

Package ‘RoBTT’

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Title Robust Bayesian T-Test

Version 1.2.1

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Description An implementation of Bayesian model-averaged t-test that allows users to draw inference about the presence vs absence of the effect, heterogeneity of variances, and outliers. The 'RoBTT' packages estimates model ensembles of models created as a combination of the competing hypotheses and uses Bayesian model-averaging to combine the models using posterior model probabilities. Users can obtain the model-averaged posterior distributions and inclusion Bayes factors which account for the uncertainty in the data generating process (Maier et al., 2022, <doi:10.31234/osf.io/d5zwc>). Users can define a wide range of informative priors for all parameters of interest. The package provides convenient functions for summary, visualizations, and fit diagnostics.

URL <https://fbartos.github.io/RoBTT/>

BugReports <https://github.com/FBartos/RoBTT/issues>

License GPL-3

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RoBTT-package

RoBTT: Robust Bayesian t-test

Description

RoBTT: Bayesian model-averaged t-test extends the Bayesian t-test by incorporating inference about heterogeneity of variances and outliers.

User guide

See Maier et al. (2022) for details regarding the RoBTT methodology.

More details regarding customization of the Bayesian model-averaged t-test are provided in **Introduction to RoBTT** vignette. Please, use the "Issues" section in the GitHub repository to ask any further questions.

Author(s)

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References

Maier M, Bartoš F, Quintana DS, van den Bergh D, Marsman M, Ly A, Wagenmakers E (2022). “Model-averaged Bayesian t-tests.” doi:10.31234/osf.io/d5zwc, PsyArxiv Preprint.

See Also

Useful links:

- <https://fbartos.github.io/RoBTT/>
- Report bugs at <https://github.com/FBartos/RoBTT/issues>

check_RoBTT

Check fitted 'RoBTT' object for errors and warnings

Description

Checks fitted 'RoBTT' object for warnings and errors and prints them to the console.

Usage

```
check_RoBTT(fit)
```

Arguments

`fit` a fitted 'RoBTT' object.

Value

check_RoBTT returns a vector of error and warning messages.

 check_setup

Prints summary of "RoBTT" ensemble implied by the specified priors

Description

check_setup prints summary of "RoBTT" ensemble implied by the specified prior distributions. It is useful for checking the ensemble configuration prior to fitting all of the models.

Usage

```
check_setup(
  prior_delta = prior(distribution = "cauchy", parameters = list(location = 0, scale =
    sqrt(2)/2)),
  prior_rho = prior(distribution = "beta", parameters = list(alpha = 1, beta = 1)),
  prior_nu = prior(distribution = "exp", parameters = list(rate = 1)),
  prior_delta_null = prior(distribution = "spike", parameters = list(location = 0)),
  prior_rho_null = prior(distribution = "spike", parameters = list(location = 0.5)),
  prior_nu_null = prior_none(),
  models = FALSE,
  silent = FALSE
)
```

Arguments

prior_delta	prior distributions for the effect size delta parameter that will be treated as belonging to the alternative hypothesis. Defaults to <code>prior(distribution = "Cauchy", parameters = list(location = 0, scale = sqrt(2)/2))</code> .
prior_rho	prior distributions for the precision allocation rho parameter that will be treated as belonging to the alternative hypothesis. Defaults to <code>prior(distribution = "beta", parameters = list(alpha = 1, beta = 1))</code> .
prior_nu	prior distribution for the degrees of freedom + 2 nu parameter that will be treated as belonging to the alternative hypothesis. Defaults to <code>prior(distribution = "exp", parameters = list(rate = 1))</code> .
prior_delta_null	prior distribution for the delta parameter that will be treated as belonging to the null hypothesis. Defaults to point distribution with location at 0 (<code>prior(distribution = "point", parameters = list(location = 0))</code>).
prior_rho_null	prior distribution for the rho parameter that will be treated as belonging to the null hypothesis. Defaults to point distribution with location at 0.5 (<code>prior(distribution = "point", parameters = list(location = 0.5))</code>).
prior_nu_null	prior distribution for the nu parameter that will be treated as belonging to the null hypothesis. Defaults to <code>prior_none</code> (i.e., normal likelihood).
models	should the models' details be printed.
silent	do not print the results.

