Package ‘momentuHMM’

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Type Package

Title Maximum Likelihood Analysis of Animal Movement Behavior Using Multivariate Hidden Markov Models

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Description Extended tools for analyzing telemetry data using generalized hidden Markov models. These include data pre-processing and visualization, fitting HMMs to location and auxiliary biotelemetry or environmental data, biased and correlated random walk movement models, multiple imputation for incorporating location measurement error and missing data, user-specified design matrices and constraints for covariate modelling of parameters, decoding of the state process, visualization of fitted models, model checking and selection, and simulation. See McClintock and Michelot (2017) <doi:10.1111/2041-210X.12995>.

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LazyData TRUE

Imports Rcpp, doParallel, foreach, numDeriv, CircStats, crawl, ggmap, ggplot2, mitools, moveHMM, raster, argosfilter, car, mvtnorm, boot, sp, MASS, Brobdingnag, gstat, conicfit, nleqslv, survival, qdapRegex, geosphere, LaplacesDemon, prodlim, dplyr, magrittr

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R topics documented:

`AIC.momentuHMM` *AIC*

Description

Akaike information criterion of momentuHMM model(s).

Usage

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

Arguments

object	A momentuHMM object.
...	Optional additional momentuHMM objects, to compare AICs of the different models.
k	Penalty per parameter. Default: 2 ; for classical AIC.
n	Optional sample size. If specified, the small sample correction AIC is used (i.e., `AICc = AIC + kp(p+1)/(n-p-1)` where p is the number of parameters).

Value

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

Examples

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

AICweights — *Calculate Akaike information criterion model weights*

Description

Calculate Akaike information criterion model weights

Usage

```
AICweights(..., k = 2, n = NULL)
```

Arguments

...	momentuHMM, HMMfits, or miHMM objects, to compare AIC weights of the different models.
k	Penalty per parameter. Default: 2 ; for classical AIC.
n	Optional sample size. If specified, the small sample correction AIC is used (i.e., `AICc = AIC + kp(p+1)/(n-p-1)` where p is the number of parameters).

Details

- Model objects must all be either of class momentuHMM or multiple imputation model objects (of class HMMfits and/or miHMM).
- AIC is only valid for comparing models fitted to the same data. The data for each model fit must therefore be identical. For multiple imputation model objects, respective model fits must have identical data.

Value

The AIC weights of the models. If multiple imputation objects are provided, then the mean model weights (and standard deviations) are provided.

Examples

```
## Not run:
# HMM specifications
nbStates <- 2
stepDist <- "gamma"
angleDist <- "vm"
mu0 <- c(20,70)
sigma0 <- c(10,30)
kappa0 <- c(1,1)
stepPar0 <- c(mu0,sigma0)
anglePar0 <- c(-pi/2,pi/2,kappa0)
formula <- ~cov1+cov2

# example$m is a momentuHMM object (as returned by fitHMM), automatically loaded with the package
mod1 <- fitHMM(example$m$data,nbStates=nbStates,dist=list(step=stepDist,angle=angleDist),
                Par0=list(step=stepPar0,angle=anglePar0),
                formula=~1,estAngleMean=list(angle=TRUE))

Par0 <- getPar0(mod1,formula=formula)
mod2 <- fitHMM(example$m$data,nbStates=nbStates,dist=list(step=stepDist,angle=angleDist),
                Par0=Par0$Par,beta0=Par0$beta,
                formula=formula,estAngleMean=list(angle=TRUE))

AICweights(mod1,mod2)

## End(Not run)
```

---

allProbs *Matrix of all probabilities*

Description

Used in functions viterbi, logAlpha, logBeta.

Usage

```
allProbs(m, nbStates)
```

Arguments

m	Object momentuHMM or miSum.
nbStates	Number of states of the HMM.

Value

Matrix of all probabilities.

Examples

```
## Not run:
P <- momentuHMM:::allProbs(m=example$m,nbStates=2)

## End(Not run)
```

---

checkPar0 *Check parameter length and order for a fitHMM (or MIfitHMM) model*

Description

Prints parameters with labels based on DM, formula, and/or formulaDelta. See fitHMM for further argument details.

Usage

```
checkPar0(data, nbStates, dist, Par0 = NULL, beta0 = NULL, delta0 = NULL,
  estAngleMean = NULL, circularAngleMean = NULL, formula = ~1,
  formulaDelta = ~1, stationary = FALSE, DM = NULL, cons = NULL,
  userBounds = NULL, workBounds = NULL, workcons = NULL,
  stateNames = NULL, fixPar = NULL)
```

Arguments

data	momentuHMMData object or a data frame containing the data stream and covariate values
nbStates	Number of states of the HMM.
dist	A named list indicating the probability distributions of the data streams.
Par0	Optional named list containing vectors of state-dependent probability distribution parameters for each data stream specified in dist. If Par0 is not provided, then ordered parameter indices are returned.
beta0	Optional matrix of regression coefficients for the transition probabilities. If beta0 is not provided, then ordered parameter indices are returned.
delta0	Optional values or regression coefficients for the initial distribution of the HMM. If delta0 is not provided, then ordered parameter indices are returned.
estAngleMean	An optional named list indicating whether or not to estimate the angle mean for data streams with angular distributions ('vm' and 'wrpcauchy').
circularAngleMean	An optional named list indicating whether to use circular-linear (FALSE) or circular-circular (TRUE) regression on the mean of circular distributions ('vm' and 'wrpcauchy') for turning angles.

formula	Regression formula for the transition probability covariates.
formulaDelta	Regression formula for the initial distribution.
stationary	FALSE if there are covariates in formula or formulaDelta. If TRUE, the initial distribution is considered equal to the stationary distribution. Default: FALSE.
DM	An optional named list indicating the design matrices to be used for the probability distribution parameters of each data stream.
cons	Deprecated: please use workBounds instead. An optional named list of vectors specifying a power to raise parameters corresponding to each column of the design matrix for each data stream.
userBounds	An optional named list of 2-column matrices specifying bounds on the natural (i.e, real) scale of the probability distribution parameters for each data stream.
workBounds	An optional named list of 2-column matrices specifying bounds on the working scale of the probability distribution, transition probability, and initial distribution parameters.
workcons	Deprecated: please use workBounds instead. An optional named list of vectors specifying constants to add to the regression coefficients on the working scale for each data stream.
stateNames	Optional character vector of length nbStates indicating state names.
fixPar	An optional list of vectors indicating parameters which are assumed known prior to fitting the model.

See Also

fitHMM, MIfitHMM

Examples

```
m <- example$m
checkPar0(data=m$data, nbStates=2, dist=m$conditions$dist,
          estAngleMean = m$conditions$estAngleMean,
          formula = m$conditions$formula)

par <- getPar(m)
checkPar0(data=m$data, nbStates=2, dist=m$conditions$dist,
          estAngleMean = m$conditions$estAngleMean,
          formula = m$conditions$formula,
          Par0=par$Par, beta0=par$beta, delta0=par$delta)

dummyDat <- data.frame(step=0,angle=0,cov1=0,cov2=0)
checkPar0(data=dummyDat, nbStates=2, dist=m$conditions$dist,
          estAngleMean = m$conditions$estAngleMean,
          formula = m$conditions$formula)

## Not run:
simDat <- simData(nbStates=2, dist=m$conditions$dist, Par = par$Par,
                  spatialCovs = list(forest=forest),
                  centers = matrix(0,1,2),
                  nbCovs = 2)
```

```
checkPar0(data = simDat, nbStates=2, dist=m$conditions$dist,
          formula = ~forest,
          DM = list(step=list(mean=~cov1, sd=~cov2),
                    angle=list(mean=~center1.angle,concentration=~1)),
          estAngleMean=list(angle=TRUE),
          circularAngleMean=list(angle=TRUE))

par <- list(step=rnorm(8),angle=rnorm(4))
beta0 <- matrix(rnorm(4),2,2)
delta0 <- c(0.5,0.5)
checkPar0(data = simDat, nbStates=2, dist=m$conditions$dist,
          Par0 = par, beta0 = beta0, delta0 = delta0,
          formula = ~forest,
          DM = list(step=list(mean=~cov1, sd=~cov2),
                    angle=list(mean=~center1.angle,concentration=~1)),
          estAngleMean=list(angle=TRUE),
          circularAngleMean=list(angle=TRUE))

## End(Not run)
```

CIbeta *Confidence intervals for working (i.e., beta) parameters*

Description

Computes the standard errors and confidence intervals on the beta (i.e., working) scale of the data stream probability distribution parameters, as well as for the transition probabilities regression parameters. Working scale depends on the real (i.e., natural) scale of the parameters. For non-circular distributions or for circular distributions with `estAngleMean`=FALSE:

Usage

```
CIbeta(m, alpha = 0.95)
```

Arguments

`m`	A `momentuHMM` object
`alpha`	Significance level of the confidence intervals. Default: 0.95 (i.e. 95% CIs).

Details

1) if both lower and upper bounds are finite then logit is the working scale; 2) if lower bound is finite and upper bound is infinite then log is the working scale.

For circular distributions with `estAngleMean`=TRUE and no constraints imposed by a design matrix (DM) or bounds (userBounds), then the working parameters are complex functions of both the angle mean and concentrations/sd natural parameters (in this case, it's probably best just to focus on the real parameter estimates!). However, if constraints are imposed by DM or userBounds on circular distribution parameters with `estAngleMean`=TRUE and `circularAngleMean`=FALSE:

1) if the natural bounds are (-pi,pi] then tangent is the working scale, otherwise if both lower and upper bounds are finite then logit is the working scale; 2) if lower bound is finite and upper bound is infinite then log is the working scale.

When circular-circular regression is specified using `circularAngleMean`, the working scale for the mean turning angle is not as easily interpretable, but the link function is atan2(sin(X)*B,1+cos(X)*B), where X are the angle covariates and B the angle coefficients. Under this formulation, the reference turning angle is 0 (i.e., movement in the same direction as the previous time step). In other words, the mean turning angle is zero when the coefficient(s) B=0.

