

Package ‘MultiBD’

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Type Package

Title Multivariate Birth-Death Processes

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Description Computationally efficient functions to provide direct likelihood-based inference for partially-observed multivariate birth-death processes. Such processes range from a simple Yule model to the complex susceptible-infectious-removed model in disease dynamics. Efficient likelihood evaluation facilitates maximum likelihood estimation and Bayesian inference.

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Depends R (>= 3.1.0)

Imports Rcpp (>= 0.11.2), RcppParallel

LinkingTo Rcpp, BH, RcppParallel

Suggests testthat, knitr, rmarkdown, MCMCpack, ggplot2, matrixStats,
plotrix

RoxygenNote 5.0.1

VignetteBuilder knitr

NeedsCompilation yes

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bbd_prob	<i>Transition probabilities of a birth/birth-death process</i>
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Description

Computes the transition pobabilities of a birth/birth-death process using the continued fraction representation of its Laplace transform

Usage

```
bbd_prob(t, a0, b0, lambda1, lambda2, mu2, gamma, A, B, nblocks = 256,
        tol = 1e-12, computeMode = 0, nThreads = 4, maxdepth = 400)
```

Arguments

t	time
a0	total number of type 1 particles at $t = 0$
b0	total number of type 2 particles at $t = 0$
lambda1	birth rate of type 1 particles (a two variables function)
lambda2	birth rate of type 2 particles (a two variables function)
mu2	death rate function of type 2 particles (a two variables function)
gamma	transition rate from type 2 particles to type 1 particles (a two variables function)
A	upper bound for the total number of type 1 particles
B	upper bound for the total number of type 2 particles
nblocks	number of blocks
tol	tolerance
computeMode	computation mode
nThreads	number of threads
maxdepth	maximum number of iterations for Lentz algorithm

Value

a matrix of the transition probabilities

References

Ho LST et al. 2015. "Birth(death)/birth-death processes and their computable transition probabilities with statistical applications". In review.

Examples

```
## Not run:
data(Eyam)

# (R, I) in the SIR model forms a birth/birth-death process

loglik_sir <- function(param, data) {
  alpha <- exp(param[1]) # Rates must be non-negative
  beta  <- exp(param[2])
  N <- data$S[1] + data$I[1] + data$R[1]

  # Set-up SIR model with (R, I)

  brates1 <- function(a, b) { 0 }
  brates2 <- function(a, b) { beta * max(N - a - b, 0) * b }
  drates2 <- function(a, b) { 0 }
  trans21 <- function(a, b) { alpha * b }

  sum(sapply(1:(nrow(data) - 1), # Sum across all time steps k
    function(k) {
      log(
        bbd_prob( # Compute the transition probability matrix
          t = data$time[k + 1] - data$time[k], # Time increment
          a0 = data$R[k], b0 = data$I[k],      # From: R(t_k), I(t_k)
          brates1, brates2, drates2, trans21,
          A = data$R[k + 1], B = data$R[k + 1] + data$I[k] - data$R[k],
          computeMode = 4, nblocks = 80        # Compute using 4 threads
        )[data$R[k + 1] - data$R[k] + 1,
          data$I[k + 1] + 1]                  # To: R(t_(k+1)), I(t_(k+1))
      )
    })
  )
}

loglik_sir(log(c(3.204, 0.019)), Eyam) # Evaluate at mode

## End(Not run)
```

dbd_prob

*Transition probabilities of a death/birth-death process***Description**

Computes the transition probabilities of a death/birth-death process using the continued fraction representation of its Laplace transform

Usage

```
dbd_prob(t, a0, b0, mu1, lambda2, mu2, gamma, a = 0, B, nblocks = 256,
  tol = 1e-12, computeMode = 0, nThreads = 4, maxdepth = 400)
```

Arguments

t	time
a0	total number of type 1 particles at $t = 0$
b0	total number of type 2 particles at $t = 0$
mu1	death rate of type 1 particles (a two variables function)
lambda2	birth rate of type 2 particles (a two variables function)
mu2	death rate function of type 2 particles (a two variables function)
gamma	transition rate from type 2 particles to type 1 particles (a two variables function)
a	lower bound for the total number of type 1 particles (default $a = 0$)
B	upper bound for the total number of type 2 particles
nblocks	number of blocks
tol	tolerance
computeMode	computation mode
nThreads	number of threads
maxdepth	maximum number of iterations for Lentz algorithm

Value

a matrix of the transition probabilities

References

Ho LST et al. 2016. "Birth(death)/birth-death processes and their computable transition probabilities with statistical applications". In review.

