Package: bennu (via r-universe)

October 26, 2024

Title Bayesian Estimation of Naloxone Kit Number Under-Reporting

Version 0.3.0.9000

Description Bayesian model and associated tools for generating
estimates of total naloxone kit numbers distributed and used
from naloxone kit orders data. Provides functions for
generating simulated data of naloxone kit use and functions for
generating samples from the posterior.

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Encoding UTF-8

LazyData true

Roxygen list(markdown = TRUE)

RoxygenNote 7.2.3

Biarch true

Depends R (>= 3.4.0)

Imports dplyr, generics, ggplot2, glue, lifecycle, magrittr, methods,
Rcpp (>= 0.12.0), RcppParallel (>= 5.0.1), rlang, rstan (>=
2.26.0), rstantools (>= 2.2.0), scales, tidybayes, tidyr

LinkingTo BH (>= 1.66.0), Rcpp (>= 0.12.0), RcppEigen (>= 0.3.3.3.0),
RcppParallel (>= 5.0.1), rstan (>= 2.26.0), StanHeaders (>=
2.26.0)

SystemRequirements GNU make

Suggests bayesplot, covr, knitr, latex2exp, posterior, progress,
rmarkdown, stringr, testthat (>= 3.0.0)

Config/testthat/edition 3

URL https://sempwn.github.io/bennu/

BugReports https://github.com/sempwn/bennu/issues

VignetteBuilder knitr

Repository https://sempwn.r-universe.dev

RemoteUrl https://github.com/sempwn/bennu

RemoteRef HEAD

RemoteSha 8b7fd8aea89ee8a73e670f0dbdaca969f0fc0c58

Contents

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bennu-package   *The 'bennu' package.*

Description

Bayesian Estimation of Naloxone use Number Under-reporting

References

Stan Development Team (2020). RStan: the R interface to Stan. R package version 2.21.2. https://mc-stan.org

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est_naloxone   *Run Bayesian estimation of naloxone number under-reporting*

Description

Samples from Bayesian model using input from data frame

Usage

```
est_naloxone(
  d,
  psi_vec = c(0.7, 0.2, 0.1),
  max_delays = 3,
  delay_alpha = 2,
  delay_beta = 1,
  priors = the$default_priors,
  run_estimation = TRUE,
  rw_type = 1,
  chains = 4,
  iter = 2000,
```

```
    seed = 42,
    adapt_delta = 0.85,
    pars = the$default_outputs,
    include = TRUE,
    ...
)
```

Arguments

d	data frame with format
	regions unique id for region
	times time in months
	Orders Kits ordered
	Reported_Used Kits reported as used
	Reported_Distributed Kits reported as distributed
	region_name Optional label for region
psi_vec	reporting delay distribution
max_delays	maximum delay from kit ordered to kit distributed
delay_alpha	shape parameter for order to distributed delay distribution
delay_beta	shape parameter for order to distributed delay distribution
priors	list of prior values including their mean (mu) and standard deviation (sigma)
run_estimation	if TRUE will sample from posterior otherwise will sample from prior only
rw_type	1 - random walk of order one. 2 - random walk of order 2.
chains	A positive integer specifying the number of Markov chains. The default is 4.
iter	A positive integer specifying the number of iterations for each chain (including warmup). The default is 2000.
seed	Seed for random number generation
adapt_delta	(double, between 0 and 1, defaults to 0.8)
pars	A vector of character strings specifying parameters of interest. The default is NA indicating all parameters in the model. If include = TRUE, only samples for parameters named in pars are stored in the fitted results. Conversely, if include = FALSE, samples for all parameters *except* those named in pars are stored in the fitted results.
include	Logical scalar defaulting to TRUE indicating whether to include or exclude the parameters given by the pars argument. If FALSE, only entire multidimensional parameters can be excluded, rather than particular elements of them.
...	other parameters to pass to rstan::sampling

Value

An S4 rstan::stanfit class object containing the fitted model

See Also

Other inference: [est_naloxone_vec()](est_naloxone_vec)

