

Package ‘moveHMM’

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Type Package

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Description Provides tools for animal movement modelling using hidden Markov models.
These include processing of tracking data, fitting HMMs to movement data, visualization of data and fitted model, decoding of the state process...

URL <https://github.com/TheoMichelot/moveHMM>,
<https://cran.r-project.org/package=moveHMM>

License GPL-3

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AIC.moveHMM

AIC

Description

Akaike information criterion of a moveHMM model.

Usage

```
## S3 method for class 'moveHMM'
AIC(object, ..., k = 2)
```

Arguments

object	A moveHMM object.
...	Optional additional moveHMM objects, to compare AICs of the different models.
k	Penalty per parameter. Default: 2 ; for classical AIC.

Value

The AIC of the model(s) provided. If several models are provided, the AICs are output in ascending order.

Examples

```
# m is a moveHMM object (as returned by fitHMM), automatically loaded with the package
m <- example$m
AIC(m)
```

allProbs	<i>Matrix of all probabilities</i>
----------	------------------------------------

Description

Used in functions [viterbi](#), [logAlpha](#), [logBeta](#).

Usage

```
allProbs(data, nbStates, stepDist, angleDist, stepPar, anglePar = NULL,
         zeroInflation = FALSE)
```

Arguments

data	Object moveData.
nbStates	Number of states of the HMM.
stepDist	Name of the distribution of the step lengths.
angleDist	Name of the distribution of the turning angles. Set to "none" if the angle distribution should not be estimated.
stepPar	Parameters of the step length distribution. Must be provided in a matrix with one row for each parameter (in the order expected by the pdf of stepDist), and one column for each state.
anglePar	Parameters of the turning angle distribution. Must be provided in a matrix with one row for each parameter (in the order expected by the pdf of angleDist), and one column for each state. Default: NULL ; if the turning angles distribution is not estimated.
zeroInflation	TRUE if the step length distribution is inflated in zero. Default: FALSE.

Value

Matrix of all probabilities.

Examples

```
## Not run:
stepPar <- c(1,10,1,5,0.2,0.3)
anglePar <- c(0,pi,0.5,2)
stepDist <- "gamma"
angleDist <- "vm"
data <- simData(nbAnimals=5,nbStates=2,stepDist=stepDist,angleDist=angleDist,stepPar=stepPar,
               anglePar=anglePar,nbCovs=2,zeroInflation=TRUE)
P <- allProbs(data=data,nbStates=2,stepDist=stepDist,angleDist=angleDist,
              stepPar=matrix(stepPar,ncol=2,byrow=TRUE),anglePar=matrix(anglePar,ncol=2,
                                byrow=TRUE),zeroInflation=TRUE)

## End(Not run)
```

angleCI

Confidence intervals for angle parameters

Description

Simulation-based computation of confidence intervals for the parameters of the angle distribution. Used in [CI](#).

Usage

```
angleCI(m, alpha, nbSims = 10^6)
```

Arguments

m	A moveHMM object
alpha	Range of the confidence intervals. Default: 0.95 (i.e. 95% CIs).
nbSims	Number of simulations. Default: 10 ⁶ .

Value

A list of the following objects:

lower	Lower bound of the confidence interval for the parameters of the angle distribution
upper	Upper bound of the confidence interval for the parameters of the angle distribution

CI	<i>Confidence intervals</i>
----	-----------------------------

Description

Computes the confidence intervals of the step length and turning angle parameters, as well as for the transition probabilities regression parameters.

Usage

```
CI(m, alpha = 0.95, nbSims = 10^6)
```

Arguments

m	A moveHMM object
alpha	Range of the confidence intervals. Default: 0.95 (i.e. 95% CIs).
nbSims	Number of simulations in the computation of the CIs for the angle parameters. Default: 10^6 .

Value

A list of the following objects:

stepPar	Confidence intervals for the parameters of the step lengths distribution
anglePar	Confidence intervals for the parameters of the turning angles distribution
beta	Confidence intervals for the regression coefficients of the transition probabilities.

Examples

```
# m is a moveHMM object (as returned by fitHMM), automatically loaded with the package  
m <- example$m
```

```
CI(m)
```

`dexp_rcpp`*Exponential density function*

Description

Probability density function of the exponential distribution (written in C++)

Usage

```
dexp_rcpp(x, rate, foo = 0)
```

Arguments

<code>x</code>	Vector of quantiles
<code>rate</code>	Rate
<code>foo</code>	Unused (for compatibility with template)

Value

Vector of densities

`dgamma_rcpp`*Gamma density function*

Description

Probability density function of the gamma distribution (written in C++)

Usage

```
dgamma_rcpp(x, mu, sigma)
```

Arguments

<code>x</code>	Vector of quantiles
<code>mu</code>	Mean
<code>sigma</code>	Standard deviation