Value

check_setup invisibly returns list of summary tables.

See Also

[RoBTT\(\)](#)

diagnostics

Checks a fitted RoBTT object

Description

diagnostics creates visual checks of individual models convergence. Numerical overview of individual models can be obtained by `summary(object, type = "models", diagnostics = TRUE)`, or even more detailed information by `summary(object, type = "individual")`.

Usage

```
diagnostics(
  fit,
  parameter,
  type,
  show_models = NULL,
  lags = 30,
  title = is.null(show_models) | length(show_models) > 1,
  ...
)
```

```
diagnostics_autocorrelation(
  fit,
  parameter = NULL,
  show_models = NULL,
  lags = 30,
  title = is.null(show_models) | length(show_models) > 1,
  ...
)
```

```
diagnostics_trace(
  fit,
  parameter = NULL,
  show_models = NULL,
  title = is.null(show_models) | length(show_models) > 1,
  ...
)
```

```
diagnostics_density(
  fit,
```

```

parameter = NULL,
show_models = NULL,
title = is.null(show_models) | length(show_models) > 1,
...
)

```

Arguments

<code>fit</code>	a fitted <code>RoBTT</code> object
<code>parameter</code>	a parameter to be plotted. Either "delta", "rho", "nu", "mu", or "sigma".
<code>type</code>	type of MCMC diagnostic to be plotted. Options are "chains" for the chains' trace plots, "autocorrelation" for autocorrelation of the chains, and "densities" for the overlaying densities of the individual chains. Can be abbreviated to first letters.
<code>show_models</code>	MCMC diagnostics of which models should be plotted. Defaults to <code>NULL</code> which plots MCMC diagnostics for a specified parameter for every model that is part of the ensemble.
<code>lags</code>	number of lags to be shown for <code>type = "autocorrelation"</code> . Defaults to 30.
<code>title</code>	whether the model number should be displayed in title. Defaults to <code>TRUE</code> when more than one model is selected.
<code>...</code>	additional arguments to be passed to <code>par</code> if <code>plot_type = "base"</code> .

Details

The visualization functions are based on `stan_plot` function and its color schemes.

Value

`diagnostics` returns either `NULL` if `plot_type = "base"` or an object/list of objects (depending on the number of parameters to be plotted) of class `'ggplot2'` if `plot_type = "ggplot2"`.

See Also

`RoBTT()`, `summary.RoBTT()`

Examples

```

## Not run:
# using the example data from Darwin
data("fertilization", package = "RoBTT")
fit <- RoBTT(
  x1      = fertilization$Self,
  x2      = fertilization$Crossed,
  prior_delta = prior("cauchy", list(0, 1/sqrt(2))),
  prior_rho  = prior("beta", list(3, 3)),
  seed      = 1,
  chains     = 1,
  warmup    = 1000,
  iter      = 2000,
)

```

```
  control      = set_control(adapt_delta = 0.95)
)

### ggplot2 version of all of the plots can be obtained by adding 'model_type = "ggplot"
# diagnostics function allows to visualize diagnostics of a fitted RoBTT object, for example,
# the trace plot for the mean parameter in each model model
diagnostics(fit, parameter = "delta", type = "chain")

# in order to show the trace plot only for the 11th model, add show_models parameter
diagnostics(fit, parameter = "delta", type = "chain", show_models = 11)

# furthermore, the autocorrelations
diagnostics(fit, parameter = "delta", type = "autocorrelation")

# and overlying densities for each plot can also be visualize
diagnostics(fit, parameter = "delta", type = "densities")

## End(Not run)
```

fertilization

Height of 15 plant pairs collected by Darwin

Description

The data set contains heights of self fertilized and cross fertilized plants as coded by Darwin.

Usage

```
fertilization
```

Format

A data.frame with 2 columns and 15 observations.

Value

a data.frame.

interpret	<i>Interprets results of a 'RoBTT' model.</i>
-----------	---

Description

interpret creates a brief textual summary of a fitted 'RoBTT' object.

