...	Additional arguments (currently unused).

**Value**

Invisibly returns the input object x.

---

```
print.qbrmsformula  Print method for qbrms formulas
```

---

**Description**

Print method for qbrms formulas

**Usage**

```
## S3 method for class 'qbrmsformula'
print(x, ...)
```

**Arguments**

x	A qbrmsformula object
...	Unused

**Value**

Invisibly returns the input object x.

---

```
print.qbrms_diagnostics
```

*Print Method for Diagnostics*

---

**Description**

Print Method for Diagnostics

**Usage**

```
## S3 method for class 'qbrms_diagnostics'  
print(x, ...)
```

**Arguments**

x	A qbrms_diagnostics object
...	Additional arguments (unused)

**Value**

Invisibly returns the input object x.

---

```
print.qbrms_fit
```

*Print Method for qbrms\_fit Objects*

---

**Description**

Prints a summary of a fitted qbrms model object.

**Usage**

```
## S3 method for class 'qbrms_fit'  
print(x, digits = 2, ...)
```

**Arguments**

x	A qbrms_fit object.
digits	Number of decimal places for output (default: 2).
...	Additional arguments (currently unused).

**Value**

Invisibly returns the input object x.

**Examples**

```
if (requireNamespace("INLA", quietly = TRUE)) {  
  fit <- qbrms(mpg ~ hp, data = mtcars, family = gaussian(), verbose = FALSE)  
  print(fit)  
}
```

---

print.qbrms\_kfold      *Print Method for qbrms\_kfold Objects*

---

**Description**

Print Method for qbrms\_kfold Objects

**Usage**

```
## S3 method for class 'qbrms_kfold'  
print(x, ...)
```

**Arguments**

x                    A qbrms\_kfold object  
...                   Additional arguments (unused)

**Value**

Invisibly returns the input object x.

---

print.qbrms\_loo\_compare  
*Print Method for qbrms\_loo\_compare Objects*

---

**Description**

Print Method for qbrms\_loo\_compare Objects

**Usage**

```
## S3 method for class 'qbrms_loo_compare'  
print(x, ...)
```

**Arguments**

x                    A qbrms\_loo\_compare object  
...                   Additional arguments (unused)

**Value**

Invisibly returns the input object *x*.

---

```
print.qbrms_model_spec
    Print Method for qbrms_model_spec
```

---

**Description**

Print Method for *qbrms\_model\_spec*

**Usage**

```
## S3 method for class 'qbrms_model_spec'
print(x, ...)
```

**Arguments**

<i>x</i>	A <i>qbrms_model_spec</i> object
...	Additional arguments (unused)

**Value**

Invisibly returns the input object *x*.

---

```
print.qbrms_multinomial_fit
    Print method for multinomial qbrms fits
```

---

**Description**

Shorthand print method that delegates to `summary.qbrms_multinomial_fit()`.

**Usage**

```
## S3 method for class 'qbrms_multinomial_fit'
print(x, digits = 2, ...)
```

**Arguments**

<i>x</i>	A <i>qbrms_multinomial_fit</i> .
<i>digits</i>	Integer; number of decimal places to display.
...	Unused.

**Value**

The input *x*, returned invisibly.

---

```
print.qbrms_prior_build
```

*Print method for qbrms\_prior\_build objects*

---

## Description

Nicely formats the result of `prior_build_from_beliefs()`, showing the elicited beliefs, implied prior distributions, and (optionally) the corresponding prior code.

## Usage

```
## S3 method for class 'qbrms_prior_build'
print(
  x,
  digits = 3,
  show_data = FALSE,
  show_code = TRUE,
  code_object_name = "priors",
  max_terms = 12,
  ...
)
```

## Arguments

<code>x</code>	An object of class "qbrms_prior_build" as returned by <a href="#">prior_build_from_beliefs</a> .
<code>digits</code>	Integer scalar giving the number of decimal places to display for numeric summaries (default: 3).
<code>show_data</code>	Logical; if TRUE, print a compact summary of the elicitation data used to construct the priors.
<code>show_code</code>	Logical; if TRUE, print the corresponding prior code that can be copied into a modelling script.
<code>code_object_name</code>	Character string giving the name that will be used for the prior object in the displayed code (default: "priors").
<code>max_terms</code>	Integer scalar giving the maximum number of individual terms to display before truncating the printed output (default: 12).
<code>...</code>	Currently ignored. Included for method compatibility.

## Value

Invisibly returns the input object `x`.

```
print.qbrms_prior_code
```

*Print method for qbrms\_prior\_code objects*

---

**Description**

Print method for qbrms\_prior\_code objects

**Usage**

```
## S3 method for class 'qbrms_prior_code'  
print(x, ...)
```

**Arguments**

x	A qbrms_prior_code object
...	Additional arguments passed to cat

**Value**

Invisibly returns the input object x.

---

```
print.qbrms_prior_diagnostics
```

*Print method for qbrms\_prior\_diagnostics objects*

---

**Description**

Print method for qbrms\_prior\_diagnostics objects

**Usage**

```
## S3 method for class 'qbrms_prior_diagnostics'  
print(x, digits = 3, ...)
```

**Arguments**

x	A qbrms_prior_diagnostics object
digits	Number of decimal places to display (default 3) # <- ADD THIS LINE
...	Additional arguments (unused)

**Value**

The input object, returned invisibly

---

`print.qbrms_prior_dist`  
*Print Prior Distribution Objects*

---

**Description**

Print Prior Distribution Objects

**Usage**

```
## S3 method for class 'qbrms_prior_dist'  
print(x, ...)
```

**Arguments**

<code>x</code>	A <code>qbrms_prior_dist</code> object
<code>...</code>	Unused

**Value**

Invisibly returns `x`.