Value

Vector of densities

dlnorm_rcpp	<i>Log-normal density function</i>
-------------	------------------------------------

Description

Probability density function of the log-normal distribution (written in C++)

Usage

```
dlnorm_rcpp(x, meanlog, sdlog)
```

Arguments

x	Vector of quantiles
meanlog	Mean of the distribution on the log-scale
sdlog	Standard deviation of the distribution on the log-scale

Value

Vector of densities

dvm_rcpp	<i>Von Mises density function</i>
----------	-----------------------------------

Description

Probability density function of the Von Mises distribution, defined as a function of the modified Bessel function of order 0 (written in C++)

Usage

```
dvm_rcpp(x, mu, kappa)
```

Arguments

x	Vector of quantiles
mu	Mean
kappa	Concentration

Value

Vector of densities

`dweibull_rcpp`*Weibull density function*

Description

Probability density function of the Weibull distribution (written in C++)

Usage

```
dweibull_rcpp(x, shape, scale)
```

Arguments

<code>x</code>	Vector of quantiles
<code>shape</code>	Shape
<code>scale</code>	Scale

Value

Vector of densities

`dwrpcauchy_rcpp`*Wrapped Cauchy density function*

Description

Probability density function of the wrapped Cauchy distribution (written in C++)

Usage

```
dwrpcauchy_rcpp(x, mu, rho)
```

Arguments

<code>x</code>	Vector of quantiles
<code>mu</code>	Mean
<code>rho</code>	Concentration

Value

Vector of densities

example	<i>Example dataset</i>
---------	------------------------

Description

This data is generated by the function [exGen](#), and used in the examples and tests of other functions to keep them as short as possible.

Usage

```
example
```

Details

It is a list of the following objects:

- data A [moveData](#) object
- m A [moveHMM](#) object
- simPar The parameters used to simulate data
- par0 The initial parameters in the optimization to fit m

exGen	<i>Example data simulation</i>
-------	--------------------------------

Description

Generate the file `data/example.RData`, used in other functions' examples and unit tests.

Usage

```
exGen()
```

fitHMM

*Fit an HMM to the data***Description**

Fit an hidden Markov model to the data provided, using numerical optimization of the log-likelihood function.

Usage

```
fitHMM(data, nbStates, stepPar0, anglePar0, beta0 = NULL, delta0 = NULL,
        formula = ~1, stepDist = c("gamma", "weibull", "lnorm", "exp"),
        angleDist = c("vm", "wrpcauchy", "none"), angleMean = NULL,
        stationary = FALSE, verbose = 0, nlmPar = NULL, fit = TRUE)
```

Arguments

data	An object moveData.
nbStates	Number of states of the HMM.
stepPar0	Vector of initial state-dependent step length distribution parameters. The parameters should be in the order expected by the pdf of stepDist, and the zero-mass parameter should be the last. Note that zero-mass parameters are mandatory if there are steps of length zero in the data. For example, for a 2-state model using the gamma distribution and including zero-inflation, the vector of initial parameters would be something like: c(mu1, mu2, sigma1, sigma2, zeromass1, zeromass2).
anglePar0	Vector of initial state-dependent turning angle distribution parameters. The parameters should be in the order expected by the pdf of angleDist. For example, for a 2-state model using the Von Mises (vm) distribution, the vector of initial parameters would be something like: c(mu1, mu2, kappa1, kappa2).
beta0	Initial matrix of regression coefficients for the transition probabilities (more information in "Details"). Default: NULL. If not specified, beta0 is initialized such that the diagonal elements of the transition probability matrix are dominant.
delta0	Initial value for the initial distribution of the HMM. Default: rep(1/nbStates, nbStates).
formula	Regression formula for the covariates. Default: ~1 (no covariate effect).
stepDist	Name of the distribution of the step lengths (as a character string). Supported distributions are: gamma, weibull, lnorm, exp. Default: gamma.
angleDist	Name of the distribution of the turning angles (as a character string). Supported distributions are: vm, wrpcauchy. Set to "none" if the angle distribution should not be estimated. Default: vm.
angleMean	Vector of means of turning angles if not estimated (one for each state). Default: NULL (the angle mean is estimated).
stationary	FALSE if there are covariates. If TRUE, the initial distribution is considered equal to the stationary distribution. Default: FALSE.

<code>verbose</code>	Determines the print level of the optimizer. The default value of 0 means that no printing occurs, a value of 1 means that the first and last iterations of the optimization are detailed, and a value of 2 means that each iteration of the optimization is detailed.
<code>nlmPar</code>	List of parameters to pass to the optimization function <code>nlm</code> (which should be either <code>'gradtol'</code> , <code>'stepmax'</code> , <code>'steptol'</code> , or <code>'iterlim'</code> – see <code>nlm</code> 's documentation for more detail)
<code>fit</code>	TRUE if an HMM should be fitted to the data, FALSE otherwise. If <code>fit=FALSE</code> , a model is returned with the MLE replaced by the initial parameters given in input. This option can be used to assess the initial parameters. Default: TRUE.