Examples

```
## Not run:
library(rstan)
library(bayesplot)

rstan_options(auto_write = TRUE)
options(mc.cores = parallel::detectCores(logical = FALSE))

d <- generate_model_data()
priors <- list(
  c = list(mu = 0, sigma = 1),
  ct0 = list(mu = 0, sigma = 1),
  zeta = list(mu = 0, sigma = 1),
  mu0 = list(mu = 0, sigma = 1),
  sigma = list(mu = 0, sigma = 1)
  )
fit <- est_naloxone(d, priors = priors, iter = 100, chains = 1)
mcmc_pairs(fit,
  pars = c("sigma", "mu0"),
  off_diag_args = list(size = 1, alpha = 0.5)
)

## End(Not run)
```

---

est_naloxone_vec   *Run Bayesian estimation of naloxone number under-reporting*

Description

Samples from Bayesian model

Usage

```
est_naloxone_vec(
  N_region,
  N_t,
  N_distributed,
  regions,
  times,
  Orders2D,
  Reported_Distributed,
  Reported_Used,
  region_name,
  psi_vec = c(0.7, 0.2, 0.1),
  max_delays = 3,
  delay_alpha = 2,
  delay_beta = 1,
  priors = the$default_priors,
```

```
    run_estimation = TRUE,
    rw_type = 1,
    chains = 4,
    iter = 2000,
    seed = 42,
    adapt_delta = 0.85,
    pars = the$default_outputs,
    include = TRUE,
    ...
)
```

Arguments

N_region	Number of regions
N_t	number of time steps
N_distributed	Number of samples of reporting for distribution of kits
regions	vector (time, region) of regions (coded 1 to N_region)
times	vector (time, region) of regions (coded 1 to N_t)
Orders2D	vector (time, region) of orders
Reported_Distributed	
	vector (time, region) reported as distributed
Reported_Used	vector (time, region) reported as used
region_name	bring in region names
psi_vec	reporting delay distribution
max_delays	maximum delay from kit ordered to kit distributed
delay_alpha	shape parameter for order to distributed delay distribution
delay_beta	shape parameter for order to distributed delay distribution
priors	list of prior values including their mean (mu) and standard deviation (sigma)
run_estimation	if TRUE will sample from posterior otherwise will sample from prior only
rw_type	1 - random walk of order one. 2 - random walk of order 2.
chains	A positive integer specifying the number of Markov chains. The default is 4.
iter	A positive integer specifying the number of iterations for each chain (including warmup). The default is 2000.
seed	Seed for random number generation
adapt_delta	(double, between 0 and 1, defaults to 0.8)
pars	A vector of character strings specifying parameters of interest. The default is NA indicating all parameters in the model. If include = TRUE, only samples for parameters named in pars are stored in the fitted results. Conversely, if include = FALSE, samples for all parameters *except* those named in pars are stored in the fitted results.
include	Logical scalar defaulting to TRUE indicating whether to include or exclude the parameters given by the pars argument. If FALSE, only entire multidimensional parameters can be excluded, rather than particular elements of them.
...	other parameters to pass to rstan::sampling

Value

An S4 [rstan::stanfit](#) class object containing the fitted model

See Also

Other inference: [est_naloxone](#)()

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experimental_validation_data

Experimental validation results

Description

Generated data from validation experiments of simulated data

Usage

```
experimental_validation_data
```

Format

experimental_validation_data:

A data frame with 200 rows and 8 columns:

.variable Model variable

p50 Median of the posterior

p25, p75 2nd and 3rd quartiles of the posterior

p05, p95 1st and 19th ventiles of the posterior

true_value The value used to generate the simulation

experiment Experiment number index

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generate_model_data   *generate model data for testing purposes*

Description

[Deprecated]

Simulate kits ordered and kits distributed for a set number of regions and time-points.

The kits ordered simulation is a simple square-term multiplied by region_coeffs. For example if region_coeffs = c(1,2) then the number of kits ordered at month 12 are c(1,2) * 12^2 = c(144,288).