Value

A list of the following objects:

`...` List(s) of estimates ('est'), standard errors ('se'), and confidence intervals ('lower', 'upper') for the working parameters of the data streams

`beta` List of estimates ('est'), standard errors ('se'), and confidence intervals ('lower', 'upper') for the working parameters of the transition probabilities

Examples

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

CIbeta(m)
```

---

circAngles — *Convert standard direction angles (in radians relative to the x-axis) to turning angle covariates suitable for circular-circular regression on the angle mean*

Description

This function can be used to convert angular covariates (e.g., ocean currents, wind direction) measured in radians relative to the x-axis to turning angle covariates sutiable for circular-circular regression in `fitHMM` or `MIfitHMM`.

Usage

```
circAngles(refAngle, data, coordNames = c("x", "y"))
```

Arguments

`refAngle` Numeric vector of standard direction angles (in radians) relative to the x-axis, where 0 = east, pi/2 = north, pi = west, -pi/2 = south

`data` data frame containing fields for the x- and y-coordinates (identified by `coordNames`) and 'ID' (if more than one individual)

`coordNames` Names of the columns of coordinates in `data`. Default: `c("x","y")`.

Value

A vector of turning angles between the movement direction at time step t-1 and `refAngle` at time t

Examples

```
# extract data from momentuHMM example
data<-example$m$data

# generate fake angle covariates
u <- rnorm(nrow(data)) # horizontal component
v <- rnorm(nrow(data)) # vertical component
refAngle <- atan2(v,u)

# add turning angle covariate to data
data$cov3 <- circAngles(refAngle=refAngle,data=data)
```

`CIreal` *Confidence intervals for the natural (i.e., real) parameters*

Description

Computes the standard errors and confidence intervals on the real (i.e., natural) scale of the data stream probability distribution parameters, as well as for the transition probabilities parameters. If covariates are included in the probability distributions or TPM formula, the mean values of non-factor covariates are used for calculating the natural parameters. For any covariate(s) of class 'factor', then the value(s) from the first observation in the data are used.

Usage

```
CIreal(m, alpha = 0.95, covs = NULL)
```

Arguments

`m`	A `momentuHMM` object
`alpha`	Significance level of the confidence intervals. Default: 0.95 (i.e. 95% CIs).
`covs`	Data frame consisting of a single row indicating the covariate values to be used in the calculations. For any covariates that are not specified using `covs`, the means of the covariate(s) are used (unless the covariate is a factor, in which case the first factor in the data is used). By default, no covariates are specified.

Value

A list of the following objects:

`...`	List(s) of estimates ('est'), standard errors ('se'), and confidence intervals ('lower', 'upper') for the natural parameters of the data streams

gamma	List of estimates ('est'), standard errors ('se'), and confidence intervals ('lower', 'upper') for the transition probabilities
delta	List of estimates ('est'), standard errors ('se'), and confidence intervals ('lower', 'upper') for the initial state probabilities

Examples

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

ci1<-CIreal(m)

# specify 'covs'
ci2<-CIreal(m,covs=data.frame(cov1=mean(m$data$cov1),cov2=mean(m$data$cov2)))

all.equal(ci1,ci2)
```

`crawlMerge` *Merge crwData object with additional data streams and/or covariates*

Description

This function can be used to merge `crwData` objects (as returned by `crawlWrap`) with additional data streams and/or covariates that are unrelated to location.

Usage

```
crawlMerge(crwData, data, Time.name)
```

Arguments

crwData	A `crwData` object
data	A data frame containing required columns `ID` and `Time.name`, plus any additional data streams and/or covariates to merge with `crwData`.
Time.name	Character string indicating name of the time column to be used for merging

Details

Specifically, the function merges the `crwData$crwPredict` data frame with `data` based on the `ID` and `Time.name` columns. Thus both `crwData$crwPredict` and `data` must contain `ID` and `Time.name` columns.

Only rows of `data` with `ID` and `Time.name` values that exactly match `crwData$crwPredict` are merged. Typically, the `Time.name` column in `data` should match predicted times of locations in `crwData$crwPredict` (i.e. those corresponding to `crwData$crwPredict$locType=="p"`)

Value

A crwData object

Examples

```
## Not run:
# extract simulated obsData from example data
obsData <- miExample$obsData

# extract crwMLE inputs from example data
inits <- miExample$inits # initial state
err.model <- miExample$err.model # error ellipse model

# Fit crwMLE models to obsData and predict locations
# at default intervals for both individuals
crwOut <- crawlWrap(obsData=obsData,
         theta=c(4,0),fixPar=c(1,1,NA,NA),
         initial.state=inits,
         err.model=err.model,attempts=100)

# create data frame with fake data stream
data <- data.frame(ID=rep(factor(c(1,2)),times=c(753,652)),
                   time=c(1:753,1:652),
                   fake=rpois(753+652,5))

# merge fake data stream with crwOut
crwOut <- crawlMerge(crwOut,data,"time")

## End(Not run)
```

---

crawlWrap *Fit and predict tracks for using crawl*

Description

Wrapper function for fitting crawl::crwMLE models and predicting locations with crawl::crwPredict for multiple individuals.

Usage

```
crawlWrap(obsData, timeStep = 1, ncores = 1, retryFits = 0,
  mov.model = ~1, err.model = NULL, activity = NULL, drift = NULL,
  coord = c("x", "y"), Time.name = "time", initial.state, theta, fixPar,
  method = "L-BFGS-B", control = NULL, constr = NULL, prior = NULL,
  need.hess = TRUE, initialSANN = list(maxit = 200), attempts = 1,
  predTime = NULL, fillCols = FALSE)
```

Arguments

obsData	data.frame object containing fields for animal ID ('ID'), time of observation (identified by Time.name, must be numeric or POSIXct), and observed locations (x- and y- coordinates identified by coord), such as that returned by simData when temporally-irregular observed locations or measurement error are included. Alternatively, a 'SpatialPointsDataFrame' object from the package 'sp' will also be accepted, in which case the coord values will be taken from the spatial data set and ignored in the arguments. Note that crwMLE requires that longitude/latitude coordinates be projected to UTM (i.e., easting/northing). For further details see crwMLE.
timeStep	Length of the time step at which to predict regular locations from the fitted model. Unless predTime is specified, the sequence of times is seq(a_i,b_i,timeStep) where a_i and b_i are the times of the first and last observations for individual i. timeStep can be numeric (regardless of whether obsData[[Time.name]] is numeric or POSIXct) or a character string (if obsData[[Time.name]] is of class POSIXct) containing one of "sec", "min", "hour", "day", "DSTday", "week", "month", "quarter" or "year". This can optionally be preceded by a positive integer and a space, or followed by "s" (e.g., "2 hours"; see seq.POSIXt). timeStep is not used for individuals for which predTime is specified.
ncores	Number of cores to use for parallel processing. Default: 1 (no parallel processing).
retryFits	Number of times to attempt to achieve convergence and valid (i.e., not NaN) variance estimates after the initial model fit. retryFits differs from attempts because retryFits iteratively uses random perturbations of the current parameter estimates as the initial values for likelihood optimization, while attempts uses the same initial values (theta) for each attempt.
mov.model	List of mov.model objects (see crwMLE) containing an element for each individual. If only one movement model is provided, then the same movement model is used for each individual.
err.model	List of err.model objects (see crwMLE) containing an element for each individual. If only one error model is provided, then the same error model is used for each individual (in which case the names of the err.model components corresponding to easting/longitudinal and northing/latitudinal location error must match coord).
activity	List of activity objects (see crwMLE) containing an element for each individual. If only one activity covariate is provided, then the same activity covariate is used for each individual.
drift	List of drift objects (see crwMLE) containing an element for each individual. If only one drift component is provided, then the same drift component is used for each individual.
coord	A 2-vector of character values giving the names of the "x" and "y" coordinates in data. See crwMLE.
Time.name	Character indicating name of the location time column. See crwMLE.
initial.state	List of initial.state objects (see crwMLE) containing an element for each individual. If only one initial state is provided, then the same initial states are used for each individual.

theta	List of theta objects (see crwMLE) containing an element for each individual. If only one theta is provided, then the same starting values are used for each individual.
fixPar	List of fixPar objects (see crwMLE) containing an element for each individual. If only one fixPar is provided, then the same parameters are held fixed to the given value for each individual.
method	Optimization method that is passed to optim.
control	Control list which is passed to optim.
constr	List of constr objects (see crwMLE) containing an element for each individual. If only one constr is provided, then the same box constraints for the parameters are used for each individual.
prior	List of prior objects (see crwMLE) containing an element for each individual. If only one prior is provided, then the same prior is used for each individual.
need.hess	A logical value which decides whether or not to evaluate the Hessian for parameter standard errors
initialSANN	Control list for optim when simulated annealing is used for obtaining start values. See details
attempts	The number of times likelihood optimization will be attempted using theta as the starting values. Note this is not the same as retryFits.
predTime	List of predTime objects (see crwPredict) containing an element for each individual. predTime can be specified as an alternative to the automatic sequences generated according to timeStep. If only one predTime object is provided, then the same prediction times are used for each individual.
fillCols	Logical indicating whether or not to use the crawl::fillCols function for filling in missing values in obsData for which there is a single unique value. Default: FALSE. If the output from crawlWrap is intended for analyses using fitHMM or MIfitHMM, setting fillCols=TRUE should typically be avoided.

Details

- Consult crwMLE and crwPredict for futher details about model fitting and prediction.
- Note that the names of the list elements corresponding to each individual in mov.model, err.model, activity, drift, initial.state, theta, fixPar, constr, prior, and predTime must match the individual IDs in obsData. If only one element is provided for any of these arguments, then the same element will be applied to all individuals.

Value

A crwData object, i.e. a list of:

crwFits	A list of crwFit objects returned by crawl::crwMLE. See crwMLE
crwPredict	A crwPredict data frame with obsData merged with the predicted locations. See crwPredict.

The crwData object is used in MIfitHMM analyses that account for temporal irregularity or location measurement error.