Details

- The matrix `beta` of regression coefficients for the transition probabilities has one row for the intercept, plus one row for each covariate, and one column for each non-diagonal element of the transition probability matrix. For example, in a 3-state HMM with 2 covariates, the matrix `beta` has three rows (intercept + two covariates) and six columns (six non-diagonal elements in the 3x3 transition probability matrix - filled in row-wise). In a covariate-free model (default), `beta` has one row, for the intercept.
- The choice of initial parameters is crucial to fit a model. The algorithm might not find the global optimum of the likelihood function if the initial parameters are poorly chosen.

Value

A `moveHMM` object, i.e. a list of:

<code>mle</code>	The maximum likelihood estimates of the parameters of the model (if the numerical algorithm has indeed identified the global maximum of the likelihood function), which is a list of: <code>stepPar</code> (step distribution parameters), <code>anglePar</code> (angle distribution parameters), <code>beta</code> (transition probabilities regression coefficients - more information in "Details"), and <code>delta</code> (initial distribution).
<code>data</code>	The movement data
<code>stepDist</code>	The step length distribution name
<code>angleDist</code>	The turning angle distribution name
<code>mod</code>	The object returned by the numerical optimizer <code>nlm</code>
<code>conditions</code>	A few conditions used to fit the model (<code>zeroInflation</code> , <code>estAngleMean</code> , <code>stationary</code> , and <code>formula</code>)
<code>rawCovs</code>	Raw covariate values, as found in the data (if any). Used in plot.moveHMM .

References

- Patterson T.A., Basson M., Bravington M.V., Gunn J.S. 2009. Classifying movement behaviour in relation to environmental conditions using hidden Markov models. *Journal of Animal Ecology*, 78 (6), 1113-1123.
- Langrock R., King R., Matthiopoulos J., Thomas L., Fortin D., Morales J.M. 2012. Flexible and practical modeling of animal telemetry data: hidden Markov models and extensions. *Ecology*, 93 (11), 2336-2342.

Examples

```

### 1. simulate data
# define all the arguments of simData
nbAnimals <- 2
nbStates <- 2
nbCovs <- 2
mu<-c(15,50)
sigma<-c(10,20)
angleMean <- c(pi,0)
kappa <- c(0.7,1.5)
stepPar <- c(mu,sigma)
anglePar <- c(angleMean,kappa)
stepDist <- "gamma"
angleDist <- "vm"
zeroInflation <- FALSE
obsPerAnimal <- c(50,100)

data <- simData(nbAnimals=nbAnimals,nbStates=nbStates,stepDist=stepDist,angleDist=angleDist,
               stepPar=stepPar,anglePar=anglePar,nbCovs=nbCovs,zeroInflation=zeroInflation,
               obsPerAnimal=obsPerAnimal)

### 2. fit the model to the simulated data
# define initial values for the parameters
mu0 <- c(20,70)
sigma0 <- c(10,30)
kappa0 <- c(1,1)
stepPar0 <- c(mu0,sigma0) # no zero-inflation, so no zero-mass included
anglePar0 <- kappa0 # the angle mean is not estimated, so only the concentration parameter is needed
formula <- ~cov1+cos(cov2)

m <- fitHMM(data=data,nbStates=nbStates,stepPar0=stepPar0,anglePar0=anglePar0,formula=formula,
            stepDist=stepDist,angleDist=angleDist,angleMean=angleMean)

print(m)

```

is.moveData

Is moveData

Description

Check that an object is of class `moveData`. Used in `fitHMM`.

Usage

```
is.moveData(x)
```

Arguments

x An R object

Value

TRUE if x is of class `moveData`, FALSE otherwise.

is.moveHMM	<i>Is moveHMM</i>
------------	-------------------

Description

Check that an object is of class `moveHMM`. Used in `CI`, `plotPR`, `plotStates`, `pseudoRes`, `stateProbs`, and `viterbi`.

Usage

```
is.moveHMM(x)
```

Arguments

x An R object

Value

TRUE if x is of class `moveHMM`, FALSE otherwise.

logAlpha	<i>Forward log-probabilities</i>
----------	----------------------------------

Description

Used in `stateProbs` and `pseudoRes`.

Usage

```
logAlpha(m)
```

Arguments

m A `moveHMM` object.

Value

The matrix of forward log-probabilities.

