

Package: BayesRTMB (via r-universe)

October 11, 2026

Type Package

Title Bayesian Inference Using 'RTMB'

Version 0.4.0

Description Provides tools for Markov chain Monte Carlo (MCMC) and Maximum A Posteriori (MAP) estimation utilizing the 'RTMB' package. It supports various statistical models including generalized linear mixed models, factor analysis, item response theory, and multidimensional unfolding. The package allows users to easily transition between frequentist and Bayesian paradigms using a unified interface. Automatic differentiation and Laplace approximation follow Kristensen et al. (2016) <[doi:10.18637/jss.v070.i05](https://doi.org/10.18637/jss.v070.i05)>, and MCMC sampling uses the No-U-Turn Sampler described by Hoffman and Gelman (2014) <<https://jmlr.org/papers/v15/hoffman14a.html>>.

License MIT + file LICENSE

Encoding UTF-8

Language en-US

LazyData true

Depends R (>= 4.1.0), RTMB

Imports R6, MASS

URL <https://github.com/norimune/BayesRTMB>,
<https://norimune.github.io/BayesRTMB/>

BugReports <https://github.com/norimune/BayesRTMB/issues>

Suggests knitr, rmarkdown, GPArotation, future

VignetteBuilder knitr

Config/roxygen2/version 8.0.0

RoxygenNote 7.3.3

Repository <https://norimune.r-universe.dev>

Date/Publication 2026-09-10 10:48:23 UTC

RemoteUrl <https://github.com/norimune/bayesrtmb>

RemoteRef HEAD

RemoteSha 7761adfa5c8884db7cf067a9d93c142bfa7c0ee8

Contents

ADVI_method	4
bayes_factor	6
beverage	6
BigFive	7
center_grand_mean	8
center_within_cluster	9
Classic_Fit	9
conditional_effects	17
conditional_effects.mcmc_fit	18
debate	19
diffusion_lpdf	19
Dim	20
distance	21
distributions	21
ess_basic	23
ess_bulk	23
ess_tail95	24
exp_mod_normal_lpdf	24
fabs	25
gaussian_process_lpdf	25
generate_random_init	26
inv_logit	27
item_curve	27
item_curve.RTMB_Fit_Base	28
item_info	28
item_info.RTMB_Fit_Base	29
log_det_chol	29
log_mix	30
log_softmax	30
log_sum_exp	31
log_sum_exp_matrix	31
log1m	32
log1m_exp	32
log1p_exp	33
logit	33
lsmeans	34
make_bw_from_ydif	34
make_glmer_re_terms	35
make_glmer_Z_matrix	36
make_init_mdu	36
make_ydif_from_bw	37
map_est	38

MAP_Fit	38
math_functions	43
MCMC_Fit	45
parameter_types	53
parameters_code	54
plot.ce_rtmb	55
plot.rtmb_lsmeans	55
plot_acf	56
plot_conditional_effects	56
plot_dens	57
plot_forest	58
plot_item_curve	58
plot_item_info	59
plot_lsmeans	59
plot_mdu	60
plot_pairs	61
plot_test_info	62
plot_trace	62
posterior_predict	63
pp_check	63
print.bayes_factor	65
print.bayes_factor_rtmb	65
print.ce_rtmb	66
print.ce_simple	66
print.summary_BayesRTMB	67
prior_flat	67
prior_jzs	68
prior_normal	68
prior_rhs	69
prior_ssp	70
prior_uniform	70
prior_weak	71
quad_form_chol	71
quad_form_diag	72
quantile95	72
r_hat	73
read_mcmc_csv	73
rhat_summary	74
rtmb_array	75
rtmb_code	75
rtmb_corr	77
rtmb_fa	79
RTMB_Fit_Base	80
rtmb_glm	85
rtmb_glmer	87
rtmb_irt	90
rtmb_lm	92
rtmb_lmer	95

rtmb_loglinear	98
rtmb_lrt	99
rtmb_mdu	100
rtmb_mediation	102
rtmb_mixture	104
rtmb_model	105
RTMB_Model-class	108
rtmb_syntax	119
rtmb_table	120
rtmb_ttest	121
rtmb_vector	123
rtmb_wrappers	123
safe_rtmb_model	124
simple_effects	125
simple_effects.mcmc_fit	126
softmax	127
sort_loadings	127
squared_distance	128
stz_basis	128
sum_to_zero	129
summary.ce_rtmb	129
summary_mcmc	130
test_info	131
to_centered_matrix	131
to_centered_tri	132
to_long	132
to_lower_tri	133
to_wide	134
training	134
transform_code	135
upgrade_fit	136
validate_data	136
VB_Fit	137

Index**144**

ADVI_method

*Automatic Differentiation Variational Inference (ADVI)***Description**

Automatic Differentiation Variational Inference (ADVI)

Usage

```
ADVI_method(
  model,
  par_list,
  pl_full,
  iter = 3000,
  tol_rel_obj = 0.001,
  window_size = 100,
  num_samples = 1000,
  alpha = 0.01,
  laplace = FALSE,
  print_freq = 500,
  method = c("meanfield", "fullrank", "hybrid"),
  update_progress = NULL,
  update_interval = 100
)
```

Arguments

<code>model</code>	An RTMB objective function object ('ad_obj').
<code>par_list</code>	A list defining the structure of parameters to be estimated.
<code>pl_full</code>	A list defining the full structure of parameters including random effects.
<code>iter</code>	Integer; fixed number of iterations for the optimization. Default is 3000.
<code>tol_rel_obj</code>	Numeric; relative tolerance for the ELBO to check convergence. Default is 0.001.
<code>window_size</code>	Integer; size of the moving window to calculate the median ELBO. Default is 100.
<code>num_samples</code>	Integer; number of posterior draws to generate after optimization. Default is 1000.
<code>alpha</code>	Numeric; learning rate (step size) for the Adam optimizer. Default is 0.01.
<code>laplace</code>	Logical; whether Laplace approximation is used. Default is FALSE.
<code>print_freq</code>	Integer; frequency of printing progress to the console. Set to 0 to disable. Default is 500.
<code>method</code>	Character; type of variational distribution. One of "meanfield", "fullrank", or "hybrid". Default is "meanfield".
<code>update_progress</code>	Optional function for progress reporting.
<code>update_interval</code>	Integer; interval for progress updates. Default is 100.

Value

A list containing 'fit', 'random_fit', 'elbo_history', 'elbo_final', 'rel_obj_final', and 'converged'.

bayes_factor	<i>Calculate Bayes Factor</i>
--------------	-------------------------------

Description

Compare two models by calculating the Bayes Factor based on their marginal likelihoods.

Usage

```
bayes_factor(logml1, logml2, error_threshold = 0.2)
```

Arguments

logml1	The first model fit (e.g., 'mcmc_fit') or its log-marginal likelihood.
logml2	The second model fit (e.g., 'mcmc_fit') or its log-marginal likelihood.
error_threshold	Threshold for warning about high bridge-sampling error (default 0.2).

Value

An object of class 'bayes_factor' containing the Bayes factor, log Bayes factor, approximate estimation error, and interpretation.

Examples

```
# Compare two models using Bayes Factor
data(debate, package = "BayesRTMB")
fit1 <- rtmb_lm(sat ~ talk, data = debate)
fit2 <- rtmb_lm(sat ~ talk + perf, data = debate)
map1 <- fit1$optimize()
map2 <- fit2$optimize()
bf <- bayes_factor(map1, map2)
print(bf)
```

beverage	<i>Beverage Preference Data</i>
----------	---------------------------------

Description

A dataset containing preference ratings for various beverages. This data was used to demonstrate a random effect model in metric multidimensional unfolding.

Usage

```
beverage
```

Format

A data frame (or matrix) with [INSERT NUMBER OF ROWS] rows and [INSERT NUMBER OF COLUMNS] columns.

AJ Apple Juice preference rating

BT Black Tea preference rating

CF Coffee preference rating

CL Cola preference rating

GT Green Tea preference rating

OJ Orange Juice preference rating

OT Oolong Tea preference rating

Source

Adachi, K. (2000). A Random Effect Model in Metric Multidimensional Unfolding. *The Japanese Journal of Behaviormetrics*, 27(1), 12-23. doi:10.2333/jbhmk.27.12

BigFive

Big Five Personality Traits Data

Description

A dataset containing responses to 20 items measuring the Big Five personality traits. This dataset was originally collected by the package author. The items are arranged in a cyclical order representing the five factors: Extraversion, Neuroticism, Openness, Agreeableness, and Conscientiousness.

Usage

BigFive

Format

A data frame with 10 rows and 20 columns:

BF1 Extraversion item 1

BF2 Neuroticism item 1

BF3 Openness item 1

BF4 Agreeableness item 1

BF5 Conscientiousness item 1

BF6 Extraversion item 2

BF7 Neuroticism item 2

BF8 Openness item 2

BF9 Agreeableness item 2

BF10 Conscientiousness item 2
BF11 Extraversion item 3
BF12 Neuroticism item 3
BF13 Openness item 3
BF14 Agreeableness item 3
BF15 Conscientiousness item 3
BF16 Extraversion item 4
BF17 Neuroticism item 4
BF18 Openness item 4
BF19 Agreeableness item 4
BF20 Conscientiousness item 4

Source

Originally collected by the package author.

center_grand_mean	<i>Center a Numeric Variable Around Its Grand Mean</i>
-------------------	--

Description

Subtracts the overall mean from a numeric vector. This helper is used by the regression wrappers in their generated ‘setup’ code and can also be used in hand-written ‘rtmb_code()’ models.

Usage

```
center_grand_mean(x, na.rm = TRUE)
```

Arguments

x	Numeric vector to center.
na.rm	Logical; whether missing values are removed when calculating the mean.

Value

A numeric vector with the same length as ‘x’.

Examples

```
center_grand_mean(c(1, 2, 3))
```

center_within_cluster *Center a Numeric Variable Within Clusters*

Description

Subtracts each cluster mean from a numeric vector. Missing cluster values produce missing centered values. This helper is used by the regression wrappers in their generated ‘setup’ code and can also be used in hand-written ‘rtmb_code()’ models.

Usage

```
center_within_cluster(x, cluster, na.rm = TRUE)
```

Arguments

x	Numeric vector to center.
cluster	Vector identifying the cluster for each element of ‘x’.
na.rm	Logical; whether missing values are removed when calculating cluster means.

Value

A numeric vector with the same length as ‘x’.

Examples

```
center_within_cluster(c(1, 3, 2, 6), c("a", "a", "b", "b"))
```

Classic_Fit *Classic fit object*

Description

An R6 class representing the results of a classical (frequentist) estimation.

Super class

[BayesRTMB::RTMB_Fit_Base](#) -> Classic_Fit

Public fields

model The 'RTMB_Model' object used for estimation.
fit The result of the estimation (dataframe or lm object).
par a named list of parameter estimates.
vcov Variance-covariance matrix of fixed effects.
se_method Character string specifying the method used for standard errors.
cluster Character string specifying the cluster variable name, if any.
robust_type Character string specifying the robust standard error correction type, if used.
bootstrap_results A matrix containing bootstrap samples, if applicable.
test_results List of additional test results (e.g., `chisq.test`).
view Character vector of parameter names to prioritize in summary.
par_vec Numeric vector of parameter estimates.
objective Final objective value.
log_lik Log-likelihood.
restricted_log_lik Restricted log-likelihood, if classical estimation used REML-style marginalization.
rss Residual sum of squares for classical linear models, if available.
df_residual Residual degrees of freedom for classical linear models, if available.
convergence Convergence code.
sd_rep TMB `sdreport` object.
df_fixed Dataframe of fixed effects results.
random_effects Dataframe of random effects results.
df_transform Dataframe of transformed parameters.
df_generate Dataframe of generated quantities.
opt_history Dataframe of optimization history.
transform List of transformed parameters.
generate List of generated quantities.
se_samples List of simulated samples for SE estimation.
par_unc Numeric vector of unconstrained parameter estimates.
vcov_unc Variance-covariance matrix of parameters in unconstrained space.
ci_method Method used for CI estimation.
laplace Whether Laplace approximation was used.
map Parameter mapping used.
df_method Character string specifying the degrees of freedom calculation method.
idx_fix_active Numeric vector; mapping between active parameters and full unconstrained vector.
show_df Logical; whether to display degrees of freedom in the summary output.

Methods**Public methods:**

- `Classic_Fit$get_point_estimate()`
- `Classic_Fit$new()`
- `Classic_Fit$robust_se()`
- `Classic_Fit$compute_robust()`
- `Classic_Fit$bootstrap()`
- `Classic_Fit$compute_bootstrap()`
- `Classic_Fit$AIC()`
- `Classic_Fit$BIC()`
- `Classic_Fit$WAIC()`
- `Classic_Fit$diagnose()`
- `Classic_Fit$print()`
- `Classic_Fit$logLik()`
- `Classic_Fit$EAP()`
- `Classic_Fit$MAP()`
- `Classic_Fit$summary()`
- `Classic_Fit$anova()`
- `Classic_Fit$lsmeans()`
- `Classic_Fit$.calc_contrast()`
- `Classic_Fit$.get_lsmeans_df()`
- `Classic_Fit$.construct_par_list()`
- `Classic_Fit$clone()`

Method `get_point_estimate()`: Get point estimate for a target parameter.

Usage:

```
Classic_Fit$get_point_estimate(target, ...)
```

Arguments:

`target` Target parameter name.

`...` Additional arguments, ignored for classic fits.

Returns: Matrix, array, vector, or scalar point estimate.

Method `new()`: Create a new 'Classic_Fit' object.

Usage:

```
Classic_Fit$new(  
  model,  
  par_vec = NULL,  
  par = NULL,  
  objective = NULL,  
  log_lik = NULL,  
  restricted_log_lik = NULL,  
  convergence = NULL,  
  sd_rep = NULL,
```

```

df_fixed = NULL,
random_effects = NULL,
df_transform = NULL,
df_generate = NULL,
opt_history = NULL,
transform = NULL,
generate = NULL,
se_samples = NULL,
par_unc = NULL,
vcov_unc = NULL,
ci_method = "wald",
laplace = TRUE,
map = NULL,
test_results = list(),
view = NULL,
fit = NULL,
vcov = NULL,
df_method = "auto",
idx_fix_active = NULL,
show_df = TRUE,
rss = NULL,
df_residual = NULL,
...
)

```

Arguments:

`model` The 'RTMB_Model' object.

`par_vec` Numeric vector of parameter estimates.

`par` List of parameter estimates.

`objective` Final objective value.

`log_lik` Full log-likelihood used for information criteria.

`restricted_log_lik` Restricted log-likelihood, if classical estimation used REML-style marginalization.

`convergence` Convergence code.

`sd_rep` TMB sdreport object.

`df_fixed` Dataframe of fixed effects results.

`random_effects` Dataframe of random effects results.

`df_transform` Dataframe of transformed parameters.

`df_generate` Dataframe of generated quantities.

`opt_history` Dataframe of optimization history.

`transform` List of transformed parameters.

`generate` List of generated quantities.

`se_samples` List of simulated samples for SE estimation.

`par_unc` Parameter vector on unconstrained scale.

`vcov_unc` Covariance matrix on unconstrained scale.

`ci_method` Method used for CI estimation.

laplace Whether Laplace approximation was used.
 map Parameter mapping used.
 test_results List of additional test results (e.g., `chisq.test`).
 view Character vector of parameter names to prioritize in summary.
 fit Legacy argument for backward compatibility (maps to `df_fixed`).
 vcov Variance-covariance matrix of parameters.
 df_method Method for degrees of freedom calculation.
 idx_fix_active Numeric vector; mapping between active parameters and full unconstrained vector.
 show_df Logical; whether to display degrees of freedom in the summary output.
 rss Residual sum of squares for classical linear models, if available.
 df_residual Residual degrees of freedom for classical linear models, if available.
 ... Additional arguments passed to the constructor.

Method `robust_se()`: Compute robust standard errors (sandwich estimator).

Usage:

```
Classic_Fit$robust_se(
  cluster = NULL,
  type = c("HC3", "HC0", "HC1", "CR1", "CR0"),
  inplace = FALSE,
  ...
)
```

Arguments:

cluster Character; variable name for clustering.
 type Character; "HC3" (default), "HC0", or "HC1" for non-clustered robust SE; "CR1" or "CR0" for clustered robust SE.
 inplace Logical; if FALSE, return a robust-SE copy without modifying the original fit. If TRUE, update the object in place.
 ... Additional arguments.

Returns: Self.

Method `compute_robust()`: (Deprecated) Use `robust_se()` instead.

Usage:

```
Classic_Fit$compute_robust(...)
```

Arguments:

... Arguments passed to `robust_se()`, including `inplace`.

Returns: Self.

Method `bootstrap()`: Compute nonparametric bootstrap standard errors and confidence intervals. Currently implemented only for mediation models. Bootstrap refits mediation equations with base R `lm.fit()/glm.fit()` when possible, and falls back to RTMB refits for unsupported families.

Usage:

```
Classic_Fit$bootstrap(n_boot = 1000, seed = NULL, inplace = FALSE, ...)
```

Arguments:

`n_boot` Integer; number of bootstrap samples.

`seed` Optional integer random seed.

`inplace` Logical; if FALSE, return a bootstrap-SE copy without modifying the original fit. If TRUE, update the object in place.

... Additional arguments.

Returns: A `Classic_Fit` object.

Method `compute_bootstrap()`: Compute nonparametric bootstrap standard errors and confidence intervals. Currently implemented only for mediation models. Bootstrap refits mediation equations with base R `lm.fit()/glm.fit()` when possible, and falls back to RTMB refits for unsupported families.

Usage:

```
Classic_Fit$compute_bootstrap(n_boot = 1000, seed = NULL, inplace = FALSE, ...)
```

Arguments:

`n_boot` Integer; number of bootstrap samples.

`seed` Optional integer random seed.

`inplace` Logical; if FALSE, return a bootstrap-SE copy without modifying the original fit. If TRUE, update the object in place.

... Additional arguments.

Returns: A `Classic_Fit` object.

Method `AIC()`: Get the AIC of the fitted model.

Usage:

```
Classic_Fit$AIC()
```

Method `BIC()`: Get the BIC of the fitted model.

Usage:

```
Classic_Fit$BIC()
```

Method `WAIC()`: WAIC is not defined for classical fits.

Usage:

```
Classic_Fit$WAIC()
```

Method `diagnose()`: Run basic diagnostics for the classical fit.

Usage:

```
Classic_Fit$diagnose(...)
```

Arguments:

... Additional arguments passed to `'diagnose_classic_fit()'`.

Returns: A `'diagnose_BayesRTMB'` object.

Method `print()`: Print the fit results.

Usage:

```
Classic_Fit$print(...)
```

Arguments:

... Additional arguments passed to 'summary()'.

Method logLik(): Get the Log-Likelihood of the fitted model.

Usage:

```
Classic_Fit$logLik()
```

Method EAP(): EAP estimates are not available for Classic_Fit.

Usage:

```
Classic_Fit$EAP(...)
```

Arguments:

... Ignored.

Method MAP(): MAP estimates are not available for Classic_Fit.

Usage:

```
Classic_Fit$MAP(...)
```

Arguments:

... Ignored.

Method summary(): Display a summary of the estimation results.

Usage:

```
Classic_Fit$summary(view = NULL, digits = 5, max_rows = 10, ranef = FALSE)
```

Arguments:

view Character vector of parameter names to prioritize or filter by.

digits Number of digits to print for estimates.

max_rows Maximum number of rows to display in the coefficient table.

ranef Logical; whether to show random effects in the summary.

Method anova(): Perform ANOVA (Wald F-tests / Chisq-tests) on the fitted model.

Usage:

```
Classic_Fit$anova(method = c("reml", "ls"), type = 3)
```

Arguments:

method Character; "reml" (standard) or "ls" (experimental).

type Integer; Type of Sum of Squares (only Type III supported currently).

Returns: A data frame containing the ANOVA table.

Method lsmeans(): Calculate Least Squares Means (Marginal Means) and contrasts.

Usage:

```
Classic_Fit$lsmeans(
  specs = NULL,
  pairwise = FALSE,
  simple = NULL,
  adjust = "holm",
  protect = FALSE
)
```

Arguments:

`specs` Character vector of factors to calculate means for.
`pairwise` Logical; whether to perform pairwise comparisons.
`simple` Character vector of factors to hold constant for simple main effects.
`adjust` Character; p-value adjustment method (e.g., "bonferroni", "holm", "none").
`protect` Logical; whether to use hierarchical (protected) testing.

Returns: A data frame containing the marginal means or contrasts.

Method `.calc_contrast()`: (Internal) Calculate metrics for a contrast.

Usage:

```
Classic_Fit$.calc_contrast(L, specs)
```

Arguments:

`L` Contrast matrix.
`specs` Variable names for lsmeans.

Returns: A data frame with estimate, SE, df, t-value, and p-value.

Method `.get_lsmeans_df()`: (Internal) Get representative DF for lsmeans.

Usage:

```
Classic_Fit$.get_lsmeans_df(specs)
```

Arguments:

`specs` Variable names for lsmeans.

Returns: Degrees of freedom.

Method `.construct_par_list()`: (Internal) Construct a list of parameters from the fit.

Usage:

```
Classic_Fit$.construct_par_list(fit)
```

Arguments:

`fit` The fit result (dataframe or lm object).

Returns: A named list of parameters.

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

```
Classic_Fit$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

conditional_effects *Calculate Conditional Effects*

Description

Calculate and visualize the predicted values (marginal effects) of a variable, potentially conditional on the levels of another variable (interaction).

Usage

```
conditional_effects(
  fit,
  effect,
  prob = 0.95,
  sd_multiplier = 1,
  sd_slice = NULL,
  ...
)
```

Arguments

<code>fit</code>	Model fit object (e.g., 'mcmc_fit', 'map_fit').
<code>effect</code>	Name of the variable to visualize (e.g., "X1" or "X1:X2").
<code>prob</code>	Probability for the credible/confidence interval (default is 0.95).
<code>sd_multiplier</code>	Numeric. Multiplier for standard deviation when splitting continuous moderators (default is 1).
<code>sd_slice</code>	Logical or NULL. If TRUE, continuous moderators are evaluated at mean - SD, mean, and mean + SD. If FALSE, all observed moderator values are used. If NULL (default), sd slicing is used automatically when the moderator has 6 or more unique values.
<code>...</code>	Additional arguments.

Value

An object of class 'ce_rtmb' containing the predicted values and their credible intervals.

Examples

```
data(debate, package = "BayesRTMB")
fit <- rtmb_lm(sat ~ talk * perf, data = debate)
map_fit <- fit$optimize()
ce <- conditional_effects(map_fit, effect = "talk:perf")
plot(ce)
summary(ce)
```

conditional_effects.mcmc_fit

Calculate conditional effects for MCMC fit objects

Description

Calculate conditional effects for MCMC fit objects

Usage

```
## S3 method for class 'mcmc_fit'
conditional_effects(
  fit,
  effect,
  prob = 0.95,
  sd_multiplier = 1,
  sd_slice = NULL,
  resolution = 100,
  ...
)
```

Arguments

fit	An object of class 'MCMC_Fit'.
effect	Name of the explanatory variable to visualize (e.g., "X1" or "X1:X2").
prob	Probability for the credible/confidence interval (default is 0.95).
sd_multiplier	Numeric. Multiplier for standard deviation when splitting continuous moderators (default is 1).
sd_slice	Logical or NULL. If TRUE, continuous moderators are evaluated at mean - SD, mean, and mean + SD. If FALSE, all observed moderator values are used. If NULL (default), sd slicing is used automatically when the moderator has 6 or more unique values.
resolution	Grid resolution to calculate for continuous variables (default is 100).
...	Additional arguments.

Value

A 'ce_rtmb' object.

debate

*Debate Simulation Data***Description**

A simulated dataset containing individual satisfaction scores and related variables from a 3-person group debate experiment. This dummy data was created by the package author to demonstrate hierarchical (multilevel) modeling.

Usage

debate

Format

A data frame with 300 rows and 6 columns:

group Group identifier. Each group consists of 3 members.

sat Self-reported satisfaction level of the individual after the debate.

talk Amount of talk or utterances by the individual during the debate.

perf Evaluated performance of the group debate (group-level variable).

skill Evaluated conversation skill of the individual.

cond Experimental condition indicator (e.g., 0 = control, 1 = treatment).

Source

Simulated dummy data created by the package author.

diffusion_lpdf

*Diffusion model log-probability density function***Description**

Log-likelihood for a two-boundary drift diffusion model. The first argument is the response time and the second argument is the binary response. Positive response values are treated as upper-boundary responses; zero or negative values are treated as lower-boundary responses.

If x is a matrix, rows are treated as independent units and columns as repeated trials. In that case, `sum = FALSE` returns one log-likelihood contribution per row. If x is a vector, `sum = FALSE` returns one contribution per observation.

Usage