See Also

MIfitHMM, simData

Examples

```
## Not run:
# extract simulated obsData from example data
obsData <- miExample$obsData

# extract crwMLE inputs from example data
inits <- miExample$inits # initial state
err.model <- miExample$err.model # error ellipse model

# Fit crwMLE models to obsData and predict locations
# at default intervals for both individuals
crwOut1 <- crawlWrap(obsData=obsData,
         theta=c(4,0),fixPar=c(1,1,NA,NA),
         initial.state=inits,
         err.model=err.model,attempts=100)

# Fit the same crwMLE models and predict locations
# at same intervals but specify for each individual using lists
crwOut2 <- crawlWrap(obsData=obsData,
         theta=list(c(4,0),c(4,0)), fixPar=list(c(1,1,NA,NA),c(1,1,NA,NA)),
         initial.state=list(inits,inits),
         err.model=list(err.model,err.model),
         predTime=list('1'=seq(1,633),'2'=seq(1,686)))

## End(Not run)
```

---

crwData *Constructor of* `crwData` *objects*

Description

Constructor of `crwData` objects

Usage

```
crwData(m)
```

Arguments

m	A list of attributes of crawl output: `crwFits` (a list of crwFit objects) and `crwPredict` (a crwPredict object)

Value

An object `crwData`.

See Also

crawlWrap, MIfitHMM

crwSim *Constructor of crwSim objects*

Description

Constructor of crwSim objects

Usage

```
crwSim(m)
```

Arguments

m	A list of attributes required for multiple imputation data generated from a crwData object using MIfitHMM: miData (a list of momentuHMMData objects), and crwSimulator (a list of crwSimulator objects). crwSim objects are returned by MIfitHMM when argument miData is a crwData object and argument fit=FALSE.

Value

An object crwSim.

dbern_rcpp *Bernoulli density function*

Description

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

Usage

```
dbern_rcpp(x, prob, foo)
```

Arguments

x	Vector of quantiles
prob	success probability
foo	Unused (for compatibility with template)

Value

Vector of densities

`dbeta_rcpp` *Probability density function of the beta distribution (written in C++)*

Description

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

Usage

```
dbeta_rcpp(x, shape1, shape2)
```

Arguments

`x`	Vector of quantiles
`shape1`	Shape1
`shape2`	Shape2

Value

Vector of densities

`dexp_rcpp` *Exponential density function*

Description

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

Usage

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

Arguments

`x`	Vector of quantiles
`rate`	Rate
`foo`	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

`x`	Vector of quantiles
`mu`	Mean
`sigma`	Standard deviation

Value

Vector of densities

`distAngle` *Calculate distance between points y and z and turning angle between points x, y, and z*

Description

Calculate distance between points y and z and turning angle between points x, y, and z

Usage

```
distAngle(x, y, z, type = "UTM", angleCov = TRUE)
```

Arguments

`x`	location 1
`y`	location 2
`z`	location 3
`type`	`'UTM'` if easting/northing provided (the default), `'LL'` if longitude/latitude
`angleCov`	logical indicating to not return NA when x=y or y=z. Default: TRUE (i.e. NA is not returned if x=y or y=z).

Details

Used in prepData and simData to get distance and turning angle covariates between locations (x1,x2), (y1,y2) and activity center (z1,z2).

If type='LL' then distance is calculated as great circle distance using spDistsN1, and turning angle is calculated based on initial bearings using bearing.

Value

2-vector with first element the distance between y and z and second element the turning angle between (x,y) and (y,z).

---

dlnorm_rcpp *Log-normal density function*

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

---

dnorm_rcpp *Normal density function*

Description

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

Usage

```
dnorm_rcpp(x, mean, sd)
```

Arguments

x	Vector of quantiles
mean	Mean of the distribution
sd	Standard deviation of the distribution

Value

Vector of densities

---

dpois_rcpp *Poisson density function*

Description

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

Usage

```
dpois_rcpp(x, rate, foo)
```

Arguments

x	Vector of quantiles
rate	Rate
foo	Unused (for compatibility with template)

Value

Vector of densities

---

dvm_rcpp *Von Mises density function*

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

x	Vector of quantiles
shape	Shape
scale	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

`x`	Vector of quantiles
`mu`	Mean
`rho`	Concentration

Value

Vector of densities

`example` *Example dataset*

Description

These data are 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

`example` is a list of the following objects for demonstrating `fitHMM`:

- `m` A `momentuHMM` object
- `simPar` The parameters used to simulate `data`
- `par0` The initial parameters in the optimization to fit `m`

`miExample` is a list of the following objects for demonstrating `crawlWrap`, `MIfitHMM`, and `MIpool`:

- `obsData` Simulated observation data with measurement error and temporal irregularity (generated by `simData`)
- `inits` initial states for `crawlWrap` example
- `err.model` Error ellipse model for `crawlWrap` example

`forest` is a simulated spatial covariate raster layer

`exGen` *Example data simulation*

Description

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

Usage

```
exGen()
```

fitHMM *Fit a multivariate HMM to the data*

Description

Fit a (multivariate) hidden Markov model to the data provided, using numerical optimization of the log-likelihood function.

Usage

```
fitHMM(data, nbStates, dist, Par0, beta0 = NULL, delta0 = NULL,
  estAngleMean = NULL, circularAngleMean = NULL, formula = ~1,
  formulaDelta = ~1, stationary = FALSE, verbose = NULL,
  nlmPar = list(), fit = TRUE, DM = NULL, cons = NULL,
  userBounds = NULL, workBounds = NULL, workcons = NULL,
  stateNames = NULL, knownStates = NULL, fixPar = NULL, retryFits = 0,
  retrySD = NULL, optMethod = "nlm", control = list(), prior = NULL,
  modelName = NULL)
```

Arguments

`data` A `momentuHMMData` object.

`nbStates` Number of states of the HMM.

`dist` A named list indicating the probability distributions of the data streams. Currently supported distributions are 'bern', 'beta', 'exp', 'gamma', 'lnorm', 'norm', 'pois', 'vm', 'vmConsensus', 'weibull', and 'wrpcauchy'. For example, `dist=list(step='gamma', ang` indicates 3 data streams ('step', 'angle', and 'dives') and their respective probability distributions ('gamma', 'vm', and 'pois'). The names of the data streams (e.g., 'step', 'angle', 'dives') must match component names in `data`.

`Par0` A named list containing vectors of initial state-dependent probability distribution parameters for each data stream specified in `dist`. The parameters should be in the order expected by the pdfs of `dist`, and any zero-mass and/or one-mass parameters should be the last (if both are present, then zero-mass parameters must preceed one-mass parameters). Note that zero-mass parameters are mandatory if there are zeros in data streams with a 'gamma','weibull','exp','lnorm', or 'beta' distribution, and one-mass parameters are mandatory if there are ones in data streams with a 'beta' distribution. For example, for a 2-state model using the Von Mises (vm) distribution for a data stream named 'angle' and the zero-inflated gamma distribution for a data stream named 'step', the vector of initial parameters would be something like: `Par0=list(step=c(mean_1,mean_2,sd_1,sd_2,zeromass_1,ze`

If `DM` is not specified for a given data stream, then `Par0` is on the natural (i.e., real) scale of the parameters. However, if `DM` is specified for a given data stream, then `Par0` must be on the working (i.e., beta) scale of the parameters, and the length of `Par0` must match the number of columns in the design matrix. See details below.

`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)`. If `formulaDelta` includes covariates, then `delta0` must be specified as a k x (`nbStates`-1) matrix, where k is the number of covariates and the columns correspond to states 2:`nbStates`. See details below.

`estAngleMean` An optional named list indicating whether or not to estimate the angle mean for data streams with angular distributions ('vm' and 'wrpcauchy'). For example, `estAngleMean=list(angle=TRUE)` indicates the angle mean is to be estimated for 'angle'. Default is `NULL`, which assumes any angle means are fixed to zero and are not to be estimated. Any `estAngleMean` elements corresponding to data streams that do not have angular distributions are ignored. `estAngleMean` is also ignored for any 'vmConsensus' data streams (because the angle mean must be estimated in consensus models).

`circularAngleMean`
An optional named list indicating whether to use circular-linear (FALSE) or circular-circular (TRUE) regression on the mean of circular distributions ('vm' and 'wrpcauchy') for turning angles. For example, `circularAngleMean=list(angle=TRUE)` indicates the angle mean is be estimated for 'angle' using circular-circular regression. Whenever circular-circular regression is used for an angular data stream, a corresponding design matrix (`DM`) must be specified for the data stream, and the previous movement direction (i.e., a turning angle of zero) is automatically used as the reference angle (i.e., the intercept). Any circular-circular regression covariates in `data` should therefore be relative to the previous direction of movement (instead of standard directions relative to the x-axis; see `prepData` and `circAngles`). See Duchesne et al. (2015) for specifics on the circular-circular regression model using previous movement direction as the reference angle. Default is `NULL`, which assumes circular-linear regression is used for any angular distributions for which the mean angle is to be estimated. `circularAngleMean` elements corresponding to angular data streams are ignored unless the corresponding element of `estAngleMean` is `TRUE`. Any `circularAngleMean` elements corresponding to data streams that do not have angular distributions are ignored. `circularAngleMean` is also ignored for any 'vmConsensus' data streams (because the consensus model is a circular-circular regression model).

`formula` Regression formula for the transition probability covariates. Default: `~1` (no covariate effect). In addition to allowing standard functions in R formulas (e.g., `cos(cov)`, `cov1*cov2`, `I(cov^2)`), special functions include `cosinor(cov,period)` for modeling cyclical patterns, spline functions (`bs`, `ns`, `bSpline`, `cSpline`, `iSpline`, and `mSpline`), and state- or parameter-specific formulas (see details). Any formula terms that are not state- or parameter-specific are included on all of the transition probabilities.

`formulaDelta` Regression formula for the initial distribution. Default: `~1` (no covariate effect). Standard functions in R formulas are allowed (e.g., `cos(cov)`, `cov1*cov2`, `I(cov^2)`).

`stationary` `FALSE` if there are covariates in `formula` or `formulaDelta`. If `TRUE`, the initial distribution is considered equal to the stationary distribution. Default: `FALSE`.