Usage

```
interpret(object)
```

Arguments

object a fitted 'RoBTT' object

Value

interpret returns a character.

is.RoBTT	<i>Reports whether x is a 'RoBTT' object</i>
----------	--

Description

Reports whether x is a 'RoBTT' object

Usage

```
is.RoBTT(x)
```

Arguments

x an object to test

Value

is.RoBTT returns a boolean.

plot.RoBTT *Plots a fitted 'RoBTT' object*

Description

plot.RoBTT allows to visualize different "RoBTT" object parameters in various ways. See `type` for the different model types.

Usage

```
## S3 method for class 'RoBTT'
plot(
  x,
  parameter = "mu",
  transform_rho = FALSE,
  conditional = FALSE,
  plot_type = "base",
  prior = FALSE,
  dots_prior = NULL,
  ...
)
```

Arguments

<code>x</code>	a fitted 'RoBTT' object
<code>parameter</code>	a parameter to be plotted. Defaults to "delta" (for the effect size). The additional options are "rho" (for the heterogeneity), "nu" (for the degrees of freedom).
<code>transform_rho</code>	whether rho parameter should be translated into log standard deviation ratio
<code>conditional</code>	whether conditional estimates should be plotted. Defaults to FALSE which plots the model-averaged estimates.
<code>plot_type</code>	whether to use a base plot "base" or ggplot2 "ggplot" for plotting. Defaults to "base".
<code>prior</code>	whether prior distribution should be added to figure. Defaults to FALSE.
<code>dots_prior</code>	list of additional graphical arguments to be passed to the plotting function of the prior distribution. Supported arguments are <code>lwd</code> , <code>lty</code> , <code>col</code> , and <code>col.fill</code> , to adjust the line thickness, line type, line color, and fill color of the prior distribution respectively.
<code>...</code>	list of additional graphical arguments to be passed to the plotting function. Supported arguments are <code>lwd</code> , <code>lty</code> , <code>col</code> , <code>col.fill</code> , <code>xlab</code> , <code>ylab</code> , <code>main</code> , <code>xlim</code> , <code>ylim</code> to adjust the line thickness, line type, line color, fill color, x-label, y-label, title, x-axis range, and y-axis range respectively.

Value

plot.RoBTT returns either NULL if plot_type = "base" or an object object of class 'ggplot2' if plot_type = "ggplot2".

See Also

[RoBTT\(\)](#)

Examples

```
## Not run:
data("fertilization", package = "RoBTT")
fit <- RoBTT(
  x1      = fertilization$Self,
  x2      = fertilization$Crossed,
  prior_delta = prior("cauchy", list(0, 1/sqrt(2))),
  prior_rho  = prior("beta", list(3, 3)),
  seed      = 1,
  chains    = 1,
  warmup    = 1000,
  iter      = 2000,
  control   = set_control(adapt_delta = 0.95)
)

# plot the model-averaged effect size estimate
plot(fit, parameter = "delta")

# plot prior and posterior of the conditional effect size estimate
plot(fit, parameter = "delta", conditional = TRUE, prior = TRUE)

## End(Not run)
```

print.RoBTT

Prints a fitted 'RoBTT' object

Description

Prints a fitted 'RoBTT' object

Usage

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

Arguments

x a fitted 'RoBTT' object.
... additional arguments.

Value

`print.RoBTT` invisibly returns the print statement.

See Also

[RoBTT\(\)](#)

`print.summary.RoBTT` *Prints summary object for 'RoBTT' method*

Description

Prints summary object for 'RoBTT' method

Usage

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

Arguments

`x` a summary of a 'RoBTT' object
`...` additional arguments

Value

`print.summary.RoBTT` invisibly returns the print statement.

See Also

[RoBTT\(\)](#)

`prior` *Creates a prior distribution*

Description

`prior` creates a prior distribution. The prior can be visualized by the `plot` function.

