Package ‘bennu’

June 23, 2023

Title  Bayesian Estimation of Naloxone Kit Number Under-Reporting

Version  0.2.1

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.

License  MIT + file LICENSE

Encoding  UTF-8

RoxygenNote  7.1.1

Biarch  true

Depends  R (>= 3.4.0)

Imports  dplyr, ggplot2, magrittr, methods, Rcpp (>= 0.12.0),
  RcppParallel (>= 5.0.1), rstan (>= 2.18.1), 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 (>= 2.18.1), StanHeaders (>=
  2.18.0)

SystemRequirements  GNU make

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

Config/testthat/edition  3

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

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

VignetteBuilder  knitr

NeedsCompilation  yes

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bennu-package  

The 'bennu' package.

Description

Bayesian Estimation of Naloxone use Number Under-reporting

References


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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

```r
est_naloxone(
  d,
  psi_vec = c(0.7, 0.2, 0.1),
  max_delays = 3,
  delay_alpha = 2,
  delay_beta = 1,
  run_estimation = TRUE,
  rw_type = 1,
  chains = 4,
  iter = 2000,
  seed = 42,
  adapt_delta = 0.85,
  ...
)
```
est_naloxone

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  
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)  
...  other parameters to pass to rstan::sampling

Value

An S4 stanfit class object containing the fitted model

See Also

Other inference: 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()
fit <- est_naloxone(d, 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

```r
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,
  run_estimation = TRUE,
  rw_type = 1,
  chains = 4,
  iter = 2000,
  seed = 42,
  adapt_delta = 0.85,
  ...
)
```

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
generate_model_data

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
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)
...  other parameters to pass to rstan::sampling

Value

An S4 stanfit class object containing the fitted model

See Also

Other inference: est_naloxone()

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generate_model_data  generate model data for testing purposes

Description

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) ~ 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
)
plot_kit_use

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

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)

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.

Value

ggplot2 object
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