Package ‘RoBTT’

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Title  Robust Bayesian T-Test
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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.

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BugReports  https://github.com/FBartos/RoBTT/issues
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Suggests  parallel, testthat, vdifffr, knitr, rmarkdown, covr
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.

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References


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.

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**

*Interprets results of a 'RoBTT' model.*

**Description**

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

**Usage**

```r
interpret(object)
```

**Arguments**

- **object**
  - a fitted 'RoBTT' object

**Value**

interpret returns a character.

---

**is.RoBTT**

*Reports whether x is a 'RoBTT' object*

**Description**

Reports whether x is a 'RoBTT' object

**Usage**

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

**Arguments**

- **x**
  - an object to test

**Value**

is.RoBTT returns a boolean.
Description

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

Usage

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

Arguments

- `x` a fitted 'RoBTT' object
- `parameter` 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).
- `conditional` whether conditional estimates should be plotted. Defaults to FALSE which plots the model-averaged estimates.
- `plot_type` whether to use a base plot "base" or ggplot2 "ggplot" for plotting. Defaults to "base".
- `prior` whether prior distribution should be added to figure. Defaults to FALSE.
- `dots_prior` list of additional graphical arguments to be passed to the plotting function of the prior distribution. Supported arguments are lwd, lty, col, and col.fill, to adjust the line thickness, line type, line color, and fill color of the prior distribution respectively.
- `...` list of additional graphical arguments to be passed to the plotting function. Supported arguments are lwd, lty, col, col.fill, xlab, ylab, main, xlim, ylim 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

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)),
  likelihood = "normal",
  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)

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.

... 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 list(lower = -Inf, upper = Inf). 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)

---

**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**

```r
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 = NULL,
  likelihood = c("normal", if (!is.null(prior_nu)) "t"),
  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 prior(distribution = "Cauchy", parameters = list(location = 0, scale = sqrt(2)/2)).
- **prior_rho**: prior distributions for the precision allocation rho parameter that will be treated as belonging to the alternative hypothesis. Defaults to prior(distribution = "beta", parameters = list(alpha = 1, beta = 1)).
- **prior_nu**: prior distribution for the degrees of freedom + 2 nu parameter that will be treated as belonging to the alternative hypothesis. Defaults to prior(distribution = "exp", parameters = list(rate = 1)).
- **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 (prior(distribution = "point", parameters = list(location = 0))).
- **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 (prior(distribution = "point", parameters = list(location = 0.5))).
- **prior_nu_null**: prior distribution for the nu parameter that will be treated as belonging to the null hypothesis. Defaults to NULL (NULL, i.e., normal distribution).
- **likelihood**: types of likelihood to be used. Defaults to c("normal", "t") for a normal and t likelihoods.
- **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 `set_control()` function. See `?set_control` for options and default settings.
- **convergence_checks**: automatic convergence checks to assess the fitted models, passed with `set_convergence_checks()` function. See `?set_convergence_checks` 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 di-
agnostics and further manipulation with the object will not be possible.

seed a seed to be set before model fitting, marginal likelihood computation, and pos-
terior 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 parallel = TRUE 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 facili-
tate manipulation with the ensemble.

Value

RoBTT returns an object of class "RoBTT".

References


See Also

summary.RoBTT(), prior()

Examples

# 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)),
  likelihood = "normal",
  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)
RoBTT_options

---

**RoBTT_control**

*Convergence checks of the fitting process*

**Description**

Set values for the convergence checks of the fitting process.

**Usage**

```r
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**

*Options for the 'RoBTT' package*

**Description**

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

**Usage**

```r
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

Summarize fitted 'RoBTT' object

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(0.025, 0.975)

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

```r
# using the example data from Darw
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)),
  likelihood = "normal",
  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")
```
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