---

`print.qbrms_prior_list`  
*Print Prior List Objects*

---

**Description**

Print Prior List Objects

**Usage**

```
## S3 method for class 'qbrms_prior_list'  
print(x, ...)
```

**Arguments**

<code>x</code>	A <code>qbrms_prior_list</code> object
<code>...</code>	Unused

**Value**

Invisibly returns `x`.

---

```
print.qbrms_prior_spec
```

*Print Prior Specification Objects*

---

### Description

Print Prior Specification Objects

### Usage

```
## S3 method for class 'qbrms_prior_spec'
print(x, ...)
```

### Arguments

x	A qbrms_prior_spec object
...	Unused

### Value

Invisibly returns x.

---

```
print.qbrms_p_significance
```

*Print Method for Enhanced p\_significance*

---

### Description

Print results from probability of practical significance analysis.

### Usage

```
## S3 method for class 'qbrms_p_significance'
print(x, digits = 3, ...)
```

```
## S3 method for class 'qbrms_p_significance'
print(x, digits = 3, ...)
```

### Arguments

x	A qbrms_p_significance object from p_significance().
digits	Number of decimal places to display (default 3).
...	Additional arguments passed to print.data.frame().

**Value**

Invisibly returns the input object.  
Invisibly returns the input object.

---

`print.summary.qbrms_fit`  
*Print Method for summary.qbrms\_fit Objects*

---

**Description**

Print Method for summary.qbrms\_fit Objects

**Usage**

```
## S3 method for class 'summary.qbrms_fit'  
print(x, ...)
```

**Arguments**

`x`                    A summary.qbrms\_fit object.  
`...`                Additional arguments (currently unused).

**Value**

Invisibly returns the input object `x`.

---

`print.tmb_ordinal_qbrms_fit`  
*Print Method for TMB Ordinal Fits*

---

**Description**

Print Method for TMB Ordinal Fits

**Usage**

```
## S3 method for class 'tmb_ordinal_qbrms_fit'  
print(x, digits = 2, ...)
```

**Arguments**

`x`                    A tmb\_ordinal\_qbrms\_fit object  
`digits`              Number of decimal places for output  
`...`                Additional arguments

**Value**

Invisibly returns the object

---

prior	<i>Specify Prior for Model Parameters</i>
-------	---

---

**Description**

Specify Prior for Model Parameters

**Usage**

```
prior(prior, class = "b", coef = NULL, group = NULL)
```

**Arguments**

prior	A prior distribution object.
class	Parameter class ("Intercept", "b", "sd", etc.)
coef	Specific coefficient name (optional)
group	Specific group name for random effects (optional)

**Value**

A prior specification object

---

priors	<i>Prior Distribution Specifications</i>
--------	--

---

**Description**

Functions to specify prior distributions for qbrms models

---

`prior_build_from_beliefs`*Prior Build from Beliefs*

---

**Description**

Build priors from elicited beliefs (GLM-aware)

**Usage**

```
prior_build_from_beliefs(  
  formula,  
  data,  
  family = gaussian(),  
  beliefs = list(),  
  outcome_location = NULL,  
  outcome_interval = NULL,  
  outcome_level = 0.95,  
  outcome_sd = NULL,  
  standardise = TRUE,  
  plausible_range = NULL,  
  target_coverage = 0.8,  
  tune = FALSE,  
  seed = NULL  
)
```

**Arguments**

<code>formula</code>	Model formula
<code>data</code>	Data frame
<code>family</code>	Model family
<code>beliefs</code>	List of beliefs about parameters
<code>outcome_location</code>	Expected outcome location
<code>outcome_interval</code>	Expected outcome interval
<code>outcome_level</code>	Confidence level for outcome interval
<code>outcome_sd</code>	Outcome standard deviation
<code>standardise</code>	Whether to standardise predictors
<code>plausible_range</code>	Plausible range for outcomes
<code>target_coverage</code>	Target coverage probability
<code>tune</code>	Whether to tune priors
<code>seed</code>	Random seed

**Value**

An object of class "qbrms\_prior\_build" containing:

- priors: A list of prior specifications.
- prior\_code: Character string of R code to reproduce the priors.
- formula: The (possibly modified) model formula.
- data: The (possibly standardised) data.
- diagnostics: Prior predictive diagnostic information.

---

prior\_code

*Format priors as qbrms prior() code*

---

**Description**

Format priors as qbrms prior() code

**Usage**

```
prior_code(build, object_name = "priors", digits = 3, include_comments = TRUE)
```

**Arguments**

build	A 'qbrms_prior_build' returned by prior_build_from_beliefs()
object_name	Name of the object on the left-hand side (default "priors")
digits	Number of decimal places to print
include_comments	Logical; if TRUE, prepend a short comment header

**Value**

A single character string containing formatted R code

---

prior\_pp\_diagnostics *Prior predictive diagnostics and sensibility report*

---

## Description

Summarise prior predictive draws to check basic support, scale and shape, and (optionally) how simple statistics of the observed data compare with the prior-predictive distribution. Returns an object with a concise verdict.