Usage

```
prior(  
  distribution,  
  parameters,  
  truncation = list(lower = -Inf, upper = Inf),  
  prior_weights = 1  
)
```

Arguments

distribution	name of the prior distribution. The possible options are "point" for a point density characterized by a location parameter. "normal" for a normal distribution characterized by a mean and sd parameters. "lognormal" for a lognormal distribution characterized by a meanlog and sdlog parameters. "cauchy" for a Cauchy distribution characterized by a location and scale parameters. Internally converted into a generalized t-distribution with df = 1. "t" for a generalized t-distribution characterized by a location, scale, and df parameters. "gamma" for a gamma distribution characterized by either shape and rate, or shape and scale parameters. The later is internally converted to the shape and rate parametrization "invgamma" for an inverse-gamma distribution characterized by a shape and scale parameters. The JAGS part uses a 1/gamma distribution with a shape and rate parameter. "beta" for a beta distribution characterized by an alpha and beta parameters. "exp" for an exponential distribution characterized by either rate or scale parameter. The later is internally converted to rate. "uniform" for a uniform distribution defined on a range from a to b
parameters	list of appropriate parameters for a given distribution.
truncation	list with two elements, lower and upper, that define the lower and upper truncation of the distribution. Defaults to <code>list(lower = -Inf, upper = Inf)</code> . The truncation is automatically set to the bounds of the support.
prior_weights	prior odds associated with a given distribution. The value is passed into the model fitting function, which creates models corresponding to all combinations of prior distributions for each of the model parameters and sets the model priors odds to the product of its prior distributions.

Value

`prior` and `prior_none` return an object of class `'prior'`. A named list containing the distribution name, parameters, and prior weights.

See Also

[plot.prior\(\)](#), [Normal](#), [Lognormal](#), [Cauchy](#), [Beta](#), [Exponential](#), [LocationScaleT](#), [InvGamma](#).

Examples

```
# create a standard normal prior distribution
p1 <- prior(distribution = "normal", parameters = list(mean = 1, sd = 1))

# create a half-normal standard normal prior distribution
p2 <- prior(distribution = "normal", parameters = list(mean = 1, sd = 1),
```

```
truncation = list(lower = 0, upper = Inf))

# the prior distribution can be visualized using the plot function
# (see ?plot.prior for all options)
plot(p1)
```

prior_none	<i>Creates a prior distribution</i>
------------	-------------------------------------

Description

prior creates a prior distribution. The prior can be visualized by the plot function.

Usage

```
prior_none(prior_weights = 1)
```

Arguments

prior_weights prior odds associated with a given distribution. The value is passed into the model fitting function, which creates models corresponding to all combinations of prior distributions for each of the model parameters and sets the model priors odds to the product of its prior distributions.

Value

prior and prior_none return an object of class 'prior'. A named list containing the distribution name, parameters, and prior weights.

See Also

[plot.prior\(\)](#), [Normal](#), [Lognormal](#), [Cauchy](#), [Beta](#), [Exponential](#), [LocationScaleT](#), [InvGamma](#).

Examples

```
# create a standard normal prior distribution
p1 <- prior(distribution = "normal", parameters = list(mean = 1, sd = 1))

# create a half-normal standard normal prior distribution
p2 <- prior(distribution = "normal", parameters = list(mean = 1, sd = 1),
truncation = list(lower = 0, upper = Inf))

# the prior distribution can be visualized using the plot function
# (see ?plot.prior for all options)
plot(p1)
```

 rho2logsdr

rho to log standard deviation ratio transformations

Description

A list containing the transformation function, inverse transformation function, and the jacobian function.

Usage

```
rho2logsdr
```

Format

An object of class `list` of length 3.

Value

a list with the corresponding functions

RoBTT

Estimate a Robust Bayesian T-Test

Description

RoBTT is used to estimate a Robust Bayesian T-Test. The input either requires the vector of observations for each group, x_1 , x_2 , or the summary statistics (in case only the "normal" likelihood is used).