Examples

```
## Not run:  
# m is a moveHMM object (as returned by fithMM), automatically loaded with the package  
m <- example$m  
  
la <- logAlpha(m)  
  
## End(Not run)
```

logBeta

Backward log-probabilities

Description

Used in [stateProbs](#).

Usage

```
logBeta(m)
```

Arguments

m A moveHMM object.

Value

The matrix of backward log-probabilities.

Examples

```
## Not run:  
# m is a moveHMM object (as returned by fithMM), automatically loaded with the package  
m <- example$m  
  
lb <- logBeta(m)  
  
## End(Not run)
```

moveData	<i>Constructor of moveData objects</i>
----------	--

Description

Constructor of moveData objects

Usage

```
moveData(data)
```

Arguments

data	A dataframe containing: ID (the ID(s) of the observed animal(s)), step (the step lengths), angle (the turning angles, if any), x (either easting or longitude), y (either northing or latitude), and covariates, if any.
------	--

Value

An object moveData.

moveHMM	<i>Constructor of moveHMM objects</i>
---------	---------------------------------------

Description

Constructor of moveHMM objects

Usage

```
moveHMM(m)
```

Arguments

m	A list of attributes of the fitted model: mle (the maximum likelihood estimates of the parameters of the model), data (the movement data), mod (the object returned by the numerical optimizer nlm), conditions (a few conditions used to fit the model: stepDist, angleDist, zeroInflation, estAngleMean, stationary, and formula), rawCovs (optional – only if there are covariates in the data).
---	---

Value

An object moveHMM.

n2w

*Scaling function: natural to working parameters.***Description**

Scales each parameter from its natural interval to the set of real numbers, to allow for unconstrained optimization. Used during the optimization of the log-likelihood.

Usage

```
n2w(par, bounds, beta, delta = NULL, nbStates, estAngleMean)
```

Arguments

par	Vector of state-dependent distributions parameters.
bounds	Matrix with 2 columns and as many rows as there are elements in par. Each row contains the lower and upper bound for the corresponding parameter.
beta	Matrix of regression coefficients for the transition probabilities.
delta	Initial distribution. Default: NULL ; if the initial distribution is not estimated.
nbStates	The number of states of the HMM.
estAngleMean	TRUE if the angle mean is estimated, FALSE otherwise.

Value

A vector of unconstrained parameters.

Examples

```
## Not run:
nbStates <- 3
par <- c(0.001,0.999,0.5,0.001,1500.3,7.1)
bounds <- matrix(c(0,1, # bounds for first parameter
                  0,1, # bounds for second parameter
                  0,1, # ...
                  0,Inf,
                  0,Inf,
                  0,Inf),
                byrow=TRUE, ncol=2)
beta <- matrix(rnorm(18), ncol=6, nrow=3)
delta <- c(0.6,0.3,0.1)

# vector of working parameters
wpar <- n2w(par=par, bounds=bounds, beta=beta, delta=delta, nbStates=nbStates,
           estAngleMean=FALSE)

## End(Not run)
```

nLogLike	<i>Negative log-likelihood function</i>
----------	---

Description

Negative log-likelihood function

Usage

```
nLogLike(wpar, nbStates, bounds, parSize, data, stepDist = c("gamma",
  "weibull", "lnorm", "exp"), angleDist = c("vm", "wrpcauchy", "none"),
  angleMean = NULL, zeroInflation = FALSE, stationary = FALSE)
```

Arguments

wpar	Vector of working parameters.
nbStates	Number of states of the HMM.
bounds	Matrix with 2 columns and as many rows as there are elements in wpar. Each row contains the lower and upper bound for the corresponding parameter.
parSize	Vector of two values: number of parameters of the step length distribution, number of parameters of the turning angle distribution.
data	An object moveData.
stepDist	Name of the distribution of the step lengths (as a character string). Supported distributions are: gamma, weibull, lnorm, exp. Default: gamma.
angleDist	Name of the distribution of the turning angles (as a character string). Supported distributions are: vm, wrpcauchy. Set to "none" if the angle distribution should not be estimated. Default: vm.
angleMean	Vector of means of turning angles if not estimated (one for each state). Default: NULL (the angle mean is estimated).
zeroInflation	TRUE if the step length distribution is inflated in zero. Default: FALSE. If TRUE, initial values for the zero-mass parameters should be included in stepPar0.
stationary	FALSE if there are covariates. If TRUE, the initial distribution is considered equal to the stationary distribution. Default: FALSE.

Value

The negative log-likelihood of the parameters given the data.