## Usage

```
prior_pp_diagnostics(
  object,
  level = 0.95,
  support = NULL,
  lower = NULL,
  upper = NULL,
  trials = NULL,
  plausible_lower = NULL,
  plausible_upper = NULL,
  include_observed = TRUE,
  seed = NULL
)
```

## Arguments

object	A qbrms prior object: qbrms_prior_fit, qbrms_prior_only, or a qbrms_fit that contains prior_samples.
level	Credible level for central intervals (default 0.95). Reserved.
support	Optional override of the implied support: one of "real", "positive", "proportion", or "bounded". If NULL, an attempt is made to infer from the family.
lower, upper	Optional numeric bounds used when support = "bounded". If support = "proportion", the default is $c(0, 1)$ .
trials	Optional integer vector for binomial data (bounds helper).
plausible_lower, plausible_upper	Optional numeric bounds defining a user-declared "plausible range" for the outcome on the response scale. When both are supplied, the function reports the fraction of prior-predictive mass that falls in $[plausible\_lower, plausible\_upper]$ and incorporates this into the verdict.
include_observed	Logical; if TRUE and the object contains data, the report compares simple statistics of $y$ to their prior-predictive reference distributions.
seed	Optional seed for reproducibility.

**Value**

An object of class `qbrms_prior_diagnostics`.

---

<code>prior_pp_summary</code>	<i>A convenience wrapper mirroring <code>pp_check</code>'s <code>show_observed</code> flag</i>
-------------------------------	--

---

**Description**

A convenience wrapper mirroring `pp_check`'s `show_observed` flag

**Usage**

```
prior_pp_summary(
  object,
  show_observed = FALSE,
  plausible_lower = NULL,
  plausible_upper = NULL,
  ...
)
```

**Arguments**

<code>object</code>	A <code>qbrms</code> prior object.
<code>show_observed</code>	Logical; compare observed summaries when available.
<code>plausible_lower</code> , <code>plausible_upper</code>	Optional plausible range bounds to score coverage.
<code>...</code>	Passed to <code>prior_pp_diagnostics()</code> .

**Value**

The diagnostics object, invisibly, after printing a summary.

---

<code>prior_predictive_check</code>	<i>Create Prior Predictive Distribution Plot</i>
-------------------------------------	--

---

**Description**

Generate predictions from the prior distribution to assess whether priors are reasonable before seeing the data.

**Usage**

```
prior_predictive_check(formula, data, family, prior, n_samples = 1000)
```

**Arguments**

formula	Model formula
data	Data frame (used for structure, not values)
family	Model family
prior	Prior specification
n_samples	Number of prior predictive samples (default: 1000)

**Value**

A ggplot object showing the prior predictive distribution

**Examples**

```
## Not run:
prior_predictive_check(
  mpg ~ hp + wt,
  data = mtcars,
  family = gaussian(),
  prior = prior(normal(0, 10), class = "b")
)

## End(Not run)
```

---

prior\_to\_posterior\_workflow  
*Complete Prior-to-Posterior Workflow*

---

**Description**

Fit a model with priors sampled, then produce a comparison density plot that overlays posterior, prior, and observed distributions where available.

**Usage**

```
prior_to_posterior_workflow(
  formula,
  data,
  family = gaussian(),
  prior = NULL,
  verbose = TRUE,
  ...
)
```

**Arguments**

<code>formula</code>	Model formula.
<code>data</code>	Data frame.
<code>family</code>	Model family (default <code>gaussian()</code> ).
<code>prior</code>	Prior specification (default <code>NULL</code> ).
<code>verbose</code>	Logical; print progress messages.
<code>...</code>	Additional arguments forwarded to <code>qbrms()</code> .

**Value**

A list of class `qbrms_workflow_result` with elements `fit` and `plot`.

---

<code>p_direction</code>	<i>Probability of Direction (pd)</i>
--------------------------	--------------------------------------

---

**Description**

Estimate the probability that a parameter is strictly positive (or strictly negative) under the posterior, based on simulated draws from a `qbrms_fit`.

**Usage**

```
p_direction(object, parameters = NULL, nsim = 4000, null = 0)
```

**Arguments**

<code>object</code>	A <code>qbrms_fit</code> object.
<code>parameters</code>	Optional character vector of parameter names. If <code>NULL</code> , all fixed-effect coefficients are used.
<code>nsim</code>	Number of draws to simulate from the fitted summary.
<code>null</code>	Numeric value defining the reference for direction (default 0).

**Value**

A data frame of class `qbrms_p_direction`.

---

p_significance	<i>Probability of Practical Significance (Enhanced bayestestR-style)</i>
----------------	--

---

### Description

Compute the probability that each parameter is above a threshold in the median's direction, similar to `bayestestR::p_significance()`. This represents the proportion of the posterior distribution that indicates a "significant" effect in the median's direction.

### Usage

```
p_significance(
  object,
  parameters = NULL,
  threshold = "default",
  nsim = 1000,
  verbose = TRUE
)
```

### Arguments

<code>object</code>	A <code>qbrms_fit</code> object.
<code>parameters</code>	Optional character vector of parameter names; if <code>NULL</code> , all fixed-effect coefficients are used.
<code>threshold</code>	The threshold value that separates significant from negligible effect: <ul style="list-style-type: none"> <li>• "default": Uses 0.1 as threshold range around zero</li> <li>• A single numeric value (e.g., 0.1): Creates symmetric range around zero (-0.1, 0.1)</li> <li>• A numeric vector of length two (e.g., <code>c(-0.2, 0.1)</code>): Asymmetric threshold</li> <li>• A list of numeric vectors: Each vector corresponds to a parameter</li> <li>• A named list: Names correspond to parameter names</li> </ul>
<code>nsim</code>	Number of draws to simulate for the approximation.
<code>verbose</code>	Logical; print progress information.