`verbose` — Deprecated: please use `print.level` in `nlmPar` argument. Determines the print level of the `nlm` 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. Ignored unless `optMethod="nlm"`.

`nlmPar` — List of parameters to pass to the optimization function `nlm` (which should be either `print.level`, `gradtol`, `stepmax`, `steptol`, `iterlim`, or `hessian` – see `nlm`'s documentation for more detail). Ignored unless `optMethod="nlm"`.

`fit` — `TRUE` if an HMM should be fitted to the data, `FALSE` otherwise. If fit=`FALSE`, 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, parameter bounds, etc. Default: `TRUE`.

`DM` — An optional named list indicating the design matrices to be used for the probability distribution parameters of each data stream. Each element of `DM` can either be a named list of linear regression formulas or a "pseudo" design matrix. For example, for a 2-state model using the gamma distribution for a data stream named 'step', `DM=list(step=list(mean=~cov1, sd=~1))` specifies the mean parameters as a function of the covariate 'cov1' for each state. This model could equivalently be specified as a 4x6 "pseudo" design matrix using character strings for the covariate: `DM=list(step=matrix(c(1,0,0,0,'cov1',0,0,0,0,1,0,0,0,'cov1',0,0,0,0,1,0,0` where the 4 rows correspond to the state-dependent paramaters (mean_1,mean_2,sd_1,sd_2) and the 6 columns correspond to the regression coefficients.

Design matrices specified using formulas allow standard functions in R formulas (e.g., `cos(cov)`, `cov1*cov2`, `I(cov^2)`). Special formula functions include `cosinor(cov,period)` for modeling cyclical patterns, spline functions (`bs`, `ns`, `bSpline`, `cSpline`, `iSpline`, and `mSpline`), `angleFormula(cov,strength)` for the angle mean of circular-circular regression models, and state-specific formulas (see details). Any formula terms that are not state-specific are included on the parameters for all `nbStates` states.

`cons` — Deprecated: please use `workBounds` instead. An optional named list of vectors specifying a power to raise parameters corresponding to each column of the design matrix for each data stream. While there could be other uses, primarily intended to constrain specific parameters to be positive. For example, `cons=list(step=c(1,2,1,1))` raises the second parameter to the second power. Default=NULL, which simply raises all parameters to the power of 1. `cons` is ignored for any given data stream unless `DM` is specified.

`userBounds` — An optional named list of 2-column matrices specifying bounds on the natural (i.e, real) scale of the probability distribution parameters for each data stream. For each matrix, the first column pertains to the lower bound and the second column the upper bound. For example, for a 2-state model using the wrapped Cauchy ('wrpcauchy') distribution for a data stream named 'angle' with `estAngleMean$angle=TRUE)`, `userBounds=list(angle=matrix(c(-pi,-pi,-1,-1,pi,pi,1,1)` specifies (-1,1) bounds for the concentration parameters instead of the default [0,1) bounds.

`workBounds` — An optional named list of 2-column matrices specifying bounds on the working scale of the probability distribution, transition probability, and initial distribution parameters. For each matrix, the first column pertains to the lower bound and the second column the upper bound. For data streams, each element of workBounds should be a k x 2 matrix with the same name of the corresponding element of Par0, where k is the number of parameters. For transition probability parameters, the corresponding element of workBounds must be a k x 2 matrix named "beta", where k=length(beta0). For initial distribution parameters, the corresponding element of workBounds must be a k x 2 matrix named "delta", where k=length(delta0). workBounds is ignored for any given data stream unless DM is also specified.

workcons
: Deprecated: please use workBounds instead. An optional named list of vectors specifying constants to add to the regression coefficients on the working scale for each data stream. Warning: use of workcons is recommended only for advanced users implementing unusual parameter constraints through a combination of DM, cons, and workcons. workcons is ignored for any given data stream unless DM is specified.

stateNames
: Optional character vector of length nbStates indicating state names.

knownStates
: Vector of values of the state process which are known prior to fitting the model (if any). Default: NULL (states are not known). This should be a vector with length the number of rows of 'data'; each element should either be an integer (the value of the known states) or NA if the state is not known.

fixPar
: An optional list of vectors indicating parameters which are assumed known prior to fitting the model. Default: NULL (no parameters are fixed). For data streams, each element of fixPar should be a vector of the same name and length as the corresponding element of Par0. For transition probability parameters, the corresponding element of fixPar must be named "beta" and have the same dimensions as beta0. For initial distribution parameters, the corresponding element of fixPar must be named "delta" and have the same dimensions as delta0. Each parameter should either be numeric (the fixed value of the parameter) or NA if the parameter is to be estimated. Corresponding fixPar parameters must be on the same scale as Par0 (e.g. if DM is specified for a given data stream, any fixed parameters for this data stream must be on the working scale), beta0, and delta0.

retryFits
: Non-negative integer indicating the number of times to attempt to iteratively fit the model using random perturbations of the current parameter estimates as the initial values for likelihood optimization. Normal(0,retrySD^2) perturbations are used on the working scale parameters. Default: 0. When retryFits>0, the model with the largest log likelihood value is returned. Ignored if fit=FALSE.

retrySD
: An optional list of scalars or vectors indicating the standard deviation to use for normal perturbations of each working scale parameter when retryFits>0. For data streams, each element of retrySD should be a vector of the same name and length as the corresponding element of Par0 (if a scalar is provided, then this value will be used for all working parameters of the data stream). For transition probability parameters, the corresponding element of retrySD must be named "beta" and have the same dimensions as beta0. For initial distribution parameters, the corresponding element of retrySD must be named "delta" and have the same dimensions as delta0 (if delta0 is on the working scale) or be of length nbStates-1 (if delta0 is on the natural scale). Default: NULL (in which case

retrySD=1 for data stream parameters and retrySD=10 for initial distribution and state transition probabilities). Ignored unless retryFits>0.

optMethod
: The optimization method to be used. Can be "nlm" (the default; see nlm), "Nelder-Mead" (see optim), or "SANN" (see optim).

control
: A list of control parameters to be passed to optim (ignored unless optMethod="Nelder-Mead" or optMethod="SANN").

prior
: A function that returns the log-density of the working scale parameter prior distribution(s). See 'Details'.

modelName
: An optional character string providing a name for the fitted model. If provided, modelName will be returned in print.momentuHMM, AIC.momentuHMM, AICweights, and other functions.

Details

- The matrix beta0 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 formula 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), beta0 has one row, for the intercept.
- When covariates are not included in formulaDelta (i.e. formulaDelta=~1), then delta0 (and fixPar$delta) are specified as a vector of length nbStates that sums to 1. When covariates are included in formulaDelta, then delta0 (and fixPar$delta) must be specified as a k x (nbStates-1) matrix of working parameters, where k is the number of regression coefficients and the columns correspond to states 2:nbStates. For example, in a 3-state HMM with formulaDelta=~cov1+cov2, the matrix delta0 has three rows (intercept + two covariates) and 2 columns (corresponding to states 2 and 3). The initial distribution working parameters are transformed to the real scale as exp(covsDelta*Delta)/rowSums(exp(covsDelta*Delta)), where covsDelta is the N x k design matrix, Delta=cbind(rep(0,k),delta0) is a k x nbStates matrix of working parameters, and N=length(unique(data$ID)).
- The choice of initial parameters (particularly Par0 and beta0) 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.
- If DM is specified for a particular data stream, then the initial values are specified on the working (i.e., beta) scale of the parameters. The working scale of each parameter is determined by the link function used. If a parameter P is bound by (0,Inf) then the working scale is the log(P) scale. If the parameter bounds are (-pi,pi) then the working scale is tan(P/2) unless circular-circular regression is used. Otherwise if the parameter bounds are finite then logit(P) is the working scale. However, when both zero- and one-inflation are included, then a multinomial logit link is used because the sum of the zeromass and onemass probability parameters cannot exceed 1. The function getParDM is intended to help with obtaining initial values on the working scale when specifying a design matrix and other parameter constraints (see example below). When circular-circular regression is specified using circularAngleMean, the working scale for the mean turning angle is not as easily interpretable, but the link function is atan2(sin(X)*B,1+cos(X)*B), where X are the angle covariates and B the angle coefficients (see Duchesne et al. 2015). Under this formulation, the reference turning angle is 0 (i.e.,

movement in the same direction as the previous time step). In other words, the mean turning angle is zero when the coefficient(s) B=0.

- Circular-circular regression in `momentuHMM` is designed for turning angles (not bearings) as computed by `simData` and `prepData`. Any circular-circular regression angle covariates for time step t should therefore be relative to the previous direction of movement for time step t-1. In other words, circular-circular regression covariates for time step t should be the turning angle between the direction of movement for time step t-1 and the standard direction of the covariate relative to the x-axis for time step t. If provided standard directions in radians relative to the x-axis (where 0 = east, pi/2 = north, pi = west, and -pi/2 = south), `circAngles` or `prepData` can perform this calculation for you.

  When the circular-circular regression model is used, the special function `angleStrength(cov,strength,by)` can be used in `DM` for the mean of angular distributions (i.e. 'vm', 'vmConsensus', and 'wrpcauchy'), where `cov` is an angle covariate (e.g. wind direction), `strength` is a positive real covariate (e.g. wind speed), and `by` is an optional factor variable for individual- or group-level effects (e.g. ID, sex). This allows angle covariates to be weighted based on their relative strength or importance at time step t as in Rivest et al. (2016). In this case, the link function for the mean angle is atan2((Z * sin(X)) %*% B,1+(Z * cos(X)) %*% B), where X are the angle covariates, Z the strength covariates, and B the angle coefficients (see Rivest et al. 2016).

- State-specific formulas can be specified in `DM` using special formula functions. These special functions can take the names `paste0("state",1:nbStates)` (where the integer indicates the state-specific formula). For example, `DM=list(step=list(mean=~cov1+state1(cov2),sd=~cov2+state2(cov1)))` includes `cov1` on the mean parameter for all states, `cov2` on the mean parameter for state 1, `cov2` on the sd parameter for all states, and `cov1` on the sd parameter for state 2.

