

Package ‘smam’

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Type Package

Title Statistical Modeling of Animal Movements

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Imports stats, methods, Matrix, numDeriv, Rcpp (>= 0.12.2)

LinkingTo Rcpp

Description Animal movement models including moving-resting process
with embedded Brownian motion, Brownian motion with measurement error.

License GPL (>= 3.0)

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R topics documented:

dtm	2
fitBmme	3
fitMovRes	4
integr.control	6
rbmme	6
rMovRes	7
Index	9

dtm

Density for Time Spent in Moving or Resting

Description

Density for time spent in moving or resting in a time interval, unconditional or conditional on the initial state.

Usage

```
dtm(w, t, lamM, lamR, s0 = NULL)
```

```
dtr(w, t, lamM, lamR, s0 = NULL)
```

Arguments

w	time points at which the density is to be evaluated
t	length of the time interval
lamM	rate parameter of the exponentially distributed duration in moving
lamR	rate parameter of the exponentially distributed duration in resting
s0	initial state. If NULL, the unconditional density is returned; otherwise, it is one of "m" or "s", standing for moving and resting, respectively, and the conditional density is returned given the initial state.

Details

dtm returns the density for time in moving; dtr returns the density for time in resting.

Value

a vector of the density evaluated at w.

Functions

- dtr: Density of time spent in resting

References

Yan, J., Chen, Y., Lawrence-Apfel, K., Ortega, I. M., Pozdnyakoc, V., Williams, S., and Meyer, T. (2014) A moving-resting process with an embedded Brownian motion for animal movements. *Population Ecology*. 56(2): 401–415.

Examples

```

lamM <- 1
lamR <- c(1/2, 1, 2)
lr <- length(lamR)
totalT <- 10
old.par <- par(no.readonly=TRUE)
par(mfrow=c(1, 2), mar=c(2.5, 2.5, 1.1, 0.1), mgp=c(1.5, 0.5, 0), las=1)
curve(dtm(x, totalT, 1, 1/2, "m"), 0, totalT, lty=1, ylim=c(0, 0.34),
      xlab="M(10)", ylab="density")
curve(dtm(x, totalT, 1, 1, "m"), 0, totalT, lty=2, add=TRUE)
curve(dtm(x, totalT, 1, 2, "m"), 0, totalT, lty=3, add=TRUE)
mtext(expression("S(0) = 1"))
legend("topleft", legend = expression(lambda[r] == 1/2, lambda[r] == 1,
                                       lambda[r] == 2), lty = 1:lr)
curve(dtm(x, totalT, 1, 1/2, "r"), 0, totalT, lty=1, ylim=c(0, 0.34),
      xlab="M(10)", ylab="density")
curve(dtm(x, totalT, 1, 1, "r"), 0, totalT, lty=2, add=TRUE)
curve(dtm(x, totalT, 1, 2, "r"), 0, totalT, lty=3, add=TRUE)
mtext(expression("S(0) = 0"))
legend("topleft", legend = expression(lambda[r] == 1/2, lambda[r] == 1,
                                       lambda[r] == 2), lty = 1:lr)
par(old.par)

```

fitBmme

*Fit a Brownian Motion with Measurement Error***Description**

Given discretely observed animal movement locations, fit a Brownian motion model with measurement errors.

Usage

```

fitBmme(data, start = NULL, method = "Nelder-Mead",
        optim.control = list())

```

Arguments

data	a data.frame whose first column is the observation time, and other columns are location coordinates.
start	starting value of the model, a vector of two component, one for sigma (sd of BM) and the other for delta (sd for measurement error). If unspecified (NULL), a moment estimator will be used assuming equal sigma and delta.
method	the method argument to feed optim.
optim.control	a list of control that is passed down to optim.

Details

The joint density of the increment data is multivariate normal with a sparse (tri-diagonal) covariance matrix. Sparse matrix operation from package Matrix is used for computing efficiency in handling large data.

Value

A list of the following components:

estimate	the estimated parameter vector
var.est	variance matrix of the estimator
loglik	loglikelihood evaluated at the estimate
convergence	convergence code from optim

References

Pozdnyakov V., Meyer, TH., Wang, Y., and Yan, J. (2013) On modeling animal movements using Brownian motion with measurement error. Ecology 95(2): p247–253. doi:doi:10.1890/13-0532.1.

See Also

[fitMovRes](#)

Examples

```
set.seed(123)
tgrid <- seq(0, 500, by = 1)
dat <- rbmme(tgrid, sigma = 1, delta = 0.5)
fit <- fitBmme(dat)
fit
```

fitMovRes

Fit a Moving-Resting Model with Embedded Brownian Motion

Description

Fit a Moving-Resting Model with Embedded Brownian Motion with animal movement data at discretely observation times by maximizing a composite likelihood constructed from the marginal density of increment.