### Value

A data frame of class `qbrms_p_significance` with columns `Parameter`, `ps`, `Median`, `CI_low`, `CI_high`, `Threshold_low`, `Threshold_high`, and `Interpretation`.

---

qbrm	<i>Alias for qbrms()</i>
------	--------------------------

---

### Description

qbrm() is a shorter alias for qbrms() with identical functionality.

Enhanced interface to qbrms with all required parameters and built-in diagnostics.

### Usage

```
qbrm(
  formula,
  data,
  family = gaussian(),
  prior = NULL,
  sample_prior = "no",
  verbose = TRUE,
  ...
)
```

```
qbrm(
  formula,
  data,
  family = gaussian(),
  prior = NULL,
  sample_prior = "no",
  verbose = TRUE,
  ...
)
```

### Arguments

formula	Model formula in lme4/brms style.
data	Data frame containing the variables in the model.
family	Model family (default: gaussian()).
prior	Prior specifications (default: NULL).
sample_prior	Whether to sample from priors ("no", "yes", "only"). Default: "no".
verbose	Logical; print diagnostic information (default: TRUE).
...	Additional arguments passed to qbrms().

### Value

An object of class "qbrms\_fit", same as qbrms().

A qbrms\_fit object with model results.

**See Also**[qbrms](#)

qbrmb

*Enhanced binomial mixed-effects modelling***Description**

Fits a regularised binomial (or Bernoulli) mixed-effects model using INLA, with enhanced diagnostics, stability checks and strategy selection.

**Usage**

```
qbrmb(
  formula,
  data,
  family = "binomial",
  strategy = "auto",
  regularisation_strength = 0.1,
  use_data_augmentation = TRUE,
  min_group_size = 5,
  verbose = FALSE,
  diagnostics = FALSE,
  silent = FALSE,
  ...
)
```

**Arguments**

formula	Model formula with random effects in lme4-style syntax.
data	Data frame containing the variables in the model.
family	Model family (currently "binomial" or "bernoulli"; default "binomial").
strategy	Fitting strategy: "auto", "enhanced", "aggressive", or "minimal".
regularisation_strength	Regularisation strength in the interval $[0, 1]$ (default 0.1).
use_data_augmentation	Logical; if TRUE, add pseudo-observations for additional numerical stability.
min_group_size	Minimum group size before triggering diagnostic warnings.
verbose	Logical; if TRUE, show detailed progress and diagnostics while fitting.
diagnostics	Logical; if TRUE, compute and store extended diagnostics in the returned object.
silent	Logical; if TRUE, suppress printed output except errors.
...	Additional arguments passed to <code>INLA::inla()</code> .

**Value**

An object of class `c("qbrmb_fit", "qbrms_fit", "list")` containing the fitted model, diagnostics and metadata.

---

qbrmb_aggressive	<i>Aggressively regularised binomial mixed-effects model</i>
------------------	--

---

**Description**

Convenience wrapper around `qbrmb` using the "aggressive" strategy with a higher default regularisation strength.

**Usage**

```
qbrmb_aggressive(formula, data, verbose = FALSE, ...)
```

**Arguments**

formula	Model formula with random effects (lme4-style).
data	Data frame containing the variables in the model.
verbose	Logical; if TRUE, show detailed diagnostics.
...	Additional arguments passed to <code>qbrmb</code> .

**Value**

An object of class `c("qbrmb_fit", "qbrms_fit", "list")`.

**Examples**

```
if (requireNamespace("INLA", quietly = TRUE)) {
  set.seed(123)
  data <- data.frame(
    y = rbinom(100, 1, 0.2),
    x = rnorm(100),
    group = factor(rep(1:10, each = 10))
  )
  # qbrmb_aggressive requires a mixed model with random intercepts
  fit <- qbrmb_aggressive(y ~ x + (1 | group), data = data, verbose = FALSE)
}
```

---

qbrmb_regularised	<i>Regularised binomial mixed-effects (enhanced strategy)</i>
-------------------	---

---

**Description**

Convenience wrapper around [qbrmb](#) using the "enhanced" regularisation strategy and a stronger default regularisation strength.

**Usage**

```
qbrmb_regularised(formula, data, verbose = FALSE, ...)
```

**Arguments**

formula	Model formula with random effects (lme4-style).
data	Data frame containing the variables in the model.
verbose	Logical; if TRUE, show detailed diagnostics.
...	Additional arguments passed to <a href="#">qbrmb</a> .

**Value**

An object of class c("qbrmb\_fit", "qbrms\_fit", "list").

---

qbrm0	<i>Quick Bayesian Ordinal Regression Models with Adaptive Centering</i>
-------	---

---

**Description**

Fits ordinal regression models using Template Model Builder (TMB) with Laplace approximation and adaptive threshold centering to match brms output.

**Usage**

```
qbrm0(
  formula,
  data,
  family = cumulative(),
  prior = NULL,
  verbose = FALSE,
  threshold_method = "quantile",
  control = list(),
  ...
)
```

**Arguments**

formula	Model formula with ordinal response on the left-hand side.
data	Data frame containing the variables in the model.
family	Ordinal family specification. Currently supports cumulative().
prior	Prior specifications using qbrms prior syntax.
verbose	Logical; print progress messages during fitting.
threshold_method	Method for threshold centering ("quantile" or "cumulative_mean").
control	List of control parameters for TMB optimization.
...	Additional arguments passed to TMB functions.