Usage

```
RoBTT(
  x1 = NULL,
  x2 = NULL,
  mean1 = NULL,
  mean2 = NULL,
  sd1 = NULL,
  sd2 = NULL,
  N1 = NULL,
  N2 = NULL,
  prior_delta = prior(distribution = "cauchy", parameters = list(location = 0, scale =
    sqrt(2)/2)),
  prior_rho = prior(distribution = "beta", parameters = list(alpha = 1, beta = 1)),
  prior_nu = prior(distribution = "exp", parameters = list(rate = 1)),
  prior_delta_null = prior(distribution = "spike", parameters = list(location = 0)),
  prior_rho_null = prior(distribution = "spike", parameters = list(location = 0.5)),
```

```

prior_nu_null = prior_none(),
chains = 4,
iter = 10000,
warmup = 5000,
thin = 1,
parallel = FALSE,
control = set_control(),
convergence_checks = set_convergence_checks(),
save = "all",
seed = NULL,
silent = TRUE,
...
)

```

Arguments

x1	vector of observations of the first group
x2	vector of observations of the second group
mean1	mean of the first group
mean2	mean of the first group
sd1	standard deviation of the first group
sd2	standard deviation of the first group
N1	sample size of the first group
N2	sample size of the first group
prior_delta	prior distributions for the effect size delta parameter that will be treated as belonging to the alternative hypothesis. Defaults to <code>prior(distribution = "Cauchy", parameters = list(location = 0, scale = sqrt(2)/2))</code> .
prior_rho	prior distributions for the precision allocation rho parameter that will be treated as belonging to the alternative hypothesis. Defaults to <code>prior(distribution = "beta", parameters = list(alpha = 1, beta = 1))</code> .
prior_nu	prior distribution for the degrees of freedom + 2 nu parameter that will be treated as belonging to the alternative hypothesis. Defaults to <code>prior(distribution = "exp", parameters = list(rate = 1))</code> .
prior_delta_null	prior distribution for the delta parameter that will be treated as belonging to the null hypothesis. Defaults to point distribution with location at 0 (<code>prior(distribution = "point", parameters = list(location = 0))</code>).
prior_rho_null	prior distribution for the rho parameter that will be treated as belonging to the null hypothesis. Defaults to point distribution with location at 0.5 (<code>prior(distribution = "point", parameters = list(location = 0.5))</code>).
prior_nu_null	prior distribution for the nu parameter that will be treated as belonging to the null hypothesis. Defaults to <code>prior_none</code> (i.e., normal likelihood).
chains	a number of chains of the MCMC algorithm.
iter	a number of sampling iterations of the MCMC algorithm. Defaults to 10000, with a minimum of 4000.

warmup	a number of warmup iterations of the MCMC algorithm. Defaults to 5000.
thin	a thinning of the chains of the MCMC algorithm. Defaults to 1.
parallel	whether the individual models should be fitted in parallel. Defaults to FALSE. The implementation is not completely stable and might cause a connection error.
control	allows to pass control settings with the <code>set_control()</code> function. See <code>?set_control</code> for options and default settings.
convergence_checks	automatic convergence checks to assess the fitted models, passed with <code>set_convergence_checks()</code> function. See <code>?set_convergence_checks</code> for options and default settings.
save	whether all models posterior distributions should be kept after obtaining a model-averaged result. Defaults to "all" which does not remove anything. Set to "min" to significantly reduce the size of final object, however, some model diagnostics and further manipulation with the object will not be possible.
seed	a seed to be set before model fitting, marginal likelihood computation, and posterior mixing for reproducibility of results. Defaults to NULL - no seed is set.
silent	whether all print messages regarding the fitting process should be suppressed. Defaults to TRUE. Note that <code>parallel = TRUE</code> also suppresses all messages.
...	additional arguments.

Details

See Maier et al. (2022) for more details regarding the methodology.

Generic `summary.RoBTT()`, `print.RoBTT()`, and `plot.RoBTT()` functions are provided to facilitate manipulation with the ensemble.

Value

RoBTT returns an object of class "RoBTT".

References

Maier M, Bartoš F, Quintana DS, van den Bergh D, Marsman M, Ly A, Wagenmakers E (2022). "Model-averaged Bayesian t-tests." doi:10.31234/osf.io/d5zwc, PsyArxiv Preprint.

See Also

`summary.RoBTT()`, `prior()`

Examples

```
## Not run:
# using the example data from Darwin
data("fertilization", package = "RoBTT")
fit <- RoBTT(
  x1      = fertilization$Self,
  x2      = fertilization$Crossed,
  prior_delta = prior("cauchy", list(0, 1/sqrt(2))),
  prior_rho  = prior("beta", list(3, 3)),
```



```

seed      = 1,
chains    = 1,
warmup    = 1000,
iter      = 2000,
control   = set_control(adapt_delta = 0.95)
)

# summary can provide many details about the model
summary(fit)

## End(Not run)

```

RoBTT_control

Convergence checks of the fitting process

Description

Set values for the convergence checks of the fitting process.