Examples

```
## Not run:
# data is a moveData object (as returned by prepData), automatically loaded with the package
data <- example$data
simPar <- example$simPar
par0 <- example$par0
```

```

estAngleMean <- is.null(simPar$angleMean)
bounds <- parDef(simPar$stepDist,simPar$angleDist,simPar$nbStates,
                 estAngleMean,simPar$zeroInflation)$bounds
parSize <- parDef(simPar$stepDist,simPar$angleDist,simPar$nbStates,
                 estAngleMean,simPar$zeroInflation)$parSize

par <- c(par0$stepPar0,par0$anglePar0)
wpar <- n2w(par,bounds,par0$beta0,par0$delta0,simPar$nbStates,FALSE)

l <- nLogLike(wpar=wpar,nbStates=simPar$nbStates,bounds=bounds,parSize=parSize,data=data,
             stepDist=simPar$stepDist,angleDist=simPar$angleDist,angleMean=simPar$angleMean,
             zeroInflation=simPar$zeroInflation)

## End(Not run)

```

nLogLike_rcpp

Negative log-likelihood

Description

Computation of the negative log-likelihood (forward algorithm - written in C++)

Usage

```
nLogLike_rcpp(nbStates, beta, covs, data, stepDist, angleDist, stepPar,
              anglePar, delta, aInd, zeroInflation = FALSE, stationary = FALSE)
```

Arguments

nbStates	Number of states
beta	Matrix of regression coefficients for the transition probabilities
covs	Covariates
data	A moveData object of the observations
stepDist	The name of the step length distribution
angleDist	The name of the turning angle distribution
stepPar	State-dependent parameters of the step length distribution
anglePar	State-dependent parameters of the turning angle distribution
delta	Stationary distribution
aInd	Vector of indices of the rows at which the data switches to another animal
zeroInflation	true if zero-inflation is included in the step length distribution, false otherwise.
stationary	false if there are covariates. If true, the initial distribution is considered equal to the stationary distribution. Default: false.

Value

Negative log-likelihood

parDef	<i>Parameters definition</i>
--------	------------------------------

Description

Parameters definition

Usage

```
parDef(stepDist, angleDist, nbStates, estAngleMean, zeroInflation)
```

Arguments

stepDist	Name of the distribution of the step lengths.
angleDist	Name of the distribution of the turning angles. Set to "none" if the angle distribution should not be estimated.
nbStates	Number of states of the HMM.
estAngleMean	TRUE if the mean of the turning angles distribution is estimated, FALSE otherwise.
zeroInflation	TRUE if the step length distribution is inflated in zero.

Value

A list of:

parSize	Vector of two values: number of parameters of the step length distribution, number of parameters of the turning angle distribution
bounds	Matrix with 2 columns and <code>sum(parSize)</code> rows - each row contains the lower and upper bound for the corresponding parameter)
parNames	Names of parameters of step distribution (the names of the parameters of the angle distribution are always the same).

plot.moveData	<i>Plot</i> moveData
---------------	----------------------

Description

Plot moveData

Usage

```
## S3 method for class 'moveData'
plot(x, animals = NULL, compact = FALSE, ask = TRUE,
     breaks = "Sturges", ...)
```

Arguments

x	An object moveData
animals	Vector of indices or IDs of animals for which information will be plotted. Default: NULL ; all animals are plotted.
compact	TRUE for a compact plot (all individuals at once), FALSE otherwise (default – one individual at a time).
ask	If TRUE, the execution pauses between each plot.
breaks	Histogram parameter. See hist documentation.
...	Currently unused. For compatibility with generic method.

Examples

```
# data is a moveData object (as returned by prepData), automatically loaded with the package
data <- example$data

plot(data, compact=TRUE, breaks=20, ask=FALSE)
```

plot.moveHMM	<i>Plot</i> moveHMM
--------------	---------------------

Description

Plot the fitted step and angle densities over histograms of the data, transition probabilities as functions of the covariates, and maps of the animals' tracks colored by the decoded states.

Usage

```
## S3 method for class 'moveHMM'
plot(x, animals = NULL, ask = TRUE, breaks = "Sturges",
     hist.ylim = NULL, sepAnimals = FALSE, sepStates = FALSE, col = NULL,
     ...)
```

Arguments

x	Object moveHMM
animals	Vector of indices or IDs of animals for which information will be plotted. Default: NULL ; all animals are plotted.
ask	If TRUE, the execution pauses between each plot.
breaks	Histogram parameter. See hist documentation.
hist.ylim	Parameter ylim for the step length histograms. See hist documentation. Default: NULL ; the function sets default values.
sepAnimals	If TRUE, the data is split by individuals in the histograms. Default: FALSE.
sepStates	If TRUE, the data is split by states in the histograms. Default: FALSE.
col	Vector or colors for the states (one color per state).
...	Currently unused. For compatibility with generic method.

Details

The state-dependent densities are weighted by the frequency of each state in the most probable state sequence (decoded with the function `viterbi`). For example, if the most probable state sequence indicates that one third of observations correspond to the first state, and two thirds to the second state, the plots of the densities in the first state are weighted by a factor 1/3, and in the second state by a factor 2/3.