**Value**

An object of class `c("tmb_ordinal_qbrms_fit", "qbrms_fit")`

---

qbrms

*Quick Bayesian Regression Models with Automatic Routing*


---

**Description**

Enhanced qbrms interface with automatic routing to specialised implementations. Supports ordinal regression via TMB, quantile regression, and all standard INLA families.

**Usage**

```
qbrms(
  formula,
  data,
  family = gaussian(),
  prior = NULL,
  sample_prior = "no",
  quantile = 0.5,
  control.compute = list(dic = TRUE, waic = TRUE, cpo = TRUE),
  verbose = getOption("qbrms.verbose", FALSE),
  ...
)
```

**Arguments**

formula	Model formula in lme4/brms style
data	Data frame containing the variables in the model
family	Model family (default: gaussian()). Ordinal families automatically route to qbrmO()
prior	Prior specifications (default: NULL)

sample_prior	Whether to sample from priors ("no", "yes", "only"). Default: "no"
quantile	For asymmetric_laplace family, which quantile to estimate (default: 0.5)
control.compute	INLA control settings for model information criteria
verbose	Logical; print diagnostic information (default: getOption("qbrms.verbose", FALSE))
...	Additional arguments passed to fitting functions

**Value**

An object of class "qbrms\_fit" (or "qbrm0\_fit" for ordinal models). The object is a list containing:

- fit: The internal model fit (INLA or TMB object).
- model\_type: String indicating the type of model fitted.
- data: The data used for fitting.
- original\_formula: The formula used.
- prior\_samples: Prior predictive samples (if requested).

**See Also**

[qbrm0](#) for direct ordinal model fitting

---

qbrms-model-criteria    *Model comparison criteria for qbrms models*

---

**Description**

Compute approximate DIC, LOO and WAIC for qbrms model fits.

**Usage**

```
waic(object, ...)

loo(object, ...)

dic(object, ...)

## S3 method for class 'qbrms_fit'
waic(object, ...)

## S3 method for class 'qbrms_fit'
loo(object, ...)

## S3 method for class 'qbrms_fit'
dic(object, ...)
```

**Arguments**

object            A qbrms\_fit object.  
 ...              Additional arguments passed to internal methods or underlying tools.

**Details**

These functions provide generic interfaces (`dic()`, `loo()`, `waic()`) and S3 methods for `qbrms_fit` objects that extract the corresponding criteria from the underlying INLA fit where available.

**Value**

For `dic()`, `loo()` and `waic()` methods on `qbrms_fit` objects, a list containing the corresponding criterion (for example, `list(dic = ...)`, `list(looic = ..., elpd_loo = ...)`, or `list(waic = ...)`). If the criterion cannot be computed, `NA_real_` is returned.

---

`qbrms_bayesian_analysis`

*Bayesian Analysis Functions (qbrms)*

---

**Description**

Posterior analysis tools for qbrms models: Bayes factors, probability of direction, ROPE, HDI, and estimated marginal means.

---

`qbrms_binomial_regularised`

*Fixed Regularised Binomial Mixed Effects Fitting*

---

**Description**

Fits binomial mixed effects models with regularisation, with all parameters handled correctly.

**Usage**

```
qbrms_binomial_regularised(
  formula,
  data,
  regularise = TRUE,
  sample_prior = "no",
  verbose = TRUE,
  ...
)
```

**Arguments**

formula	Model formula with mixed effects structure.
data	Data frame containing the variables.
regularise	Logical; if TRUE, apply regularisation techniques.
sample_prior	Whether to sample from priors ("no", "yes", "only"). Default: "no".
verbose	Logical; print progress information.
...	Additional arguments passed to qbrms().

**Value**

A qbrms\_fit object with additional regularisation metadata.

---

qbrms_emmeans	<i>Estimated Marginal Means for qbrms models</i>
---------------	--

---

**Description**

Compute estimated marginal means (least-squares means) for factor terms and their combinations for a qbrms\_fit, using a multivariate-normal approximation to the posterior of the fixed effects.

**Usage**

```
qbrms_emmeans(object, specs, at = NULL, nsim = 1000, prob = 0.95, ...)
```

**Arguments**

object	A qbrms_fit.
specs	Character vector naming factor(s) for EMMs, or a string containing a formula with a right-hand side (for example, "~ group" or "y ~ group"). If multiple terms are provided, a full grid is used.
at	Optional named list giving values at which to hold other predictors. Numerics are fixed at their means if not supplied; factors at their modal level.
nsim	Number of posterior draws for uncertainty.
prob	Interval mass (default 0.95).
...	Additional arguments (currently not used).

**Value**

A data frame of class qbrms\_emmeans.

---

qbrms\_fit\_log      *Get captured fit log from a qbrms object (if available)*

---

**Description**

Get captured fit log from a qbrms object (if available)

**Usage**

```
qbrms_fit_log(x)
```

**Arguments**

x                    A qbrms\_fit / qbrmO\_fit object returned by qbrm()/qbrms()

**Value**

A character vector of captured console lines, or NULL if none

---

qbrms\_ordinal\_binary      *Ordinal regression via binary decomposition (fallback)*

---

**Description**

Splits an ordered response with K levels into K-1 binary problems (thresholds  $y > c_j$ ) and fits a simple binomial GLM for each split.

