

Package: ssrhom (via r-universe)

September 11, 2024

Title Hierarchical ordinal models for analyzing single subject designs

Version 0.0.3.9001

Description Hierarchical ordinal models for analyzing single subject designs using Bayesian models fit with Stan.

License GPL (>= 3)

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.1

Biarch true

Depends R (>= 3.4.0)

Imports methods, posterior, Rcpp (>= 0.12.0), RcppParallel (>= 5.0.1), rstan (>= 2.18.1), rstantools (>= 2.4.0), splines2

LinkingTo BH (>= 1.66.0), Rcpp (>= 0.12.0), RcppEigen (>= 0.3.3.3.0), RcppParallel (>= 5.0.1), rstan (>= 2.18.1), StanHeaders (>= 2.18.0)

SystemRequirements GNU make

LazyData true

Suggests testthat (>= 3.0.0)

Config/testthat.edition 3

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

RemoteUrl <https://github.com/jamesuanhoro/ssrhom>

RemoteRef HEAD

RemoteSha 2f7ce15f69ff0f5d19da5d657f46cce8a2ec2ef7

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ssrhom-package *The 'ssrhom' package.*

Description

The 'ssrhom' package.

References

Stan Development Team (NA). RStan: the R interface to Stan. R package version 2.32.6. <https://mc-stan.org>

ssrhom_get_effect *Report an effect of interest*

Description

Report an effect of interest

Usage

```
ssrhom_get_effect(res_obj, stat = "nap", interval = 0.95, return_draws = FALSE)
```

Arguments

<code>res_obj</code>	Object returned by main function
<code>stat</code>	One of "mean", "median", "mean-diff", "median-diff", "lrr", "lor", "nap", "tau", "pem", "smd_c", or "smd_p". lrr or log rate ratio is only computed when the outcome variable is non-negative or has a minimum greater than 0. lor or log odds ratio is only computed when the outcome variable falls entirely in the 0-1 interval, inclusive of both 0 and 1.
<code>interval</code>	Some quantile interval between 0 and 1
<code>return_draws</code>	If TRUE, do not summarize the posterior samples. If FALSE, summarize the posterior samples.

Value

Returns dataset.

<code>ssrhom_list_stats</code>	<i>Function to list out effects computed by package.</i>
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Description

Function to list out effects computed by package.

Usage

```
ssrhom_list_stats(table = TRUE)
```

Arguments

<code>table</code>	If TRUE, report statistics in a table describing each statistic. If FALSE, simply return statistics as a list.
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<code>ssrhom_model_ab</code>	<i>Analyze AB design</i>
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Description

Analyze AB design

Usage

```
ssrhom_model_ab(
  data,
  grouping = NA_character_,
  condition = NA_character_,
  time = NA_character_,
  outcome = NA_character_,
  case = NA_character_,
  increase = TRUE,
  warmup = 750,
  sampling = 750,
  refresh = max((warmup + sampling)%%10, 1),
  adapt_delta = 0.9,
  max_treedepth = 10,
  chains = 3,
  cores = min(chains, max(parallel::detectCores() - 2, 1)),
  seed = sample.int(.Machine$integer.max, 1),
  show_messages = TRUE
)
```

Arguments

<code>data</code>	A dataset, ideally a data.frame.
<code>grouping</code>	The name of the grouping variable in the dataset.
<code>condition</code>	The level of the grouping variable that identifies the treatment condition.
<code>time</code>	The name of the time variable. This must be a series of positive whole numbers signifying the time the outcome was measured.
<code>outcome</code>	The name of the outcome variable.
<code>case</code>	The name of the variable that identifies different cases in the dataset.
<code>increase</code>	TRUE (Default) if increase in outcome is desirable. Set FALSE if increase in outcome is undesirable.
<code>warmup</code>	Number of iterations used to warmup the sampler, per chain.
<code>sampling</code>	Number of iterations retained for inference, per chain.
<code>refresh</code>	(Positive whole number) How often to print the status of the sampler.
<code>adapt_delta</code>	Number in (0,1). Increase to resolve divergent transitions.
<code>max_treedepth</code>	(Positive whole number) Increase to resolve problems with maximum tree depth.
<code>chains</code>	Number of chains to use.
<code>cores</code>	Number of cores to use.
<code>seed</code>	Random seed.
<code>show_messages</code>	(Logical) If TRUE, show messages from Stan sampler, if FALSE, hide messages.

Value

Object containing analysis results.

Examples

```
## Not run:
tasky_model <- ssrhom_model_ab(
  data = tasky,
  grouping = "phase", condition = "B",
  time = "time", outcome = "count", case = "person"
)
ssrhom_get_effect(tasky_model, stat = "nap")

## End(Not run)
```

tasky *Dataset from Tasky et al. (2008)*

Description

Dataset from Tasky et al. (2008)

Usage

tasky

Format

tasky:

A data frame with 70 rows and 5 columns:

person The case label

phase Intervention phase where "B" is treatment

count The count of on-task intervals out of 6

proportion The count as a proportion

time Session number

Source

Tasky et al. (2008). Using Choice to Increase On-Task Behavior in Individuals with Traumatic Brain Injury. Journal of Applied Behavior Analysis, 41(2), 261–265. <https://doi.org/10.1901/jaba.2008.41-261>

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