Examples

```
# m is a moveHMM object (as returned by fithMM), automatically loaded with the package
m <- example$m

plot(m,ask=TRUE,animals=1,breaks=20)
```

plotPR

Plot pseudo-residuals

Description

Plots time series, qq-plots (against the standard normal distribution), and sample ACF functions of the pseudo-residuals

Usage

```
plotPR(m)
```

Arguments

m	A <code>moveHMM</code> object
---	-------------------------------

Details

- If some turning angles in the data are equal to π , the corresponding pseudo-residuals will not be included. Indeed, given that the turning angles are defined on $(-\pi, \pi]$, an angle of π results in a pseudo-residual of $+\text{Inf}$ (check Section 6.2 of reference for more information on the computation of pseudo-residuals).
- If some steps are of length zero (i.e. if there is zero-inflation), the corresponding pseudo-residuals are shown as segments, because pseudo-residuals for discrete data are defined as segments (see Zucchini and MacDonald, 2009, Section 6.2).

References

Zucchini, W. and MacDonald, I.L. 2009. Hidden Markov Models for Time Series: An Introduction Using R. Chapman & Hall (London).

Examples

```
# m is a moveHMM object (as returned by fithMM), automatically loaded with the package
m <- example$m

plotPR(m)
```

plotStates

Plot states

Description

Plot the states and states probabilities.

Usage

```
plotStates(m, animals = NULL, ask = TRUE)
```

Arguments

m	A moveHMM object
animals	Vector of indices or IDs of animals for which states will be plotted.
ask	If TRUE, the execution pauses between each plot.

Examples

```
# m is a moveHMM object (as returned by fithMM), automatically loaded with the package
m <- example$m

# plot states for first and second animals
plotStates(m, animals=c(1,2))
```

```
prepData
```

Preprocessing of the tracking data

Description

Preprocessing of the tracking data

Usage

```
prepData(trackData, type = c("LL", "UTM"), coordNames = c("x", "y"))
```

Arguments

trackData	A dataframe of the tracking data, including at least coordinates (either longitude/latitude values or cartesian coordinates), and optionnaly a field ID (identifiers for the observed individuals). Additionnal fields are considered as covariates. Note that, if the names of the coordinates are not "x" and "y", the coordNames argument should specified.
type	'LL' if longitude/latitude provided (default), 'UTM' if easting/northing.
coordNames	Names of the columns of coordinates in the data frame. Default: c("x", "y").

Value

An object moveData, i.e. a dataframe of:

ID	The ID(s) of the observed animal(s)
step	The step lengths - in kilometers if longitude/latitude provided, and in the metrics of the data otherwise
angle	The turning angles (if any) - in radians
x	Either easting or longitude
y	Either northing or latitude
...	Covariates (if any)

Examples

```
coord1 <- c(1,2,3,4,5,6,7,8,9,10)
coord2 <- c(1,1,1,2,2,2,1,1,1,2)
trackData <- data.frame(coord1=coord1, coord2=coord2)
d <- prepData(trackData, type='UTM', coordNames=c("coord1", "coord2"))
```

```
print.moveHMM          Print moveHMM
```

Description

Print moveHMM

Usage

```
## S3 method for class 'moveHMM'
print(x, ...)
```

Arguments

```
x                A moveHMM object.
...              Currently unused. For compatibility with generic method.
```

Examples

```
# m is a moveHMM object (as returned by fitHMM), automatically loaded with the package
m <- example$m

print(m)
```

```
pseudoRes            Pseudo-residuals
```

Description

The pseudo-residuals of a moveHMM model, as described in Zucchini and McDonad (2009).

Usage

```
pseudoRes(m)
```

Arguments

```
m                A moveHMM object.
```

Details

If some turning angles in the data are equal to π , the corresponding pseudo-residuals will not be included. Indeed, given that the turning angles are defined on $(-\pi, \pi]$, an angle of π results in a pseudo-residual of $+\text{Inf}$ (check Section 6.2 of reference for more information on the computation of pseudo-residuals).

Value

A list of:

stepRes	The pseudo-residuals for the step lengths
angleRes	The pseudo-residuals for the turning angles

References

Zucchini, W. and MacDonald, I.L. 2009. Hidden Markov Models for Time Series: An Introduction Using R. Chapman & Hall (London).

Examples

```
# m is a moveHMM object (as returned by fithMM), automatically loaded with the package
m <- example$m
res <- pseudoRes(m)
qqnorm(res$stepRes)
qqnorm(res$angleRes)
```

 simData

Simulation tool

Description

Simulates movement data from an HMM.