Usage

```

set_convergence_checks(max_Rhat = 1.05, min_ESS = 500)

set_control(adapt_delta = 0.8, max_treedepth = 15, bridge_max_iter = 1000)

```

Arguments

max_Rhat	maximum value of the R-hat diagnostic. Defaults to 1.05.
min_ESS	minimum estimated sample size. Defaults to 500.
adapt_delta	tuning parameter of HMC. Defaults to 0.80.
max_treedepth	tuning parameter of HMC. Defaults to 15.
bridge_max_iter	maximum number of iterations for the bridge_sampler function. Defaults to 10000

Value

set_control returns a list of control settings and set_convergence_checks returns a list of convergence checks settings.

RoBTT_options	<i>Options for the 'RoBTT' package</i>
---------------	--

Description

A placeholder object and functions for the 'RoBTT' package. (adapted from the runjags R package).

Usage

```
RoBTT.options(...)

RoBTT.get_option(name)
```

Arguments

...	named option(s) to change - for a list of available options, see details below.
name	the name of the option to get the current value of - for a list of available options, see details below.

Value

The current value of all available 'RoBTT' options (after applying any changes specified) is returned invisibly as a named list.

summary.RoBTT	<i>Summarize fitted 'RoBTT' object</i>
---------------	--

Description

summary.RoBTT creates summary tables for a RoBTT object.

Usage

```
## S3 method for class 'RoBTT'
summary(
  object,
  type = "ensemble",
  conditional = FALSE,
  group_estimates = FALSE,
  probs = c(0.025, 0.975),
  logBF = FALSE,
  BF01 = FALSE,
  short_name = FALSE,
  remove_spike_0 = FALSE,
  ...
)
```

Arguments

object	a fitted 'RoBTT' object
type	whether to show the overall 'RoBTT' results ("ensemble"), an overview of the individual models ("models"), an overview of the individual models MCMC diagnostics ("diagnostics"), or a detailed summary of the individual models ("individual"). Can be abbreviated to first letters.
conditional	show the conditional estimates (assuming that the alternative is true). Defaults to FALSE. Only available for type == "conditional".
group_estimates	show the model-averaged mean and standard deviation estimates for each group.
probs	quantiles of the posterior samples to be displayed. Defaults to c(.025, .975)
logBF	show log of Bayes factors. Defaults to FALSE.
BF01	show Bayes factors in support of the null hypotheses. Defaults to FALSE.
short_name	whether priors names should be shortened to the first (couple) of letters. Defaults to FALSE.
remove_spike_0	whether spike prior distributions with location at zero should be omitted from the summary. Defaults to FALSE.
...	additional arguments

Value

summary.RoBTT returns a list of tables of class 'BayesTools_table'.

See Also

[RoBTT\(\)](#)

Examples

```
## Not run:
# using the example data from Darwin
data("fertilization", package = "RoBTT")
fit <- RoBTT(
  x1      = fertilization$Self,
  x2      = fertilization$Crossed,
  prior_delta = prior("cauchy", list(0, 1/sqrt(2))),
  prior_rho  = prior("beta", list(3, 3)),
  seed      = 1,
  chains    = 1,
  warmup    = 1000,
  iter      = 2000,
  control   = set_control(adapt_delta = 0.95)
)

# summary can provide many details about the model
summary(fit)
```

```
# estimates from the conditional models can be obtained with
summary(fit, conditional = TRUE)

# overview of the models and their prior and posterior probability, marginal likelihood,
# and inclusion Bayes factor can be obtained with
summary(fit, type = "models")

# diagnostics overview, containing the maximum R-hat, minimum ESS, maximum MCMC error, and
# maximum MCMC error / sd across parameters for each individual model can be obtained with
summary(fit, type = "diagnostics")

# summary of individual models and their parameters can be further obtained by
summary(fit, type = "individual")

## End(Not run)
```

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