

# Package ‘spatialSPsurv’

May 29, 2020

**Type** Package  
**Title** Bayesian Spatial Split Population Survival Model  
**Version** 0.1.0.9000  
**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:

|                         |          |
|-------------------------|----------|
| frailtySPsurv . . . . . | 1        |
| spatialSPsurv . . . . . | 2        |
| SPsurv . . . . .        | 4        |
| <b>Index</b>            | <b>5</b> |

---

|               |                      |
|---------------|----------------------|
| frailtySPsurv | <i>frailtySPsurv</i> |
|---------------|----------------------|

---

## Description

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

**Usage**

```

frailtySPsurv(
  duration,
  immune,
  Y0,
  LY,
  S,
  data,
  N,
  burn,
  thin,
  w = c(1, 1, 1),
  m = 10,
  form,
  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 |
| 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 | ...  |

**Value**

chain of the variables of interest

---

spatialSPsurv

*spatialSPsurv*


---

**Description**

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

**Usage**

```

spatialSPsurv(
  duration,
  immune,
  Y0,
  LY,
  S,
  data = list(),
  A,
  N,
  burn,
  thin,
  w = c(1, 1, 1),
  m = 10,
  form,
  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 |
| data     | ...  |
| A        | Spatial Matrix (load separate spatial weights matrix file)   |
| 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

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 = list(),
  N,
  S,
  burn,
  thin,
  w = c(1, 1, 1),
  m = 10,
  form
)
```

**Arguments**

|          |   |
|----------|---|
| duration | ...   |
| immune   | ...   |
| Y0       | the elapsed time since inception until the beginning of time period (t-1)                             |
| LY       | last observation year   |
| data     | ...   |
| N        | number of MCMC iterations   |
| S        | ...   |
| 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)   |

**Value**

chain of the variables of interest

# Index

frailtySPsurv, [1](#)

spatialSPsurv, [2](#)

SPsurv, [4](#)