Usage

```
fitMovRes(data, start, likelihood = c("full", "composite"), logtr = FALSE,
  method = "Nelder-Mead", optim.control = list(),
  integrControl = integr.control())
```

Arguments

data	a data.frame whose first column is the observation time, and other columns are location coordinates.
start	starting value of the model, a vector of three components in the order of rate for moving, rate for resting, and volatility.
likelihood	a character string specifying the likelihood type to maximize in estimation. This can be "full" for full likelihood or "composite" for composite likelihood. full loglikelihood from hidden Markov model approach.
logtr	logical, if TRUE parameters are estimated on the log scale.
method	the method argument to feed optim.
optim.control	a list of control to be passed to optim.
integrControl	a list of control parameters for the integrate function: rel.tol, abs.tol, subdivision.

Value

a list of the following components:

estimate	the estimated parameter vector
loglik	maximized loglikelihood or composite loglikelihood evaluated at the estimate
convergence	convergence code from optim
likelihood	likelihood type (full or composite) from the input

References

Yan, J., Chen, Y., Lawrence-Apfel, K., Ortega, I. M., Pozdnyakoc, V., Williams, S., and Meyer, T. (2014) A moving-resting process with an embedded Brownian motion for animal movements. *Population Ecology*. 56(2): 401–415.

Examples

```
tgrid <- seq(0, 10, length=500)
set.seed(123)
## make it irregularly spaced
tgrid <- sort(sample(tgrid, 30)) # change to 400 for a larger sample
dat <- rMovRes(tgrid, 1, 2, 25, "m")

fit.fl <- fitMovRes(dat, start=c(2, 2, 20), likelihood = "full")
fit.fl

fit.cl <- fitMovRes(dat, start=c(2, 2, 20), likelihood = "composite")
fit.cl
## Not run:
## old, very slow, unexported R code
fit.<- smam::fitMovRes.cl(dat, start=c(2, 2, 2))
fit.cpp

## End(Not run)
```

integr.control	<i>Auxiliary for Controlling Numerical Integration</i>
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Description

Auxiliary function for the numerical integration used in the likelihood and composite likelihood functions. Typically only used internally by 'fitMovRes'.

Usage

```
integr.control(rel.tol = .Machine$double.eps^0.25, abs.tol = rel.tol,
  subdivisions = 100L)
```

Arguments

rel.tol	relative accuracy requested.
abs.tol	absolute accuracy requested.
subdivisions	the maximum number of subintervals.

Details

The arguments are the same as `integrate`, but passed down to the C API of `Rdqags` used by `integrate`.

Value

A list with components named as the arguments.

rbmme	<i>Sampling from Brown Motion with Measurement Error</i>
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Description

Given the volatility parameters of a Brownian motion and normally distributed measurement errors, generate the process at discretely observed time points of a given dimension.

Usage

```
rbmme(time, dim = 2, sigma = 1, delta = 1)
```

Arguments

time	vector of time points at which observations are to be sampled
dim	(integer) dimension of the Brownian motion
sigma	volatility parameter (sd) of the Brownian motion
delta	sd parameter of measurement error

Value

A data.frame whose first column is the time points and whose other columns are coordinates of the locations.

References

Pozdnyakov V., Meyer, TH., Wang, Y., and Yan, J. (2013) On modeling animal movements using Brownian motion with measurement error. *Ecology* 95(2): p247–253. doi:doi:10.1890/13-0532.1.

Examples

```
tgrid <- seq(0, 10, length = 1001)
## make it irregularly spaced
tgrid <- sort(sample(tgrid, 800))
dat <- rbmme(tgrid, 1, 1)
plot(dat[,1], dat[,2], xlab="t", ylab="X(t)", type="l")
```

rMovRes

Sampling from a Moving-Resting Process with Embedded Brownian Motion

Description

A moving-resting process consists of two states: moving and resting. The transition between the two states is modeled by an alternating renewal process, with exponentially distributed duration. An animal stays at the same location while resting, and moves according to a Brownian motion while moving.

Usage

```
rMovRes(time, lamM, lamR, sigma, s0, dim = 2)
```

Arguments

time	time points at which observations are to be simulated
lamM	rate parameter of the exponential duration while moving
lamR	rate parameter of the exponential duration while resting
sigma	volatility parameter of the Brownian motion while moving
s0	the state at time 0, must be one of "m" or "r", for moving and resting, respectively
dim	(integer) dimension of the Brownian motion

Value

A data.frame whose first column is the time points and whose other columns are coordinates of the locations.

References

Yan, J., Chen, Y., Lawrence-Apfel, K., Ortega, I. M., Pozdnyakoc, V., Williams, S., and Meyer, T. (2014) A moving-resting process with an embedded Brownian motion for animal movements. *Population Ecology*. 56(2): 401–415.

Examples

```
tgrid <- seq(0, 10, length=1001)
## make it irregularly spaced
tgrid <- sort(sample(tgrid, 800))
dat <- rMovRes(tgrid, 1, 1, 1, "m")
plot(dat[,1], dat[,2], xlab="t", ylab="X(t)", type='l')
```


Index

dtm, [2](#)

dtr (dtm), [2](#)

fitBmme, [3](#)

fitMovRes, [4](#), [4](#)

integr.control, [6](#)

rbmme, [6](#)

rMovRes, [7](#)