The probability of kit use in time is assumed to increase linearly in inverse logit space at a constant rate 0.1. The probability of reporting for each month and region is iid distributed $logit^{-1}(p) \sim N(2,5)$ which produces a mean reporting rate of approximately 88%

Usage

```
generate_model_data(
  N_t = 24,
  region_coeffs = c(5, 0.5),
  c_region = c(-1, 2),
  reporting_freq = NULL
)
```

Arguments

N_t	number of time-points
region_coeffs	vector of coefficients for regions determining kit orders
c_region	logit probability of kit use per region
reporting_freq	The frequency that distribution data is provided. If NULL distribution frequency matches orders frequency

Value

A [tibble](#)

Orders Kit orders per time and region

regions Numeric index indicating region of orders and distributions

Reported_Used Number of kits reported as used

Reported_Distributed Number of kits reported as distributed

p_use Probability that a kit was used

p_reported Probability that a distributed kit was reported

times Index for time

region_name String index for the region

See Also

Other data generation: [model_random_walk_data](#)()

---

kit_summary_table	*Summarize model fit*

Description

Provides a summary of:

- Estimated kits distributed
- Percentage of kits distributed that are reported
- Estimated kits used
- percentage of kits used that are reported
- percentage of kits orders that are used
- probability kit used if distributed

Usage

```
kit_summary_table(
  fit,
  ...,
  data = NULL,
  accuracy = 0.01,
  cri_range = 0.95,
  ndraws = NULL
)
```

Arguments

`fit`	stanfit object
`...`	variables to group by in estimate
`data`	data used for model fitting. Can also include p_use column which can be used to plot true values if derived from simulated data.
`accuracy`	A number to round to. Use (e.g.) 0.01 to show 2 decimal places of precision. If NULL, the default, uses a heuristic that should ensure breaks have the minimum number of digits needed to show the difference between adjacent values.
`cri_range`	The range of the credible interval e.g. 0.95
`ndraws`	Number of draws to use in estimate

Value

A tibble::tibble

- Probability of kit use if distributed
- Estimated as distributed
- Proportion kits distributed that are reported
- Estimated kits used
- Proportion kits used that are reported
- Proportion kits ordered that are used

See Also

Other plots: plot_kit_use()

Examples

```
## Not run:
  fit <- est_naloxone(d)
  kit_summary_table(fit,regions,data = d)

## End(Not run)
```

---

missing_data_validation
Missing data experimental validation results

Description

Generated data from validation experiments of simulated data

Usage

```
missing_data_validation
```

Format

missing_data_validation:

A data frame with 10 rows and 6 columns:

p50 Median of the posterior

p25, p75 2nd and 3rd quartiles of the posterior

p05, p95 1st and 19th ventiles of the posterior

reporting_freq The reporting frequency in months

---

model_random_walk_data
generate model data for testing purposes

Description

Model generating process using random walk to match data generating model in Bayesian framework

Usage

```
model_random_walk_data(
  N_t = 24,
  region_coeffs = c(5, 0.5),
  c_region = c(-1, 2),
  sigma = 2,
  zeta = 0.5,
  mu0 = -1,
  Orders = NULL,
  reporting_freq = NULL
)
```

Arguments

`N_t`	number of time-points
`region_coeffs`	vector of coefficients for regions determining kit orders
`c_region`	logit probability of kit use per region
`sigma`	standard deviation of error in logit probability of kit use
`zeta`	standard deviation of random walk in logit space
`mu0`	initial condition of random walk in logit space
`Orders`	A 2D matrix of shape `length(region_coeffs)` by `N_t`
`reporting_freq`	The frequency that distribution data is provided. If `NULL` distribution frequency matches orders frequency

Value

A tibble

Orders Kit orders per time and region

regions Numeric index indicating region of orders and distributions

Reported_Used Number of kits reported as used

Reported_Distributed Number of kits reported as distributed

p_use Probability that a kit was used

p_reported Probability that a distributed kit was reported

times Index for time

region_name String index for the region

See Also

Other data generation: [generate_model_data](#)()

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plot_kit_use	*Plot of probability of naloxone kit use*

Description

plot can compare between two different model fits or a single model fit by region. If data are simulated then can also include in plot. For more details see the introduction vignette: `vignette("Introduction", package = "bennu")`

Usage

```
plot_kit_use(..., data = NULL, reported = FALSE, regions_to_plot = NULL)
```

Arguments

`...`	named list of [stanfit](#) objects
`data`	data used for model fitting. Can also include `p_use` column which can be used to plot true values if derived from simulated data.
`reported`	if `TRUE` then produces a plot of the reported kits which is equivalent to the predictive check.
`regions_to_plot`	
	Optional list to filter which regions are plotted

Value

[ggplot2](#) object

See Also

Other plots: [`kit_summary_table()`](#)

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