```
diffusion_lpdf(x, response, alpha, tau, beta, delta, K_diff = 20, sum = TRUE)
```

Arguments

x	Response times. A vector, or a matrix with units in rows and trials in columns.
response	Binary responses with the same shape as x. Positive values indicate the upper boundary.
alpha	Boundary separation. A scalar, row-wise vector, trial-wise vector, or matrix compatible with x.
tau	Non-decision time. A scalar, row-wise vector, trial-wise vector, or matrix compatible with x.
beta	Initial bias as a proportion of the boundary separation. A scalar, row-wise vector, trial-wise vector, or matrix compatible with x.
delta	Drift rate. A scalar, row-wise vector, trial-wise vector, or matrix compatible with x.
K_diff	Number of terms in the truncated infinite-series approximation.
sum	Logical; if TRUE (default), returns the summed log-likelihood.

Value

The summed log-likelihood, row-wise log-likelihoods for matrix input, or observation-wise log-likelihoods for vector input.

Dim

Define parameter dimensions and types

Description

Define parameter dimensions and types

Usage

```
Dim(dim = 1, type = NULL, lower = NULL, upper = NULL, random = FALSE)
```

Arguments

dim	Dimensions of the parameter.
type	Type of the parameter.
lower	Lower bound.
upper	Upper bound.
random	Logical; whether it is a random effect.

distance	<i>Euclidean distance</i>
----------	---------------------------

Description

Euclidean distance

Usage

```
distance(x, y, eps = 1e-08)
```

Arguments

x	A numeric vector.
y	A numeric vector.
eps	A small value added for numerical stability (default is 1e-8).

Value

The Euclidean distance between x and y.

distributions	<i>Probability Distributions for RTMB Models</i>
---------------	--

Description

This page summarizes the probability distributions available within the ‘rtmb_code’ block. These functions are designed to be used with the Stan-like sampling syntax (‘~’), which internally adds the log-density to the model’s total log-posterior.

Details

Syntax Styles: In ‘rtmb_code’, you can specify distributions in two ways:

- **Sampling Syntax (Recommended):** `y ~ normal(mu, sigma)`
- **Explicit Function Call:** `lp <- lp + normal_lpdf(y, mu, sigma)`

Continuous Distributions (LPDF):

- `normal(mean, sd)`: Normal distribution.
- `lognormal(meanlog, sdlog)`: Lognormal distribution.
- `exp_mod_normal(mu, sigma, lambda)`: Exponentially modified normal distribution.
- `exponential(rate)`: Exponential distribution.
- `cauchy(location, scale)`: Cauchy distribution.

- `student_t(df, mu, sigma)`: Student's t-distribution.
- `gamma(shape, rate)`: Gamma distribution.
- `inverse_gamma(shape, scale)`: Inverse-gamma distribution.
- `beta(a, b)`: Beta distribution.

Discrete Distributions (LPMF):

- `bernoulli(prob)` / `bernoulli_logit(eta)`: Binary outcomes.
- `binomial(size, prob)` / `binomial_logit(size, eta)`: Binomial outcomes.
- `poisson(mean)`: Poisson count data.
- `neg_binomial_2(mu, size)`: Negative binomial (mean/dispersion parameterization).
- `ordered_logistic(eta, cutpoints)`: Ordered categorical outcomes.
- `sequential_logistic(eta, cutpoints)`: Sequential ordered categorical outcomes.

Multivariate and Matrix Distributions:

- `multi_normal(mean, Sigma)`: Standard multivariate normal distribution.
- `multi_student_t(df, mean, Sigma)`: Multivariate Student's t-distribution.
- `multi_cauchy(mean, Sigma)`: Multivariate Cauchy distribution (Student-t with $df=1$).
- `gaussian_process(x, mean, magnitude, smoothing, noise)`: Gaussian process prior with a squared exponential kernel.
- `lkj_corr(eta)`: LKJ prior for correlation matrices.
- `dirichlet(alpha)`: Dirichlet distribution for simplexes.
- `lower_tri_normal(mean, sd)`: Normal distribution for elements of a lower-triangular matrix.
- `centered_tri_multi_normal(sigma)`: Multivariate normal for centered triangular matrices (used in identification constraints).
- `sufficient_multi_normal_fa(S_mat, N, y_bar, mu, psi, Lambda)`: Factor analysis likelihood using sufficient statistics (highly efficient for large sample sizes).

Response-time Distributions:

- `diffusion(alpha, tau, beta, delta)`: Drift diffusion model likelihood for response times and binary choices. Use with `obs(RT, Choice) ~ diffusion(...)`.

Vectorization: Most univariate distributions are vectorized. If y and μ are vectors, `y ~ normal(mu, sigma)` will calculate the sum of log-densities for all elements efficiently.

`ess_basic`*Basic Effective Sample Size for a single chain or pooled chains*

Description

Basic Effective Sample Size for a single chain or pooled chains

Usage

```
ess_basic(sims)
```

Arguments

`sims` A numeric vector or matrix of samples.

Value

A numeric value.

`ess_bulk`*Calculate Bulk Effective Sample Size*

Description

Calculate Bulk Effective Sample Size

Usage

```
ess_bulk(sims)
```

Arguments

`sims` A matrix of samples (iterations x chains).

Value

A numeric value.

ess_tail95	<i>Calculate Tail Effective Sample Size (at 2.5% and 97.5% quantiles)</i>
------------	---

Description

Calculate Tail Effective Sample Size (at 2.5% and 97.5% quantiles)

Usage

```
ess_tail95(sims)
```

Arguments

sims	A matrix of samples (iterations x chains).
------	--

Value

A numeric value.

exp_mod_normal_lpdf	<i>Exponentially modified normal log-probability density function</i>
---------------------	---

Description

Log-density for $X = Z + E$, where Z follows a normal distribution with mean μ and standard deviation σ , and E follows an exponential distribution with rate λ .

Usage

```
exp_mod_normal_lpdf(x, mu, sigma, lambda, sum = TRUE)
```

Arguments

x	Vector of quantiles.
mu	Mean of the normal component.
sigma	Standard deviation of the normal component.
lambda	Rate of the exponential component.
sum	Logical; if TRUE (default), returns the sum of log-densities. If FALSE, returns element-wise log-densities.

Value

The sum of the log-density or a vector of log-densities.

fabs	<i>Smooth absolute value function</i>
------	---------------------------------------

Description

Smooth absolute value function

Usage

```
fabs(x, eps = 1e-08)
```

Arguments

x	A numeric vector.
eps	A small value added for numerical stability (default is 1e-8).

Value

The smooth absolute value of x.

gaussian_process_lpdf	<i>Gaussian Process Log-Density (Squared Exponential Kernel)</i>
-----------------------	--

Description

Calculates the log-density of a Gaussian Process with a Squared Exponential (RBF) kernel.

Usage

```
gaussian_process_lpdf(
  y,
  x,
  mean = 0,
  magnitude = 1,
  smoothing = 1,
  noise = 0.01,
  sum = TRUE
)
```

Arguments

y	Observation vector (N), or matrix (M x N) whose rows are independent GP realizations on the same coordinates.
x	Coordinate vector or matrix (N x D), where N matches length(y) for vector y or ncol(y) for matrix y.
mean	Mean vector (scalar, length N, or M x N matrix for matrix y).
magnitude	Signal standard deviation (alpha).
smoothing	Length-scale (rho).
noise	Measurement noise standard deviation (sigma).
sum	Logical; whether to return the sum of log-densities. If FALSE and y is a matrix, returns one log-density per row.

Value

Log-density value.

generate_random_init *Generate Random Initial Values*

Description

Generates random initial values for model parameters by drawing from a uniform distribution on the unconstrained scale and then transforming them to the constrained scale.

Usage

```
generate_random_init(pl_full, par_list, range = 2)
```

Arguments

pl_full	A list containing the full parameter structure, including the 'init' field which serves as a template.
par_list	A list defining the structure and constraints of the parameters, including 'unc_length'.
range	Numeric; the range for the uniform distribution '[-range, range]' used for generating unconstrained values. Default is 2.

Value

A numeric vector of initial values where 'NA' elements are replaced with randomly generated constrained values.

inv_logit	<i>Inverse logit function</i>
-----------	-------------------------------

Description

Inverse logit function

Usage

```
inv_logit(x)
```

Arguments

x	A numeric vector.
---	-------------------

Value

The inverse logit of x.

item_curve	<i>Calculate Item Response Curve / Category Response Curve</i>
------------	--

Description

Calculate Item Response Curve / Category Response Curve

Usage

```
item_curve(x, ...)
```

Arguments

x	An object of class
...	Additional arguments.

```
item_curve.RTMB_Fit_Base
```

Item Response Curve for RTMB_Fit_Base

Description

Item Response Curve for RTMB_Fit_Base

Usage

```
## S3 method for class 'RTMB_Fit_Base'
item_curve(x, theta_seq = seq(-4, 4, length.out = 100), items = NULL, ...)
```

Arguments

x	An object of class RTMB_Fit_Base.
theta_seq	Sequence of trait values (ability) to evaluate.
items	Index or item names to restrict the calculation to specific items (optional).
...	Additional arguments.

Examples

```
fit <- rtmb_irt(data = BigFive[, 1:5], model = "2PL", type = "ordered")
map_fit <- fit$optimize()
ic <- item_curve(map_fit)
plot(ic)
```

```
item_info
```

Calculate Item Information Function

Description

Calculate Item Information Function

Usage

```
item_info(x, ...)
```

Arguments

x	An object of class RTMB_Fit_Base
...	Additional arguments.

Examples

```
fit <- rtmb_irt(data = BigFive[, 1:5], model = "2PL", type = "ordered")
map_fit <- fit$optimize()
ii <- item_info(map_fit)
plot(ii)
```

item_info.RTMB_Fit_Base

Item Information Function for RTMB_Fit_Base

Description

Item Information Function for RTMB_Fit_Base

Usage

```
## S3 method for class 'RTMB_Fit_Base'
item_info(x, theta_seq = seq(-4, 4, length.out = 100), items = NULL, ...)
```

Arguments

x	An object of class RTMB_Fit_Base.
theta_seq	Sequence of trait values (ability) to evaluate.
items	Index or item names to restrict the calculation to specific items (optional).
...	Additional arguments.

log_det_chol

Log determinant of a Cholesky factor

Description

Log determinant of a Cholesky factor

Usage

```
log_det_chol(L)
```

Arguments

L	A lower triangular Cholesky factor matrix.
---	--

Value

The log determinant of the corresponding covariance matrix.

log_mix	<i>Log mixture of two probabilities</i>
---------	---

Description

Log mixture of two probabilities

Usage

```
log_mix(theta, lp1, lp2)
```

Arguments

theta	Mixing proportion (between 0 and 1).
lp1	Log-probability of the first component.
lp2	Log-probability of the second component.

Value

The log-probability of the mixture.

log_softmax	<i>Log-softmax function</i>
-------------	-----------------------------

Description

Log-softmax function

Usage

```
log_softmax(x)
```

Arguments

x	A numeric vector.
---	-------------------

Value

A numeric vector of log-softmax probabilities.

log_sum_exp	<i>Log-sum-exp function</i>
-------------	-----------------------------

Description

Log-sum-exp function

Usage

```
log_sum_exp(x, y = NULL)
```

Arguments

x	A numeric vector or scalar.
y	An optional numeric scalar.

Value

The log of the sum of the exponentials.

log_sum_exp_matrix	<i>Log-sum-exp function for matrices (row-wise)</i>
--------------------	---

Description

Log-sum-exp function for matrices (row-wise)

Usage

```
log_sum_exp_matrix(M)
```

Arguments

M	A numeric matrix or advector matrix.
---	--------------------------------------

Value

A numeric vector of row-wise log-sum-exp.

log1m	<i>Log of one minus x</i>
-------	---------------------------

Description

Log of one minus x

Usage

log1m(x)

Arguments

x A numeric vector.

Value

The natural logarithm of 1 - x.

log1m_exp	<i>Log of one minus exponential of x</i>
-----------	--

Description

Log of one minus exponential of x

Usage

log1m_exp(x)

Arguments

x A numeric vector.

Value

The natural logarithm of 1 - exp(x).

log1p_exp	<i>Log of one plus exponential of x</i>
-----------	---

Description

Log of one plus exponential of x

Usage

log1p_exp(x)

Arguments

x A numeric vector.

Value

The natural logarithm of $1 + \exp(x)$.

logit	<i>Logit function</i>
-------	-----------------------

Description

Logit function

Usage

logit(x)

Arguments

x A numeric vector of probabilities.

Value

The logit of x.

lsmeans	<i>Least Squares Means (Marginal Means)</i>
---------	---

Description

Calculate least squares means (also known as marginal means or predicted means) for categorical factors in a fitted model. It also supports pairwise comparisons and simple main effects.

Usage

```
lsmeans(object, specs, ...)
```

Arguments

object	A fitted model object (e.g., 'Classic_Fit').
specs	A character vector of factor names to calculate means for.
...	Additional arguments passed to the method.

make_bw_from_ydif	<i>Make Best and Worst Responses from Best-Worst Pair Indices</i>
-------------------	---

Description

Converts a matrix of Best-Worst pair indices ('Y_dif') into separate 'Best' and 'Worst' data frames. The returned values are positions within each row of 'sets', not the item labels stored in 'sets'.

Usage

```
make_bw_from_ydif(Y_dif, sets)

restore_bw_from_ydif(Y_dif, sets)
```

Arguments

Y_dif	Matrix or data frame of pair indices (N persons x P tasks). Each value must be an integer from 1 to 'C * (C - 1)', where 'C' is the number of items per task.
sets	Matrix or data frame of presented item sets (P tasks x C items).

Value

A list with two data frames: 'Best' and 'Worst'.

make_glmer_re_terms	<i>Prepare GLMM Formula Components</i>
---------------------	--

Description

Builds the response, fixed-effect model matrix, and lme4-style random-effect design components used by `'rtmb_glmer()'`. This is the user-facing helper that reproduces what the wrapper places in the generated `'setup'` block.

Usage

```
make_glmer_re_terms(  
  formula,  
  data = NULL,  
  family = "gaussian",  
  resid_group = NULL,  
  resid_time = NULL,  
  within = NULL,  
  factors = NULL,  
  missing = "listwise",  
  contrasts = NULL  
)
```

Arguments

<code>formula</code>	lme4-style formula.
<code>data</code>	Optional data frame. If omitted, variables are resolved from the formula environment. This is useful inside an <code>'rtmb_code()'</code> <code>'setup'</code> block, where data-frame columns are available as individual variables.
<code>family</code>	Character string of the distribution family.
<code>resid_group</code>	Optional residual-correlation grouping variable.
<code>resid_time</code>	Optional residual-correlation time variable.
<code>within</code>	Optional list for wide-to-long conversion when the response is written as <code>'cbind(...)'</code> .
<code>factors</code>	Optional character vector of variables to treat as factors.
<code>missing</code>	Missing value handling strategy: "listwise".
<code>contrasts</code>	Optional contrast type, either <code>"treatment"</code> or <code>"sum"</code> .

Value

A list containing `'Y'`, `'X'`, `'trials'`, `'offset'`, `'N'`, fixed-effect metadata, and random-effect terms.

make_glmer_Z_matrix	<i>Reconstruct an Observation-Level Random-Effect Design Matrix</i>
---------------------	---

Description

Converts the transposed block random-effect design matrix used internally by ‘rtmb_glmer()’ into an observation-level matrix. This is kept as a small utility for users who want to work from the block matrix returned by ‘make_glmer_re_terms()’.

Usage

```
make_glmer_Z_matrix(Zt, group_idx, N = length(group_idx))
```

Arguments

Zt	Transposed block random-effect design matrix.
group_idx	Integer group index for each observation.
N	Number of observations. Defaults to ‘length(group_idx)’.

Value

A matrix with ‘N’ rows and one column per random-effect coefficient.

make_init_mdu	<i>Create Initial Values for Multidimensional Unfolding</i>
---------------	---

Description

Create Initial Values for Multidimensional Unfolding

Usage

```
make_init_mdu(
  Y,
  D,
  distance = c("squared", "euclidean"),
  alpha = c("random", "fix"),
  distance_eps = 1e-04,
  min_sigma = 0.1
)
```

Arguments

Y	Numeric matrix or data frame (N rows x M items).
D	Number of unfolding dimensions.
distance	Character; "squared" or "euclidean".
alpha	Character; "random" for item-specific alpha initial values or "fix" for a common alpha initial value.
distance_eps	Small positive constant added to the distance.
min_sigma	Minimum initial residual standard deviation.

Value

A named list of initial values.

make_ydif_from_bw	<i>Make Best-Worst Pair Indices from Best and Worst Responses</i>
-------------------	---

Description

Converts separate 'Best' and 'Worst' response matrices into 'Y_dif' pair indices for Best-Worst MDU models. The returned index is the position of the ordered '(best, worst)' pair among all 'C * (C - 1)' position pairs generated from each row of 'sets'.

Usage

```
make_ydif_from_bw(Best, Worst, sets)
```

Arguments

Best	Matrix or data frame of best responses (N persons x P tasks). Values must be positions within the corresponding row of 'sets', from '1' to 'ncol(sets)'.
Worst	Matrix or data frame of worst responses (N persons x P tasks). Values must be positions within the corresponding row of 'sets', from '1' to 'ncol(sets)'.
sets	Matrix or data frame of presented item sets (P tasks x C items).

Value

An integer matrix of pair indices ('Y_dif').

map_est	<i>Maximum A Posteriori (MAP) Estimate</i>
---------	--

Description

Maximum A Posteriori (MAP) Estimate

Usage

```
map_est(z)
```

Arguments

z A numeric vector of samples.

Value

A numeric value.

MAP_Fit	<i>MAP fit object</i>
---------	-----------------------

Description

MAP fit object
MAP fit object

Details

An R6 class storing optimization results from maximum a posteriori (MAP) estimation.

Super class

`BayesRTMB::RTMB_Fit_Base` -> `map_fit`

Public fields

- `model` The 'RTMB_Model' object used for estimation.
- `par_vec` Parameter vector on the unconstrained scale (constrained values unlisted).
- `par` Parameter list on the constrained scale.
- `par_unc` Parameter vector on the unconstrained scale (raw unconstrained values).
- `ci_method` Method used for CI estimation ("wald", "sampling", or "none").
- `objective` RTMB objective function object.
- `log_ml` Log marginal likelihood or related model criterion.

convergence Optimizer convergence code.
 sd_rep Standard deviation report object.
 df_fixed Summary table for fixed-effect parameters.
 random_effects Random effect estimates.
 df_transform Summary table for transformed parameter estimates.
 df_generate Summary table for generated quantity estimates.
 opt_history A vector of optimize objective history.
 transform List of transformed parameters maintaining their original dimensions.
 generate List of generated quantities maintaining their original dimensions.
 se_samples List of simulated samples for standard error estimation.
 laplace Logical; whether Laplace approximation was used.
 vcov_unc Variance-covariance matrix of parameters in unconstrained space.
 map List; the parameter mapping used.
 marginal_vars Character vector of parameter names requested through 'optimize(marginal = ...)'.
 laplace_random_vars Character vector of all parameter names passed to 'MakeADFun(random = ...)' during Laplace approximation.
 idx_fix_active Numeric vector; mapping between active parameters and full unconstrained vector.
 show_df Logical; whether to display degrees of freedom in the summary output.
 view Character vector of parameter names to prioritize in summary.
 fallback_needed Logical; whether Hessian/SE fallback was used during optimization.

Methods

Public methods:

- `MAP_Fit$get_point_estimate()`
- `MAP_Fit$new()`
- `MAP_Fit$ranef()`
- `MAP_Fit$draws()`
- `MAP_Fit$summary()`
- `MAP_Fit$print()`
- `MAP_Fit$generated_quantities()`
- `MAP_Fit$WAIC()`
- `MAP_Fit$diagnose()`
- `MAP_Fit$profile()`
- `MAP_Fit$clone()`

Method `get_point_estimate()`: Get point estimate for a target parameter.

Usage:

```
MAP_Fit$get_point_estimate(target, ...)
```

Arguments:

`target` Target parameter name.
 ... Additional arguments, ignored for MAP fits.
Returns: Matrix, array, vector, or scalar point estimate.

Method `new()`: Create a new 'MAP_Fit' object.

Usage:

```
MAP_Fit$new(
  model,
  par_vec = NULL,
  par = NULL,
  objective = NULL,
  log_ml = NULL,
  convergence = NULL,
  sd_rep = NULL,
  df_fixed = NULL,
  random_effects = NULL,
  df_transform = NULL,
  df_generate = NULL,
  opt_history = NULL,
  transform = NULL,
  generate = NULL,
  se_samples = NULL,
  par_unc = NULL,
  ci_method = "wald",
  laplace = TRUE,
  map = NULL,
  vcov_unc = NULL,
  marginal_vars = NULL,
  laplace_random_vars = NULL,
  idx_fix_active = NULL,
  show_df = TRUE,
  view = NULL,
  fallback_needed = NULL
)
```

Arguments:

`model` The 'RTMB_Model' object used for estimation.
`par_vec` Parameter vector on the unconstrained scale (constrained values unlisted).
`par` Parameter list on the constrained scale.
`objective` The objective function value at the optimum.
`log_ml` Log marginal likelihood.
`convergence` Optimizer convergence code.
`sd_rep` The 'sdreport' object from TMB.
`df_fixed` Data frame of fixed effects estimates and CIs.
`random_effects` Data frame of random effects estimates and CIs.
`df_transform` Data frame of transformed parameters.
`df_generate` Data frame of generated quantities.

opt_history Data frame of optimization history.
 transform List of transformed parameters maintaining their original dimensions.
 generate List of generated quantities maintaining their original dimensions.
 se_samples List of simulated samples for standard error estimation.
 par_unc Parameter vector on the unconstrained scale (raw values).
 ci_method Method used for CI estimation ("wald", "sampling", or "none").
 laplace Logical; whether Laplace approximation was used.
 map List; the parameter mapping used.
 vcov_unc Variance-covariance matrix of parameters in unconstrained space.
 marginal_vars Character vector of parameter names requested through 'optimize(marginal = ...)'.
 laplace_random_vars Character vector of all parameter names passed to 'MakeADFun(random = ...)' during Laplace approximation.
 idx_fix_active Numeric vector; mapping between active parameters and full unconstrained vector.
 show_df Logical; whether to display degrees of freedom in the summary output. Default is TRUE.
 view Character vector of parameter names to prioritize in summary.
 fallback_needed Logical; whether Hessian/SE fallback was used during optimization.

Method ranef(): Return random effect estimates as a named list.

Usage:

```
MAP_Fit$ranef()
```

Returns: A named list of random effect estimates.

Method draws(): Extract samples from the asymptotic posterior distribution.

Usage:

```
MAP_Fit$draws(
  pars = NULL,
  inc_random = FALSE,
  inc_transform = TRUE,
  inc_generate = TRUE,
  ...
)
```

Arguments:

pars Character or numeric vector specifying the names or indices of parameters to extract.
 inc_random Logical; whether to include random effects.
 inc_transform Logical; whether to include transformed parameters.
 inc_generate Logical; whether to include generated quantities.
 ... Ignored.

Returns: An array of samples [iterations, 1, parameters].

Method summary(): Summarize MAP estimates.

Usage:

```
MAP_Fit$summary(
  pars = NULL,
  max_rows = 10,
  digits = 5,
  ranef = FALSE,
  view = NULL
)
```

Arguments:

pars Character vector specifying the names of parameters to summarize. If NULL, all available parameters are summarized.

max_rows Maximum number of rows to print in summaries. Default is 10.

digits Number of digits to print.

ranef Logical; whether to also display random effect estimates. Default is FALSE.

view Character vector of parameter names to prioritize or filter by.

Returns: A summary object, typically a data frame.

Method print(): Print a brief summary of the fitted object.

Usage:

```
MAP_Fit$print(pars = NULL, max_rows = 10, digits = 5, ...)
```

Arguments:

pars Character vector specifying the names of parameters to summarize.

max_rows Maximum number of rows to print in summaries.

digits Number of digits to print.

... Additional arguments passed to the ‘summary’ method.

Returns: The object itself, invisibly.

Method generated_quantities(): Compute generated quantities from the MAP estimate.

Usage:

```
MAP_Fit$generated_quantities(code)
```

Arguments:

code An ‘rtmb_code({ ... })’ or ‘{ ... }’ block containing the logic to be calculated using the MAP estimate.

Returns: The ‘MAP_Fit’ object itself (invisibly). Results are added or updated in the ‘generate’ list and ‘df_generate’.

Method WAIC(): Compute an approximate WAIC from sampling-based uncertainty propagation.

Usage:

```
MAP_Fit$WAIC()
```

Returns: A ‘waic_BayesRTMB’ object.

Method diagnose(): Run basic diagnostics for the MAP fit.

Usage:

```
MAP_Fit$diagnose(...)
```

Arguments:

... Additional arguments passed to 'diagnose_map_fit()'.

Returns: A 'diagnose_BayesRTMB' object.

Method `profile()`: Calculate Profile Likelihood confidence intervals for specific parameters.

Usage:

```
MAP_Fit$profile(
  pars = NULL,
  level = 0.95,
  trace = FALSE,
  digits = 5,
  show_plot = FALSE,
  quiet = FALSE,
  jacobian = "none",
  ...
)
```

Arguments:

`pars` Character vector of parameter names to profile. If NULL, all fixed parameters are profiled.

`level` Confidence level (default is 0.95).

`trace` Logical; whether to print profiling progress. Default is FALSE.

`digits` Integer; number of decimal places to print. Default is 5.

`show_plot` Logical; whether to plot the profile likelihood curves. Default is FALSE.

`quiet` Logical; whether to suppress text output. Default is FALSE.

`jacobian` Character; "none" (default), "random", or "all". Whether to include Jacobian adjustments for transformations.

... Additional arguments passed to `TMB::tmbprofile` (e.g., `ytol`).

Returns: A data frame containing the profile-based confidence intervals, with the raw profile objects stored in the "profiles" attribute.

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

```
MAP_Fit$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

Description

This page summarizes the utility functions provided to assist in writing efficient and numerically stable model code within 'rtmb_code'. These functions are specifically designed to be compatible with RTMB's Automatic Differentiation (AD).