- State- and parameter-specific formulas can be specified for transition probabilities in `formula` using special formula functions. These special functions can take the names `paste0("state",1:nbStates)` (where the integer indicates the current state from which transitions occur), `paste0("toState",1:nbStates)` (where the integer indicates the state to which transitions occur), or `paste0("betaCol",nbStates*(nbStates-1))` (where the integer indicates the column of the `beta` matrix). For example with `nbStates=3`, `formula=~cov1+betaCol1(cov2)+state3(cov3)+toState1(cov4)` includes `cov1` on all transition probability parameters, `cov2` on the `beta` column corresponding to the transition from state 1->2, `cov3` on transition probabilities from state 3 (i.e., `beta` columns corresponding to state transitions 3->1 and 3->2), and `cov4` on transition probabilities to state 1 (i.e., `beta` columns corresponding to state transitions 2->1 and 3->1).

- Cyclical relationships (e.g., hourly, monthly) may be modeled in `DM` or `formula` using the `cosinor(x,period)` special formula function for covariate `x` and sine curve period of time length `period`. For example, if the data are hourly, a 24-hour cycle can be modeled using `~cosinor(cov1,24)`, where the covariate `cov1` is a repeating sequential series of integers indicating the hour of day `(0,1,...,23,0,1,...,23,0,1,...)` (note that `fitHMM` will not do this for you, the appropriate covariate must be included in `data`; see example below). The `cosinor(x,period)` function converts `x` to 2 covariates `cosinorCos(x)=cos(2*pi*x/period)` and `cosinorSin(x)=sin(2*pi*x/period` for inclusion in the model (i.e., 2 additional parameters per state). The amplitude of the sine wave is thus `sqrt(B_cos^2 + B_sin^2)`, where `B_cos` and `B_sin` are the working parameters correponding to `cosinorCos(x)` and `cosinorSin(x)`, respectively (e.g., see Cornelissen 2014).

- Similar to that used in `crawlWrap`, the `prior` argument is a user-specified function that returns the log-density of the working scale parameter prior distribution(s). In addition to including prior information about parameters, one area where priors can be particularly useful is for handling numerical issues that can arise when parameters are near a boundary. When parameters are near boundaries, they can wander into the "nether regions" of the parameter space during optimization. For example, setting `prior=function(par) {sum(dnorm(par,0,sd,log=TRUE))}` with a reasonably large `sd` (e.g. 100 or 1000) can help prevent working parameters from straying too far along the real line. Here `par` is the vector of working scale parameters (as returned by `fitHMM`, e.g., see `example$m$mod$estimate`) in the following order: data stream working parameters (in order `names(dist)`), beta working parameters, and delta working parameters. Instead of specifying the same prior on all parameters, different priors could be specified on different parameters (and not all parameters must have user-specified priors). For example, `prior=function(par){dnorm(par[3],0,100,log=TRUE)}` would only specify a prior for the third working parameter. Note that the `prior` function must return a scalar on the log scale. See 'harbourSealExample.R' in the "vignettes" source directory for an example using the `prior` argument.

Value

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

`mle`	A named list of the maximum likelihood estimates of the parameters of the model (if the numerical algorithm has indeed identified the global maximum of the likelihood function). Elements are included for the parameters of each data strea, as well as `beta` (transition probabilities regression coefficients - more information in 'Details'), `gamma` (transition probabilities on real scale, based on mean covariate values if `formula` includes covariates), and `delta` (initial distribution).
`CIreal`	Standard errors and 95% confidence intervals on the real (i.e., natural) scale of parameters
`CIbeta`	Standard errors and 95% confidence intervals on the beta (i.e., working) scale of parameters
`data`	The momentuHMMData object
`mod`	The object returned by the numerical optimizer `nlm` or `optim`
`conditions`	Conditions used to fit the model, e.g., `bounds` (parameter bounds), distributions, `zeroInflation`, `estAngleMean`, `stationary`, `formula`, `DM`, `fullDM` (full design matrix), etc.
`rawCovs`	Raw covariate values for transition probabilities, as found in the data (if any). Used in `plot.momentuHMM`.
`stateNames`	The names of the states.
`knownStates`	Vector of values of the state process which are known.
`covsDelta`	Design matrix for initial distribution.

References

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McClintock B.T., King R., Thomas L., Matthiopoulos J., McConnell B.J., Morales J.M. 2012. A general discrete-time modeling framework for animal movement using multistate random walks. Ecological Monographs, 82 (3), 335-349.

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Rivest, LP, Duchesne, T, Nicosia, A, Fortin, D, 2016. A general angular regression model for the analysis of data on animal movement in ecology. Journal of the Royal Statistical Society: Series C (Applied Statistics), 65(3):445-463.

See Also

getParDM, prepData, simData

Examples

```
nbStates <- 2
stepDist <- "gamma" # step distribution
angleDist <- "vm" # turning angle distribution

# extract data from momentuHMM example
data <- example$m$data

### 1. 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)
stepPar <- c(mu0,sigma0) # no zero-inflation, so no zero-mass included
anglePar <- kappa0 # not estimating angle mean, so not included
formula <- ~cov1+cos(cov2)

m <- fitHMM(data=data,nbStates=nbStates,dist=list(step=stepDist,angle=angleDist),
            Par0=list(step=stepPar,angle=anglePar),formula=formula)

print(m)

## Not run:
### 2. fit the exact same model to the simulated data using DM formulas
# Get initial values for the parameters on working scale
Par0 <- getParDM(data=data,nbStates=nbStates,dist=list(step=stepDist,angle=angleDist),
        Par=list(step=stepPar,angle=anglePar),
        DM=list(step=list(mean=~1,sd=~1),angle=list(concentration=~1)))
```

```
mDMf <- fitHMM(data=data,nbStates=nbStates,dist=list(step=stepDist,angle=angleDist),
              Par0=Par0,formula=formula,
              DM=list(step=list(mean=~1,sd=~1),angle=list(concentration=~1)))

print(mDMf)

### 3. fit the exact same model to the simulated data using DM matrices
# define DM
DMm <- list(step=diag(4),angle=diag(2))

# user-specified dimnames not required but are recommended
dimnames(DMm$step) <- list(c("mean_1","mean_2","sd_1","sd_2"),
                   c("mean_1:(Intercept)","mean_2:(Intercept)",
                   "sd_1:(Intercept)","sd_2:(Intercept)"))
dimnames(DMm$angle) <- list(c("concentration_1","concentration_2"),
                    c("concentration_1:(Intercept)","concentration_2:(Intercept)"))

mDMm <- fitHMM(data=data,nbStates=nbStates,dist=list(step=stepDist,angle=angleDist),
              Par0=Par0,formula=formula,
              DM=DMm)

print(mDMm)

### 4. fit step mean parameter covariate model to the simulated data using DM
stepDMf <- list(mean=~cov1,sd=~1)
Par0 <- getParDM(data,nbStates,list(step=stepDist,angle=angleDist),
                 Par=list(step=stepPar,angle=anglePar),
                 DM=list(step=stepDMf,angle=DMm$angle))
mDMfcov <- fitHMM(data=data,nbStates=nbStates,dist=list(step=stepDist,angle=angleDist),
              Par0=Par0,
              formula=formula,
              DM=list(step=stepDMf,angle=DMm$angle))

print(mDMfcov)

### 5. fit the exact same step mean parameter covariate model using DM matrix
stepDMm <- matrix(c(1,0,0,0,"cov1",0,0,0,0,1,0,0,0,"cov1",0,0,
                 0,0,1,0,0,0,0,1),4,6,dimnames=list(c("mean_1","mean_2","sd_1","sd_2"),
                c("mean_1:(Intercept)","mean_1:cov1","mean_2:(Intercept)","mean_2:cov1",
                 "sd_1:(Intercept)","sd_2:(Intercept)")))
Par0 <- getParDM(data,nbStates,list(step=stepDist,angle=angleDist),
                 Par=list(step=stepPar,angle=anglePar),
                 DM=list(step=stepDMm,angle=DMm$angle))
mDMmcov <- fitHMM(data=data,nbStates=nbStates,dist=list(step=stepDist,angle=angleDist),
              Par0=Par0,
              formula=formula,
              DM=list(step=stepDMm,angle=DMm$angle))

print(mDMmcov)

### 6. fit circular-circular angle mean covariate model to the simulated data using DM

# Generate fake circular covariate using circAngles
```

```
data$cov3 <- circAngles(refAngle=2*atan(rnorm(nrow(data))),data)

# Fit circular-circular regression model for angle mean
# Note no intercepts are estimated for angle means because these are by default
# the previous movement direction (i.e., a turning angle of zero)
mDMcircf <- fitHMM(data=data,nbStates=nbStates,dist=list(step=stepDist,angle=angleDist),
                 Par0=list(step=stepPar,angle=c(0,0,Par0$angle)),
                  formula=formula,
                  estAngleMean=list(angle=TRUE),
                  circularAngleMean=list(angle=TRUE),
                  DM=list(angle=list(mean=~cov3,concentration=~1)))

print(mDMcircf)

### 7. fit the exact same circular-circular angle mean model using DM matrices

# Note no intercept terms are included in DM for angle means because the intercept is
# by default the previous movement direction (i.e., a turning angle of zero)
mDMcircm <- fitHMM(data=data,nbStates=nbStates,dist=list(step=stepDist,angle=angleDist),
                 Par0=list(step=stepPar,angle=c(0,0,Par0$angle)),
                  formula=formula,
                  estAngleMean=list(angle=TRUE),
                  circularAngleMean=list(angle=TRUE),
                DM=list(angle=matrix(c("cov3",0,0,0,0,"cov3",0,0,0,0,1,0,0,0,0,1),4,4)))

print(mDMcircm)

### 8. Cosinor and state-dependent formulas
nbStates<-2
dist<-list(step="gamma")
Par<-list(step=c(100,1000,50,100))

# include 24-hour cycle on all transition probabilities
# include 12-hour cycle on transitions from state 2
formula=~cosinor(hour24,24)+state2(cosinor(hour12,12))

# specify appropriate covariates
covs<-data.frame(hour24=0:23,hour12=0:11)

beta<-matrix(c(-1.5,1,1,NA,NA,-1.5,-1,-1,1,1),5,2)
# row names for beta not required but can be helpful
rownames(beta)<-c("(Intercept)",
                  "cosinorCos(hour24, 24)",
                  "cosinorSin(hour24, 24)",
                  "cosinorCos(hour12, 12)",
                  "cosinorSin(hour12, 12)")
data.cos<-simData(nbStates=nbStates,dist=dist,Par=Par,
                      beta=beta,formula=formula,covs=covs)

m.cosinor<-fitHMM(data.cos,nbStates=nbStates,dist=dist,Par0=Par,formula=formula)
m.cosinor

### 9. Piecewise constant B-spline on step length mean and angle concentration
```

```
library(splines2)
nObs <- 1000 # length of simulated track
cov <- data.frame(time=1:nObs) # time covariate for splines
dist <- list(step="gamma",angle="vm")
stepDM <- list(mean=~bSpline(time,df=3,degree=0),sd=~1)
angleDM <- list(mean=~1,concentration=~bSpline(time,df=3,degree=0))
DM <- list(step=stepDM,angle=angleDM)
Par <- list(step=c(log(1000),1,-1,log(100)),angle=c(0,log(10),2,-5))

data.spline<-simData(obsPerAnimal=nObs,nbStates=1,dist=dist,Par=Par,DM=DM,covs=cov)

Par0 <- list(step=Par$step,angle=Par$angle[-1])
m.spline<-fitHMM(data.spline,nbStates=1,dist=dist,Par0=Par0,
                 DM=list(step=stepDM,
                         angle=list(concentration=~bSpline(time,df=3,degree=0))))

### 10. Initial state (delta) based on covariate
nObs <- 100
dist <- list(step="gamma",angle="vm")
Par <- list(step=c(100,1000,50,100),angle=c(0,0,0.01,0.75))

# create sex covariate
cov <- data.frame(sex=factor(rep(c("F","M"),each=nObs))) # sex covariate
formulaDelta <- ~ sex + 0

# Female begins in state 1, male begins in state 2
delta <- matrix(c(-100,100),2,1,dimnames=list(c("sexF","sexM"),"state 2"))

data.delta<-simData(nbAnimals=2,obsPerAnimal=nObs,nbStates=2,dist=dist,Par=Par,
                    delta=delta,formulaDelta=formulaDelta,covs=cov)

Par0 <- list(step=Par$step, angle=Par$angle[3:4])
m.delta <- fitHMM(data.delta, nbStates=2, dist=dist, Par0 = Par0,
                  formulaDelta=formulaDelta)

## End(Not run)
```