**Usage**

```
qbrms_ordinal_binary(formula, data, verbose = FALSE, ...)
```

**Arguments**

formula            Model formula with an ordered response on the LHS.  
 data                Data frame.  
 verbose            Logical; print progress messages.  
 ...                Ignored (compat).

**Value**

An object of class `c("ordinal_binary_qbrms_fit", "qbrms_fit")` with:

- binary\_models: list of length K-1 of fitted glm objects
- thresholds: character vector of thresholds used
- response: response variable name
- levels: factor levels of the ordered response
- ordinal\_levels: factor levels (for test compatibility)

---

qbrms\_set\_verbosity    *Set qbrms verbosity for the current session*

---

**Description**

Set qbrms verbosity for the current session

**Usage**

```
qbrms_set_verbosity(verbose = FALSE)
```

**Arguments**

verbose            Logical. If TRUE, fitting prints progress; if FALSE, fitting is silent.

**Value**

Invisibly returns the previous value.

---

quick\_density\_comparison  
*Quick Density Comparison*

---

**Description**

Quick Density Comparison

**Usage**

```
quick_density_comparison(object, parameter = NULL, ...)
```

**Arguments**

object            A qbrms\_fit object.  
parameter        Optional parameter name to focus the comparison.  
...                Additional arguments forwarded to density\_plot().

**Value**

A ggplot2 object.

---

random\_walk\_families *Random Walk Families*

---

### Description

Random Walk Families

### Usage

```
rw1(scale.model = "log", diagonal = 1e-06)
```

```
rw2(scale.model = "log", diagonal = 1e-06)
```

### Arguments

scale.model	Scaling model for precision
diagonal	Diagonal precision matrix structure

### Value

A family object of class "family".

---

residuals.qbrms\_fit *Extract residuals from qbrms models*

---

### Description

Extract residuals from qbrms models

### Usage

```
## S3 method for class 'qbrms_fit'
residuals(object, type = "response", ...)
```

### Arguments

object	A qbrms_fit object
type	Character string indicating type of residuals (default: "response")
...	Additional arguments (currently unused)

### Value

Numeric vector of residuals

**Examples**

```
## Not run:
fit <- qbrms(mpg ~ hp, data = mtcars, family = gaussian())
resid_values <- residuals(fit, type = "response")

## End(Not run)
```

---

rope_analysis	<i>ROPE analysis</i>
---------------	----------------------

---

**Description**

Compute the posterior mass inside a Region Of Practical Equivalence (ROPE) for selected parameters.

**Usage**

```
rope_analysis(object, parameters = NULL, rope = c(-0.1, 0.1), nsim = 4000)
```

**Arguments**

object	A qbrms_fit.
parameters	Optional character vector of parameter names. If NULL, all fixed-effect coefficients are used.
rope	Numeric length-2 vector c(lower, upper).
nsim	Number of posterior draws to simulate.

**Value**

A data frame of class qbrms\_rope.

---

simplex	<i>Simplex Family for Compositional Data</i>
---------	--

---

**Description**

Simplex Family for Compositional Data

**Usage**

```
simplex(link = "logit", link.precision = "log")
```

**Arguments**

link                    Link function for the mean (default: "logit")  
link.precision        Link function for precision parameter (default: "log")

**Value**

A family object of class "family".

---

skew_normal	<i>Skew Normal Family</i>
-------------	---------------------------

---

**Description**

Skew Normal Family

**Usage**

```
skew_normal()
```

**Value**

An object of class "family" representing the Skew Normal distribution.

---

student_t	<i>Student's t Family for Robust Regression</i>
-----------	---

---

**Description**

Student's t-distribution family for robust regression with heavier tails than Gaussian to handle outliers.

Functions that act as both family constructors (for qbrm) and prior specifications (for prior), depending on arguments.

**Usage**

```
student_t(
  link_or_df = "identity",
  location = 0,
  scale = 1,
  link = NULL,
  link.sigma = "log",
  link.nu = "log",
  ...
)
```

```
student()  
  
student_t(  
  link_or_df = "identity",  
  location = 0,  
  scale = 1,  
  link = NULL,  
  link.sigma = "log",  
  link.nu = "log",  
  ...  
)  
  
student_t_prior(  
  link_or_df = 3,  
  location = 0,  
  scale = 1,  
  link.sigma = "log",  
  link.nu = "log"  
)
```

### Arguments

link_or_df	For family: link function (character). For prior: degrees of freedom (numeric).
location	Location parameter (prior only).
scale	Scale parameter (prior only).
link	Optional link function (if acting as family).
link.sigma	Link for sigma (family only).
link.nu	Link for nu (family only).
...	Additional arguments.

### Value

An object of class "family" specifying the Student-t distribution.  
An object of class "family" specifying the Student-t distribution.  
A family object or prior object depending on inputs.

### Examples

```
# Create a Student-t family object  
fam <- student_t()  
print(fam$family)
```

---

summary.qbrmb\_fit      *Summary Method for qbrmb\_fit Objects*

---

### Description

Provides a detailed summary of a regularised binomial qbrms model.

### Usage

```
## S3 method for class 'qbrmb_fit'
summary(object, digits = 2, ...)
```

### Arguments

object	A qbrmb_fit object.
digits	Number of decimal places for output (default: 2).
...	Additional arguments (currently unused).

### Value

An object of class "summary.qbrmb\_fit" containing model summary information.

---

summary.qbrms\_fit      *Summary Method for qbrms\_fit Objects*

---

### Description

Provides a detailed summary of a fitted qbrms model.