Details

1. Link and Inverse Functions:

- `logit(x)`: Computes the logit transformation $\log(x/(1-x))$.
- `inv_logit(x)`: Computes the inverse logit (logistic) transformation $1/(1+\exp(-x))$.

2. Numerical Stability Utilities:

These functions use specialized algorithms to prevent overflow/underflow in AD calculations.

- `log_sum_exp(x)`: Safely computes $\log(\sum(\exp(x)))$ using the log-sum-exp trick.
- `log1p_exp(x)`: Computes $\log(1 + \exp(x))$ stably.
- `log1m_exp(x)`: Computes $\log(1 - \exp(x))$ stably for $x < 0$.
- `log_softmax(x)`: Computes the log of the softmax function.
- `fabs(x)`: A smooth version of the absolute value function $\text{abs}(x)$ to ensure differentiability at zero.

3. Matrix and Vector Transformations:

Used to convert unconstrained vectors into structured matrices (e.g., for factor analysis or identification constraints).

- `sum_to_zero(x)`: Transforms a vector of length $K-1$ into a vector of length K that sums to zero.
- `to_lower_tri(x, M, D)`: Fills a matrix of size $M \times D$ with elements from vector x in a lower-triangular fashion.
- `to_centered_matrix(x, R, C)`: Creates an $R \times C$ matrix where each column sums to zero.
- `to_centered_tri(x, R, C)`: Creates an $R \times C$ matrix with column-wise sum-to-zero constraints on the lower elements (useful for identification in factor analysis).
- `rtmb_vector(value, length)`: Creates an AD-compatible vector initialized with `value`.
- `rtmb_array(value, dim)`: Creates an AD-compatible array initialized with `value`.

4. Linear Algebra for AD:

- `log_det_chol(L)`: Calculates the log-determinant of a covariance matrix from its Cholesky factor L .
- `quad_form_chol(x, L)`: Computes the quadratic form $x^T \Sigma^{-1} x$ using the Cholesky factor L .
- `distance(x, y)`: Computes the Euclidean distance between two vectors with a small epsilon for stability.

MCMC_Fit

*MCMC fit object***Description**

MCMC fit object

MCMC fit object

Details

An R6 class storing posterior samples and related information from MCMC estimation.

Bayes factors are computed as ratios of marginal likelihoods estimated by bridge sampling. The comparison model can be constructed by fixing parameters with ‘fixed = list(...)’, or supplied as an already fitted ‘MCMC_Fit’ object via ‘comparison_fit’. Bayes factors are computed only by marginal-likelihood model comparison.

Super class

`BayesRTMB::RTMB_Fit_Base` -> `mcmc_fit`

Public fields

`model` An ‘RTMB_Model’ object used for estimation.

`fit` Posterior draws for model parameters.

`random_fit` Posterior draws for random effects.

`transform_fit` Posterior draws for transformed parameters.

`transform_dims` Dimension information for transformed parameters.

`generate_fit` Posterior draws for generated quantities.

`generate_dims` Dimension information for generated quantities.

`eps` Step size used by the sampler.

`accept` Acceptance statistics from sampling.

`treedepth` Tree depth used in HMC/NUTS sampling.

`n_leapfrog` Number of leapfrog steps for retained draws.

`divergent` Logical matrix indicating divergent transitions.

`energy` Hamiltonian energy for retained draws.

`metric` Per-chain inverse mass matrix used by NUTS.

`metric_type` Effective mass matrix adaptation type used by NUTS.

`metric_requested` Mass matrix adaptation type requested by the user.

`metric_effective` Effective mass matrix adaptation type by chain.

`metric_auto` Automatic metric selection details by chain, if used.

`metric_init` Initial metric source used by NUTS.

metric_adaptation Metric learning mode used during warmup.
nuts_variant NUTS proposal selection variant used for sampling.
warmup_diagnostics Per-chain warmup diagnostics.
chain_state Final unconstrained sampler position for each chain.
sampler_config Sampling settings required to continue the chains.
laplace Logical; whether Laplace approximation was used.
posterior_mean Posterior mean estimates.
log_ml Numeric value storing the calculated log marginal likelihood from bridge sampling.
comparison_fit An MCMC_Fit object containing the fitted comparison model.
max_treedepth Maximum tree depth requested for NUTS/HMC.
pd_error_count Positive-definite/singularity errors treated as $lp = -\text{Inf}$ by chain.

Methods

Public methods:

- `MCMC_Fit$get_point_estimate()`
- `MCMC_Fit$new()`
- `MCMC_Fit$print()`
- `MCMC_Fit$continue_sampling()`
- `MCMC_Fit$draws()`
- `MCMC_Fit$summary()`
- `MCMC_Fit$rhat_summary()`
- `MCMC_Fit$unconstrain_draws()`
- `MCMC_Fit$log_prob()`
- `MCMC_Fit$bridgesampling()`
- `MCMC_Fit$WAIC()`
- `MCMC_Fit$diagnose()`
- `MCMC_Fit$bayes_factor()`
- `MCMC_Fit$transformed_draws()`
- `MCMC_Fit$generated_quantities()`
- `MCMC_Fit$resolve_switching()`
- `MCMC_Fit$clone()`

Method `get_point_estimate()`: Get point estimate for a target parameter.

Usage:

```
MCMC_Fit$get_point_estimate(target, chains = NULL, best_chains = NULL)
```

Arguments:

`target` Target parameter name.

`chains` Numeric vector of chains to include. If `NULL`, all chains are used.

`best_chains` Integer; number of best chains to retain based on mean log-posterior.

Returns: Matrix, array, vector, or scalar point estimate.

Method `new()`: Create a new ‘MCMC_Fit’ object.

Usage:

```
MCMC_Fit$new(
  model,
  fit,
  random_fit,
  eps,
  accept,
  treedepth,
  laplace,
  posterior_mean,
  max_treedepth = NULL,
  pd_error_count = NULL,
  n_leapfrog = NULL,
  divergent = NULL,
  energy = NULL,
  metric = NULL,
  metric_type = NULL,
  metric_init = NULL,
  metric_requested = NULL,
  metric_effective = NULL,
  metric_auto = NULL,
  metric_adaptation = NULL,
  nuts_variant = NULL,
  warmup_diagnostics = NULL,
  chain_state = NULL,
  sampler_config = NULL
)
```

Arguments:

`model` An ‘RTMB_Model’ object used for estimation.
`fit` Posterior draws for model parameters.
`random_fit` Posterior draws for random effects, if available.
`eps` Step size used by the sampler.
`accept` Acceptance statistics from sampling.
`treedepth` Tree depth used in HMC/NUTS sampling.
`laplace` Logical; whether Laplace approximation was used.
`posterior_mean` Posterior mean estimates.
`max_treedepth` Maximum tree depth requested for NUTS/HMC.
`pd_error_count` Positive-definite/singularity errors treated as ‘lp = -Inf’ by chain.
`n_leapfrog` Number of leapfrog steps for retained draws.
`divergent` Logical matrix indicating divergent transitions.
`energy` Hamiltonian energy for retained draws.
`metric` Per-chain inverse mass matrix used by NUTS.
`metric_type` Effective mass matrix adaptation type used by NUTS.
`metric_init` Initial metric source used by NUTS.

metric_requested Mass matrix adaptation type requested by the user.
 metric_effective Effective mass matrix adaptation type by chain.
 metric_auto Automatic metric selection details by chain, if used.
 metric_adaptation Metric learning mode used during warmup.
 nuts_variant NUTS proposal selection variant used for sampling.
 warmup_diagnostics Per-chain warmup diagnostics.
 chain_state Final unconstrained sampler position for each chain.
 sampler_config Sampling settings required to continue the chains.

Method print(): Print a brief summary of the fitted object.

Usage:

```
MCMC_Fit$print(...)
```

Arguments:

... Additional arguments.

Returns: The object itself, invisibly.

Method continue_sampling(): Continue all NUTS chains from their saved final states.

The adapted mass matrix and step size from each chain are reused, so no additional warmup is performed. New posterior draws and diagnostics are appended along the iteration dimension.

Usage:

```
MCMC_Fit$continue_sampling(
  sampling = 1000,
  thin = NULL,
  seed = sample.int(1e+06, 1),
  max_treedepth = NULL,
  parallel = FALSE,
  inplace = TRUE,
  globals = FALSE,
  progress = c("auto", "none", "bar", "message")
)
```

Arguments:

sampling Positive integer; number of additional post-warmup NUTS transitions per chain before thinning. Default is 1000.

thin Optional positive integer thinning interval. 'NULL' reuses the interval from the original sampling run.

seed Integer random seed.

max_treedepth Optional positive integer maximum tree depth. 'NULL' reuses the value from the original sampling run.

parallel Logical; whether to continue chains in parallel.

inplace Logical; if 'TRUE', append draws to this object. If 'FALSE', return an independently cloned and extended object.

globals Logical; if 'TRUE', let 'future' discover globals when 'parallel = TRUE'.

progress Progress reporting style: "auto", "none", "bar", or "message".

Returns: The extended 'MCMC_Fit' object, invisibly when 'inplace = TRUE'.

Method `draws()`: Extract posterior draws for selected parameters.

Usage:

```
MCMC_Fit$draws(
  pars = NULL,
  chains = NULL,
  best_chains = NULL,
  inc_random = FALSE,
  inc_transform = TRUE,
  inc_generate = TRUE
)
```

Arguments:

`pars` Character or numeric vector specifying the names or indices of parameters to extract. If NULL, all available parameters are extracted.

`chains` Numeric vector specifying the chains to extract. If NULL, draws from all chains are returned.

`best_chains` Integer; number of best chains to retain based on mean log-posterior (lp).

`inc_random` Logical; whether to include random effects in the output. Default is FALSE.

`inc_transform` Logical; whether to include transformed parameters in the output. Default is TRUE.

`inc_generate` Logical; whether to include generated quantities in the output. Default is TRUE.

Returns: Posterior draws.

Method `summary()`: Summarize posterior draws.

Usage:

```
MCMC_Fit$summary(
  pars = NULL,
  chains = NULL,
  best_chains = NULL,
  max_rows = 10,
  digits = 2,
  inc_random = FALSE,
  inc_transform = TRUE,
  inc_generate = TRUE
)
```

Arguments:

`pars` Character or numeric vector specifying the names or indices of parameters to summarize. If NULL, all available parameters are summarized.

`chains` Numeric vector specifying the chains to extract. If NULL, draws from all chains are used.

`best_chains` Integer; number of best chains to retain based on mean log-posterior (lp).

`max_rows` Integer; maximum number of rows to print in the summary table. Default is 10.

`digits` Integer; number of decimal places to print. Default is 2.

`inc_random` Logical; whether to include random effects in the summary. Default is FALSE.

`inc_transform` Logical; whether to include transformed parameters in the summary. Default is TRUE.

`inc_generate` Logical; whether to include generated quantities in the summary. Default is TRUE.

Returns: A summary object.

Method `rhat_summary()`: Summarize R-hat values.

Usage:

```
MCMC_Fit$rhat_summary(
  pars = NULL,
  chains = NULL,
  best_chains = NULL,
  inc_random = FALSE,
  inc_transform = TRUE,
  inc_generate = FALSE,
  finite = TRUE,
  ...
)
```

Arguments:

`pars` Character or numeric vector specifying parameters to include.

`chains` Numeric vector specifying chains to include.

`best_chains` Integer; number of best chains to retain based on mean log-posterior.

`inc_random` Logical; whether to include random effects. Default is FALSE.

`inc_transform` Logical; whether to include transformed parameters. Default is TRUE.

`inc_generate` Logical; whether to include generated quantities. Default is FALSE.

`finite` Logical; whether to drop non-finite or missing R-hat values. Default is TRUE.

... Additional arguments.

Returns: A numeric vector of R-hat values with class "rhat_summary".

Method `unconstrain_draws()`: Transform posterior draws to the unconstrained scale.

Usage:

```
MCMC_Fit$unconstrain_draws()
```

Returns: Posterior draws on the unconstrained scale.

Method `log_prob()`: Evaluate log-probability values.

Usage:

```
MCMC_Fit$log_prob(safe = FALSE)
```

Arguments:

`safe` Logical; whether to wrap the evaluation in a tryCatch block. Default is FALSE for speed.

Returns: Numeric vector of log-probability values.

Method `bridgesampling()`: Estimate the marginal likelihood by bridge sampling.

Usage:

```
MCMC_Fit$bridgesampling(
  method = "normal",
  use_neff = TRUE,
  seed = NULL,
  max_iter = 100
)
```

Arguments:

method Character; the method to use for bridge sampling (e.g., "warp3", "normal"). Default is "warp3".

use_neff Logical; whether to use the effective sample size (ESS) to adjust for autocorrelation. Default is TRUE.

seed Integer; random seed for reproducibility. Default is NULL.

max_iter Integer; maximum number of iterations for the estimation algorithm. Default is 100.

Returns: Bridge sampling result.

Method `WAIC()`: Compute WAIC from pointwise generated log likelihood.

Usage:

```
MCMC_Fit$WAIC(...)
```

Arguments:

... Additional arguments passed to `'draws()'`, such as `'chains'` or `'best_chains'`.

Returns: A `'waic_BayesRTMB'` object.

Method `diagnose()`: Run basic diagnostics for the MCMC fit.

Usage:

```
MCMC_Fit$diagnose(...)
```

Arguments:

... Additional arguments passed to `'diagnose_mcmc_fit()'`.

Returns: A `'diagnose_BayesRTMB'` object.

Method `bayes_factor()`: Calculate the Bayes factor by marginal-likelihood model comparison.

Usage:

```
MCMC_Fit$bayes_factor(
  fixed = NULL,
  comparison_fit = NULL,
  bs_method = "normal",
  error_threshold = 0.2,
  ...
)
```

Arguments:

fixed Named list of parameter values used to construct the comparison model. For example, `fixed = list(delta = 0)` or `fixed = list("b[x]" = 0)`.

comparison_fit Optional `'MCMC_Fit'` object for an already fitted comparison model.

`bs_method` Character; the method to use for bridge sampling ("normal" or "warp3").
`error_threshold` Numeric; threshold for the approximate error warning.
 ... Additional arguments passed to 'sample()' when fitting the comparison model (e.g., `chains = 4`, `sampling = 4000`).

Returns: A list of class `bayes_factor_rtmb` containing Bayes factor results.

Method `transformed_draws()`: Compute transformed parameters from posterior draws.

Usage:

```
MCMC_Fit$transformed_draws(
  tran_fn = NULL,
  progress = c("auto", "none", "bar", "message"),
  tape = c("auto", "none", "force")
)
```

Arguments:

`tran_fn` A function for transformed parameters.
`progress` Progress reporting style: "auto", "none", "bar", or "message". "auto" and "bar" use line-based messages.
`tape` Derived-quantity evaluation mode. "auto" tries RTMB tape evaluation and falls back to R evaluation on error; "none" always uses R evaluation; "force" requires tape evaluation and errors if it fails.

Returns: Transformed parameter draws.

Method `generated_quantities()`: Compute generated quantities from posterior draws.

Usage:

```
MCMC_Fit$generated_quantities(
  code,
  progress = c("auto", "none", "bar", "message"),
  tape = c("auto", "none", "force")
)
```

Arguments:

`code` An 'rtmb_code({ ... })' or '{ ... }' block containing the logic to be calculated using posterior samples.
`progress` Progress reporting style: "auto", "none", "bar", or "message". "auto" and "bar" use line-based messages.
`tape` Derived-quantity evaluation mode. "auto" tries RTMB tape evaluation and falls back to R evaluation on error; "none" always uses R evaluation; "force" requires tape evaluation and errors if it fails.

Returns: The 'MCMC_Fit' object itself (invisibly). Results are appended to the 'generate_fit' field.

Method `resolve_switching()`: Resolve label switching in posterior draws.

Usage:

```
MCMC_Fit$resolve_switching(
  target,
  linked = NULL,
  overwrite = TRUE,
  scalar_fns = list()
)
```

Arguments:

target Character string specifying the target variable to base the relabeling on.

linked Character vector of variable names to be relabeled in the same order as the target. Default is NULL.

overwrite Logical; whether to overwrite the stored draws in the current object. Default is TRUE.

scalar_fns A named list of functions to apply to scalar variables for relabeling. Default is an empty list.

Returns: Relabeled draws or updated object.

Method clone(): The objects of this class are cloneable with this method.

Usage:

```
MCMC_Fit$clone(deep = FALSE)
```

Arguments:

deep Whether to make a deep clone.

parameter_types

Parameter Types and Constraints in RTMB Models

Description

When declaring parameters in the parameters block using `Dim()`, you can specify a type to automatically apply structural constraints. These constraints ensure that parameters remain within their valid mathematical space during estimation.

Details

Standard Types:

- "vector", "matrix", "array": Standard unconstrained containers. Use lower and upper for element-wise bounds.

Ordering Constraints:

- "ordered": A vector where $x_1 < x_2 < \dots < x_K$.
- "positive_ordered": A vector where $0 < x_1 < x_2 < \dots < x_K$.

Constrained Vectors:

- "simplex": A vector where all elements are ≥ 0 and $\text{sum}(x) = 1$.

- "centered": A vector of length K where $\text{sum}(x) = 0$. (Estimated using K-1 degrees of freedom).

Correlation and Covariance Matrices:

- "corr_matrix": A symmetric, positive-definite correlation matrix (diagonal elements are 1).
- "cov_matrix": A symmetric, positive-definite covariance matrix.
- "CF_corr": The Cholesky factor of a correlation matrix.
- "CF_cov": The Cholesky factor of a covariance matrix (diagonal elements are positive).

Special Structural Matrices:

- "lower_tri": A lower-triangular matrix.
- "positive_lower_tri": A lower-triangular matrix with positive diagonal elements.
- "centered_matrix": A matrix where each column sums to zero.
- "centered_tri": A triangular matrix with column-wise sum-to-zero constraints (often used for identification in factor analysis).

See Also

[rtmb_code](#), [math_functions](#), [distributions](#)

parameters_code

Code block for parameter definitions

Description

Defines the list of parameters to be passed to 'rtmb_model'. By writing in the format 'variable_name = Dim(...)' within a block enclosed in "", evaluation is delayed, enabling strict error checking during model construction.

Usage

```
parameters_code(expr)
```

Arguments

expr A parameter definition expression enclosed in "".

Value

A lazily evaluated list of parameters.

plot.ce_rtmb	<i>Plot method for ce_rtmb class (Base R)</i>
--------------	---

Description

Plot method for ce_rtmb class (Base R)

Usage

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

Arguments

x	An object of class ce_rtmb
...	Additional arguments.

plot.rtmb_lsmeans	<i>Plot marginal means with error bars</i>
-------------------	--

Description

Plot method for rtmb_lsmeans objects.

Usage

```
## S3 method for class 'rtmb_lsmeans'
plot(
  x,
  y,
  error_bar = "se",
  col = NULL,
  main = NULL,
  xlab = NULL,
  ylab = NULL,
  ...
)
```

Arguments

x	An rtmb_lsmeans object.
y	Ignored.
error_bar	Type of error bar ("se" or "ci").
col	Color of the bars.

main	Plot title.
xlab	X axis label.
ylab	Y axis label.
...	Additional arguments passed to barplot.

plot_acf	<i>Plot autocorrelation for one variable across chains</i>
----------	--

Description

Draw autocorrelation plots for a selected parameter across all chains.

Usage

```
plot_acf(x, var_idx = 1)
```

Arguments

x	A 3D array of posterior samples with dimensions ‘(iterations, chains, variables)’.
var_idx	Integer. Index of the variable to plot.

Value

No return value. This function is called for its side effect of plotting.

plot_conditional_effects	<i>Plot conditional effects</i>
--------------------------	---------------------------------

Description

Calculate and plot conditional effects for a fitted model.

Usage

```
plot_conditional_effects(
  fit,
  effect,
  prob = 0.95,
  sd_multiplier = 1,
  sd_slice = NULL,
  resolution = 100,
  ...
)
```

Arguments

fit	A fitted model object (e.g., 'MCMC_Fit', 'MAP_Fit', 'VB_Fit').
effect	Name of the variable to visualize (e.g., "X1" or "X1:X2").
prob	Probability for the credible/confidence interval.
sd_multiplier	Numeric multiplier for standard deviation when splitting continuous moderators.
sd_slice	Logical or NULL; controls whether continuous moderators are evaluated at mean - SD, mean, and mean + SD.
resolution	Grid resolution to calculate for continuous variables.
...	Additional arguments passed to the plot method.

Value

Invisibly returns the plotted object of class `ce_rtmf`.

plot_dens	<i>Plot posterior densities for MCMC samples</i>
-----------	--

Description

Draw kernel density plots for each parameter across chains.

Usage

```
plot_dens(x, mono = FALSE)
```

Arguments

x	A 3D array of posterior samples with dimensions '(iterations, chains, variables)'. A 2D matrix '(iterations, chains)' is also allowed and is treated as a single variable.
mono	Logical. If 'TRUE', plot in monochrome. If 'FALSE', use blue shades.

Value

No return value. This function is called for its side effect of plotting.

plot_forest	<i>Plot parameter estimates and credible intervals (Forest Plot)</i>
-------------	--

Description

Plot parameter estimates and credible intervals (Forest Plot)

Usage

```
plot_forest(  
  x,  
  prob = 0.95,  
  point_estimate = c("median", "EAP", "mean", "MAP", "marginal_map", "joint_map")  
)
```

Arguments

- x A 3D array of posterior samples with dimensions ‘(iterations, chains, variables)’.
- prob Numeric. Probability mass for the credible interval (default is 0.95).
- point_estimate Character. Point estimate shown as dots. One of “median” (default), “EAP”/“mean”, “MAP”/“marginal_map”, or “joint_map”. “joint_map” uses the draw with the largest ‘lp’ variable.

Value

No return value.

plot_item_curve	<i>Plot item/category response curves</i>
-----------------	---

Description

Calculate and plot item/category response curves for a fitted IRT model.

Usage

```
plot_item_curve(fit, ...)
```

Arguments

- fit A fitted IRT model object.
- ... Additional arguments passed to [item_curve](#) or the plot method.

Value

Invisibly returns the plotted object of class `rtmb_item_curve`.

plot_item_info	<i>Plot item information functions</i>
----------------	--

Description

Calculate and plot item information functions for a fitted IRT model.

Usage

```
plot_item_info(fit, ...)
```

Arguments

fit	A fitted IRT model object.
...	Additional arguments passed to item_info or the plot method.

Value

Invisibly returns the plotted object of class `rtmb_item_info`.

plot_lsmeans	<i>Plot least-squares marginal means</i>
--------------	--

Description

Calculate and plot marginal means for a fitted model.

Usage

```
plot_lsmeans(fit, specs, ...)
```

Arguments

fit	A fitted model object (e.g. 'Classic_Fit').
specs	Character vector specifying the variables for which marginal means are calculated.
...	Additional arguments passed to lsmeans or the plot method.

Value

Invisibly returns the plotted object.

plot_mdu

*Plot Multidimensional Unfolding Configuration***Description**

Draws an item-person map for multidimensional unfolding models. Item locations are shown as labels, optional blue circles show item alpha/radius values, and the respondent locations are summarized by a two- dimensional kernel density contour.

Usage

```
plot_mdu(
  delta,
  theta = NULL,
  item_alpha = NULL,
  phi = NULL,
  dims = c(1, 2),
  radius = NULL,
  signs = c(1, 1),
  item_labels = NULL,
  show_radius = TRUE,
  show_density = TRUE,
  circle_scale = 1,
  alpha = 0.2,
  contour_n = 60,
  distance = c("auto", "euclidean", "squared"),
  point_estimate = c("EAP", "MAP", "mean", "marginal_map", "joint_map"),
  prefer_rotated = TRUE,
  show_phi = NULL,
  main = "MDU Configuration",
  xlab = NULL,
  ylab = NULL,
  ...
)
```

Arguments

delta	Item coordinate matrix (M items x D dimensions), or a fitted object with an 'EAP()' method.
theta	Person coordinate matrix (N persons x D dimensions). If 'delta' is a fitted object and 'theta' is 'NULL', it is extracted from the fit.
item_alpha	Optional item alpha vector used for item radii. If 'delta' is a fitted object and 'item_alpha' is 'NULL', 'alpha' is extracted when available.
phi	Deprecated alias for 'item_alpha'.
dims	Integer vector of length 2 specifying dimensions to plot.

radius	Numeric plot radius. If 'NULL', a radius is chosen from the coordinates.
signs	Numeric vector of length 2. Use '-1' to flip an axis.
item_labels	Optional item labels. Defaults to row names or item numbers.
show_radius	Logical; whether to draw radius circles based on item alpha.
show_density	Logical; whether to draw density contours for 'theta'.
circle_scale	Numeric multiplier for item radii.
alpha	Circle transparency.
contour_n	Grid size passed to 'MASS::kde2d()'.
distance	Character; "auto", "euclidean", or "squared". Used to transform item alpha values into plotted radii. "auto" uses the fit's stored distance when available and otherwise falls back to "euclidean".
point_estimate	Character; point estimate used when 'delta' is a fit object. Passed to 'estimate()'.
prefer_rotated	Logical; when 'delta' is a fitted object, prefer rotated generated quantities ('delta_rot' and 'theta_rot') if available.
show_phi	Deprecated alias for 'show_radius'.
main, xlab, ylab	Plot title and axis labels.
...	Additional arguments passed to 'plot()'.

