Package 'spatialSPsurv'

June 1, 2020

| туре гаскаде |
|--|
| Title Bayesian Spatial Split Population Survival Model |
| Version 0.1.3 |
| Description Contains functions to fit Bayesian spatial survival model for split population. |
| License MIT + file LICENSE |
| Encoding UTF-8 |
| LazyData true |
| RoxygenNote 7.1.0 |
| LinkingTo Rcpp, RcppArmadillo |
| Imports MCMCpack, FastGP, stats, Rcpp, RcppArmadillo, coda |
| R topics documented: |
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Description

Markov Chain Monte Carlo (MCMC) to run Bayesian non-spatial frailty split population survival model

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Usage

```
frailtySPsurv(
   duration,
   immune,
   Y0,
   LY,
   S,
   data,
   N,
   burn,
   thin,
   w = c(1, 1, 1),
   m = 10,
   form = c("Weibull", "exponential", "loglog"),
   prop.var
)
```

Arguments

duration

immune Υ0 the elapsed time since inception until the beginning of time period (t-1) LY last observation year spatial information (e.g. district ID) for each observation that matches the spatial S matrix row/column information data number of MCMC iterations Ν burn burn-in to be discarded thin thinning to prevent from autocorrelation size of the slice in the slice sampling for (betas, gammas, rho). Write it as a vector. E.g. c(1,1,1)

limit on steps in the slice sampling. A vector of values for beta, gamma, rho.

Value

m

form prop.var

chain of the variables of interest

type of parametric model (Exponential or Weibull)

Description

Markov Chain Monte Carlo (MCMC) to run Bayesian spatial split population survival model

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Usage

```
spatialSPsurv(
  duration,
  immune,
  Υ0,
  LY,
  S,
  Α,
  data,
  N,
  burn,
  thin,
  w = c(1, 1, 1),
  m = 10,
  form = c("Weibull", "exponential", "loglog"),
  prop.var
)
```

Arguments

| duration | |
|----------|--|
| immune | |
| Y0 | the elapsed time since inception until the beginning of time period (t-1) |
| LY | last observation year |
| S | spatial information (e.g. district ID) for each observation that matches the spatial matrix row/column information $\frac{1}{2}$ |
| A | Spatial Matrix (load separate spatial weights matrix file) |
| data | |
| N | number of MCMC iterations |
| burn | burn-in to be discarded |
| thin | thinning to prevent from autocorrelation |
| W | size of the slice in the slice sampling for (betas, gammas, rho). Write it as a vector. E.g. $c(1,1,1)$ |
| m | limit on steps in the slice sampling. A vector of values for beta, gamma, rho. |
| form | type of parametric model (Exponential or Weibull) |
| prop.var | proposal variance for Metropolis-Hastings |

Value

chain of the variables of interest

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| surv | SPsurv | SPsurv |
|------|--------|--------|
|------|--------|--------|

Description

Markov Chain Monte Carlo (MCMC) to run Bayesian split population survival model with no frailties

Usage

```
SPsurv(
   duration,
   immune,
   Y0,
   LY,
   data,
   N,
   burn,
   thin,
   w = c(1, 1, 1),
   m = 10,
   form = c("Weibull", "exponential", "loglog")
)
```

Arguments

duration immune ... Υ0 the elapsed time since inception until the beginning of time period (t-1) LY last observation year data number of MCMC iterations Ν burn-in to be discarded burn thin thinning to prevent from autocorrelation size of the slice in the slice sampling for (betas, gammas, rho). Write it as a vector. E.g. c(1,1,1)limit on steps in the slice sampling. A vector of values for beta, gamma, rho. m type of parametric model (Exponential or Weibull) form

Value

chain of the variables of interest

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