### Usage

```
## S3 method for class 'qbrms_fit'
summary(object, ..., digits = 2)
```

```
## S3 method for class 'qbrms_fit'
summary(object, ..., digits = 2)
```

### Arguments

object	A qbrms_fit object
...	Additional arguments
digits	Number of digits for output (default 2)

**Value**

An object of class "summary.qbrms\_fit" containing:

- formula: The model formula.
- family: The distribution family.
- nobs: Number of observations.
- fixed: Data frame of fixed effects estimates.
- random: Random effects summary (if applicable).

**Examples**

```
if (requireNamespace("INLA", quietly = TRUE)) {
  fit <- qbrms(mpg ~ hp, data = mtcars, family = gaussian(), verbose = FALSE)
  summary(fit)
}
```

---

summary.qbrms\_multinomial\_fit

*Summary method for multinomial qbrms fits*

---

**Description**

Print a readable summary of a qbrms\_multinomial\_fit, including its reference category, the list of categories, and per-category fixed-effect summaries when available.

**Usage**

```
## S3 method for class 'qbrms_multinomial_fit'
summary(object, digits = 2, ...)
```

**Arguments**

object	A qbrms_multinomial_fit.
digits	Integer; number of decimal places to display.
...	Unused.

**Value**

The input object, returned invisibly.

---

```
summary.qbrms_p_significance
```

*Summary Method for Enhanced p\_significance*

---

### Description

Provide a summary of probability of practical significance results.

### Usage

```
## S3 method for class 'qbrms_p_significance'
summary(object, ...)
```

```
## S3 method for class 'qbrms_p_significance'
summary(object, ...)
```

### Arguments

object	A qbrms_p_significance object from p_significance().
...	Additional arguments (currently unused).

### Value

Invisibly returns the input object.

Invisibly returns the input object.

---

```
summary.tmb_ordinal_qbrms_fit
```

*Summary Method for TMB Ordinal Fits*

---

### Description

Summary Method for TMB Ordinal Fits

### Usage

```
## S3 method for class 'tmb_ordinal_qbrms_fit'
summary(object, digits = 2, ...)
```

### Arguments

object	A tmb_ordinal_qbrms_fit object
digits	Number of decimal places for output
...	Additional arguments

**Value**

Invisibly returns the object

---

tab_model	<i>Create HTML Table for qbrms Models with Enhanced Styling</i>
-----------	---

---

**Description**

Generate APA-style HTML tables for qbrms model outputs with customizable styling options.

**Usage**

```
tab_model(
  ...,
  show.ci = TRUE,
  ci.lvl = 0.95,
  show.ropc = FALSE,
  rope = c(-0.1, 0.1),
  show.p_sig = FALSE,
  show.pd = FALSE,
  show.bf = FALSE,
  digits = 2,
  title = "Model Results",
  file = NULL,
  CSS = NULL,
  dv.labels = NULL,
  pred.labels = NULL,
  show.intercept = TRUE,
  show.r2 = FALSE,
  show.icc = FALSE,
  show.nobs = TRUE,
  bootstrap = TRUE,
  table.style = "default",
  font.family = "system-ui, -apple-system, sans-serif",
  font.size = "14px",
  header.bg = "#f8f9fa",
  stripe.bg = "#f9f9f9",
  verbose = FALSE
)
```

**Arguments**

...	One or more qbrms_fit objects to display in the table
show.ci	Logical; show credible intervals (default TRUE)
ci.lvl	Credible interval level (default 0.95)
show.ropc	Logical; show ROPE analysis (default FALSE)

rope	Numeric vector c(lower, upper) for ROPE bounds
show.p_sig	Logical; show probability of practical significance (default FALSE)
show.pd	Logical; show probability of direction (default FALSE)
show.bf	Logical; show Bayes factors (default FALSE)
digits	Number of decimal places (default 2)
title	Character; table title
file	Character; file path to save HTML output (optional)
CSS	Character; custom CSS styling (optional)
dv.labels	Character vector of dependent variable labels
pred.labels	Named character vector for predictor labels
show.intercept	Logical; show intercept row (default TRUE)
show.r2	Logical; show R-squared if available (default FALSE)
show.icc	Logical; show ICC for mixed models (default FALSE)
show.nobs	Logical; show number of observations (default TRUE)
bootstrap	Logical; use Bootstrap CSS framework (default TRUE)
table.style	Character; table style theme. Options: "default", "minimal", "academic", "modern"
font.family	Character; CSS font family (default "system-ui")
font.size	Character; base font size (default "14px")
header.bg	Character; header background colour (default "#f8f9fa")
stripe.bg	Character; striped row background colour (default "#f9f9f9")
verbose	Logical; print progress (default FALSE)

**Value**

An object of class "qbrms\_html\_table" containing the HTML code

---

test\_corrected\_bayes\_R2

*Test the corrected implementation with a mixed-effects example*

---

**Description**

Test the corrected implementation with a mixed-effects example

**Usage**

test\_corrected\_bayes\_R2()