---

getCovNames *Get names of any covariates used in probability distribution parameters*

Description

Get names of any covariates used in probability distribution parameters

Usage

```
getCovNames(m, p, distname)
```

Arguments

m	momentuHMM object
p	list returned by parDef
distname	Name of the data stream

Value

A list of:

DMterms	Names of all covariates included in the design matrix for the data stream
DMpartems	A list of the names of all covariates for each of the probability distribution parameters

---

getDM_rcpp *Get design matrix*

Description

Loop for creating full design matrix (X) from pseudo-design matrix (DM). Written in C++. Used in getDM.

Usage

```
getDM_rcpp(X, covs, DM, nr, nc, cov, nbObs)
```

Arguments

X	full design matrix
covs	matrix of covariates
DM	pseudo design matrix
nr	number of rows in design matrix
nc	number of column in design matrix
cov	covariate names
nbObs	number of observations

Value

full design matrix (X)

getPar — *Get starting values from momentuHMM, miHMM, or miSum object returned by fitHMM, MIfitHMM, or MIpool*

Description

Get starting values from momentuHMM, miHMM, or miSum object returned by fitHMM, MIfitHMM, or MIpool

Usage

```
getPar(m)
```

Arguments

m	A momentuHMM, miHMM, or miSum object.

Value

A list of parameter values (Par, beta, delta) that can be used as starting values in fitHMM or MIfitHMM

See Also

getPar0, getParDM

Examples

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

getPar0 — *Get starting values for new model from existing* momentuHMM *model fit*

Description

For nested models, this function will extract starting parameter values (i.e., Par0 in fitHMM or MIfitHMM) from an existing momentuHMM model fit based on the provided arguments for the new model. Any parameters that are not in common between model and the new model (as specified by the arguments) are set to 0. This function is intended to help users incrementally build and fit more complicated models from simpler nested models (and vice versa).

Usage

```
getPar0(model, nbStates = NULL, estAngleMean = NULL,
  circularAngleMean = NULL, formula = NULL, formulaDelta = NULL,
  DM = NULL, stateNames = NULL)
```

Arguments

model	A momentuHMM, miHMM, or miSum object (as returned by fitHMM, MIfitHMM, or MIpool)
nbStates	Number of states in the new model. If nbStates=NULL (the default), then nbStates=length(model$stateNames)
estAngleMean	Named list indicating whether or not the angle mean for data streams with angular distributions ('vm' and 'wrpcauchy') are to be estimated in the new model. If estAngleMean=NULL (the default), then estAngleMean=model$conditions$estAngleMean
circularAngleMean	Named list indicating whether circular-linear (FALSE) or circular-circular (TRUE) regression on the mean of circular distributions ('vm' and 'wrpcauchy') for turning angles are to be used in the new model. If circularAngleMean=NULL (the default), then circularAngleMean=model$conditions$circularAngleMean
formula	Regression formula for the transition probability covariates of the new model (see fitHMM). If formula=NULL (the default), then formula=model$conditions$formula.
formulaDelta	Regression formula for the initial distribution covariates of the new model (see fitHMM). If formulaDelta=NULL (the default), then formulaDelta=model$conditions$formulaDelta.
DM	Named list indicating the design matrices to be used for the probability distribution parameters of each data stream in the new model (see fitHMM). Only parameters with design matrix column names that match those in model$conditions$fullDM are extracted, so care must be taken in naming columns if any elements of DM are specified as matrices instead of formulas. If DM=NULL (the default), then DM=model$conditions$DM.
stateNames	Character vector of length nbStates indicating the names and order of the states in the new model. If stateNames=NULL (the default), then stateNames=model$stateNames[1:nbStates

Value

A named list containing starting values suitable for Par0 and beta0 arguments in fitHMM or MIfitHMM:

Par	A list of vectors of state-dependent probability distribution parameters for each data stream specified in model$conditions$dist
beta	Matrix of regression coefficients for the transition probabilities
delta	Initial distribution of the HMM. Only returned if stateNames has the same membership as the state names for model

.

All other fitHMM (or MIfitHMM) model specifications (e.g., dist, userBounds, workBounds, etc.) and data are assumed to be the same for model and the new model (as specified by estAngleMean, circularAngleMean, formula, formulaDelta, DM, and stateNames).

See Also

getPar, getParDM, fitHMM, MIfitHMM

Examples

```
# model is a momentuHMM object, automatically loaded with the package
model <- example$m
data <- model$data
dist <- model$conditions$dist
nbStates <- length(model$stateNames)
estAngleMean <- model$conditions$estAngleMean

newformula <- ~cov1+cov2
Par0 <- getPar0(model,formula=newformula)

## Not run:
newModel <- fitHMM(model$data,dist=dist,nbStates=nbStates,
                   Par0=Par0$Par,beta0=Par0$beta,
                   formula=newformula,
                   estAngleMean=estAngleMean)

## End(Not run)

newDM1 <- list(step=list(mean=~cov1,sd=~cov1))
Par0 <- getPar0(model,DM=newDM1)

## Not run:
newModel1 <- fitHMM(model$data,dist=dist,nbStates=nbStates,
                   Par0=Par0$Par,beta0=Par0$beta,
                   formula=model$conditions$formula,
                   estAngleMean=estAngleMean,
                   DM=newDM1)

## End(Not run)

# same model but specify DM for step using matrices
newDM2 <- list(step=matrix(c(1,0,0,0,
                             "cov1",0,0,0,
                             0,1,0,0,
                             0,"cov1",0,0,
                             0,0,1,0,
                             0,0,"cov1",0,
                             0,0,0,1,
                             0,0,0,"cov1"),nrow=nbStates*2))

# to be extracted, new design matrix column names must match
# column names of model$conditions$fullDM
colnames(newDM2$step)<-paste0(rep(c("mean_","sd_"),each=2*nbStates),
                      rep(1:nbStates,each=2),
                      rep(c(":(Intercept)",":cov1"),2*nbStates))
Par0 <- getPar0(model,DM=newDM2)
```

```
## Not run:
newModel2 <- fitHMM(model$data,dist=dist,nbStates=nbStates,
                    Par0=Par0$Par,beta0=Par0$beta,
                    formula=model$conditions$formula,
                    estAngleMean=estAngleMean,
                    DM=newDM2)

## End(Not run)
```

getParDM *Get starting values on working scale based on design matrix and other parameter constraints*

Description

Convert starting values on the natural scale of data stream probability distributions to a feasible set of working scale parameters based on a design matrix and other parameter constraints.