Examples

```
## Not run:
data(Eyam)

loglik_sir <- function(param, data) {
  alpha <- exp(param[1]) # Rates must be non-negative
  beta  <- exp(param[2])

  # Set-up SIR model
  drates1 <- function(a, b) { 0 }
  brates2 <- function(a, b) { 0 }
  drates2 <- function(a, b) { alpha * b }
  trans12 <- function(a, b) { beta * a * b }

  sum(sapply(1:(nrow(data) - 1), # Sum across all time steps k
    function(k) {
      log(
        dbd_prob( # Compute the transition probability matrix
          t = data$time[k + 1] - data$time[k], # Time increment
          a0 = data$S[k], b0 = data$I[k],      # From: S(t_k), I(t_k)
```

```

        drates1, brates2, drates2, trans12,
        a = data$S[k + 1], B = data$S[k] + data$I[k] - data$S[k + 1],
        computeMode = 4, nblocks = 80          # Compute using 4 threads
      )[1, data$I[k + 1] + 1]                  # To: S(t_(k+1)), I(t_(k+1))
    )
  })
}

loglik_sir(log(c(3.204, 0.019)), Eyam) # Evaluate at mode

## End(Not run)

# Birth-death-shift model for transposable elements

lam = 0.0188; mu = 0.0147; v = 0.00268; # birth, death, shift rates

drates1 <- function(a, b) { mu * a }
brates2 <- function(a, b) { lam * (a + b) }
drates2 <- function(a, b) { mu * b }
trans12 <- function(a, b) { v * a }

# Get transition probabilities
p <- dbd_prob(t = 1, a0 = 10, b0 = 0,
              drates1, brates2, drates2, trans12,
              a = 0, B = 50)

```

Eyam

Eyam plague.

Description

A dataset containing the number of susceptible, infectious and removed individuals during the Eyam plague from June 18 to October 20, 1666.

Usage

```
data(Eyam)
```

Format

A data frame with 8 rows and 4 variables:

time Months past June 18 1666

S Susceptible

I Infectious

R Removed

References

Ragget G (1982). A stochastic model of the Eyam plague. *Journal of Applied Statistics* 9, 212-226.

MultiBD	<i>Multivariate birth-death processes</i>
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Description

The MultiBD package computes the transition probabilities of several multivariate birth-death processes.

References

Ho LST et al. 2016. "Birth(death)/birth-death processes and their computable transition probabilities with statistical applications". In review.

SIR_prob	<i>Transition probabilities of an SIR process</i>
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Description

Computes the transition probabilities of an SIR process using the bivariate birth process representation

Usage

```
SIR_prob(t, alpha, beta, S0, I0, nSI, nIR, direction = c("Forward",
  "Backward"), nblocks = 20, tol = 1e-12, computeMode = 0, nThreads = 4)
```

Arguments

t	time
alpha	removal rate
beta	infection rate
S0	initial susceptible population
I0	initial infectious population
nSI	number of infection events
nIR	number of removal events
direction	direction of the transition probabilities (either Forward or Backward)
nblocks	number of blocks
tol	tolerance
computeMode	computation mode
nThreads	number of threads

Value

a matrix of the transition probabilities

Examples

```
data(Eyam)

loglik_sir <- function(param, data) {
  alpha <- exp(param[1]) # Rates must be non-negative
  beta  <- exp(param[2])

  if(length(unique(rowSums(data[, c("S", "I", "R")])))) > 1) {
    stop ("Please make sure the data conform with a closed population")
  }

  sum(sapply(1:(nrow(data) - 1), # Sum across all time steps k
    function(k) {
      log(
        SIR_prob( # Compute the forward transition probability matrix
          t = data$time[k + 1] - data$time[k], # Time increment
          alpha = alpha, beta = beta,
          S0 = data$S[k], I0 = data$I[k],      # From: R(t_k), I(t_k)
          nSI = data$S[k] - data$S[k + 1], nIR = data$R[k + 1] - data$R[k],
          computeMode = 4, nblocks = 80        # Compute using 4 threads
        )[data$S[k] - data$S[k + 1] + 1,
          data$R[k + 1] - data$R[k] + 1]      # To: R(t_(k+1)), I(t_(k+1))
      )
    }
  ))

  loglik_sir(log(c(3.204, 0.019)), Eyam) # Evaluate at mode
```

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