**Examples**

```
## Not run:
# Test with mixed-effects model
library(qbrms)

# Create sample data with strong group effects
set.seed(123)
n_groups <- 10
n_per_group <- 20
n_total <- n_groups * n_per_group

data <- data.frame(
  group = factor(rep(1:n_groups, each = n_per_group)),
  x = rnorm(n_total),
  group_effect = rep(rnorm(n_groups, 0, 2), each = n_per_group)
)

# Generate response with strong group effects
data$y <- 2 + 0.5 * data$x + data$group_effect + rnorm(n_total, 0, 0.5)

# Fit mixed-effects model
fit_mixed <- qbrms(y ~ x + (1|group), data = data, family = gaussian())

# Compute Bayesian R-squared (should now match brms closely)
r2_corrected <- bayes_R2(fit_mixed, verbose = TRUE)
print(r2_corrected)

# Should show high R-squared due to strong group effects

## End(Not run)
```

---

uniform

*Specify Uniform Prior Distribution*


---

**Description**

Specify Uniform Prior Distribution

**Usage**

```
uniform(min = -Inf, max = Inf)
```

**Arguments**

min	Lower bound (default -Inf)
max	Upper bound (default Inf)

**Value**

A prior distribution object

---

 validate\_family\_quantile

*Validate Family Quantile Combination*


---

**Description**

Check if a family supports quantile regression with a given quantile value. Throws informative errors for invalid combinations.

**Usage**

```
validate_family_quantile(family_name, quantile)
```

**Arguments**

family_name	Character string specifying the family name.
quantile	Numeric quantile value (or NULL).

**Value**

TRUE if the combination is valid (invisibly), throws error otherwise.

---

 vcov.qbrms\_fit

*Extract Variance-Covariance Matrix from qbrms Models*


---

**Description**

Extract Variance-Covariance Matrix from qbrms Models

**Usage**

```
## S3 method for class 'qbrms_fit'
vcov(object, ...)
```

**Arguments**

object	A qbrms_fit object
...	Additional arguments (unused)

**Value**

Variance-covariance matrix

---

`vcov.tmb_ordinal_qbrms_fit`*Variance-Covariance Matrix Method for TMB Ordinal Fits*

---

**Description**

Variance-Covariance Matrix Method for TMB Ordinal Fits

**Usage**

```
## S3 method for class 'tmb_ordinal_qbrms_fit'  
vcov(object, ...)
```

**Arguments**

<code>object</code>	A <code>tmb_ordinal_qbrms_fit</code> object
<code>...</code>	Additional arguments

**Value**

Variance-covariance matrix

---

`view_table`*Display HTML Table in Viewer*

---

**Description**

Display HTML Table in Viewer

**Usage**`view_table(x)`**Arguments**

<code>x</code>	A <code>qbrms_html_table</code> created by <code>tab_model()</code> .
----------------	---

---

**visualise\_prior**      *Visualise Prior Distributions*

---

**Description**

Create visual representations of prior distributions to aid in prior specification and sensitivity analysis.

**Usage**

```
visualise_prior(  
  prior,  
  parameter = NULL,  
  xlim = NULL,  
  add_reference = TRUE,  
  samples = 10000  
)
```

**Arguments**

<code>prior</code>	Prior specification in qbrms format, or a list of prior specifications to compare
<code>parameter</code>	Character string specifying which parameter to visualise (e.g., "b", "sd", "sigma"). If NULL, visualises all priors.
<code>xlim</code>	Numeric vector of length 2 specifying x-axis limits. If NULL, automatically determined.
<code>add_reference</code>	Logical; if TRUE, adds reference distributions for comparison (default: TRUE)
<code>samples</code>	Number of samples to draw for visualisation (default: 10000)

**Details**

This function helps users:

- Visualise the implications of their prior choices
- Compare different prior specifications
- Identify overly informative or vague priors
- Understand prior-data conflict potential

Supported prior distributions include:

- Normal: `normal(mean, sd)`
- Student t: `student_t(df, mean, scale)`
- Cauchy: `cauchy(location, scale)`
- Exponential: `exponential(rate)`
- Gamma: `gamma(shape, rate)`
- Uniform: `uniform(lower, upper)`

**Value**

A ggplot object showing the prior distribution(s)

**Examples**

```
## Not run:
# Visualise a single prior
prior <- prior(normal(0, 10), class = "b")
visualise_prior(prior)

# Compare different priors
prior_list <- list(
  "Weak" = prior(normal(0, 10), class = "b"),
  "Medium" = prior(normal(0, 5), class = "b"),
  "Strong" = prior(normal(0, 1), class = "b")
)
visualise_prior(prior_list)

# Visualise with custom limits
visualise_prior(prior, xlim = c(-20, 20))

## End(Not run)
```

---

weibull

*Weibull Survival Family*

---

**Description**

Weibull Survival Family

**Usage**

```
weibull(link = "log", link.shape = "log")
```

**Arguments**

link	Link function for scale (default: "log")
link.shape	Link function for shape (default: "log")

**Value**

A family object of class "family".

---

zero\_inflated\_negbinomial

*Zero-Inflated Negative Binomial Family*

---

**Description**

Zero-Inflated Negative Binomial Family

**Usage**

```
zero_inflated_negbinomial(link = "log", link.zi = "logit")
```

```
zinb(link = "log", link.zi = "logit")
```

**Arguments**

link            Link function for mean (default: "log")

link.zi        Link function for zero-inflation (default: "logit")

**Value**

A family object of class "family".

---

zero\_inflated\_poisson *Zero-Inflated Poisson Family*

---

**Description**

Zero-Inflated Poisson Family

**Usage**

```
zero_inflated_poisson(link = "log", link.zi = "logit")
```

```
zip()
```

**Arguments**

link            Link function for mean (default: "log")

link.zi        Link function for zero-inflation (default: "logit")

**Value**

A family object of class "family".

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