Value

Invisibly returns a list with plotted 'delta', 'theta', and 'item_alpha'.

plot_pairs	<i>Plot pairs for posterior samples</i>
------------	---

Description

Draw a scatterplot matrix to examine posterior correlations between parameters.

Usage

```
plot_pairs(x, pars = NULL)
```

Arguments

x	A 3D array of posterior samples with dimensions '(iterations, chains, variables)'.
pars	Character vector or integer vector specifying which parameters to plot. If NULL (default), up to the first 10 parameters are plotted to prevent overplotting.

Value

No return value.

plot_test_info	<i>Plot test information function</i>
----------------	---------------------------------------

Description

Calculate and plot test information function for a fitted IRT model.

Usage

```
plot_test_info(fit, ...)
```

Arguments

fit	A fitted IRT model object.
...	Additional arguments passed to <code>test_info</code> or the plot method.

Value

Invisibly returns the plotted object of class `rtmb_test_info`.

plot_trace	<i>Plot MCMC trace plots</i>
------------	------------------------------

Description

Draw trace plots for each parameter across chains.

Usage

```
plot_trace(x, mono = FALSE)
```

Arguments

x	A 3D array of posterior samples with dimensions ‘(iterations, chains, variables)’. A 2D matrix ‘(iterations, chains)’ is also allowed and is treated as a single variable.
mono	Logical. If ‘TRUE’, plot in monochrome. If ‘FALSE’, use blue shades.

Value

No return value. This function is called for its side effect of plotting.

posterior_predict	<i>Posterior predictive simulation</i>
-------------------	--

Description

Generate replicated outcomes from an estimated BayesRTMB model. Regression wrappers provide an automatic simulator. For a custom model, supply an `'rtmb_code()'` object containing a `'generate'` block that creates and reports one replicated outcome vector. MCMC and variational fits use posterior draws. A MAP fit uses sampling-based uncertainty when available and otherwise conditions on its point estimate.

Usage

```
posterior_predict(object, ...)

## S3 method for class 'RTMB_Fit_Base'
posterior_predict(object, ...)
```

Arguments

<code>object</code>	A BayesRTMB fit object.
<code>...</code>	Arguments passed to the fit object's <code>'posterior_predict()'</code> method.

Value

A numeric matrix with posterior predictive draws in rows and observations in columns.

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

Description

Compare observed data with replicated outcomes from an estimated BayesRTMB model. Density overlays are used for continuous outcomes and binned bar plots for discrete outcomes. When `'type = "auto"'`, the display is selected from the likelihood's `'_lpdf'` or `'_lpmf'` implementation.

Usage

```
pp_check(object, ...)

## S3 method for class 'RTMB_Fit_Base'
pp_check(object, ...)

## S3 method for class 'rtmb_pp_check'
plot(
```

```

    x,
    main = NULL,
    xlab = NULL,
    ylab = NULL,
    observed_col = "#1B1B1B",
    predictive_col = "#2C7FB8",
    show_legend = TRUE,
    legend_position = c("auto", "topleft", "topright", "bottomleft", "bottomright"),
    legend_cex = 0.78,
    interval = 0.95,
    ...
  )

```

Arguments

<code>object</code>	A BayesRTMB fit object.
<code>...</code>	Arguments passed to the fit object's <code>'pp_check()'</code> method or to the plotting method.
<code>x</code>	An <code>'rtmb_pp_check'</code> object.
<code>main</code>	Optional plot title.
<code>xlab</code>	Optional x-axis label.
<code>ylab</code>	Optional y-axis label.
<code>observed_col</code>	Color for observed data.
<code>predictive_col</code>	Color for predictive data and intervals.
<code>show_legend</code>	Logical; display the plot legend.
<code>legend_position</code>	Legend position. <code>"auto"</code> moves scatter-plot legends away from the fitted trend; the other values are passed to <code>'legend()'</code> .
<code>legend_cex</code>	Relative text and symbol size for the legend.
<code>interval</code>	Probability covered by posterior predictive intervals.

Details

Supplying `'x'` to the fit object's `'pp_check()'` method switches to a scatter-based check. Observed outcomes are compared with posterior predictive means and 95 value `'x = ".fitted"'` uses the posterior predictive mean on the horizontal axis for a model-wide calibration check.

Value

An object of class `'rtmb_pp_check'`, returned invisibly after plotting.

print.bayes_factor	<i>Print method for bayes_factor objects</i>
--------------------	--

Description

Print method for bayes_factor objects

Usage

```
## S3 method for class 'bayes_factor'
print(x, digits = 4, ...)
```

Arguments

x	An object of class bayes_factor.
digits	Number of decimal places to display (default is 4).
...	Additional arguments.

print.bayes_factor_rtmb	<i>Print method for bayes_factor_rtmb objects</i>
-------------------------	---

Description

Print method for bayes_factor_rtmb objects

Usage

```
## S3 method for class 'bayes_factor_rtmb'
print(x, digits = 4, ...)
```

Arguments

x	An object of class bayes_factor_rtmb.
digits	Number of decimal places to display (default is 4).
...	Additional arguments.

print.ce_rtmb	<i>Print method for ce_rtmb class (automatically calls plot)</i>
---------------	--

Description

Print method for ce_rtmb class (automatically calls plot)

Usage

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

Arguments

x	An object of class ce_rtmb
...	Additional arguments.

print.ce_simple	<i>Print simple effects</i>
-----------------	-----------------------------

Description

Print simple effects

Usage

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

Arguments

x	A 'ce_simple' object.
digits	Number of digits to print.
...	Additional arguments.

```
print.summary_BayesRTMB
      print for summary_BayesRTMB class
```

Description

print for summary_BayesRTMB class

Usage

```
## S3 method for class 'summary_BayesRTMB'
print(x, digits = NULL, ...)
```

Arguments

x	An object of class summary_BayesRTMB
digits	integer
...	Additional arguments.

prior_flat	<i>Specify a flat prior</i>
------------	-----------------------------

Description

'prior_flat()' specifies that no additional prior density is added by the wrapper. This is the only prior type allowed for 'classic()'.

Usage

```
prior_flat()
```

Value

A list with class '"rtmb_prior"' and 'type = "flat"'.

prior_jzs	<i>Specify a JZS (Jeffrey-Zellner-Siow) prior for t-tests</i>
-----------	---

Description

Specify a JZS (Jeffrey-Zellner-Siow) prior for t-tests

Usage

```
prior_jzs(r = 0.707)
```

Arguments

r	Numeric; scale parameter for the Cauchy prior on effect size delta. Default is 0.707.
---	---

Value

A list with class "rtmb_prior"

prior_normal	<i>Specify normal/exponential priors for MAP and Bayesian inference</i>
--------------	---

Description

'prior_normal()' specifies normal priors for location parameters and exponential priors for scale parameters. It is intended for MAP and Bayesian inference, not for 'classic()'.

Usage

```
prior_normal(
  Intercept_sd = 10,
  mu_sd = 10,
  b_sd = 10,
  sigma_rate = 1/5,
  tau_rate = 1/5,
  ...
)
```

Arguments

Intercept_sd	Standard deviation for the intercept prior. If 'NULL', no intercept prior is added.
mu_sd	Standard deviation for mean/intercept priors. If 'NULL', no mean prior is added.
b_sd	Standard deviation for coefficient priors. If 'NULL', no coefficient prior is added.
sigma_rate	Rate for residual standard deviation priors. The default '1 / 5' gives an exponential prior with mean 5. If 'NULL', no sigma prior is added.
tau_rate	Rate for random-effect standard deviation priors. The default '1 / 5' gives an exponential prior with mean 5. If 'NULL', no tau prior is added.
...	Optional wrapper-specific hyperparameters.

Value

A list with class "rtmb_prior" and 'type = "normal"'.

prior_rhs	<i>Specify a Regularized Horseshoe prior for continuous shrinkage</i>
-----------	---

Description

Specify a Regularized Horseshoe prior for continuous shrinkage

Usage

```
prior_rhs(expected_vars = 3, slab_scale = 2, slab_df = 4, ...)
```

Arguments

expected_vars	Expected number of non-zero variables. Default is 3.
slab_scale	Scale parameter for the slab distribution. Default is 2.0.
slab_df	Degrees of freedom for the slab distribution. Default is 4.0.
...	Optional hyperparameters for other distributions.

Value

A list with class "rtmb_prior"

prior_ssp	<i>Specify a Spike-and-Slab prior for variable selection</i>
-----------	--

Description

Specify a Spike-and-Slab prior for variable selection

Usage

```
prior_ssp(ssp_ratio = 0.25, max_beta = 1, ...)
```

Arguments

ssp_ratio	Prior probability of inclusion for each variable. Default is 0.25.
max_beta	Maximum expected effect size. Default is 1.0.
...	Optional hyperparameters for other distributions.

Value

A list with class "rtmb_prior"

prior_uniform	<i>Specify a flat prior</i>
---------------	-----------------------------

Description

Deprecated alias of 'prior_flat()'.

Usage

```
prior_uniform()
```

Value

A list with class "'rtmb_prior'" and 'type = "flat"'.

prior_weak	<i>Specify a weakly informative prior</i>
------------	---

Description

Specify a weakly informative prior

Usage

```
prior_weak(sd_ratio = 0.5, max_beta = 1, ...)
```

Arguments

sd_ratio	Ratio of the prior standard deviation to the half-range of the response variable. Default is 0.5.
max_beta	Maximum expected effect size. Default is 1.0.
...	Optional hyperparameters for other distributions.

Value

A list with class "rtmb_prior"

quad_form_chol	<i>Quadratic form using a Cholesky factor</i>
----------------	---

Description

Quadratic form using a Cholesky factor

Usage

```
quad_form_chol(x, L)
```

Arguments

x	A numeric vector.
L	A lower triangular Cholesky factor matrix.

Value

The value of the quadratic form.

quad_form_diag	<i>Quadratic form with a diagonal matrix</i>
----------------	--

Description

Quadratic form with a diagonal matrix

Usage

```
quad_form_diag(m, v)
```

Arguments

m	A numeric matrix.
v	A numeric vector representing the diagonal elements.

Value

The value of the quadratic form.

quantile95	<i>Calculate 95% Quantiles</i>
------------	--------------------------------

Description

Calculate 95% Quantiles

Usage

```
quantile95(x)
```

Arguments

x	A numeric vector.
---	-------------------

Value

A numeric vector of length 2.

r_hat	<i>Calculate Rank-normalized Split-R-hat</i>
-------	--

Description

Calculate Rank-normalized Split-R-hat

Usage

```
r_hat(sims)
```

Arguments

sims A matrix of samples (iterations x chains).

Value

A numeric value.

read_mcmc_csv	<i>Restore MCMC Fit from CSV</i>
---------------	----------------------------------

Description

Restore MCMC Fit from CSV

Usage

```
read_mcmc_csv(model, name, dir = "BayesRTMB_mcmc", chains = 4, laplace = FALSE)
```

Arguments

model	An RTMB_Model object.
name	Base name of the saved CSVs.
dir	Directory where CSVs are saved. Default is "BayesRTMB_mcmc".
chains	Number of chains. Default is 4.
laplace	Logical; whether Laplace approximation was used. Default is FALSE.

Value

An MCMC_Fit object.

rhat_summary	<i>Summarize MCMC R-hat Values</i>
--------------	------------------------------------

Description

Extract R-hat values from a fitted MCMC object as a numeric vector. The returned object prints a compact convergence summary and can be passed directly to functions such as [hist](#).

Usage

```
rhat_summary(fit, ...)

## Default S3 method:
rhat_summary(fit, ...)

## S3 method for class 'mcmc_fit'
rhat_summary(
  fit,
  pars = NULL,
  chains = NULL,
  best_chains = NULL,
  inc_random = FALSE,
  inc_transform = TRUE,
  inc_generate = FALSE,
  finite = TRUE,
  ...
)
```

Arguments

<code>fit</code>	A fitted model object.
<code>...</code>	Additional arguments passed to methods.
<code>pars</code>	Character or numeric vector specifying parameters to include. If NULL, all available parameters are summarized.
<code>chains</code>	Numeric vector specifying chains to include.
<code>best_chains</code>	Integer; number of best chains to retain based on mean log-posterior.
<code>inc_random</code>	Logical; whether to include random effects. Default is FALSE.
<code>inc_transform</code>	Logical; whether to include transformed parameters. Default is TRUE.
<code>inc_generate</code>	Logical; whether to include generated quantities. Default is FALSE.
<code>finite</code>	Logical; whether to drop non-finite or missing R-hat values. Default is TRUE.

Value

A numeric vector of R-hat values with class "rhat_summary".

Examples

```
data(debate, package = "BayesRTMB")
mdl <- rtmb_lm(sat ~ talk + perf, data = debate)
fit <- mdl$sample(sampling = 200, warmup = 200, chains = 2)
r <- rhat_summary(fit)
r
hist(r)
```

rtmb_array	Create an AD-compatible array
------------	-------------------------------

Description

Creates a fixed-size vector, matrix, or higher-dimensional array that is safe to use inside ‘rtmb_code()’ when subsequent assignments may involve RTMB automatic-differentiation values. This is a safer alternative to ‘array(value, dim)’ or ‘matrix(value, ...)’ in model code.

Usage

```
rtmb_array(value = 0, dim, seed = NULL)
```

Arguments

value	Initial value. Usually a scalar such as ‘0’.
dim	Integer dimension vector.
seed	Optional AD value used to create the container. See ‘rtmb_vector()’.

Value

An AD-compatible array.

rtmb_code	Define an RTMB Model with Stan-like Syntax
-----------	--

Description

rtmb_code is the primary interface for defining Bayesian or Frequentist models within the RTMB framework. It allows you to organize model logic into functional blocks while utilizing a Stan-like ~ operator for specifying priors and likelihoods.

Usage

```
rtmb_code(...)
```

Arguments

... Model definition blocks.

Details

Key Blocks and Logic:

- **setup:** Pre-compilation data processing.
- **parameters:** Declaration of estimated parameters. See [parameter_types](#) for available constraints.
- **transform:** Definition of intermediate variables. Use [math_functions](#) for stable AD calculations.
- **model:** Likelihood and Priors. Refer to [distributions](#) for available sampling statements.
- **generate:** Post-hoc calculation of predictions or diagnostics.

Automatic Differentiation (AD) Note: All code within parameters, transform, and model is automatically differentiated by RTMB. To ensure numerical stability, use provided utility functions like [log_sum_exp](#) or [inv_logit](#) instead of raw algebraic implementations.

Value

A list of unevaluated code blocks.

See Also

[rtmb_model](#) for building the model object. [parameter_types](#) for constraining parameters. [distributions](#) for likelihood functions. [math_functions](#) for numerical utilities.

Examples

```
# Simulate data for a linear regression
set.seed(123)
N <- 100
x <- rnorm(N)
y <- 2.0 + 1.5 * x + rnorm(N, mean = 0, sd = 1)
data_list <- list(N = N, x = x, y = y)

# Define the model using rtmb_code
code <- rtmb_code(
  setup = {
    # Center the predictor variable (executed once)
    x_centered <- x - mean(x)
  },
  parameters = {
    # Define parameters and their constraints
    alpha = Dim(1)
    beta = Dim(1)
    sigma = Dim(1, lower = 0)
  },
  transform = {
```

```

    # Calculate the linear predictor
    mu <- alpha + beta * x_centered
  },
  model = {
    # Priors
    alpha ~ normal(0, 10)
    beta ~ normal(0, 10)
    sigma ~ exponential(1)

    # Likelihood (Vectorized)
    y ~ normal(mu, sigma)
  },
  generate = {
    # Calculate generated quantities
    y_pred <- mu

    # Must return a named list
    list(y_pred = y_pred)
  }
)

# Create the model object
mod <- rtmb_model(data = data_list, code = code)

# Fit the model using MAP estimation
map_res <- mod$optimize()
map_res$summary(pars = c("alpha", "beta", "sigma"))

# The generated quantity 'y_pred' can also be summarized
map_res$summary("y_pred", max_rows = 5)

```

rtmb_corr

Fit a Correlation Model using RTMB

Description

‘rtmb_corr’ fits a correlation model to estimate means, standard deviations, and correlation structures. It supports simple correlation, multilevel correlation, and classical frequentist estimation.

Usage

```

rtmb_corr(
  x = NULL,
  data = NULL,
  ID = NULL,
  covariates = NULL,
  method = c("pearson", "spearman", "reml"),
  prior = prior_flat(),

```

```

y_range = NULL,
init = NULL,
fixed = NULL,
missing = c("listwise", "fiml", "pairwise"),
WAIC = FALSE
)

```

Arguments

<code>x</code>	A matrix, data frame, formula, or expression (e.g., <code>cbind(V1, V2)</code>) of response variables.
<code>data</code>	An optional data frame containing the variables.
<code>ID</code>	A character string or expression specifying the group ID variable for multilevel models.
<code>covariates</code>	Optional numeric matrix or data frame of covariates to be included in the joint MVN model.
<code>method</code>	Correlation method for <code>classic()</code> : "pearson", "spearman", or "reml".
<code>prior</code>	Prior configuration object: 'prior_flat()', 'prior_normal()', or 'prior_weak()'. Default is 'prior_flat()'. For 'prior_normal()', correlation models use the aliases 'mean_sd' and 'sd_rate', which override the common arguments 'mu_sd' and 'sigma_rate'. An LKJ prior with 'lkj_eta = 1' is added automatically unless 'lkj_eta' is supplied explicitly.
<code>y_range</code>	Optional numeric vector or matrix defining the theoretical range (min, max) of response variables. Required when using <code>prior_weak()</code> . Can be a vector of length 2 (applies to all variables) or a matrix/list of length P.
<code>init</code>	Optional list of initial values.
<code>fixed</code>	Optional named list of fixed values for specific parameters.
<code>missing</code>	Missing value handling strategy: "listwise" (default), "pairwise", or "fiml" (Full Information Maximum Likelihood).
<code>WAIC</code>	Logical; if TRUE, add pointwise 'log_lik' to the generate block for WAIC.

Examples

```

# Estimate the correlation between two variables in the debate dataset
data(debate, package = "BayesRTMB")

fit_corr <- rtmb_corr(cbind(sat, perf), data = debate)

mcmc_corr <- fit_corr$sample(sampling = 500, warmup = 500, chains = 2)
mcmc_corr$summary()

bf_corr <- mcmc_corr$bayes_factor(fixed = list(corr = 0))
print(bf_corr)

```

Description

Performs exploratory factor analysis (EFA) using RTMB. It supports standard rotation methods (e.g., varimax, promax) as well as regularized factor analysis using a Spike-and-Slab Prior (SSP) for estimating sparse loading matrices.

Usage

```
rtmb_fa(
  data,
  nfactors = 1,
  rotate = NULL,
  score = FALSE,
  prior = prior_flat(),
  y_range = NULL,
  init = NULL,
  fixed = NULL,
  missing = c("listwise", "fiml"),
  WAIC = FALSE
)
```

Arguments

data	Observation data frame or matrix (N x J).
nfactors	Number of factors (K).
rotate	String specifying the rotation method (e.g., "varimax", "promax", "ssp"). If NULL, no rotation is applied. Specifying "ssp" performs regularized factor analysis.
score	Logical; if TRUE, factor scores are calculated in the generate block (default is FALSE).
prior	Prior configuration: 'prior_flat()', 'prior_normal()', or 'prior_weak()'. 'prior_ssp()' is accepted when 'rotate = "ssp"'. Hyperparameters can be specified within these functions (e.g., 'prior_normal(mean_sd = 10, sd_rate = 1 / 5, loadings_sd = 10)'). Available FA aliases are 'mean_sd', 'sd_rate', and 'loadings_sd'; they override the corresponding common arguments 'mu_sd', 'sigma_rate', and 'b_sd'. 'sd_rate' is an exponential rate, so '1 / 5' gives a prior mean of 5. 'ssp_ratio' is available when 'rotate = "ssp"'.
y_range	A numeric vector of length 2 specifying the theoretical min and max values of the items. Used to construct weakly informative priors when 'prior = prior_weak()'.
init	List of initial values.
fixed	A named list of parameter values to fix (optional).

missing	Missing value handling strategy: "listwise" (default) or "fiml" (Full Information Maximum Likelihood).
WAIC	Logical; if TRUE, add pointwise 'log_lik' to the generate block for WAIC.

Examples

```
# Prepare a subset of the BigFive dataset for factor analysis
data(BigFive, package = "BayesRTMB")
fa_data <- BigFive[, 1:10]

# --- 1. Standard Exploratory Factor Analysis (1 Factor) ---
fit_fa1 <- rtmb_fa(data = fa_data, nfactors = 1)

# Maximum A Posteriori (MAP) estimation
map_fa1 <- fit_fa1$optimize()
map_fa1$summary()
```

RTMB_Fit_Base	<i>Base class for RTMB Fit objects</i>
---------------	--

Description

Base class for RTMB Fit objects

Base class for RTMB Fit objects

Details

An R6 base class providing common methods for Bayesian and MAP inference results.

Public fields

model The 'RTMB_Model' object used for estimation.

Methods

Public methods:

- `RTMB_Fit_Base$get_point_estimate()`
- `RTMB_Fit_Base$estimate()`
- `RTMB_Fit_Base$EAP()`
- `RTMB_Fit_Base$MAP()`
- `RTMB_Fit_Base$rotate()`
- `RTMB_Fit_Base$posterior_predict()`
- `RTMB_Fit_Base$pp_check()`
- `RTMB_Fit_Base$fa_rotate()`
- `RTMB_Fit_Base$clone()`

Method `get_point_estimate()`: Abstract method to get a point estimate for a target parameter.

Usage:

```
RTMB_Fit_Base$get_point_estimate(target, ...)
```

Arguments:

target Character string specifying the target parameter name.

... Additional arguments.

Returns: A numeric array or matrix of the point estimate.

Method estimate(): Get point estimates for parameters, transformed parameters, and generated quantities.

Usage:

```
RTMB_Fit_Base$estimate(
  pars = NULL,
  type = c("mean", "EAP", "marginal_map", "joint_map", "MAP"),
  component = c("all", "parameters", "transform", "generate"),
  chains = NULL,
  best_chains = NULL,
  drop = TRUE,
  ...
)
```

Arguments:

pars Optional character or numeric vector of parameter names or indices to extract. Supports special keywords: "parameters", "transform", "generate", and "all".

type Character string specifying the estimation type.

component Character string specifying the component to filter by.

chains Numeric vector of chains to include.

best_chains Number of best chains to include.

drop Logical; if TRUE and only one parameter is selected, return the value directly instead of a list.

... Additional arguments passed to draws().

Returns: A named list of point estimates, or a single value if 'drop = TRUE'.

Method EAP(): Calculate Expected A Posteriori (EAP) estimates from posterior samples.

Usage:

```
RTMB_Fit_Base$EAP(
  pars = "parameters",
  chains = NULL,
  best_chains = NULL,
  drop = TRUE,
  ...
)
```

Arguments:

pars Optional character vector of parameter names to extract.

chains Numeric vector of chains to include.

best_chains Number of best chains to include.

drop Logical; whether to drop the list if only one parameter is selected.
 ... Additional arguments passed to 'estimate()'.

Returns: A named list of EAP estimates.

Method MAP(): Calculate Maximum A Posteriori (MAP) estimates.

Usage:

```
RTMB_Fit_Base$MAP(
  pars = "parameters",
  chains = NULL,
  best_chains = NULL,
  type = c("marginal", "joint"),
  drop = TRUE,
  ...
)
```

Arguments:

pars Optional character vector of parameter names to extract.
 chains Numeric vector of chains to include.
 best_chains Number of best chains to include.
 type Character string; "marginal" or "joint" MAP.
 drop Logical; whether to drop the list if only one parameter is selected.
 ... Additional arguments passed to 'estimate()'.

Returns: A named list of MAP estimates.

Method rotate(): Rotate sampled parameters.

Usage:

```
RTMB_Fit_Base$rotate(
  target,
  reference = NULL,
  linked = NULL,
  principal = FALSE,
  suffix = "rot",
  overwrite = TRUE
)
```

Arguments:

target Character string specifying the target variable to base the rotation on.
 reference Matrix to rotate towards. If NULL, the target's point estimate is used.
 linked Character vector of variable names to be rotated in the same direction.
 principal Logical; if TRUE and 'reference' is NULL, the point estimate is first rotated to its principal axes and then used as the Procrustes reference. This is useful for MDU configurations.
 suffix Character suffix used for generated quantities. The default stores results as '<variable>_rot'.
 overwrite Logical; if TRUE, existing generated quantities with the same names are overwritten. If FALSE, a numeric suffix is appended.

Returns: The updated object invisibly.

Method `posterior_predict()`: Generate posterior predictive replications.