Usage

```
getParDM(data = data.frame(), nbStates, dist, Par, zeroInflation = NULL,
  oneInflation = NULL, estAngleMean = NULL, circularAngleMean = NULL,
  DM = NULL, cons = NULL, userBounds = NULL, workBounds = NULL,
  workcons = NULL)
```

Arguments

data	Optional momentuHMMData object or a data frame containing the covariate values. data must be specified if covariates are included in DM.
nbStates	Number of states of the HMM.
dist	A named list indicating the probability distributions of the data streams. Currently supported distributions are 'gamma','weibull','exp','lnorm','beta','pois','wrpcauchy', and 'vm'. For example, dist=list(step='gamma', angle='vm', dives='pois') indicates 3 data streams ('step', 'angle', and 'dives') and their respective probability distributions ('gamma', 'vm', and 'pois').
Par	A named list containing vectors of state-dependent probability distribution parameters for each data stream specified in dist. The parameters should be on the natural scale, in the order expected by the pdfs of dist, and any zero-mass parameters should be the last.
zeroInflation	A named list of logicals indicating whether the probability distributions of the data streams should be zero-inflated. If zeroInflation is TRUE for a given data stream, then values for the zero-mass parameters should be included in the corresponding element of Par. Ignored if data is a momentuHMMData object.

oneInflation
: Named list of logicals indicating whether the probability distributions of the data streams are one-inflated. If `oneInflation` is `TRUE` for a given data stream, then values for the one-mass parameters should be included in the corresponding element of `Par`. Ignored if `data` is a `momentuHMMData` object.

estAngleMean
: An optional named list indicating whether or not to estimate the angle mean for data streams with angular distributions ('vm' and 'wrpcauchy'). Any `estAngleMean` elements corresponding to data streams that do not have angular distributions are ignored.

circularAngleMean
: An optional named list indicating whether to use circular-linear (FALSE) or circular-circular (TRUE) regression on the mean of circular distributions ('vm' and 'wrpcauchy') for turning angles. `circularAngleMean` elements corresponding to angular data streams are ignored unless the corresponding element of `estAngleMean` is `TRUE`. Any `circularAngleMean` elements corresponding to data streams that do not have angular distributions are ignored.

DM
: A named list indicating the design matrices to be used for the probability distribution parameters of each data stream. Each element of `DM` can either be a named list of linear regression formulas or a matrix. For example, for a 2-state model using the gamma distribution for a data stream named 'step', `DM=list(step=list(mean=~cov1, sd=~1))` specifies the mean parameters as a function of the covariate 'cov1' for each state. This model could equivalently be specified as a 4x6 matrix using character strings for the covariate: `DM=list(step=matrix(c(1,0,0,0,'cov1',0,0,0,0,1,0,0,0,'cov1',0,0,0,0,1,0,0,0,0,1),4,6` where the 4 rows correspond to the state-dependent paramaters (mean_1,mean_2,sd_1,sd_2) and the 6 columns correspond to the regression coefficients.

cons
: Deprecated: please use `workBounds` instead. An optional named list of vectors specifying a power to raise parameters corresponding to each column of the design matrix for each data stream. While there could be other uses, primarily intended to constrain specific parameters to be positive. For example, `cons=list(step=c(1,2,1,1))` raises the second parameter to the second power. Default=NULL, which simply raises all parameters to the power of 1. `cons` is ignored for any given data stream unless `DM` is specified.

userBounds
: An optional named list of 2-column matrices specifying bounds on the natural (i.e, real) scale of the probability distribution parameters for each data stream. For example, for a 2-state model using the wrapped Cauchy ('wrpcauchy') distribution for a data stream named 'angle' with `estAngleMean$angle=TRUE)`, `userBounds=list(angle=matrix(c(-pi,-pi,-1,-1,pi,pi,1,1),4,2))` specifies (-1,1) bounds for the concentration parameters instead of the default [0,1) bounds.

workBounds
: An optional named list of 2-column matrices specifying bounds on the working scale of the probability distribution, transition probability, and initial distribution parameters. For each matrix, the first column pertains to the lower bound and the second column the upper bound. For data streams, each element of `workBounds` should be a k x 2 matrix with the same name of the corresponding element of `Par0`, where k is the number of parameters. For transition probability parameters, the corresponding element of `workBounds` must be a k x 2 matrix named "beta", where k=`length(beta0)`. For initial distribution parameters, the

corresponding element of workBounds must be a k x 2 matrix named "delta", where k=length(delta0).

workcons
: An optional named list of vectors specifying constants to add to the regression coefficients on the working scale for each data stream. Warning: use of workcons is recommended only for advanced users implementing unusual parameter constraints through a combination of DM, cons, and workcons. workcons is ignored for any given data stream unless DM is specified.

Details

If design matrix includes non-factor covariates, then natural scale parameters are assumed to correspond to the mean value(s) for the covariate(s) (if nrow(data)>1) and getParDM simply returns one possible solution to the system of linear equations defined by Par, DM, and any other constraints using singular value decomposition. This can be helpful for exploring relationships between the natural and working scale parameters when covariates are included, but getParDM will not necessarily return "good" starting values (i.e., Par0) for fitHMM or MIfitHMM.

Value

A list of parameter values that can be used as starting values (Par0) in fitHMM or MIfitHMM

See Also

getPar, getPar0, fitHMM, MIfitHMM

Examples

```
# data is a momentuHMMData object, automatically loaded with the package
data <- example$m$data
stepDist <- "gamma"
angleDist <- "vm"
nbStates <- 2
stepPar0 <- c(15,50,10,20) # natural scale mean_1, mean_2, sd_1, sd_2
anglePar0 <- c(0.7,1.5) # natural scale conentration_1, concentration_2

# get working parameters for 'DM' and 'cons' that constrain step length mean_1 < mean_2
stepDM <- matrix(c(1,1,0,0,0,1,0,0,0,0,1,0,0,0,0,1),4,4,
          dimnames=list(NULL,c("mean:(Intercept)","mean_2",
                               "sd_1:(Intercept)","sd_2:(Intercept)")))
stepcons <- c(1,2,1,1) # coefficient for 'mean_2' constrained to be positive
wPar0 <- getParDM(nbStates=2,dist=list(step=stepDist),
                      Par=list(step=stepPar0),
                      DM=list(step=stepDM),cons=list(step=stepcons))

## Not run:
# Fit HMM using wPar0 as initial values for the step data stream
mPar <- fitHMM(data,nbStates=2,dist=list(step=stepDist,angle=angleDist),
               Par0=list(step=wPar0$step,angle=anglePar0),
               DM=list(step=stepDM),cons=list(step=stepcons))

## End(Not run)
```

```
# get working parameters for 'DM' using 'cov1' and 'cov2' covariates
stepDM2 <- list(mean=~cov1,sd=~cov2)
wPar20 <- getParDM(data,nbStates=2,dist=list(step=stepDist),
                      Par=list(step=stepPar0),
                      DM=list(step=stepDM2))

## Not run:
# Fit HMM using wPar20 as initial values for the step data stream
mPar2 <- fitHMM(data,nbStates=2,dist=list(step=stepDist,angle=angleDist),
               Par0=list(step=wPar20$step,angle=anglePar0),
               DM=list(step=stepDM2))

## End(Not run)
```

HMMfits *Constructor of* HMMfits *objects*

Description

Constructor of HMMfits objects

Usage

```
HMMfits(m)
```

Arguments

m A list of momentuHMM objects.
HMMfits objects are returned by MIfitHMM when arguments fit=TRUE and poolEstimates=FALSE.

Value

An object HMMfits.

is.crwData *Is crwData*

Description

Check that an object is of class crwData. Used in MIfitHMM.

Usage

```
is.crwData(x)
```

Arguments

`x` An R object

Value

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

---

is.crwSim *Is crwSim*

Description

Check that an object is of class `crwSim`.

Usage

```
is.crwSim(x)
```

Arguments

`x` An R object

Value

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

---

is.HMMfits *Is HMMfits*

Description

Check that an object is of class `HMMfits`.

Usage

```
is.HMMfits(x)
```

Arguments

`x` An R object

Value

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

is.miHMM *Is miHMM*

Description

Check that an object is of class `miHMM`.

Usage

```
is.miHMM(x)
```

Arguments

`x`	An R object

Value

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

is.miSum *Is miSum*

Description

Check that an object is of class `miSum`.

Usage

```
is.miSum(x)
```

Arguments

`x`	An R object

Value

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

is.momentuHMM *Is momentuHMM*

Description

Check that an object is of class `momentuHMM`. Used in `CIreal`, `CIbeta`, `plotPR`, `plotStates`, `pseudoRes`, `stateProbs`, and `viterbi`.

Usage

```
is.momentuHMM(x)
```

Arguments

x	An R object

Value

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

is.momentuHMMData *Is momentuHMMData*

Description

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

Usage

```
is.momentuHMMData(x)
```

Arguments

x	An R object

Value

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

logAlpha *Forward log-probabilities*

Description

Used in stateProbs and pseudoRes.

Usage

```
logAlpha(m)
```

Arguments

m	A momentuHMM, miHMM, or miSum object.

Value

The matrix of forward log-probabilities.

Examples

```
## Not run:
# m is a momentuHMM object (as returned by fitHMM), automatically loaded with the package
m <- example$m

la <- momentuHMM:::logAlpha(m)

## End(Not run)
```

logBeta *Backward log-probabilities*

Description

Used in stateProbs.

Usage

```
logBeta(m)
```

Arguments

m	A momentuHMM, miHMM, or miSum object.

Value

The matrix of backward log-probabilities.

Examples

```
## Not run:
# m is a momentuHMM object (as returned by fitHMM), automatically loaded with the package
m <- example$m

lb <- momentuHMM:::logBeta(m)

## End(Not run)
```

MIfitHMM *Fit HMMs to multiple imputation data*

Description

Fit a (multivariate) hidden Markov model to multiple imputation data. Multiple imputation is a method for accommodating missing data, temporal-irregularity, or location measurement error in hidden Markov models, where pooled parameter estimates reflect uncertainty attributable to observation error.

Usage

```
MIfitHMM(miData, nSims, ncores = 1, poolEstimates = TRUE, alpha = 0.95,
  nbStates, dist, Par0, beta0 = NULL, delta0 = NULL, estAngleMean = NULL,
  circularAngleMean = NULL, formula = ~1, formulaDelta = ~1,
  stationary = FALSE, verbose = NULL, nlmPar = NULL, fit = TRUE,
  useInitial = FALSE, DM = NULL, cons = NULL, userBounds = NULL,
  workBounds = NULL, workcons = NULL, stateNames = NULL,
  knownStates = NULL, fixPar = NULL, retryFits = 0, retrySD = NULL,
  optMethod = "nlm", control = list(), prior = NULL, modelName = NULL,
  covNames = NULL, spatialCovs = NULL, centers = NULL, centroids = NULL,
  angleCovs = NULL, method = "IS", parIS = 1000, dfSim = Inf,
  grid.eps = 1, crit = 2.5, scaleSim = 1, force.quad = TRUE,
  fullPost = TRUE, dfPostIS = Inf, scalePostIS = 1, thetaSamp = NULL)
```

Arguments

miData	A crwData object, a crwSim object, or a list of momentuHMMData objects.
nSims	Number of imputations in which to fit the HMM using fitHMM. If miData is a list of momentuHMMData objects, nSims cannot exceed the length of miData.
ncores	Number of cores to use for parallel processing. Default: 1 (no parallel processing).
poolEstimates	Logical indicating whether or not to calculate pooled parameter estimates across the nSims imputations using MIpool. Default: TRUE.
alpha	Significance level for calculating confidence intervals of pooled estimates when poolEstimates=TRUE (see MIpool). Default: 0.95.
nbStates	Number of states of the HMM. See fitHMM.

dist
: A named list indicating the probability distributions of the data streams. See fitHMM.

