Package 'smam'

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Type Package

Title Statistical Modeling of Animal Movements

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Depends R (>= 3.0.0), Matrix

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

License GPL (>= 3.0)

NeedsCompilation yes

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R topics documented:

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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   the length of the time interval

lamM   the rate parameter of the exponentially distributed moving stage duration

lamR   the rate parameter of the exponentially distributed resting stage duration

s0   the 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.

Value

a vector of the density evaluated at w

Author(s)

Jun Yan <jun.yan@uconn.edu>

References

Yan, J., Chen, Y., Lawrence-Apfel, K., Ortega, I. M., Pozdnyakoc, V., Williams, S., and Meyer, T. (2013+) A moving-resting process with an embedded Brownian motion for animal movements. Population Ecology. Forthcoming.

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(dat, start = NULL, method = "Nelder-Mead", optim.control = list())
```

Arguments

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

Author(s)

Jun Yan <jun.yan@uconn.edu>

References

Pozdnyakov V., Meyer, TH., Wang, Y., and Yan, J. (2013) On modeling animal movements using Brownian motion with measurement error. Ecology 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, method = "Nelder-Mead", optim.control = list())
cllk.m1(theta, data)
```

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 component, which represents two rate parameters of moving and resting duration, and one volatility parameter for the Brownian motion.
method	the method argument to feed optim.
optim.control	a list of control that if passed down to optim.
theta	a parameter vector of three components (similar to start)

Value

fitMovRes returns a list of the following components:

estimate	the esimated parameter vector
cloglik	composite loglikelihood evaluated at the estimate
convergence	convergence code from optim

cllk.m1 returns the composite loglikelihood constructed from the marginal distribution of each increment.

Author(s)

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References

Yan, J., Chen, Y., Lawrence-Apfel, K., Ortega, I. M., Pozdnyakoc, V., Williams, S., and Meyer, T. (2013+) A moving-resting process with an embedded Brownian motion for animal movements. Population Ecology. Forthcoming.

Examples

```
tgrid <- seq(0, 10, length=2001)
## make it irregularly spaced
tgrid <- sort(sample(tgrid, 1000))
set.seed(123)
dat <- rMovRes(tgrid, 1, 1, 1, "m")
## Not run:
fit <- fitMovRes(dat, start=c(2, 2, 2))
fit

## End(Not run)
```

---

rbmme   *Sampling from Brown Motion with Measurement Error*

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	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.

Author(s)

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References

Pozdnyakov V., Meyer, TH., Wang, Y., and Yan, J. (2013) On modeling animal movements using Brownian motion with measurement error. Ecology 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 expenentially 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	the 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.

Author(s)

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References

Yan, J., Chen, Y., Lawrence-Apfel, K., Ortega, I. M., Pozdnyakoc, V., Williams, S., and Meyer, T. (2013+) A moving-resting process with an embedded Brownian motion for animal movements. Population Ecology. Forthcoming.

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