Usage:

```
RTMB_Fit_Base$posterior_predict(
  code = NULL,
  variable = NULL,
  draws = 100L,
  seed = NULL,
  random = c("conditional", "population", "simulate"),
  chains = NULL,
  best_chains = NULL,
  observed = NULL
)
```

Arguments:

`code` Optional 'rtmb_code()' object containing a 'generate' block for custom models. The block should create and report one replicated outcome.

`variable` Name of the replicated quantity returned by 'code'. If omitted, 'y_rep' or the only returned quantity is used.

`draws` Number of predictive draws, or 'NULL' to use every available posterior draw.

`seed` Optional random seed.

`random` Hierarchical prediction mode: "conditional" uses fitted random effects, "population" omits them, and "simulate" draws new random effects for the observed groups.

`chains` Optional chains to use.

`best_chains` Optional number of best chains to use.

`observed` Optional observed outcome or its name in model data. This is stored as metadata when its length matches a prediction.

Returns: A matrix with predictive draws in rows and observations in columns.

Method `pp_check()`: Plot a posterior predictive check.

Usage:

```
RTMB_Fit_Base$pp_check(
  type = c("auto", "dens", "bars"),
  stat = NULL,
  x = NULL,
  code = NULL,
  observed = NULL,
  variable = NULL,
  draws = 100L,
  seed = NULL,
  random = c("conditional", "population", "simulate"),
  chains = NULL,
  best_chains = NULL,
  plot = TRUE,
  ...
)
```

Arguments:

type Plot type: "dens", "bars", or "auto". Automatic mode uses the observation likelihood's `_lpdf` or `_lpmf` implementation.

stat Optional scalar statistic function, or its name. When supplied, the replicated statistic distribution is compared with its observed value.

x Optional predictor used for a scatter-based check. Supply a column name from the model data or a vector with one value per observation.

code Optional custom generate block; see `'posterior_predict()'`.

observed Optional observed outcome or its name in model data.

variable Name of the replicated quantity returned by `'code'`.

draws Number of posterior predictive replications.

seed Optional random seed.

random Hierarchical prediction mode; see `'posterior_predict()'`.

chains Optional chains to use.

best_chains Optional number of best chains to use.

plot Logical; draw the check immediately.

... Graphical arguments passed to the plotting method.

Returns: An `'rtmb_pp_check'` object, invisibly.

Method `fa_rotate()`: Rotate factor loadings and optional factor scores.

Usage:

```
RTMB_Fit_Base$fa_rotate(
  target = "L",
  linked = NULL,
  scores = NULL,
  rotate = "promax",
  ...,
  suffix = NULL,
  overwrite = TRUE
)
```

Arguments:

target Character string specifying the target variable to base the rotation on.

linked Character vector of variable names to be rotated in the same direction.

scores Character vector of variable names to be rotated as factor scores (inverse direction).

rotate Character string specifying the rotation method.

... Additional arguments passed to the rotation function.

suffix Character suffix used for generated quantities. If `NULL`, the rotation method name is used.

overwrite Logical; if `TRUE`, existing generated quantities with the same names are overwritten. If `FALSE`, a numeric suffix is appended.

Returns: The updated object invisibly.

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

```
RTMB_Fit_Base$clone(deep = FALSE)
```

Arguments:

deep Whether to make a deep clone.

rtmb_glm

RTMB-based GLM wrapper function (no random effects)

Description

RTMB-based GLM wrapper function (no random effects)

Usage

```
rtmb_glm(
  formula,
  data = NULL,
  family = "gaussian",
  prior = prior_flat(),
  y_range = NULL,
  init = NULL,
  fixed = NULL,
  gmc = NULL,
  centering = NULL,
  std = FALSE,
  view = NULL,
  factors = NULL,
  contrasts = "treatment",
  missing = c("listwise", "fiml"),
  WAIC = FALSE,
  ...
)
```

Arguments

formula	Formula
data	Optional data frame. If omitted, variables are resolved from the formula environment. In this mode, use bare variable names; formulas using \$, [[, or . require an explicit data argument.
family	Character string of the distribution family (e.g., "gaussian", "binomial", "poisson")
prior	An object of class "rtmb_prior". Use 'prior_flat()' for no prior, 'prior_normal()' for default normal/exponential priors, 'prior_jzs()' for continuous-family JZS priors, or 'prior_weak()', 'prior_rhs()', 'prior_ssp()' for weakly informative or regularized Bayesian inference. Default is 'prior_flat()'.
y_range	Theoretical minimum and maximum values of the response variable as a vector c(min, max). Specifying this automatically enables weakly informative priors.

<code>init</code>	List of initial values
<code>fixed</code>	Optional named list of fixed values for specific parameters.
<code>gmc</code>	Character vector of variable names for GMC
<code>centering</code>	Alias for 'gmc'.
<code>std</code>	Logical; if 'TRUE', also report post-hoc standardized fixed-effect coefficients. All fixed-effect design-matrix columns are standardized.
<code>view</code>	Optional character vector of parameter names to show first in summary.
<code>factors</code>	Character vector of variable names to be treated as factors.
<code>contrasts</code>	Character string specifying the contrast type ("treatment" or "sum").
<code>missing</code>	Missing value handling strategy: "listwise".
<code>WAIC</code>	Logical; if TRUE, add pointwise 'log_lik' to the generate block for WAIC.
<code>...</code>	Additional arguments passed to <code>rtmb_glmr()</code> .

Examples

```
# --- 1. Linear Regression (rtmb_lm) ---
# Fit a linear regression model using the debate dataset
data(debate, package = "BayesRTMB")
fit_lm <- rtmb_lm(sat ~ talk + perf, data = debate)
map_lm <- fit_lm$optimize()
map_lm$summary()

# --- 2. Generalized Linear Model (rtmb_glm) ---
# Fit a logistic regression model using the debate dataset
data(debate, package = "BayesRTMB")
fit_glm <- rtmb_glm(cond ~ talk + sat, data = debate, family = "bernoulli")
map_glm <- fit_glm$optimize()
map_glm$summary()

# --- 3. Generalized Linear Mixed Model (rtmb_glmr) ---
# Fit a linear mixed-effects model using the debate dataset
data(debate, package = "BayesRTMB")
fit_glmr <- rtmb_glmr(talk ~ cond + (1 | group), data = debate, family = "gaussian")

# MAP estimation using Laplace approximation for random effects
map_glmr <- fit_glmr$optimize(laplace = TRUE)
map_glmr$summary()

# MCMC sampling (chains and iterations reduced for faster execution)

mcmc_glmr <- fit_glmr$sample(sampling = 500, warmup = 500, chains = 2)
mcmc_glmr$summary()

# --- 4. Linear Mixed Model (rtmb_lmer) ---
# A convenient wrapper for Gaussian mixed models (identical to rtmb_glmr with family="gaussian")
fit_lmer <- rtmb_lmer(sat ~ talk + (1 | group), data = debate)
map_lmer <- fit_lmer$optimize()
```

```

map_lmer$summary()

# --- 5. Regularized Regression (Variable Selection) ---
# You can apply regularization to the fixed effects to shrink noise variables towards zero.
# Use prior = prior_rhs() for the Regularized Horseshoe prior,
# or prior_ssp() for the Spike-and-Slab prior.
# Note: When using regularization, you must specify 'y_range' (the theoretical minimum and maximum
# values of the response variable) to automatically set up the required weakly informative priors.

# Fit a linear regression using debate predictors with the Horseshoe prior
fit_rhs <- rtmb_lm(
  sat ~ talk + perf + skill,
  data = debate,
  prior = prior_rhs(),
  y_range = c(1, 5)
)
map_rhs <- fit_rhs$optimize()
# Summarize only the fixed effects (slopes)
map_rhs$summary("b")

# Fit a linear regression with the Spike-and-Slab prior
fit_ssp <- rtmb_lm(
  sat ~ talk + perf + skill,
  data = debate,
  prior = prior_ssp(),
  y_range = c(1, 5)
)
map_ssp <- fit_ssp$optimize()
map_ssp$summary("b")

```

rtmb_glmer

RTMB-based GLMM wrapper function

Description

RTMB-based GLMM wrapper function

Usage

```

rtmb_glmer(
  formula,
  data = NULL,
  family = "gaussian",
  laplace = FALSE,
  prior = prior_flat(),
  y_range = NULL,
  init = NULL,
  fixed = NULL,
  gmc = NULL,

```

```

centering = NULL,
cwc = NULL,
std = FALSE,
view = NULL,
within = NULL,
factors = NULL,
contrasts = "treatment",
sigma_by = NULL,
resid_corr = NULL,
resid_time = NULL,
resid_group = NULL,
generate = NULL,
missing = c("listwise", "fiml"),
WAIC = FALSE,
.force_sum = FALSE
)

```

Arguments

formula	lme4-style formula (e.g., $Y \sim X + (1 \text{GID})$)
data	Optional data frame. If omitted, variables are resolved from the formula environment. In this mode, use bare variable names; formulas using \$, [[, or . require an explicit data argument.
family	Character string of the distribution family (e.g., "gaussian", "binomial", "poisson", "ordered", "sequential")
laplace	Logical; whether to marginalize random effects using Laplace approximation
prior	An object of class "rtmb_prior" specifying the prior distribution. Use 'prior_flat()', 'prior_normal()', 'prior_weak()', 'prior_rhs()', or 'prior_ssp()'. 'prior_jzs()' is available for continuous families. Default is 'prior_flat()'.
y_range	Theoretical minimum and maximum values of the response variable as a vector c(min, max). Required when using weakly informative or regularized priors with continuous models.
init	List of initial values (generated automatically based on glm if omitted)
fixed	Optional named list of fixed values for specific parameters.
gmc	Character vector of variable names for Grand Mean Centering (GMC). If "all", all numeric variables are centered.
centering	Alias for 'gmc'.
cwc	List for Centering Within Cluster (CWC). Should contain cluster (group variable) and pars (variable names to center). You can also use <code>cwc = list(ID, "x")</code> or <code>cwc = list(ID, "all")</code> ; "all" centers all numeric fixed-effect variables within the cluster.
std	Logical; if 'TRUE', add post-hoc standardized fixed-effect coefficients as 'b_std'. Every column of the fixed-effect design matrix is standardized, including columns generated from factors and interactions. For Gaussian models, coefficients are scaled by both the predictor and response standard deviations. For other families, only the predictor standard deviations are used, so coefficients remain on the link scale.

view	Character vector of parameter names to prioritize in summary.
within	Optional list for wide-to-long conversion.
factors	Character vector of variable names to be treated as factors.
contrasts	Character string specifying the contrast type ("treatment" or "sum").
sigma_by	Character vector specifying variables to group residual variance by (heteroscedasticity).
resid_corr	Residual correlation structure: "ar1" (Autoregressive), "cs" (Compound Symmetry), "toep" (Toeplitz), or "un" (Unstructured).
resid_time	Variable name for time points in residual correlation.
resid_group	Variable name for grouping in residual correlation.
generate	Optional expression for generated quantities.
missing	Missing value handling strategy: "listwise".
WAIC	Logical; if TRUE, add pointwise 'log_lik' to the generate block for WAIC.
.force_sum	Logical; internal use only.

Examples

```
# --- 1. Linear Regression (rtmb_lm) ---
# Fit a linear regression model using the debate dataset
data(debate, package = "BayesRTMB")
fit_lm <- rtmb_lm(sat ~ talk + perf, data = debate)
map_lm <- fit_lm$optimize()
map_lm$summary()

# --- 2. Generalized Linear Model (rtmb_glm) ---
# Fit a logistic regression model using the debate dataset
data(debate, package = "BayesRTMB")
fit_glm <- rtmb_glm(cond ~ talk + sat, data = debate, family = "bernoulli")
map_glm <- fit_glm$optimize()
map_glm$summary()

# --- 3. Generalized Linear Mixed Model (rtmb_glmer) ---
# Fit a linear mixed-effects model using the debate dataset
data(debate, package = "BayesRTMB")
fit_glmer <- rtmb_glmer(talk ~ cond + (1 | group), data = debate, family = "gaussian")

# MAP estimation using Laplace approximation for random effects
map_glmer <- fit_glmer$optimize(laplace = TRUE)
map_glmer$summary()

# MCMC sampling (chains and iterations reduced for faster execution)

mcmc_glmer <- fit_glmer$sample(sampling = 500, warmup = 500, chains = 2)
mcmc_glmer$summary()

# --- 4. Linear Mixed Model (rtmb_lmer) ---
# A convenient wrapper for Gaussian mixed models (identical to rtmb_glmer with family="gaussian")
```

```

fit_lmer <- rtmb_lmer(sat ~ talk + (1 | group), data = debate)
map_lmer <- fit_lmer$optimize()
map_lmer$summary()

# --- 5. Regularized Regression (Variable Selection) ---
# You can apply regularization to the fixed effects to shrink noise variables towards zero.
# Use prior = prior_rhs() for the Regularized Horseshoe prior,
# or prior_ssp() for the Spike-and-Slab prior.
# Note: When using regularization, you must specify 'y_range' (the theoretical minimum and maximum
# values of the response variable) to automatically set up the required weakly informative priors.

# Fit a linear regression using debate predictors with the Horseshoe prior
fit_rhs <- rtmb_lm(
  sat ~ talk + perf + skill,
  data = debate,
  prior = prior_rhs(),
  y_range = c(1, 5)
)
map_rhs <- fit_rhs$optimize()
# Summarize only the fixed effects (slopes)
map_rhs$summary("b")

# Fit a linear regression with the Spike-and-Slab prior
fit_ssp <- rtmb_lm(
  sat ~ talk + perf + skill,
  data = debate,
  prior = prior_ssp(),
  y_range = c(1, 5)
)
map_ssp <- fit_ssp$optimize()
map_ssp$summary("b")

```

rtmb_irt

RTMB-based IRT (Item Response Theory) Wrapper

Description

Performs Item Response Theory modeling (1PL, 2PL, 3PL, and Graded Response Model) using RTMB. Missing values (NA) in the data are automatically removed internally for efficient computation.

Usage

```

rtmb_irt(
  data,
  model = c("2PL", "1PL", "3PL"),
  type = c("binary", "ordered"),
  prior = prior_flat(),
  init = NULL,

```

```

    fixed = NULL,
    view = NULL,
    missing = c("listwise", "fiml"),
    WAIC = FALSE
  )

```

Arguments

<code>data</code>	A data frame or matrix of item responses (N persons x J items).
<code>model</code>	Character string for the model type: "1PL", "2PL", or "3PL".
<code>type</code>	Character string for the data type: "binary" or "ordered".
<code>prior</code>	Prior configuration: 'prior_flat()', 'prior_normal()', or 'prior_weak()'. Hyper-parameters can be specified within these functions (e.g., 'prior_normal(b_sd = 5)'). Available parameters for IRT: 'a_rate' (discrimination; defaults to 1/2 with 'prior_normal()'), 'b_sd' (difficulty), and 'c_alpha'/'c_beta' (guessing).
<code>init</code>	List of initial values.
<code>fixed</code>	A named list of parameter values to fix (optional).
<code>view</code>	Character vector of parameter names to prioritize in summary.
<code>missing</code>	Missing value handling strategy: "listwise" (default) or "fiml" (Full Information Maximum Likelihood).
<code>WAIC</code>	Logical; if TRUE, add pointwise 'log_lik' to the generate block for WAIC.

Examples

```

# --- 1. Binary Data (e.g., correct/incorrect answers) ---
# Simulate binary response data for 100 persons and 5 items
set.seed(123)
bin_data <- matrix(rbinom(500, size = 1, prob = 0.6), nrow = 100, ncol = 5)
colnames(bin_data) <- paste0("Item", 1:5)

# Introduce some missing values (NA) to demonstrate automatic handling
#bin_data[sample(1:500, 10)] <- NA

# Fit a 2-Parameter Logistic (2PL) model
fit_2pl <- rtmb_irt(data = bin_data, model = "2PL", type = "binary")

# Maximum A Posteriori (MAP) estimation
map_2pl <- fit_2pl$optimize()
map_2pl$summary()

# --- 2. Ordered Data (e.g., Likert scale) ---
# Simulate ordered response data (categories 1 to 5) with a true latent structure
set.seed(123)
N <- 100
J <- 5
K <- 4

# True parameters
theta <- rnorm(N, 0, 1)          # Person abilities (latent traits)

```

```

a <- runif(J, 0.8, 2.0)          # Item discriminations

# Item-specific thresholds (must be strictly increasing)
b <- matrix(NA, nrow = J, ncol = K - 1)
for (j in 1:J) {
  b[j, ] <- sort(c(-1.5, 0, 1.5) + rnorm(3, 0, 0.2))
}

ord_data <- matrix(NA, nrow = N, ncol = J)
colnames(ord_data) <- paste0("Item", 1:J)

# Generate responses based on the Graded Response Model
for (i in 1:N) {
  for (j in 1:J) {
    # Latent continuous response (eta + standard logistic noise)
    eta <- a[j] * theta[i]
    y_star <- eta + rlogis(1)

    # Apply thresholds to determine the observed category (1 to 4)
    category <- 1
    for (k in 1:(K - 1)) {
      if (y_star > b[j, k]) category <- k + 1
    }
    ord_data[i, j] <- category
  }
}

# Fit a Graded Response Model (2PL for ordered data)
fit_ord <- rtmb_irt(data = ord_data, model = "2PL", type = "ordered")
fit_ord$print_code()

map_ord <- fit_ord$optimize()
map_ord$summary()

```

rtmb_lm

RTMB-based Linear Regression wrapper function

Description

RTMB-based Linear Regression wrapper function

Usage

```

rtmb_lm(
  formula,
  data = NULL,
  prior = prior_flat(),
  y_range = NULL,
  init = NULL,
  fixed = NULL,

```

```

    gmc = NULL,
    centering = NULL,
    std = FALSE,
    view = NULL,
    factors = NULL,
    contrasts = "treatment",
    missing = c("listwise", "fiml"),
    WAIC = FALSE,
    ...
  )

```

Arguments

formula	Formula (e.g., $Y \sim X1 + X2$)
data	Optional data frame. If omitted, variables are resolved from the formula environment. In this mode, use bare variable names; formulas using \$, [, or . require an explicit data argument.
prior	An object of class "rtmb_prior". Use 'prior_flat()' for no prior, 'prior_normal()' for default normal/exponential priors, 'prior_jzs()' for JZS regression priors, or 'prior_weak()', 'prior_rhs()', 'prior_ssp()' for weakly informative or regularized Bayesian inference. Default is 'prior_flat()'.
y_range	Theoretical minimum and maximum values of the response variable as a vector c(min, max). Specifying this automatically enables weakly informative priors.
init	List of initial values.
fixed	Optional named list of fixed values for specific parameters.
gmc	Character vector of variable names for GMC
centering	Alias for 'gmc'.
std	Logical; if 'TRUE', also report post-hoc standardized fixed-effect coefficients. All fixed-effect design-matrix columns are standardized.
view	Optional character vector of parameter names to show first in summary.
factors	Character vector of variable names to be treated as factors.
contrasts	Character string specifying the contrast type ("treatment" or "sum").
missing	Missing value handling strategy: "listwise".
WAIC	Logical; if TRUE, add pointwise 'log_lik' to the generate block for WAIC.
...	Additional arguments passed to rtmb_glmmer().

Examples

```

# --- 1. Linear Regression (rtmb_lm) ---
# Fit a linear regression model using the debate dataset
data(debate, package = "BayesRTMB")
fit_lm <- rtmb_lm(sat ~ talk + perf, data = debate)
map_lm <- fit_lm$optimize()
map_lm$summary()

```

```

# --- 2. Generalized Linear Model (rtmb_glm) ---
# Fit a logistic regression model using the debate dataset
data(debate, package = "BayesRTMB")
fit_glm <- rtmb_glm(cond ~ talk + sat, data = debate, family = "bernoulli")
map_glm <- fit_glm$optimize()
map_glm$summary()

# --- 3. Generalized Linear Mixed Model (rtmb_glmer) ---
# Fit a linear mixed-effects model using the debate dataset
data(debate, package = "BayesRTMB")
fit_glmer <- rtmb_glmer(talk ~ cond + (1 | group), data = debate, family = "gaussian")

# MAP estimation using Laplace approximation for random effects
map_glmer <- fit_glmer$optimize(laplace = TRUE)
map_glmer$summary()

# MCMC sampling (chains and iterations reduced for faster execution)

mcmc_glmer <- fit_glmer$sample(sampling = 500, warmup = 500, chains = 2)
mcmc_glmer$summary()

# --- 4. Linear Mixed Model (rtmb_lmer) ---
# A convenient wrapper for Gaussian mixed models (identical to rtmb_glmer with family="gaussian")
fit_lmer <- rtmb_lmer(sat ~ talk + (1 | group), data = debate)
map_lmer <- fit_lmer$optimize()
map_lmer$summary()

# --- 5. Regularized Regression (Variable Selection) ---
# You can apply regularization to the fixed effects to shrink noise variables towards zero.
# Use prior = prior_rhs() for the Regularized Horseshoe prior,
# or prior_ssp() for the Spike-and-Slab prior.
# Note: When using regularization, you must specify 'y_range' (the theoretical minimum and maximum
# values of the response variable) to automatically set up the required weakly informative priors.

# Fit a linear regression using debate predictors with the Horseshoe prior
fit_rhs <- rtmb_lm(
  sat ~ talk + perf + skill,
  data = debate,
  prior = prior_rhs(),
  y_range = c(1, 5)
)
map_rhs <- fit_rhs$optimize()
# Summarize only the fixed effects (slopes)
map_rhs$summary("b")

# Fit a linear regression with the Spike-and-Slab prior
fit_ssp <- rtmb_lm(
  sat ~ talk + perf + skill,
  data = debate,
  prior = prior_ssp(),
  y_range = c(1, 5)
)

```

```
map_ssp <- fit_ssp$optimize()
map_ssp$summary("b")
```

rtmb_lmer

RTMB-based Linear Mixed Model (LMM) wrapper function

Description

RTMB-based Linear Mixed Model (LMM) wrapper function

Usage

```
rtmb_lmer(
  formula,
  data = NULL,
  laplace = TRUE,
  prior = prior_flat(),
  y_range = NULL,
  init = NULL,
  fixed = NULL,
  gmc = NULL,
  centering = NULL,
  cwc = NULL,
  std = FALSE,
  view = NULL,
  sigma_by = NULL,
  factors = NULL,
  contrasts = "treatment",
  resid_corr = NULL,
  resid_time = NULL,
  resid_group = NULL,
  within = NULL,
  missing = c("listwise", "fiml"),
  WAIC = FALSE,
  ...
)
```

Arguments

formula	Formula
data	Optional data frame. If omitted, variables are resolved from the formula environment. In this mode, use bare variable names; formulas using \$, [[, or . require an explicit data argument.
laplace	Logical; whether to marginalize random effects using Laplace approximation

prior	An object of class "rtmb_prior". Use 'prior_flat()' for no prior, 'prior_normal()' for default normal/exponential priors, 'prior_jzs()' for JZS regression priors, or 'prior_weak()', 'prior_rhs()', 'prior_ssp()' for weakly informative or regularized Bayesian inference. Default is 'prior_flat()'.
y_range	Theoretical minimum and maximum values of the response variable
init	Initial values
fixed	Optional named list of fixed values for specific parameters.
gmc	Character vector of variable names for GMC
centering	Alias for 'gmc'.
cwc	List for CWC
std	Logical; if 'TRUE', also report post-hoc standardized fixed-effect coefficients. All fixed-effect design-matrix columns are standardized.
view	Character vector of parameter names to prioritize in summary.
sigma_by	Character vector specifying variables to group residual variance by (heteroscedasticity).
factors	Character vector of variable names to be treated as factors.
contrasts	Character string specifying the contrast type ("treatment" or "sum").
resid_corr	Residual correlation structure (e.g., "ar1", "cs", "un", "toep").
resid_time	Variable name for time points in residual correlation.
resid_group	Variable name for grouping in residual correlation.
within	Optional list for wide-to-long conversion. For repeated measures data in wide format, specify the factor names and their levels, e.g., list(Time = 4) or list(A = 2, B = 3). The total number of levels must match the number of columns in cbind() on the LHS. If omitted and the LHS is cbind(), the within-factor name is inferred from RHS variables not present in the data.
missing	Missing value handling strategy: "listwise".
WAIC	Logical; if TRUE, add pointwise 'log_lik' to the generate block for WAIC.
...	Additional arguments passed to rtmb_glm().