Usage

```
simData(nbAnimals = 1, nbStates = 2, stepDist = c("gamma", "weibull",
  "lnorm", "exp"), angleDist = c("vm", "wrpcauchy", "none"), stepPar = NULL,
  anglePar = NULL, beta = NULL, covs = NULL, nbCovs = 0,
  zeroInflation = FALSE, obsPerAnimal = c(500, 1500), model = NULL,
  states = FALSE)
```

Arguments

nbAnimals	Number of observed individuals to simulate.
nbStates	Number of behavioural states to simulate.
stepDist	Name of the distribution of the step lengths (as a character string). Supported distributions are: gamma, weibull, lnorm, exp. Default: gamma.
angleDist	Name of the distribution of the turning angles (as a character string). Supported distributions are: vm, wrpcauchy. Set to "none" if the angle distribution should not be estimated. Default: vm.
stepPar	Parameters of the step length distribution.
anglePar	Parameters of the turning angle distribution.

beta	Matrix of regression parameters for the transition probabilities (more information in "Details").
covs	Covariate values to include in the model, as a dataframe. Default: NULL. Covariates can also be simulated according to a standard normal distribution, by setting covs to NULL, and specifying nbCovs>0.
nbCovs	Number of covariates to simulate (0 by default). Does not need to be specified if covs is specified.
zeroInflation	TRUE if the step length distribution is inflated in zero. Default: FALSE. If TRUE, values for the zero-mass parameters should be included in stepPar.
obsPerAnimal	Either the number of the number of observations per animal (if single value), or the bounds of the number of observations per animal (if vector of two values). In the latter case, the numbers of observations generated for each animal are uniformly picked from this interval. Default: c(500, 1500).
model	A moveHMM object. This option can be used to simulate from a fitted model. Default: NULL. Note that, if this argument is specified, most other arguments will be ignored – except for nbAnimals, obsPerAnimal, covs (if covariate values different from those in the data should be specified), and states.
states	TRUE if the simulated states should be returned, FALSE otherwise (default).

Details

- The matrix beta of regression coefficients for the transition probabilities has one row for the intercept, plus one row for each covariate, and one column for each non-diagonal element of the transition probability matrix. For example, in a 3-state HMM with 2 covariates, the matrix beta has three rows (intercept + two covariates) and six columns (six non-diagonal elements in the 3x3 transition probability matrix - filled in row-wise). In a covariate-free model (default), beta has one row, for the intercept.
- If the length of covariate values passed (either through 'covs', or 'model') is not the same as the number of observations suggested by 'nbAnimals' and 'obsPerAnimal', then the series of covariates is either shortened (removing last values - if too long) or extended (starting over from the first values - if too short).

Value

An object moveData, i.e. a dataframe of:

ID	The ID(s) of the observed animal(s)
step	The step lengths
angle	The turning angles (if any)
x	Either easting or longitude
y	Either northing or latitude
...	Covariates (if any)

Examples

```

# 1. Pass a fitted model to simulate from
# (m is a moveHMM object - as returned by fithMM - automatically loaded with the package)
# We keep the default nbAnimals=1.
m <- example$m
obsPerAnimal=c(50,100)
data <- simData(model=m,obsPerAnimal=obsPerAnimal)

# 2. Pass the parameters of the model to simulate from
stepPar <- c(1,10,1,5,0.2,0.3) # mean1, mean2, sd1, sd2, z1, z2
anglePar <- c(pi,0,0.5,2) # mean1, mean2, k1, k2
stepDist <- "gamma"
angleDist <- "vm"
data <- simData(nbAnimals=5,nbStates=2,stepDist=stepDist,angleDist=angleDist,stepPar=stepPar,
               anglePar=anglePar,nbCovs=2,zeroInflation=TRUE,obsPerAnimal=obsPerAnimal)

stepPar <- c(1,10,1,5) # mean1, mean2, sd1, sd2
anglePar <- c(pi,0,0.5,0.7) # mean1, mean2, k1, k2
stepDist <- "weibull"
angleDist <- "wrpcauchy"
data <- simData(nbAnimals=5,nbStates=2,stepDist=stepDist,angleDist=angleDist,stepPar=stepPar,
               anglePar=anglePar,obsPerAnimal=obsPerAnimal)

# step length only and zero-inflation
stepPar <- c(1,10,1,5,0.2,0.3) # mean1, mean2, sd1, sd2, z1, z2
stepDist <- "gamma"
data <- simData(nbAnimals=5,nbStates=2,stepDist=stepDist,angleDist="none",stepPar=stepPar,
               nbCovs=2,zeroInflation=TRUE,obsPerAnimal=obsPerAnimal)

# include covariates
# (note that it is useless to specify "nbCovs", which respectively determined
# by the number of columns of "cov")
cov <- data.frame(temp=rnorm(500,20,5))
stepPar <- c(1,10,1,5) # mean1, mean2, sd1, sd2
anglePar <- c(pi,0,0.5,2) # mean1, mean2, k1, k2
stepDist <- "gamma"
angleDist <- "vm"
data <- simData(nbAnimals=5,nbStates=2,stepDist=stepDist,angleDist=angleDist,stepPar=stepPar,
               anglePar=anglePar,covs=cov)

```

stateProbs

State probabilities

Description

For a given model, computes the probability of the process being in the different states at each time point.