Value

RTMB_Model object

Examples

```
# --- 1. Linear Regression (rtmb_lm) ---
# Fit a linear regression model using the debate dataset
data(debate, package = "BayesRTMB")
fit_lm <- rtmb_lm(sat ~ talk + perf, data = debate)
map_lm <- fit_lm$optimize()
map_lm$summary()

# --- 2. Generalized Linear Model (rtmb_glm) ---
# Fit a logistic regression model using the debate dataset
```

```

data(debate, package = "BayesRTMB")
fit_glm <- rtmb_glm(cond ~ talk + sat, data = debate, family = "bernoulli")
map_glm <- fit_glm$optimize()
map_glm$summary()

# --- 3. Generalized Linear Mixed Model (rtmb_glmer) ---
# Fit a linear mixed-effects model using the debate dataset
data(debate, package = "BayesRTMB")
fit_glmer <- rtmb_glmer(talk ~ cond + (1 | group), data = debate, family = "gaussian")

# MAP estimation using Laplace approximation for random effects
map_glmer <- fit_glmer$optimize(laplace = TRUE)
map_glmer$summary()

# MCMC sampling (chains and iterations reduced for faster execution)

mcmc_glmer <- fit_glmer$sample(sampling = 500, warmup = 500, chains = 2)
mcmc_glmer$summary()

# --- 4. Linear Mixed Model (rtmb_lmer) ---
# A convenient wrapper for Gaussian mixed models (identical to rtmb_glmer with family="gaussian")
fit_lmer <- rtmb_lmer(sat ~ talk + (1 | group), data = debate)
map_lmer <- fit_lmer$optimize()
map_lmer$summary()

# --- 5. Regularized Regression (Variable Selection) ---
# You can apply regularization to the fixed effects to shrink noise variables towards zero.
# Use prior = prior_rhs() for the Regularized Horseshoe prior,
# or prior_ssp() for the Spike-and-Slab prior.
# Note: When using regularization, you must specify 'y_range' (the theoretical minimum and maximum
# values of the response variable) to automatically set up the required weakly informative priors.

# Fit a linear regression using debate predictors with the Horseshoe prior
fit_rhs <- rtmb_lm(
  sat ~ talk + perf + skill,
  data = debate,
  prior = prior_rhs(),
  y_range = c(1, 5)
)
map_rhs <- fit_rhs$optimize()
# Summarize only the fixed effects (slopes)
map_rhs$summary("b")

# Fit a linear regression with the Spike-and-Slab prior
fit_ssp <- rtmb_lm(
  sat ~ talk + perf + skill,
  data = debate,
  prior = prior_ssp(),
  y_range = c(1, 5)
)
map_ssp <- fit_ssp$optimize()
map_ssp$summary("b")

```

rtmb_loglinear	<i>RTMB-based Log-linear analysis (Poisson regression)</i>
----------------	--

Description

Performs Bayesian or Frequentist log-linear analysis (Poisson regression) on a contingency table or raw data.

Usage

```
rtmb_loglinear(
  formula,
  data,
  prior = prior_flat(),
  y_range = NULL,
  fixed = NULL,
  WAIC = FALSE,
  ...
)
```

Arguments

formula	A formula (e.g., '~ A + B + A:B') or a contingency table.
data	A data frame (required if 'formula' is used).
prior	An object of class "rtmb_prior" specifying the prior distribution.
y_range	Optional theoretical minimum and maximum values of the count response. If supplied with the default flat prior, 'prior_weak()' is used.
fixed	Optional named list of fixed values for specific parameters.
WAIC	Logical; if TRUE, add pointwise 'log_lik' to the generate block for WAIC.
...	Additional arguments passed to 'rtmb_glm()'.

Value

An 'RTMB_Model' object.

Examples

```
# Create a contingency table
tab <- matrix(c(10, 20, 30, 40), nrow = 2)
dimnames(tab) <- list(A = c("A1", "A2"), B = c("B1", "B2"))

# Fit a log-linear model (independence model: ~ A + B)
fit_log <- rtmb_loglinear(~ A + B, data = tab)

# MAP estimation
map_log <- fit_log$optimize()
map_log$summary()
```

rtmb_lrt

*Fit a Latent Rank Theory (LRT) Model***Description**

Fits a Latent Rank Theory model, which is a mixture model with ordered ranks and Gaussian Process smoothing on the mean profiles.

Usage

```
rtmb_lrt(
  formula,
  k = 3,
  data = NULL,
  rank_coords = NULL,
  covariance = c("diagonal", "diagonal_equal", "full", "full_equal", "full_equal_corr"),
  magnitude = NULL,
  smoothing = NULL,
  noise = 0.01,
  probab_smoothing = FALSE,
  link = c("ordered", "sequential"),
  prior = prior_flat(),
  y_range = NULL,
  fixed = NULL,
  two_stage = FALSE,
  WAIC = FALSE,
  ...
)
```

Arguments

formula	A formula specifying the response variable(s).
k	Number of ranks (mixture components).
data	A data frame containing the variables.
rank_coords	Optional numeric vector of coordinates for each rank. Default is 1:k.
covariance	Covariance structure: "diagonal", "diagonal_equal", "full", "full_equal", or "full_equal_corr".
magnitude	Signal standard deviation for the GP prior. If NULL, it is estimated.
smoothing	Length-scale for the GP prior. If NULL, it is estimated.
noise	Measurement noise for the GP prior (default is 0.01).
probab_smoothing	Logical; whether to apply smoothing to the class membership probabilities.
link	Link function for class probabilities: "ordered" or "sequential".
prior	Prior configuration: 'prior_flat()', 'prior_normal()', 'prior_weak()', 'prior_rhs()', or 'prior_ssp()'. Default is 'prior_flat()'. If 'y_range' is supplied with the default flat prior, the wrapper automatically switches to 'prior_weak()'.

y_range	Optional theoretical range of the response variables. Use a numeric vector 'c(min, max)' for a common range, or a P x 2 matrix/list for response-specific ranges. Specifying this automatically enables 'prior_weak()' when 'prior' is 'prior_flat()' and calibrates the residual standard-deviation prior.
fixed	Optional named list of fixed values for specific parameters.
two_stage	Logical; if TRUE, estimate the latent-rank measurement model first and then estimate the rank regression with delta-method uncertainty propagation. Currently supported for '\$optimize()' only.
WAIC	Logical; if TRUE, add pointwise 'log_lik' to the generate block for WAIC.
...	Additional arguments passed to 'rtmb_model'.

Value

A RTMB_Model object.

rtmb_mdu

RTMB-based Multidimensional Unfolding Wrapper

Description

Fits a multidimensional unfolding model for preference/rating data. Rows are persons or observations and columns are stimuli/items. The model represents both row scores ('theta') and item locations ('delta') in a shared D-dimensional space.

Usage

```
rtmb_mdu(
  data,
  ndim = 2,
  distance = c("euclidean", "squared"),
  alpha = c("random", "fix"),
  lambda = c("fix", "random"),
  method = c("rating", "Best", "Best-Worst", "MDS"),
  sets = NULL,
  prior = prior_flat(),
  y_range = NULL,
  init = NULL,
  fixed = NULL,
  view = NULL,
  distance_eps = 1e-04,
  missing = c("listwise", "fiml"),
  WAIC = FALSE
)
```

Arguments

<code>data</code>	Numeric matrix or data frame (N rows x M items) for <code>'method = "rating"'</code> . For choice methods, a list containing <code>'Best'</code> and, for <code>'method = "Best-Worst"'</code> , <code>'Worst'</code> . For <code>'method = "Best-Worst"'</code> , a single matrix/data frame is treated as pre-coded <code>'Y_dif'</code> pair indices.
<code>ndim</code>	Number of unfolding dimensions.
<code>distance</code>	Character; <code>"euclidean"</code> uses Euclidean distance (default), while <code>"squared"</code> uses squared Euclidean distance.
<code>alpha</code>	Character; <code>"random"</code> estimates item-specific alpha values as random effects (default), while <code>"fix"</code> estimates a single common alpha.
<code>lambda</code>	Character; for choice methods, <code>"fix"</code> estimates a common inverse-temperature parameter (default), while <code>"random"</code> estimates person-specific inverse-temperature parameters with a log-normal hierarchy.
<code>method</code>	Character; <code>"rating"</code> for continuous ratings, <code>"Best"</code> for best-only choice tasks, <code>"Best-Worst"</code> for best-worst choice tasks, or <code>"MDS"</code> for fitting a multidimensional scaling model to a distance matrix.
<code>sets</code>	Matrix or data frame of presented item sets (P tasks x C items) for choice methods.
<code>prior</code>	Prior configuration: <code>'prior_flat()'</code> , <code>'prior_normal()'</code> , or <code>'prior_weak()'</code> . <code>'prior_flat()'</code> creates a maximum-likelihood model suitable for <code>'classic()'</code> . The latent coordinates <code>'delta'</code> and <code>'theta'</code> are always treated as random effects with normal scale priors, similarly to IRT ability parameters.
<code>y_range</code>	Optional response range for <code>'method = "rating"'</code> . If supplied with the default flat prior, <code>'prior_weak()'</code> is used. For choice methods (<code>"Best"</code> and <code>"Best-Worst"</code>), <code>'prior_weak()'</code> behaves like <code>'prior_normal()'</code> because there is no observed rating scale.
<code>init</code>	Optional named list of initial values.
<code>fixed</code>	Optional named list of parameter values to fix.
<code>view</code>	Character vector of parameter names to prioritize in summaries.
<code>distance_eps</code>	Small positive constant added to the distance.
<code>missing</code>	Missing value handling strategy: <code>"listwise"</code> (default) or <code>"fiml"</code> (Full Information Maximum Likelihood).
<code>WAIC</code>	Logical; if TRUE, add pointwise <code>'log_lik'</code> to the generate block for WAIC.

Value

An `'RTMB_Model'` object.

Examples

```
# Simulate rating data for Multidimensional Unfolding (MDU)
set.seed(123)
N <- 50 # Number of persons
M <- 10 # Number of items
```

```

D <- 2 # Number of dimensions

# True person and item coordinates in a 2D space
theta <- matrix(rnorm(N * D), N, D)
delta <- matrix(rnorm(M * D), M, D)

# Generate distance-like ratings (smaller means more preferred)
Y <- matrix(NA, N, M)
for(i in 1:N) {
  for(j in 1:M) {
    Y[i, j] <- sum((theta[i,] - delta[j,])^2) + rnorm(1, 0, 0.5)
  }
}

# Fit a 2-dimensional MDU model
fit_mdu <- rtmb_mdu(Y, ndim = 2, distance = "squared", method = "rating")

# MAP estimation
map_mdu <- fit_mdu$optimize()
map_mdu$summary()

# Note: MDU models have many parameters, so MCMC sampling might take time.

# mcmc_mdu <- fit_mdu$sample(sampling = 500, warmup = 500, chains = 2)

```

rtmb_mediation

RTMB-based Mediation Analysis Wrapper

Description

‘rtmb_mediation’ performs mediation analysis by simultaneously estimating multiple GLM regression equations. It automatically identifies mediation paths and calculates indirect, direct, and total effects.

Usage

```

rtmb_mediation(
  formula,
  data,
  family = "gaussian",
  prior = prior_flat(),
  y_range = NULL,
  fixed = NULL,
  view = NULL,
  WAIC = FALSE,
  gmc = NULL,
  centering = NULL,
  cwc = NULL,

```

```
    ...  
  )
```

Arguments

formula	A list of formulas defining the regression paths (e.g., 'list(M ~ X, Y ~ X + M)'). Each equation may optionally include one random intercept, such as '(1 ID)'.
data	A data frame containing the variables.
family	A single character string or a list of character strings specifying the error distribution for each equation (e.g., 'family = list("gaussian", "binomial)'). Default is "gaussian".
prior	An object of class "rtmb_prior" specifying the prior distribution.
y_range	Theoretical minimum and maximum values of the response variable.
fixed	A named list of parameter values to fix (optional).
view	Character vector of parameter names to prioritize in summary.
WAIC	Logical; if TRUE, add pointwise 'log_lik' to the generate block for WAIC.
gmc	Character vector naming predictors to grand-mean center, or "all" to center all numeric predictors used by the mediation equations.
centering	Alias for 'gmc'.
cwc	Centering-within-cluster specification. Use, for example, 'list(cluster = ID, pars = c("X", "M"))' or 'list(ID, "X')'. Cluster means are not added automatically.
...	Reserved; unused arguments are rejected.

Details

The function identifies mediation paths by looking for variables that are responses in one equation and predictors in another. Indirect effects are calculated as the product of coefficients along these paths ($a * b$).

Random intercepts may be included in all equations or in only a subset of equations. When more than one equation contains a random intercept, all random intercepts must use the same grouping variable and their correlations are estimated jointly. Random slopes, multiple random-effect terms within an equation, and different grouping variables across equations are not yet supported. The mediation-specific classical bootstrap is currently unavailable for random-intercept and CWC models.

'gmc' (or its alias 'centering') and 'cwc' are applied to predictor uses of the selected variables before each equation's model matrix is constructed. Their response uses remain on the original scale. Thus, if 'M' is the response in one equation and a predictor in another, 'cwc = list(ID, "M')' centers 'M' only in the latter role. When both GMC and CWC target the same variable, GMC is applied first. Between-cluster means must be created by the user and included explicitly in the formulas.

Uncertainty Estimation: When using '\$optimize(ci_method = "sampling")', the function provides asymmetric confidence intervals for indirect effects based on the distribution of products, which is more accurate than the standard Sobel test (Delta Method).

Value

An 'RTMB_Model' object.

Examples

```
# Simulate mediation data
set.seed(123)
N <- 100
X <- rnorm(N)
# M is influenced by X
M <- 0.5 * X + rnorm(N, 0, 0.5)
# Y is influenced by both X and M
Y <- 0.3 * X + 0.8 * M + rnorm(N, 0, 0.5)
dat <- data.frame(X, M, Y)

# Fit a mediation model
# The formula list specifies the two regression equations
fit_med <- rtmb_mediation(list(M ~ X, Y ~ X + M), data = dat)

# Maximum A Posteriori (MAP) estimation
map_med <- fit_med$optimize()
# The summary automatically calculates indirect, direct, and total effects
map_med$summary()
```

rtmb_mixture

Mixture Model Wrapper for RTMB

Description

Provides a user-friendly interface for fitting Gaussian mixture models with optional covariates on class membership probabilities and various covariance structures.

Usage

```
rtmb_mixture(
  formula,
  k = 2,
  data = NULL,
  covariance = c("diagonal", "diagonal_equal", "full", "full_equal", "full_equal_corr"),
  prior = prior_flat(),
  y_range = NULL,
  fixed = NULL,
  WAIC = FALSE,
  ...
)
```

Arguments

formula	A formula specifying the response variable(s). For multivariate, use <code>cbind(y1, y2) ~ 1</code> .
k	Number of mixture components.
data	A data frame containing the variables in the model.
covariance	Covariance structure: "diagonal" (default), "diagonal_equal", "full", "full_equal", or "full_equal_corr".
prior	Prior configuration: 'prior_flat()', 'prior_normal()', 'prior_weak()', 'prior_rhs()', or 'prior_ssp()'. Default is 'prior_flat()'. If 'y_range' is supplied with the default flat prior, the wrapper automatically switches to 'prior_weak()'.
y_range	Optional theoretical range of the response variables. Use a numeric vector 'c(min, max)' for a common range, or a P x 2 matrix/list for response-specific ranges. Specifying this automatically enables 'prior_weak()' when 'prior' is 'prior_flat()' and calibrates the component mean and residual standard-deviation priors.
fixed	Optional named list of fixed values for specific parameters.
WAIC	Logical; if TRUE, add pointwise 'log_lik' to the generate block for WAIC.
...	Reserved; unused arguments are rejected.

Value

A `RTMB_Model` object.

Examples

```
# Simulate 1D mixture data (2 components)
set.seed(123)
N <- 100
group <- rbinom(N, 1, 0.4)
y <- ifelse(group == 1, rnorm(N, 5, 1), rnorm(N, 0, 1))
dat <- data.frame(y)

# Fit a 1D Gaussian mixture model with 2 components
fit_mix <- rtmb_mixture(y ~ 1, k = 2, data = dat)

# MAP estimation
map_mix <- fit_mix$optimize()
map_mix$summary()
```

Description

The `rtmb_model` function acts as the core constructor for compiling and combining user-defined data with the model code (defined via `rtmb_code`). It generates an `RTMB_Model` (R6 class) instance, which serves as the foundation for performing Bayesian inference, including Maximum A Posteriori (MAP) estimation, Variational Inference (ADVI), and Markov Chain Monte Carlo (MCMC) sampling.

Usage

```
rtmb_model(
  data,
  code,
  par_names = list(),
  init = NULL,
  view = NULL,
  fixed = NULL,
  silent = FALSE,
  gr_test = FALSE
)
```

Arguments

<code>data</code>	A named list, data frame, matrix, or other object containing the observations used in the model. The original object is available as <code>.data</code> while the setup block is evaluated.
<code>code</code>	A model definition block generated by <code>rtmb_code(...)</code> (must include parameters and model blocks).
<code>par_names</code>	A named list of character vectors corresponding to the dimensions of specific parameters (optional).
<code>init</code>	A list or numeric vector of initial values for parameters (optional). If not specified, initialized randomly.
<code>view</code>	Character vector of parameter names to be displayed preferentially at the top when outputting results like <code>summary()</code> (optional).
<code>fixed</code>	A named list of parameter values to fix (optional). Useful for scoring or plug-in estimation where some parameters (e.g., item parameters) are fixed to known values.
<code>silent</code>	Logical; if TRUE, suppresses diagnostic messages during model creation. Default is FALSE.
<code>gr_test</code>	Logical; if TRUE, evaluate the gradient once after the AD tape is built. By default, model creation checks that <code>MakeADFun()</code> can build the AD tape but skips this extra gradient evaluation for speed.

Details

Model Compilation and Pre-checking: When this function is called, it evaluates the provided data and model blocks. It performs a "sandbox execution" (pre-check) using dummy initial values

to dynamically detect common structural errors, such as undefined variables, out-of-bounds indices, or incompatible matrix operations, before proceeding to the computationally expensive Automatic Differentiation (MakeADFun) phase. Cryptic backend errors are caught and translated into user-friendly hints.

Inside the setup block, the read-only reserved name `.data` refers to the original object supplied to `data`. This allows setup code such as `Y <- as.matrix(.data)` for a matrix or data frame, and `S <- as.matrix(.data$sets)` for a named list. The temporary `.data` binding is removed after setup has finished.

Writing AD-Compatible Code (Important): To ensure the model is differentiable, you must follow specific syntax rules when writing code within `rtmb_code`. Avoid discrete branching (`if`, `ifelse`) based on parameters and use numerically stable functions. See [rtmb_syntax](#) for a detailed guide on Automatic Differentiation requirements.

Initial Values (`init`): Initial parameter values can be specified as a flat numeric vector or a named list. If a partial list is provided, the unspecified parameters are automatically initialized with random values drawn from a uniform distribution on the unconstrained scale. If `init = NULL`, all parameters are initialized randomly.

Parameter Labeling (`par_names`): By default, vector or matrix parameters are displayed with numeric indices (e.g., `mu[1]`). You can pass a named list of character vectors to `par_names` to assign meaningful labels to specific dimensions (e.g., `mu[Control]`), vastly improving the readability of summary outputs and trace plots.

Available Inference Methods on the Returned Object: The returned `RTMB_Model` instance provides the following core methods:

- `$optimize(...)`: Performs Maximum A Posteriori (MAP) or Maximum Likelihood estimation. Returns a `MAP_Fit` object.
- `$sample(...)`: Draws posterior samples using the NUTS (No-U-Turn Sampler) algorithm. Returns an `MCMC_Fit` object.
- `$variational(...)`: Performs Mean-field or Full-rank Automatic Differentiation Variational Inference (ADVI). Returns a `VB_Fit` object.

Value

An `RTMB_Model` class instance with a compiled and pre-tested automatic differentiation function.

An `RTMB_Model` class instance with a compiled and pre-tested automatic differentiation function.

Examples

```
# Simulate data for 3 groups
set.seed(123)
N <- 60
group_idx <- sample(1:3, N, replace = TRUE)
group_names <- c("Control", "Treatment_A", "Treatment_B")

# True group means: Control = 0, Treatment_A = 2, Treatment_B = -1
true_means <- c(0, 2, -1)
y <- true_means[group_idx] + rnorm(N, mean = 0, sd = 0.5)

data_list <- list(N = N, K = 3, group_idx = group_idx, y = y)
```

```

# Define the model using rtmb_code
model_code <- rtmb_code(
  parameters = {
    mu      = Dim(K)          # Vector of length K (group means)
    sigma = Dim(1, lower = 0) # Scalar (residual standard deviation)
  },
  model = {
    # Priors
    for (k in 1:K) mu[k] ~ normal(0, 10)
    sigma ~ exponential(1)

    # Likelihood
    for (i in 1:N) {
      y[i] ~ normal(mu[group_idx[i]], sigma)
    }
  }
)

# --- 1. Basic Model Creation ---
# Create the RTMB_Model object
mod_basic <- rtmb_model(
  data = data_list,
  code = model_code
)

# Perform Maximum A Posteriori (MAP) estimation
map_basic <- mod_basic$optimize()
# The summary displays default parameter names: mu[1], mu[2], mu[3]
map_basic$summary()

# --- 2. Optional: Adding Custom Parameter Names and initial values ---
# You can optionally use 'par_names' to assign meaningful labels
# to vector or matrix elements for easier interpretation.
mod_named <- rtmb_model(
  data = data_list,
  code = model_code,
  init = list(mu = rep(0, 3), sigma = 1),
  par_names = list(mu = group_names)
)

map_named <- mod_named$optimize()
# The summary now displays: mu[Control], mu[Treatment_A], mu[Treatment_B]
map_named$summary()

```

Description

An R6 class representing a Bayesian model built with RTMB. This class stores model components and provides methods for building the automatic differentiation object, optimizing the posterior, and drawing posterior samples.

Public fields

`data` Named list containing observation data.

`par_list` Evaluated list of parameter definitions.

`log_prob` Executable function for likelihood and prior calculations.

`transform` Function for calculating transformed parameters.

`generate` Function for calculating generated quantities.

`par_names` List of variable names corresponding to parameter dimensions.

`pl_full` Complete parameter list with expanded constraints and dimension information used internally.

`formula` Formula used for model generation (if created via a wrapper function).

`requested_contrasts` Character; user-requested contrast setting (e.g. "treatment").

`contrasts` Character; internal contrast setting used for fitting (e.g. "sum").

`raw_data` Data frame; the original data used for the model.

`family` Character string of the distribution family (if created via a wrapper function).

`init` List or numeric vector of initial values.

`view` Character vector of variable names to prioritize in summary.

`code` Original model AST generated by `'rtmb_code()'`.

`map` A list specifying parameter mappings for fixing values (e.g., via `fixed_model()`).

`prior_correction` Numeric value for legacy or low-level marginal-likelihood correction. Fixed-parameter prior removal is handled during AD objective construction.

`fixed_prior_specs` Internal specification for removing fixed-parameter prior contributions during AD evaluation.

`type` Character; the type of the model (e.g. 'lmer', 'glm', 'table', 'ttest', 'corr', 'mediation').

`extra` List; used to store auxiliary data (like term assignments, factors, test results) needed by methods such as `classic()`.

Methods**Public methods:**

- `RTMB_Model$new()`
- `RTMB_Model$prepare_init()`
- `RTMB_Model$get_par_list()`
- `RTMB_Model$get_ad_obj()`
- `RTMB_Model$to_unconstrained()`
- `RTMB_Model$to_constrained()`

- `RTMB_Model$unconstrained_vector_to_list()`
- `RTMB_Model$constrained_vector_to_list()`
- `RTMB_Model$calculate_satterthwaite_df()`
- `RTMB_Model$calculate_reml_satterthwaite_df()`
- `RTMB_Model$build_ad_obj()`
- `RTMB_Model$optimize()`
- `RTMB_Model$classic()`
- `RTMB_Model$sample()`
- `RTMB_Model$variational()`
- `RTMB_Model$print_code()`
- `RTMB_Model$print_log_prob()`
- `RTMB_Model$print_transform()`
- `RTMB_Model$print_generate()`
- `RTMB_Model$get_n_obs()`
- `RTMB_Model$fixed_model()`
- `RTMB_Model$clone()`

Method `new()`: Create a new ‘RTMB_Model’ object.

Usage:

```
RTMB_Model$new(
  data,
  par_list,
  log_prob,
  transform = NULL,
  generate = NULL,
  par_names = NULL,
  init = NULL,
  view = NULL,
  code = NULL,
  gr_test = FALSE
)
```

Arguments:

`data` Named list containing observation data.

`par_list` Evaluated list of parameter definitions.

`log_prob` Executable function for likelihood and prior calculations.

`transform` Function for calculating transformed parameters (optional).

`generate` Function for calculating generated quantities (optional).

`par_names` List of variable names corresponding to parameter dimensions.

`init` List or numeric vector of initial values.

`view` Character vector of variable names to prioritize in summary.

`code` Original model AST generated by ‘`rtmb_code()`’.

`gr_test` Logical; if TRUE, evaluate the gradient once after the AD tape is built.

Method `prepare_init()`: Prepare and format initial values for the model parameters.

Usage:

```
RTMB_Model$prepare_init(init_arg)
```

Arguments:

init_arg Optional list or numeric vector of initial values. If NULL, defaults to 'self\$init' or random generation.

Returns: A flat numeric vector of constrained initial values.

Method `get_par_list()`: Get the current parameters as a named list.

Usage:

```
RTMB_Model$get_par_list(init = NULL)
```

Arguments:

init Optional numeric vector or list of initial values. If NULL, uses the model's current initial values.

Returns: A named list of constrained parameters.

Method `get_ad_obj()`: Get the RTMB automatic differentiation object.

Usage:

```
RTMB_Model$get_ad_obj(...)
```

Arguments:

... Arguments passed to `build_ad_obj`.

Returns: A TMB objective object (`ad_obj`).

Method `to_unconstrained()`: Convert a list of constrained parameters to unconstrained space.

Usage:

```
RTMB_Model$to_unconstrained(par_list_constrained)
```

Arguments:

par_list_constrained A named list of parameters in their natural space.

Returns: A named list of parameters in unconstrained space.

Method `to_constrained()`: Convert a list of unconstrained parameters to constrained (natural) space.

Usage:

```
RTMB_Model$to_constrained(par_list_unconstrained)
```

Arguments:

par_list_unconstrained A named list of parameters in unconstrained space.

Returns: A named list of parameters in constrained space.

Method `unconstrained_vector_to_list()`: Convert a flat unconstrained vector to a named list.

Usage:

```
RTMB_Model$unconstrained_vector_to_list(vec)
```

Arguments:

vec A numeric vector in unconstrained space.

Returns: A named list of unconstrained parameters.

Method `constrained_vector_to_list()`: Convert a flat constrained vector to a named list.

Usage:

```
RTMB_Model$constrained_vector_to_list(vec)
```

Arguments:

vec A numeric vector in constrained space.

Returns: A named list of constrained parameters.

Method `calculate_satterthwaite_df()`: Calculate Satterthwaite degrees of freedom for parameters.

Usage:

```
RTMB_Model$calculate_satterthwaite_df(
  ad_obj,
  idx_fix_active = NULL,
  L_u_total = NULL,
  opt_par = NULL,
  max_df = NULL,
  silent = FALSE,
  return_sensitivities = FALSE
)
```

Arguments:

ad_obj An RTMB objective object at the optimum.

idx_fix_active Integer vector; indices of active fixed parameters in the full unconstrained vector.

L_u_total Integer; total length of the full unconstrained parameter vector.

opt_par Optional numeric vector of optimized parameters.

max_df Numeric; maximum allowed degrees of freedom. Default is NULL.

silent Logical; whether to suppress informational messages. Default is FALSE.

return_sensitivities Logical; if TRUE, returns Hessian sensitivities and V for delta method.

Returns: A numeric vector of estimated degrees of freedom (length = *L_u_total*). Inf for random effects.

Method `calculate_reml_satterthwaite_df()`: Calculate Satterthwaite degrees of freedom for integrated fixed effects (REML).

Usage:

```
RTMB_Model$calculate_reml_satterthwaite_df(
  ad_obj,
  opt_par,
  beta_idx,
  max_df = NULL,
  silent = FALSE,
  return_sensitivities = FALSE
)
```

Arguments:

ad_obj An RTMB objective object.
 opt_par Numeric vector of optimized variance components.
 beta_idx Integer vector; indices of fixed effects within the random effects vector.
 max_df Numeric; maximum allowed degrees of freedom. Default is NULL.
 silent Logical; whether to suppress informational messages. Default is FALSE.
 return_sensitivities Logical; if TRUE, returns Hessian sensitivities and delta-method components.
 ... Additional arguments.

Returns: A numeric vector of estimated degrees of freedom for the fixed effects.

Method build_ad_obj(): Build the RTMB automatic differentiation object.

Usage:

```
RTMB_Model$build_ad_obj(
  init = NULL,
  laplace = FALSE,
  jacobian_target = "none",
  map = NULL,
  .marginal_vars = NULL
)
```

Arguments:

init Optional numeric vector or list of initial values for the parameters. Default is NULL.
 laplace Logical; whether to use Laplace approximation to marginalize random effects. Default is FALSE.
 jacobian_target Character string specifying which parameters to apply Jacobian adjustments to:
 • "all": Apply to all parameters (standard for Bayesian MCMC).
 • "random": Apply only to parameters with random = TRUE (standard for Laplace approximation/REML).
 • "none": No Jacobian adjustment (standard for Maximum Likelihood estimation).
 Default is "none".
 map Optional list specifying parameters to fix. Passed directly to MakeADFun. Default is NULL.
 .marginal_vars Internal use for profiling marginalized parameters.

Returns: An RTMB objective object (ad_obj).

Method optimize(): Perform Maximum Likelihood or Maximum A Posteriori (MAP) estimation.

Usage:

```
RTMB_Model$optimize(
  laplace = TRUE,
  init = NULL,
  num_estimate = 1,
  control = list(),
```

```

optimizer = "nllminb",
method = "BFGS",
map = NULL,
fixed = NULL,
se_method = c("wald", "sampling", "none"),
num_samples = 1000,
seed = 123,
marginal = "none",
df_method = "auto",
view = NULL,
...
)

```

Arguments:

laplace Logical; whether to use Laplace approximation for random effects. Default is TRUE.

init Optional initial values for parameters (numeric vector or list).

num_estimate Integer; Number of multi-start optimization runs. Default is 1.

control A list of control settings passed to the optimizer.

optimizer Character; The optimizer to use: "nllminb" (default) or "optim".

method Character; The method for "optim" (e.g., "BFGS", "L-BFGS-B").

map Optional list specifying parameters to fix (factors).

fixed Optional list specifying parameter values to fix.

se_method Character; method for uncertainty estimation.

- "wald": Wald standard errors and Wald confidence intervals.
- "sampling": Simulation-based error propagation.
- "none": Do not compute standard errors, confidence intervals, or degrees of freedom.

num_samples Integer; number of samples to draw when **se_method** is "sampling". Default is 1000.

seed Integer; random seed for sampling.

marginal Character vector or "auto" or "none"; specifies which parameters to marginalize out via Laplace approximation.

- "none" (default): No additional marginalization.
- "auto": Uses variables specified by the model wrapper (e.g., fixed effects in lmer).
- "all": Marginalize all parameters (advanced use).
- character vector: Specific parameter names to marginalize.

df_method Character or numeric; method for finite degrees-of-freedom approximation. Used only when 'marginal' resolves to one or more parameters and 'se_method' != "none".

- "auto": Uses Satterthwaite approximation when marginalization is active.
- "satterthwaite": Satterthwaite approximation.
- "inf" or "none": Use infinite degrees of freedom.
- numeric: Use the supplied fixed degrees of freedom.

view Character vector of parameter names to prioritize in summary display.

... Additional arguments.

Returns: A fitted 'MAP_Fit' object.

Method `classic()`: Perform frequentist inference (REML/ML) with model-appropriate degrees of freedom.

Usage:

```
RTMB_Model$classic(
  df_method = "auto",
  se_method = c("wald", "sampling"),
  num_samples = 1000,
  seed = 123,
  view = NULL,
  map = NULL,
  fixed = NULL,
  ...
)
```

Arguments:

`df_method` Character; Method for calculating degrees of freedom. Default is "auto".

- "auto": Determined based on model type (e.g., Satterthwaite for mixed models).
- "residual": Residual degrees of freedom.
- "satterthwaite": Satterthwaite approximation (robust for mixed models).
- "inf": Use z-distribution (infinite degrees of freedom).

`se_method` Character; The method for CI estimation: "wald" (default) or "sampling".

`num_samples` Integer; number of samples to draw when `se_method` is "sampling". Default is 1000.

`seed` Integer; random seed for sampling.

`view` Character vector of parameters to prioritize in the summary output.

`map` Optional list specifying parameters to fix.

`fixed` Optional list specifying parameter values to fix.

... Additional arguments.

Returns: A 'Classic_Fit' object.

Method `sample()`: Draw posterior samples from the model.

Usage:

```
RTMB_Model$sample(
  sampling = 1000,
  warmup = 1000,
  chains = 4,
  thin = 1,
  seed = sample.int(1e+06, 1),
  delta = 0.8,
  max_treedepth = 10,
  nuts_variant = c("multinomial", "slice"),
  metric = c("auto", "diag", "dense", "hybrid"),
  metric_init = c("identity", "hessian"),
  metric_adaptation = c("stan_window", "cumulative", "window"),
  metric_regularization = TRUE,
  metric_shrinkage = 5,
```

```

metric_min = 1e-06,
metric_max = 1e+06,
parallel = FALSE,
laplace = FALSE,
init = NULL,
init_jitter = 0.1,
save_csv = NULL,
map = NULL,
fixed = NULL,
globals = FALSE,
progress = c("auto", "none", "bar", "message"),
.resume = NULL
)

```

Arguments:

sampling Number of sampling iterations. Default is 1000.

warmup Number of warmup iterations. Default is 1000.

chains Number of MCMC chains. Default is 4.

thin Thinning interval. Default is 1.

seed Random seed.

delta Target acceptance rate for HMC/NUTS. Default is 0.8.

max_treedepth Maximum tree depth for HMC/NUTS. Default is 10.

nuts_variant NUTS proposal selection variant. "multinomial" uses Stan-style Hamiltonian-weighted proposal selection; "slice" uses the original slice-based implementation. Default is "multinomial".

metric Mass matrix adaptation type. "auto" starts from the hybrid strategy and falls back to "diag" during warmup when the dense covariance block is unstable or has very low correlation; "diag" adapts only marginal variances; "dense" adapts a full covariance metric for correlated parameters; "hybrid" uses a dense metric for fixed parameters and a diagonal metric for random parameters. Default is "auto".

metric_init Initial metric source. "identity" starts from the unit metric; "hessian" starts from an inverse Hessian approximation at the chain initial value when available. Default is "identity".

metric_adaptation Metric learning mode during warmup. "stan_window" uses the current expanding Stan-style slow window; "cumulative" uses all slow-window warmup draws accumulated so far; "window" uses only the current adaptation window. Default is "stan_window".

metric_regularization Logical; whether to shrink the adapted metric toward the unit metric during warmup. Default is TRUE.

metric_shrinkage Non-negative scalar controlling the strength of metric shrinkage. Larger values shrink more strongly toward 1. Default is 5.

metric_min Minimum allowed diagonal metric value. Default is 1e-6.

metric_max Maximum allowed diagonal metric value. Default is 1e6.

parallel Logical; whether to run chains in parallel. Default is FALSE.

laplace Logical; whether to use Laplace approximation. Default is FALSE.

init Optional initial values for parameters.

init_jitter sd of randomize initial values for parameters.

`save_csv` Optional list for saving MCMC results. e.g., `list(name = "model", dir = "BayesRTMB_mcmc")`.

`map` Optional list specifying parameters to fix (factors).

`fixed` Optional list specifying parameter values to fix.

`globals` Logical; if TRUE, let **future** discover globals automatically when `parallel = TRUE`. If FALSE, only the model object components required by BayesRTMB workers are exported. Default is FALSE.

`progress` Progress reporting style. "auto", "bar", and "message" use line-based progress messages; "none" suppresses detailed progress but still prints the high-level start message unless `silent = TRUE` was used when creating the model. "bar" is accepted for backward compatibility. Default is "auto".

`.resume` Internal saved sampler state used by `'MCMC_Fit$continue_sampling()'`; users should leave this as 'NULL'.

Returns: A fitted 'MCMC_Fit' object.

Method `variational()`: Run Automatic Differentiation Variational Inference (ADVI).

Usage:

```
RTMB_Model$variational(
  iter = 3000,
  tol_rel_obj = 0.005,
  window_size = 100,
  num_samples = 1000,
  num_estimate = 4,
  alpha = 0.01,
  laplace = FALSE,
  print_freq = 1000,
  method = c("meanfield", "fullrank", "hybrid"),
  parallel = FALSE,
  seed = sample.int(1e+06, 1),
  init = NULL,
  save_csv = NULL,
  map = NULL,
  fixed = NULL,
  globals = FALSE,
  progress = c("auto", "none", "bar", "message")
)
```

Arguments:

`iter` Integer; fixed number of iterations for the optimization. Default is 3000.

`tol_rel_obj` Numeric; relative tolerance for the ELBO change to determine convergence. Default is 0.005.

`window_size` Integer; window size for median smoothing in the convergence check. Default is 100.

`num_samples` Integer; number of posterior samples to generate from the fitted variational distribution. Default is 1000.

`num_estimate` Integer; number of times to run the VB estimation (treated as chains). Default is 4.

`alpha` Numeric; learning rate for the Adam optimizer. Default is 0.01.

laplace Logical; whether to use Laplace approximation to marginalize random effects. Default is FALSE.
print_freq Integer; iterations interval for progress output. Set to 0 to disable. Default is 1000.
method Character; method of Variational Inference. Default is "meanfield".
parallel Logical; whether to run estimations in parallel. Default is FALSE.
seed Integer; random seed for reproducibility.
init Optional numeric vector or list for initial parameter values. Default is NULL.
save_csv Optional list for saving VB results. e.g., list(name = "model", dir = "BayesRTMB_vb").
map Optional list specifying parameters to fix (factors).
fixed Optional list specifying parameter values to fix.
globals Logical; if TRUE, let **future** discover globals automatically when parallel = TRUE. If FALSE, only the model object components required by BayesRTMB workers are exported. Default is FALSE.
progress Progress reporting style. "auto" and "bar" use line-based progress messages; "none" suppresses detailed progress but still prints the high-level start message unless silent = TRUE was used when creating the model. Default is "auto".

Returns: A fitted 'VB_Fit' object containing posterior samples and diagnostic information.

Method print_code(): Print model code or model structure.

Usage:

```
RTMB_Model$print_code()
```

Returns: The object itself, invisibly.

Method print_log_prob(): Print the internal log-probability function.

Usage:

```
RTMB_Model$print_log_prob()
```

Returns: The object itself, invisibly.

Method print_transform(): Print the internal transformation function.

Usage:

```
RTMB_Model$print_transform()
```

Returns: The object itself, invisibly.

Method print_generate(): Print the internal generation function.

Usage:

```
RTMB_Model$print_generate()
```

Returns: The object itself, invisibly.

Method get_n_obs(): Automatically detect and count the number of independent data points (observations).

Usage:

```
RTMB_Model$get_n_obs()
```

Returns: Integer; total number of observations, or NULL if model code is missing.

Method `fixed_model()`: Create a model with fixed parameters.

Usage:

```
RTMB_Model$fixed_model(fixed = list(), silent = FALSE)
```

Arguments:

`fixed` A named list of parameter values to fix.

`silent` Logical; whether to suppress informational messages. Default is FALSE.

Returns: A new RTMB_Model object.

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

```
RTMB_Model$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

Description

Models defined in `rtmb_code` rely on Automatic Differentiation (AD) via the RTMB package. To ensure the model is differentiable and numerically stable, specific coding practices must be followed.

Details

1. Automatic Differentiation and advector: Parameters and intermediate calculations involving them are treated as advector objects. RTMB "records" all mathematical operations to compute derivatives automatically. If a function strips these attributes or is not differentiable, the gradient calculation will fail.

2. Avoid Discrete Branching: Standard R conditional statements like `if (x > 0)` or `ifelse()` based on parameter values do not provide derivatives.

- **Problem:** They create "jumps" in the likelihood surface.
- **Solution:** Use smooth approximations. For example, use `fabs` instead of `abs`, or `log_mix` for mixture logic.

3. Numerical Stability: Computations in log-space are preferred to prevent overflow or underflow. Use the following stable utilities instead of raw algebraic expressions:

- `log_sum_exp`: For summing probabilities in log-space.
- `log1p_exp`: For $\log(1 + \exp(x))$.
- `inv_logit`: For mapping real numbers to probabilities.

4. Vectorization vs. Loops:

- **Vectorization:** Highly recommended for performance. Standard R vectorized arithmetic (+, -, *, /, log, exp) works seamlessly with AD.
- **Loops:** Standard for loops are safe as long as the operations inside are differentiable.
- **Avoid apply:** Functions like apply, sapply, or lapply may sometimes strip AD attributes and should be replaced with vectorized operations or explicit loops.

5. Matrix Operations: Use specialized functions for matrix algebra to maintain efficiency:

- `quad_form_chol`: For efficient quadratic forms.
- `log_det_chol`: For log-determinants via Cholesky factors.

See Also

[math_functions](#), [distributions](#), [rtmb_code](#)

rtmb_table	<i>RTMB-based Contingency Table Analysis (Chi-squared Test)</i>
------------	---

Description

‘rtmb_table’ performs a chi-squared test of independence between two categorical variables. It provides both classic (frequentist) Pearson chi-squared tests and Bayesian multinomial-style models.

Usage

```
rtmb_table(  
  x,  
  y = NULL,  
  data = NULL,  
  correct = TRUE,  
  prior = prior_flat(),  
  fixed = NULL,  
  WAIC = FALSE,  
  ...  
)
```

Arguments

x	Variable name, formula, table, or matrix.
y	Variable name (optional if x is a formula).
data	A data frame.
correct	Logical; if TRUE, apply Yates’ continuity correction for 2x2 classic analyses.
prior	Prior specification (Bayesian mode). Use ‘prior_flat()’ for a uniform Dirichlet prior or ‘prior_normal(dirichlet_alpha = ...)’ to set the Dirichlet concentration. Default is ‘prior_flat()’.
fixed	Optional named list of fixed values for specific parameters.
WAIC	Logical; if TRUE, add pointwise ‘log_lik’ to the generate block for WAIC.
...	Reserved; unused arguments are rejected.

Value

An 'RTMB_Model' object.

Examples

```
# Classic chi-squared test
data(debate, package = "BayesRTMB")
rtmb_table(skill, cond, data = debate)$classic()
rtmb_table(table(debate$skill, debate$cond))$classic()
```

rtmb_ttest

RTMB-based Bayesian two-sample t-test wrapper function

Description

Performs a Bayesian or Frequentist two-sample t-test using RTMB.

Usage

```
rtmb_ttest(
  x,
  y = NULL,
  data = NULL,
  r = 0.707,
  paired = FALSE,
  ID = NULL,
  y_range = NULL,
  prior = prior_flat(),
  init = NULL,
  fixed = NULL,
  var.equal = TRUE,
  missing = c("listwise", "fiml"),
  WAIC = FALSE,
  ...
)
```

Arguments

x	Numeric vector of responses for group 1, a formula (e.g., 'y ~ group'), or a column name (unquoted) if 'data' is provided.
y	Numeric vector of responses for group 2, or a column name (unquoted) if 'data' is provided. Required if 'x' is not a formula.
data	Data frame containing the variables.
r	Numeric; Cauchy prior scale for the effect size (delta). Default is 0.707.
paired	Logical; whether to perform a paired t-test.

ID	Character; name of the ID variable for paired t-tests (required for formula input with paired = TRUE).
y_range	Theoretical minimum and maximum values of the response variable as a vector c(min, max). Required when using weakly informative priors.
prior	An object of class "rtmb_prior". Use 'prior_flat()' for no prior, 'prior_normal()' for default normal/exponential priors, 'prior_jzs()' for JZS t-test priors, or 'prior_weak()' for weakly informative Bayesian inference. Default is 'prior_flat()'.
init	List of initial values.
fixed	Optional named list of fixed values for specific parameters.
var.equal	Logical; whether to assume equal variances. Default is TRUE.
missing	Missing value handling strategy: "listwise".
WAIC	Logical; if TRUE, add pointwise 'log_lik' to the generate block for WAIC.
...	Reserved; unused arguments are rejected.

Details

For classic inference, heteroscedastic two-sample t-tests use the same RTMB Satterthwaite machinery as 'optimize(marginal = ..., df_method = "satterthwaite")'. The result is model-based and reproducible from the printed model code. This corresponds to the Welch-type unequal-variance t-test, but the degrees of freedom are computed by the package's internal Satterthwaite procedure rather than by a separate closed-form formula. For JZS t-tests, 'prior_jzs()' places a Cauchy prior on the standardized effect size and the Jeffreys scale prior $p(\sigma) \propto 1/\sigma$ on the residual standard deviation. For paired tests, the latter is applied to the standard deviation of the pairwise differences. When 'prior_jzs()' is combined with 'var.equal = FALSE', BayesRTMB uses a Welch-style JZS extension: the effect size 'delta' is an explicit parameter with a Cauchy prior, and the group mean difference is scaled by the root-mean-square of the two group standard deviations. The Jeffreys scale prior is applied separately to both group standard deviations.

Value

An 'RTMB_Model' object.

Examples

```
# Simulate two-sample data with a true effect size
set.seed(123)
y1 <- rnorm(30, mean = 0.5, sd = 1)
y2 <- rnorm(30, mean = 0.0, sd = 1)

# Fit the Bayesian two-sample t-test model
# r = 0.707 is the standard scale for the Cauchy prior on the effect size
fit_ttest <- rtmb_ttest(y1, y2, prior = prior_jzs(r = 0.707))

# MCMC sampling (chains and iterations reduced for faster execution)
mcmc_ttest <- fit_ttest$sample(sampling = 500, warmup = 500, chains = 2)
mcmc_ttest$summary()
```

rtmb_vector	Create an AD-compatible vector
-------------	--------------------------------

Description

Creates a fixed-length vector that is safe to use inside `'rtmb_code()'` when subsequent assignments may involve RTMB automatic-differentiation values. This is a safer alternative to `'numeric(length)'` in model code.

Usage

```
rtmb_vector(value = 0, length, seed = NULL)
```

Arguments

value	Initial value. Usually a scalar such as <code>'0'</code> .
length	Length of the vector.
seed	Optional AD value used to create the container. Usually this can be left as <code>'NULL'</code> ; inside <code>'rtmb_code()'</code> , BayesRTMB automatically provides an AD seed from the model parameters when available.

Value

An AD-compatible vector.

rtmb_wrappers	Common Features and Arguments of RTMB Wrapper Functions
---------------	---

Description

The RTMB wrapper functions (`'rtmb_lm'`, `'rtmb_glm'`, `'rtmb_glmer'`, `'rtmb_fa'`, etc.) share a unified interface designed to make Bayesian and Frequentist inference accessible through familiar R formulas and standard model specifications.

Details

All wrapper functions in this package are built upon the same core engine. This ensures that regardless of the model type, the workflow for estimation, summary, and expansion remains consistent.

1. Unified Inference Methods: Every model object returned by a wrapper function provides the following methods:

- `$classic()`: Performs standard frequentist estimation (MLE/REML) using `'prior_flat()'`. Supports robust standard errors and Satterthwaite/Between-Within degrees of freedom approximations.
- `$optimize()`: Performs Maximum A Posteriori (MAP) estimation (Empirical Bayes).

- `$sample()`: Performs MCMC sampling (NUTS via `tmbstan`) for full Bayesian inference.
- `$variational()`: Performs Variational Inference (ADVI) for fast posterior approximation.

2. Prior API and Regularization: You can specify the prior distribution using the ‘prior’ argument:

- `prior_flat()`: No additional prior (default). Required for `classic()` inference.
- `prior_normal()`: Manual normal/exponential priors for parameters.
- `prior_weak()`: Weakly informative priors based on `y_range`.
- `prior_rhs()`: Regularized Horseshoe prior for continuous shrinkage.
- `prior_ssp()`: Spike-and-Slab prior for sparse variable selection.

Note: When using ‘prior_weak()’, ‘prior_rhs()’, or ‘prior_ssp()’, you must specify `y_range = c(min, max)` to let the model set appropriate global scales for the priors.

3. Model Comparison and Bayes Factors: Model comparison is performed exclusively via Bridge Sampling. To compare a full model against a nested null model, use the `$bayes_factor(fixed = list(...))` method on an MCMC fit object. For example, `fit$bayes_factor(fixed = list(b = 0))` tests the hypothesis that the fixed effect `b` is exactly zero.

4. Standard Errors and Degrees of Freedom: The `$classic()` and `$optimize()` methods provide advanced summary options:

- `se_method`: Calculate “robust” (Huber-White) or “cluster-robust” standard errors by providing a cluster variable.
- `df_method`: Use “satterthwaite” for mixed models or “bw” (Between-Within) for multi-level correlation models to obtain accurate p-values and confidence intervals.

5. Fixed parameters: Use `fixed = list(...)` during model construction to fix model parameters to specified values. For example, `fixed = list(delta = 0)` fixes the parameter `delta` to zero. This same syntax is used in `$bayes_factor()` to define the restricted model.

safe_rtmb_model

Safe RTMB model construction (with error message translation)

Description

Wraps ‘rtmb_model’ to translate cryptic error messages generated during ‘MakeADFun’ execution (originating from C++/RTMB) into user-friendly hints.

Usage

```
safe_rtmb_model(data, code, par_names = list(), init = NULL, view = NULL)
```

Arguments

data	A list of data that has passed 'validate_data'.
code	Code blocks for likelihood and priors defined with 'model_code()'.
par_names	A list of variable names corresponding to the dimensions of each parameter (optional).
init	A list or numeric vector of initial values (optional).
view	Character vector of parameter names to be displayed preferentially in summary outputs (optional).

Value

Returns an 'rtmb_model' object (R6 class instance) upon successful compilation.

simple_effects	<i>Calculate Simple Effects</i>
----------------	---------------------------------

Description

Calculate the effect of a focal variable at different levels of a moderator. For categorical focal variables, it calculates pairwise differences (contrasts). For continuous focal variables, it calculates the slope (simple slopes).

Usage

```
simple_effects(
  fit,
  effect,
  prob = 0.95,
  sd_multiplier = 1,
  sd_slice = NULL,
  ...
)
```

Arguments

fit	Model fit object (e.g., 'map_fit', 'mcmc_fit').
effect	Character string of the interaction (e.g., "A:B"). The first variable is the focal variable.
prob	Probability for the credible/confidence interval (default is 0.95).
sd_multiplier	Multiplier for SD for continuous moderators (default is 1).
sd_slice	Logical or NULL. If TRUE, continuous moderators are evaluated at mean - SD, mean, and mean + SD. If FALSE, all observed moderator values are used. If NULL (default), sd slicing is used automatically when the moderator has 6 or more unique values.
...	Additional arguments.

Value

A 'ce_simple' object (data frame) containing the estimated effects and their credible intervals. For 'Classic_Fit' objects, test columns ('df', 't value', and 'Pr') are also returned when standard errors are available.

Examples