Usage

```
stateProbs(m)
```

Arguments

`m` A moveHMM object.

Value

The matrix of state probabilities, with element $[i,j]$ the probability of being in state j in observation i .

References

Zucchini, W. and MacDonald, I.L. 2009. Hidden Markov Models for Time Series: An Introduction Using R. Chapman & Hall (London).

Examples

```
# m is a moveHMM object (as returned by fitHMM), automatically loaded with the package
m <- example$m

sp <- stateProbs(m)
```

summary.moveData	<i>Summary</i> moveData
------------------	-------------------------

Description

Summary moveData

Usage

```
## S3 method for class 'moveData'
summary(object, details = TRUE, ...)
```

Arguments

`object` A moveData object.

`details` TRUE if quantiles of the covariate values should be printed (default), FALSE otherwise.

`...` Currently unused. For compatibility with generic method.

Examples

```
# m is a moveData object (as returned by prepData), automatically loaded with the package
data <- example$data

summary(data)
```

trMatrix_rcpp	<i>Transition probability matrix</i>
---------------	--------------------------------------

Description

Computation of the transition probability matrix, as a function of the covariates and the regression parameters. Written in C++. Used in [viterbi](#).

Usage

```
trMatrix_rcpp(nbStates, beta, covs)
```

Arguments

nbStates	Number of states
beta	Matrix of regression parameters
covs	Matrix of covariate values

Value

Three dimensional array trMat, such that trMat[, , t] is the transition matrix at time t.

turnAngle	<i>Turning angle</i>
-----------	----------------------

Description

Used in [prepData](#).

Usage

```
turnAngle(x, y, z)
```

Arguments

x	First point
y	Second point
z	Third point

Value

The angle between vectors (x,y) and (y,z)

Examples

```
## Not run:  
x <- c(0,0)  
y <- c(4,6)  
z <- c(10,7)  
turnAngle(x,y,z)  
  
## End(Not run)
```

viterbi

Viterbi algorithm

Description

For a given model, reconstructs the most probable states sequence, using the Viterbi algorithm.

Usage

```
viterbi(m)
```

Arguments

m An object moveHMM

Value

The sequence of most probable states.

References

Zucchini, W. and MacDonald, I.L. 2009. Hidden Markov Models for Time Series: An Introduction Using R. Chapman & Hall (London).

Examples

```
# m is a moveHMM object (as returned by fithMM), automatically loaded with the package  
m <- example$m  
  
# reconstruction of states sequence  
states <- viterbi(m)
```

w2n *Scaling function: working to natural parameters*

Description

Scales each parameter from the set of real numbers, back to its natural interval. Used during the optimization of the log-likelihood.

Usage

```
w2n(wpar, bounds, parSize, nbStates, nbCovs, estAngleMean, stationary)
```

Arguments

wpar	Vector of state-dependent distributions unconstrained parameters.
bounds	Matrix with 2 columns and as many rows as there are elements in wpar. Each row contains the lower and upper bound for the corresponding parameter.
parSize	Vector of two values: number of parameters of the step length distribution, number of parameters of the turning angle distribution.
nbStates	The number of states of the HMM.
nbCovs	The number of covariates.
estAngleMean	TRUE if the angle mean is estimated, FALSE otherwise.
stationary	FALSE if there are covariates. If TRUE, the initial distribution is considered equal to the stationary distribution. Default: FALSE.

Value

A list of:

stepPar	Matrix of natural parameters of the step length distribution
anglePar	Matrix of natural parameters of the turning angle distribution
beta	Matrix of regression coefficients of the transition probabilities
delta	Initial distribution

Examples

```
## Not run:
nbStates <- 3
nbCovs <- 2
par <- c(0.001, 0.999, 0.5, 0.001, 1500.3, 7.1)
parSize <- c(1, 1)
bounds <- matrix(c(0, 1, 0, 1, 0, 1,
                  0, Inf, 0, Inf, 0, Inf),
                 byrow=TRUE, ncol=2)
beta <- matrix(rnorm(18), ncol=6, nrow=3)
delta <- c(0.6, 0.3, 0.1)
```

```
wpar <- n2w(par,bounds,beta,delta,nbStates,FALSE)
print(w2n(wpar,bounds,parSize,nbStates,nbCovs,estAngleMean=FALSE,stationary=FALSE))

## End(Not run)
```

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