```
data(debate, package = "BayesRTMB")
fit <- rtmb_lm(sat ~ talk * perf, data = debate)
map_fit <- fit$optimize()
# Effect of talk at different levels of performance
se <- simple_effects(map_fit, effect = "talk:perf")
print(se)
```

```
simple_effects.mcmc_fit
```

Simple effects for MCMC fit objects

Description

Simple effects for MCMC fit objects

Usage

```
## S3 method for class 'mcmc_fit'
simple_effects(
  fit,
  effect,
  prob = 0.95,
  sd_multiplier = 1,
  sd_slice = NULL,
  ...
)
```

Arguments

fit	An object of class 'MCMC_Fit'.
effect	Interaction term (e.g., "A:B").
prob	Probability for credible intervals.
sd_multiplier	Multiplier for SD for continuous moderators.
sd_slice	Logical or NULL; controls whether continuous moderators are evaluated at mean - SD, mean, and mean + SD.
...	Additional arguments.

`softmax`*Softmax function*

Description

Softmax function

Usage

```
softmax(x)
```

Arguments

`x` A numeric vector.

Value

A numeric vector of softmax probabilities.

`sort_loadings`*Sort and display factor loadings neatly*

Description

Sort and display factor loadings neatly

Usage

```
sort_loadings(loadings, cutoff = 0, round_digits = 3)
```

Arguments

`loadings` Matrix, data frame, or list of factor loadings (if list, the first element is used)

`cutoff` Absolute loadings below this value will be displayed as blank (default is 0.0)

`round_digits` Number of decimal places to display (default is 3)

Value

Sorted loading matrix (returned invisibly, allowing assignment to a variable)

squared_distance	<i>Squared Euclidean distance</i>
------------------	-----------------------------------

Description

Squared Euclidean distance

Usage

squared_distance(x, y, eps = 1e-08)

Arguments

- x A numeric vector.
- y A numeric vector.
- eps A small value added for numerical stability (default is 1e-8).

Value

The squared Euclidean distance between x and y.

stz_basis	<i>stz basis function</i>
-----------	---------------------------

Description

stz basis function

Usage

stz_basis(K)

Arguments

- K A numeric value

Value

A transformation matrix

sum_to_zero	<i>Sum-to-zero transformation</i>
-------------	-----------------------------------

Description

Transforms a vector of length K-1 to a vector of length K that sums to zero using an orthogonal basis matrix.

Usage

sum_to_zero(x)

Arguments

x A numeric vector of length K-1.

Value

A numeric vector of length K whose elements sum to zero.

summary.ce_rtmb	<i>Summary method for ce_rtmb class</i>
-----------------	---

Description

Summary method for ce_rtmb class

Usage

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

Arguments

object An object of class ce_rtmb
... Additional arguments.

summary_mcmc

*Summarize MCMC Draws Stored in an Array***Description**

Summarizes posterior draws stored in the same array layout used by [MCMC_Fit](#): iterations by chains by variables. The returned object uses the same columns and print method as `MCMC_Fit$summary()`.

Usage

```
summary_mcmc(draws, pars = NULL, chains = NULL, max_rows = 10, digits = 2)
```

Arguments

<code>draws</code>	A numeric three-dimensional array with dimensions iterations by chains by variables.
<code>pars</code>	Optional numeric or character vector selecting variables. Character values may be full variable names (for example, <code>"beta[1]"</code>) or base names (for example, <code>"beta"</code>). Prefix character names with <code>"-"</code> to exclude them.
<code>chains</code>	Optional numeric vector selecting chains. Positive and negative integer indexing are supported.
<code>max_rows</code>	Maximum number of variables to include. Use <code>'NULL'</code> to include all variables.
<code>digits</code>	Number of decimal places used when printing the result.

Value

A data frame with class `"summary_BayesRTMB"` containing posterior means, standard deviations, marginal MAP estimates, 95 percent intervals, bulk and tail effective sample sizes, and split R-hat values.

Examples

```
set.seed(123)
draws <- array(
  rnorm(200 * 2 * 2),
  dim = c(200, 2, 2),
  dimnames = list(NULL, c("chain1", "chain2"), c("alpha", "beta"))
)
summary_mcmc(draws)
```

test_info	<i>Calculate Test Information Function</i>
-----------	--

Description

Calculate Test Information Function

Usage

```
test_info(x, ...)
```

Arguments

x	An object of class RTMB_Fit_Base
...	Additional arguments.

Examples

```
fit <- rtmb_irt(data = BigFive[, 1:5], model = "2PL", type = "ordered")
map_fit <- fit$optimize()
ti <- test_info(map_fit)
plot(ti)
```

to_centered_matrix	<i>Vector to centered matrix (RTMB compatible)</i>
--------------------	--

Description

Vector to centered matrix (RTMB compatible)

Usage

```
to_centered_matrix(x, R, C)
```

Arguments

x	A numeric vector of length (R-1) * C.
R	Number of rows.
C	Number of columns.

Value

An R x C matrix where each column sums to zero.

to_centered_tri	<i>Vector to centered triangular matrix (RTMB compatible)</i>
-----------------	---

Description

Vector to centered triangular matrix (RTMB compatible)

Usage

```
to_centered_tri(x, R, C)
```

Arguments

x	A numeric vector of appropriate length.
R	Number of rows.
C	Number of columns.

Value

An R x C matrix with column-wise sum-to-zero constraints on lower elements.

to_long	<i>Convert Wide Data to Long Format</i>
---------	---

Description

A highly intuitive wrapper around `stats::reshape` designed for psychological research. It converts data from wide format to long format by identifying within-subjects factors.

Usage

```
to_long(
  data,
  within = NULL,
  label = NULL,
  value = "Value",
  id = NULL,
  sort = FALSE
)
```

Arguments

data	A data frame in wide format.
within	The columns to gather into long format. Can be: <ul style="list-style-type: none">• A character vector of column names.• A range string like "time1:time4".• A prefix string like "time" (matches all columns starting with "time").• A list of column-name vectors or range/prefix specifications to concatenate into one long value column.• Multiple range/prefix/name specifications when value has the same length.
label	The name for the new column that will contain the level names (e.g., "Time"). If NULL, it defaults to the prefix used in within or "Condition".
value	The name for the new column that will contain the measurement values. Can be a character vector for multiple measurement groups. Default is "Value".
id	The identifier columns that should be repeated for each row. If NULL (default), all columns NOT specified in within are treated as IDs.
sort	Logical; if TRUE, sort the output by id and the within label. If FALSE (default), preserve the original row order of data and the within-column order inside each row.

Value

A data frame in long format.

to_lower_tri	<i>Vector to lower triangular matrix (RTMB compatible)</i>
--------------	--

Description

Vector to lower triangular matrix (RTMB compatible)

Usage

```
to_lower_tri(x, M, D)
```

Arguments

x	A numeric or advector.
M	Number of rows.
D	Number of columns.

Value

An M x D lower triangular matrix.

to_wide	<i>Convert Long Data to Wide Format</i>
---------	---

Description

A user-friendly wrapper around `stats::reshape` to convert data from long format back to wide format.

Usage

```
to_wide(data, within = "Condition", value = "Value", id = NULL)
```

Arguments

data	A data frame in long format.
within	The name of the column containing within-subjects factor levels (e.g., "Condition").
value	The name of the column containing measurement values (e.g., "Value"). Can be a character vector for multiple measurement columns.
id	The identifier columns (e.g., "Subject", "Group"). If NULL, inferred as all columns except within and value.

Value

A data frame in wide format.

training	<i>Social Skills Training Data</i>
----------	------------------------------------

Description

A small dataset containing repeated outcome measurements from a social skills training study. The outcome was measured at four time points for participants assigned to a control or intervention condition.

Usage

```
training
```

Format

A data frame with 12 rows and 8 columns:

ID Participant identifier.

time1 Outcome score at the first measurement occasion.

time2 Outcome score at the second measurement occasion.

time3 Outcome score at the third measurement occasion.

time4 Outcome score at the fourth measurement occasion.

a Training condition indicator: 0 = control group, 1 = intervention group.

b Qualitative baseline skill classification.

age Participant age.

Source

Simulated dummy data created by the package author.

transform_code	<i>Transformed Code Wrapper for RTMB</i>
----------------	--

Description

Transformed Code Wrapper for RTMB

Usage

```
transform_code(expr, env = parent.frame(), ad_seed_name = NULL)
```

Arguments

expr A block of code containing calculations for transformed parameters.

env Environment to assign to the generated function.

ad_seed_name Optional parameter name used internally to seed RTMB's AD type.

Value

A function taking (dat, par) that returns a named list.

upgrade_fit	<i>Upgrade a saved fit object to the current BayesRTMB class definitions</i>
-------------	--

Description

'upgrade_fit()' rebuilds an existing fit object with the currently loaded BayesRTMB R6 class definitions. This is useful for saved fit objects created by older package versions when newer methods have been added to the fit classes.

Usage

```
upgrade_fit(fit, upgrade_model = TRUE)
```

Arguments

fit	A BayesRTMB fit object. Supported classes are MCMC, VB, MAP, and classic fit objects.
upgrade_model	Logical; if 'TRUE', rebuild the embedded model object from its stored data, parameter list, and model functions. If rebuilding fails, the original model is kept and a warning is issued.

Details

The function does not refit the model or recompute estimates. It only copies the stored estimation results into a new fit object. When 'upgrade_model' is 'TRUE', the embedded 'RTMB_Model' object is also rebuilt from the model components stored in the fit, so newer model methods are available as well.

Value

A fit object of the same type, using the currently loaded class definitions.

validate_data	<i>Pre-validation of data and parameters</i>
---------------	--

Description

Before passing data to 'rtmb_model', it checks for the presence of R-specific data types (such as data.frame) and missing values, and outputs errors or warnings accordingly.

Usage

```
validate_data(dat_list)
```

Arguments

`dat_list` A list of data to be passed to the model (usually containing matrices or numeric vectors).

Details

RTMB's automatic differentiation engine requires pure 'matrix' or 'numeric' types. If a user mistakenly passes a 'data.frame', incomprehensible errors occur during the construction of the computation graph. This function catches such issues in advance.

Value

Returns invisible 'NULL' on success. Interrupts execution with 'stop()' or issues 'warning()' if issues are found.

<code>VB_Fit</code>	<i>VB fit object</i>
---------------------	----------------------

Description

VB fit object

VB fit object

Details

An R6 class storing posterior samples and related information from Automatic Differentiation Variational Inference (ADVI).

Super class

`BayesRTMB::RTMB_Fit_Base -> advi_fit`

Public fields

`model` An 'RTMB_Model' object used for estimation.

`fit` A 3D array of posterior draws for fixed model parameters.

`random_fit` A 3D array of posterior draws for random effects, if available.

`transform_fit` A 3D array of posterior draws for transformed parameters, if available.

`generate_fit` A 3D array of posterior draws for generated quantities, if available.

`transform_dims` A list storing dimension information for transformed parameters.

`generate_dims` A list storing dimension information for generated quantities.

`elbo_history` A list of numeric vectors storing the Evidence Lower Bound (ELBO) history during optimization for each chain.

`laplace` Logical; whether Laplace approximation was used to marginalize random effects.

posterior_mean A named numeric vector of posterior mean estimates.
 ELBO A numeric vector of final ELBO values for each chain.
 rel_obj_vals A numeric vector of final relative objective tolerance values for each chain.
 best_chain Integer; the index of the chain with the maximum ELBO.
 mu_history Matrix of the parameter trajectory from the final window.

Methods

Public methods:

- VB_Fit\$get_point_estimate()
- VB_Fit\$estimate()
- VB_Fit\$EAP()
- VB_Fit\$MAP()
- VB_Fit\$new()
- VB_Fit\$print()
- VB_Fit\$draws()
- VB_Fit\$summary()
- VB_Fit\$plot_elbo()
- VB_Fit\$plot_trajectory()
- VB_Fit\$transformed_draws()
- VB_Fit\$generated_quantities()
- VB_Fit\$WAIC()
- VB_Fit\$diagnose()
- VB_Fit\$clone()

Method get_point_estimate(): Get point estimate for a target parameter.

Usage:

```
VB_Fit$get_point_estimate(target, chains = NULL, best_chains = NULL)
```

Arguments:

target Target parameter name.

chains Numeric vector of chains to include. If NULL, the best chain is used.

best_chains Integer; number of best chains to retain based on ELBO.

Returns: Matrix, array, vector, or scalar point estimate.

Method estimate(): Get point estimates from variational draws.

Usage:

```
VB_Fit$estimate(
  pars = NULL,
  type = c("mean", "EAP", "marginal_map", "joint_map", "MAP"),
  component = c("all", "parameters", "transform", "generate"),
  chains = NULL,
  best_chains = NULL,
  drop = TRUE,
  ...
)
```

Arguments:

pars Optional character or numeric vector of parameter names or indices to extract. Supports special keywords: "parameters", "transform", "generate", and "all".

type Character string specifying the estimation type.

component Character string specifying the component to filter by.

chains Numeric vector of chains to include. If NULL, the best chain is used.

best_chains Number of best chains to include.

drop Logical; if TRUE and only one parameter is selected, return the value directly instead of a list.

... Additional arguments passed to `draws()`.

Returns: A named list of point estimates, or a single value if 'drop = TRUE'.

Method EAP(): Calculate Expected A Posteriori (EAP) estimates from the best variational estimate by default.

Usage:

```
VB_Fit$EAP(
  pars = "parameters",
  chains = NULL,
  best_chains = NULL,
  drop = TRUE,
  ...
)
```

Arguments:

pars Optional character vector of parameter names to extract.

chains Numeric vector of chains to include. If NULL, the best chain is used.

best_chains Number of best chains to include.

drop Logical; whether to drop the list if only one parameter is selected.

... Additional arguments passed to 'estimate()'.

Returns: A named list of EAP estimates.

Method MAP(): Calculate Maximum A Posteriori (MAP) estimates from the best variational estimate by default.

Usage:

```
VB_Fit$MAP(
  pars = "parameters",
  chains = NULL,
  best_chains = NULL,
  type = c("marginal", "joint"),
  drop = TRUE,
  ...
)
```

Arguments:

pars Optional character vector of parameter names to extract.

chains Numeric vector of chains to include. If NULL, the best chain is used.

best_chains Number of best chains to include.
 type Character string; "marginal" or "joint" MAP.
 drop Logical; whether to drop the list if only one parameter is selected.
 ... Additional arguments passed to 'estimate()'.

Returns: A named list of MAP estimates.

Method new(): Create a new 'VB_Fit' object.

Usage:

```
VB_Fit$new(  
  model,  
  fit,  
  random_fit,  
  elbo_history,  
  laplace,  
  posterior_mean,  
  ELBO,  
  rel_obj_vals,  
  best_chain,  
  mu_history  
)
```

Arguments:

model An 'RTMB_Model' object.
 fit A 3D array of parameter draws.
 random_fit A 3D array of random effect draws.
 elbo_history A list of numeric vectors of ELBO values for each chain.
 laplace Logical; indicates if Laplace approximation was used.
 posterior_mean A named numeric vector of posterior means.
 ELBO A numeric vector of final ELBO values for each chain.
 rel_obj_vals A numeric vector of final relative objective tolerance values for each chain.
 best_chain Integer; the index of the chain with the maximum ELBO.
 mu_history Matrix of the parameter trajectory from the final window.

Method print(): Print a brief summary of the fitted object.

Usage:

```
VB_Fit$print(...)
```

Arguments:

... Additional arguments passed to the 'summary' method.

Returns: The object itself, invisibly.

Method draws(): Extract posterior draws for selected parameters.

Usage:

```

VB_Fit$draws(
  pars = NULL,
  chains = NULL,
  best_chains = NULL,
  inc_random = FALSE,
  inc_transform = TRUE,
  inc_generate = TRUE,
  best_only = FALSE
)

```

Arguments:

pars Character or numeric vector specifying the names or indices of parameters to extract. If NULL, all available parameters are extracted.

chains Numeric vector specifying the chains to extract. If NULL, draws from all chains are returned.

best_chains Integer; number of best chains to retain based on ELBO. If supplied, chains with the highest ELBO are retained.

inc_random Logical; whether to include random effects in the output. Default is FALSE.

inc_transform Logical; whether to include transformed parameters in the output. Default is TRUE.

inc_generate Logical; whether to include generated quantities in the output. Default is TRUE.

best_only Logical; whether to extract only from the chain with the maximum ELBO. Default is FALSE unless explicitly requested.

Returns: A 3D array of posterior draws ‘[iterations, chains, parameters]’.

Method summary(): Summarize posterior draws.

Usage:

```

VB_Fit$summary(
  pars = NULL,
  max_rows = 10,
  digits = 2,
  inc_random = FALSE,
  inc_transform = TRUE,
  inc_generate = TRUE
)

```

Arguments:

pars Character or numeric vector specifying the names or indices of parameters to summarize. If NULL, all available parameters are summarized.

max_rows Integer; maximum number of rows to print in the summary table. Default is 10.

digits Integer; number of decimal places to print. Default is 2.

inc_random Logical; whether to include random effects in the summary. Default is FALSE.

inc_transform Logical; whether to include transformed parameters in the summary. Default is TRUE.

inc_generate Logical; whether to include generated quantities in the summary. Default is TRUE.

Returns: A data frame containing the summarized posterior statistics.

Method `plot_elbo()`: Plot the ELBO history to diagnose convergence.

Usage:

```
VB_Fit$plot_elbo(tail_n = 1000, ests = NULL, type = "l", ...)
```

Arguments:

`tail_n` Integer; the number of recent iterations to plot. If `NULL`, plots the entire history. Default is 2000.

`ests` Character string `"best"`, numeric vector of estimate indices (e.g., `c(1, 3)`), or `'NULL'` to plot all. Default is `'NULL'`.

`type` Character string; the type of plot. Default is `"l"` (lines).

... Additional arguments passed to the `'plot'` function.

Returns: The object itself, invisibly.

Method `plot_trajectory()`: Plot the parameter trajectory from the final optimization window.

Usage:

```
VB_Fit$plot_trajectory(pars = NULL, type = "l", ...)
```

Arguments:

`pars` Character vector specifying the names of parameters to plot. If `NULL`, plots all available parameters.

`type` Character string; the type of plot. Default is `"l"` (lines).

... Additional arguments passed to the `'matplot'` function.

Returns: The object itself, invisibly.

Method `transformed_draws()`: Compute transformed parameters from posterior draws.

Usage:

```
VB_Fit$transformed_draws(
  tran_fn = NULL,
  progress = c("auto", "none", "bar", "message"),
  tape = c("auto", "none", "force")
)
```

Arguments:

`tran_fn` An optional user-supplied function that takes data and parameter lists to return transformed quantities.

`progress` Progress reporting style: `"auto"`, `"none"`, `"bar"`, or `"message"`. `"auto"` and `"bar"` use line-based messages.

`tape` Derived-quantity evaluation mode. `"auto"` tries RTMB tape evaluation and falls back to R evaluation on error; `"none"` always uses R evaluation; `"force"` requires tape evaluation and errors if it fails.

Returns: The `'VB_Fit'` object itself, invisibly.

Method `generated_quantities()`: Compute generated quantities from posterior draws.

Usage:

```
VB_Fit$generated_quantities(
  code,
  progress = c("auto", "none", "bar", "message"),
  tape = c("auto", "none", "force")
)
```

Arguments:

code An ‘rtmb_code({ ... })’ or ‘{ ... }’ block containing the logic to be calculated using posterior samples.

progress Progress reporting style: “auto”, “none”, “bar”, or “message”. “auto” and “bar” use line-based messages.

tape Derived-quantity evaluation mode. “auto” tries RTMB tape evaluation and falls back to R evaluation on error; “none” always uses R evaluation; “force” requires tape evaluation and errors if it fails.

Returns: The ‘VB_Fit’ object itself (invisibly). Results are appended to the ‘generate_fit’ field.

Method `WAIC()`: Compute WAIC from pointwise generated log likelihood.

Usage:

```
VB_Fit$WAIC(...)
```

Arguments:

... Additional arguments passed to ‘draws()’, such as ‘chains’ or ‘best_chains’.

Returns: A ‘waic_BayesRTMB’ object.

Method `diagnose()`: Run basic diagnostics for the variational fit.

Usage:

```
VB_Fit$diagnose(...)
```

Arguments:

... Additional arguments passed to ‘diagnose_vb_fit()’.

Returns: A ‘diagnose_BayesRTMB’ object.

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

```
VB_Fit$clone(deep = FALSE)
```

Arguments:

deep Whether to make a deep clone.

Index

- * **datasets**
 - beverage, [6](#)
 - BigFive, [7](#)
 - debate, [19](#)
 - training, [134](#)
- * **distributions**
 - distributions, [21](#)
- * **utilities**
 - math_functions, [43](#)
- * **wrappers**
 - rtmb_wrappers, [123](#)
- ADVI_method, [4](#)
- bayes_factor, [6](#)
- BayesRTMB::RTMB_Fit_Base, [9](#), [38](#), [45](#), [137](#)
- beverage, [6](#)
- BigFive, [7](#)
- center_grand_mean, [8](#)
- center_within_cluster, [9](#)
- Classic_Fit, [9](#)
- conditional_effects, [17](#)
- conditional_effects.mcmc_fit, [18](#)
- debate, [19](#)
- diffusion_lpdf, [19](#)
- Dim, [20](#)
- distance, [21](#)
- distributions, [21](#), [54](#), [76](#), [120](#)
- ess_basic, [23](#)
- ess_bulk, [23](#)
- ess_tail95, [24](#)
- exp_mod_normal_lpdf, [24](#)
- fabs, [25](#), [119](#)
- gaussian_process_lpdf, [25](#)
- generate_random_init, [26](#)
- hist, [74](#)
- inv_logit, [27](#), [76](#), [119](#)
- item_curve, [27](#), [58](#)
- item_curve.RTMB_Fit_Base, [28](#)
- item_info, [28](#), [59](#)
- item_info.RTMB_Fit_Base, [29](#)
- log1m, [32](#)
- log1m_exp, [32](#)
- log1p_exp, [33](#), [119](#)
- log_det_chol, [29](#), [120](#)
- log_mix, [30](#), [119](#)
- log_softmax, [30](#)
- log_sum_exp, [31](#), [76](#), [119](#)
- log_sum_exp_matrix, [31](#)
- logit, [33](#)
- lsmeans, [34](#), [59](#)
- make_bw_from_ydif, [34](#)
- make_glm_re_terms, [35](#)
- make_glm_Z_matrix, [36](#)
- make_init_mdu, [36](#)
- make_ydif_from_bw, [37](#)
- map_est, [38](#)
- MAP_Fit, [38](#)
- math_functions, [43](#), [54](#), [76](#), [120](#)
- MCMC_Fit, [45](#), [130](#)
- parameter_types, [53](#), [76](#)
- parameters_code, [54](#)
- plot.ce_rtmb, [55](#)
- plot.rtmb_lsmeans, [55](#)
- plot.rtmb_pp_check (pp_check), [63](#)
- plot_acf, [56](#)
- plot_conditional_effects, [56](#)
- plot_dens, [57](#)
- plot_forest, [58](#)
- plot_item_curve, [58](#)
- plot_item_info, [59](#)

plot_lsmeans, 59
 plot_mdu, 60
 plot_pairs, 61
 plot_test_info, 62
 plot_trace, 62
 posterior_predict, 63
 pp_check, 63
 print.bayes_factor, 65
 print.bayes_factor_rtmb, 65
 print.ce_rtmb, 66
 print.ce_simple, 66
 print.summary_BayesRTMB, 67
 prior_flat, 67
 prior_jzs, 68
 prior_normal, 68
 prior_rhs, 69
 prior_ssp, 70
 prior_uniform, 70
 prior_weak, 71

 quad_form_chol, 71, 120
 quad_form_diag, 72
 quantile95, 72

 r_hat, 73
 read_mcmc_csv, 73
 restore_bw_from_ydif
 (make_bw_from_ydif), 34
 rhat_summary, 74
 rtmb_array, 75
 rtmb_code, 54, 75, 120
 rtmb_corr, 77
 rtmb_fa, 79
 RTMB_Fit_Base, 80
 rtmb_glm, 85
 rtmb_glmer, 87
 rtmb_irt, 90
 rtmb_lm, 92
 rtmb_lmer, 95
 rtmb_loglinear, 98
 rtmb_lrt, 99
 rtmb_mdu, 100
 rtmb_mediation, 102
 rtmb_mixture, 104
 RTMB_Model (RTMB_Model-class), 108
 rtmb_model, 76, 105
 RTMB_Model-class, 108
 rtmb_syntax, 107, 119
 rtmb_table, 120

 rtmb_ttest, 121
 rtmb_vector, 123
 rtmb_wrappers, 123

 safe_rtmb_model, 124
 simple_effects, 125
 simple_effects.mcmc_fit, 126
 softmax, 127
 sort_loadings, 127
 squared_distance, 128
 stz_basis, 128
 sum_to_zero, 129
 summary.ce_rtmb, 129
 summary_mcmc, 130

 test_info, 62, 131
 to_centered_matrix, 131
 to_centered_tri, 132
 to_long, 132
 to_lower_tri, 133
 to_wide, 134
 training, 134
 transform_code, 135

 upgrade_fit, 136

 validate_data, 136
 VB_Fit, 137