Par0
: A named list containing vectors of initial state-dependent probability distribution parameters for each data stream specified in dist. See fitHMM. Par0 may also be a list of length nSims, where each element is a named list containing vectors of initial state-dependent probability distribution parameters for each imputation. Note that if useInitial=TRUE then Par0 is ignored after the first imputation.

beta0
: Initial matrix of regression coefficients for the transition probabilities. See fitHMM. beta0 may also be a list of length nSims, where each element is an initial matrix of regression coefficients for the transition probabilities for each imputation.

delta0
: Initial values for the initial distribution of the HMM. See fitHMM. delta0 may also be a list of length nSims, where each element is the initial values for the initial distribution of the HMM for each imputation.

estAngleMean
: An optional named list indicating whether or not to estimate the angle mean for data streams with angular distributions ('vm' and 'wrpcauchy'). See fitHMM.

circularAngleMean
: An optional named list indicating whether to use circular-linear (FALSE) or circular-circular (TRUE) regression on the mean of circular distributions ('vm' and 'wrpcauchy') for turning angles. See fitHMM.

formula
: Regression formula for the transition probability covariates. See fitHMM.

formulaDelta
: Regression formula for the initial distribution. See fitHMM.

stationary
: FALSE if there are covariates. If TRUE, the initial distribution is considered equal to the stationary distribution. See fitHMM.

verbose
: Deprecated: please use print.level in nlmPar argument. Determines the print level of the nlm 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. Ignored unless optMethod="nlm".

nlmPar
: List of parameters to pass to the optimization function nlm (which should be either print.level, gradtol, stepmax, steptol, iterlim, or hessian – see nlm's documentation for more detail). Ignored unless optMethod="nlm".

fit
: TRUE if the HMM should be fitted to the data, FALSE otherwise. See fitHMM. If fit=FALSE and miData is a crwData object, then MIfitHMM returns a list containing a momentuHMMData object (if nSims=1) or, if nSims>1, a crwSim object.

useInitial
: Logical indicating whether or not to use parameter estimates for the first model fit as initial values for all subsequent model fits. If ncores>1 then the first model is fit on a single core and then used as the initial values for all subsequent model fits on each core (in this case, the progress of the initial model fit can be followed using the verbose argument). Default: FALSE.

DM
: An optional named list indicating the design matrices to be used for the probability distribution parameters of each data stream. See fitHMM.

cons
: Deprecated: please use workBounds instead. An optional named list of vectors specifying a power to raise parameters corresponding to each column of the design matrix for each data stream. See fitHMM.

userBounds
: An optional named list of 2-column matrices specifying bounds on the natural (i.e, real) scale of the probability distribution parameters for each data stream. See fitHMM.

workBounds
: An optional named list of 2-column matrices specifying bounds on the working scale of the probability distribution, transition probability, and initial distribution parameters. See fitHMM.

workcons
: Deprecated: please use workBounds instead. An optional named list of vectors specifying constants to add to the regression coefficients on the working scale for each data stream. See fitHMM.

stateNames
: Optional character vector of length nbStates indicating state names.

knownStates
: Vector of values of the state process which are known prior to fitting the model (if any). See fitHMM. If miData is a list of momentuHMMData objects, then knownStates can alternatively be a list of vectors containing the known values for the state process for each element of miData.

fixPar
: An optional list of vectors indicating parameters which are assumed known prior to fitting the model. See fitHMM.

retryFits
: Non-negative integer indicating the number of times to attempt to iteratively fit the model using random perturbations of the current parameter estimates as the initial values for likelihood optimization. See fitHMM.

retrySD
: An optional list of scalars or vectors indicating the standard deviation to use for normal perturbations of each working scale parameter when retryFits>0. See fitHMM.

optMethod
: The optimization method to be used. Can be "nlm" (the default; see nlm), "Nelder-Mead" (see optim), or "SANN" (see optim).

control
: A list of control parameters to be passed to optim (ignored unless optMethod="Nelder-Mead" or optMethod="SANN").

prior
: A function that returns the log-density of the working scale parameter prior distribution(s). See fitHMM.

modelName
: An optional character string providing a name for the fitted model. If provided, modelName will be returned in print.momentuHMM, AIC.momentuHMM, AICweights, and other functions.

covNames
: Names of any covariates in miData$crwPredict (if miData is a crwData object; otherwise covNames is ignored). See prepData.

spatialCovs
: List of raster layer(s) for any spatial covariates not included in miData$crwPredict (if miData is a crwData object; otherwise spatialCovs is ignored). See prepData.

centers
: 2-column matrix providing the x-coordinates (column 1) and y-coordinates (column 2) for any activity centers (e.g., potential centers of attraction or repulsion) from which distance and angle covariates will be calculated based on realizations of the position process. See prepData. Ignored unless miData is a crwData object.

centroids
: List where each element is a data frame containing the x-coordinates ('x'), y-coordinates ('y'), and times (with user-specified name, e.g., 'time') for centroids (i.e., dynamic activity centers where the coordinates can change over time) from which distance and angle covariates will be calculated based on the location data. See prepData. Ignored unless miData is a crwData object.

angleCovs	Character vector indicating the names of any circular-circular regression angular covariates in miData$crwPredict that need conversion from standard direction (in radians relative to the x-axis) to turning angle (relative to previous movement direction) See prepData. Ignored unless miData is a crwData object.
method	Method for obtaining weights for movement parameter samples. See crwSimulator. Ignored unless miData is a crwData object.
parIS	Size of the parameter importance sample. See crwSimulator. Ignored unless miData is a crwData object.
dfSim	Degrees of freedom for the t approximation to the parameter posterior. See 'df' argument in crwSimulator. Ignored unless miData is a crwData object.
grid.eps	Grid size for method="quadrature". See crwSimulator. Ignored unless miData is a crwData object.
crit	Criterion for deciding "significance" of quadrature points (difference in log-likelihood). See crwSimulator. Ignored unless miData is a crwData object.
scaleSim	Scale multiplier for the covariance matrix of the t approximation. See 'scale' argument in crwSimulator. Ignored unless miData is a crwData object.
force.quad	A logical indicating whether or not to force the execution of the quadrature method for large parameter vectors. See crwSimulator. Default: TRUE. Ignored unless miData is a crwData object and method=``quadrature''.
fullPost	Logical indicating whether to draw parameter values as well to simulate full posterior. See crwPostIS. Ignored unless miData is a crwData object.
dfPostIS	Degrees of freedom for multivariate t distribution approximation to parameter posterior. See 'df' argument in crwPostIS. Ignored unless miData is a crwData object.
scalePostIS	Extra scaling factor for t distribution approximation. See 'scale' argument in crwPostIS. Ignored unless miData is a crwData object.
thetaSamp	If multiple parameter samples are available in crwSimulator objects, setting thetaSamp=n will use the nth sample. Defaults to the last. See crwSimulator and crwPostIS. Ignored unless miData is a crwData object.

Details

miData can either be a crwData object (as returned by crawlWrap), a crwSim object (as returned by MIfitHMM when fit=FALSE), or a list of momentuHMMData objects (e.g., each element of the list as returned by prepData).

If miData is a crwData object, MIfitHMM uses a combination of crwSimulator, crwPostIS, prepData, and fitHMM to draw nSims realizations of the position process and fit the specified HMM to each imputation of the data. The vast majority of MIfitHMM arguments are identical to the corresponding arguments from these functions.

If miData is a crwData object, nSims determines both the number of realizations of the position process to draw (using crwSimulator and crwPostIS) as well as the number of HMM fits.

If miData is a crwSim object or a list of momentuHMMData object(s), the specified HMM will simply be fitted to each of the momentuHMMData objects and all arguments related to crwSimulator, crwPostIS, or prepData are ignored.

Value

If nSims>1, poolEstimates=TRUE, and fit=TRUE, a miHMM object, i.e., a list consisting of:

miSum: miSum object returned by MIpool.

HMMfits: List of length nSims comprised of momentuHMM objects.

If poolEstimates=FALSE and fit=TRUE, a list of length nSims consisting of momentuHMM objects is returned.

However, if fit=FALSE and miData is a crwData object, then MIfitHMM returns a crwSim object, i.e., a list containing miData (a list of momentuHMMData objects) and crwSimulator (a list of crwSimulator objects),and most other arguments related to fitHMM are ignored.

References

Hooten M.B., Johnson D.S., McClintock B.T., Morales J.M. 2017. Animal Movement: Statistical Models for Telemetry Data. CRC Press, Boca Raton.

McClintock B.T. 2017. Incorporating telemetry error into hidden Markov movement models using multiple imputation. Journal of Agricultural, Biological, and Environmental Statistics.

See Also

crawlWrap, crwPostIS, crwSimulator, fitHMM, getParDM, MIpool, prepData

Examples

```
# Don't run because it takes too long on a single core
## Not run:
# extract simulated obsData from example data
obsData <- miExample$obsData

# extract crwMLE inputs from example data
inits <- miExample$inits # initial state
err.model <- miExample$err.model # error ellipse model

# create crwData object by fitting crwMLE models to obsData and predict locations
# at default intervals for both individuals
crwOut <- crawlWrap(obsData=obsData,
         theta=c(4,0),fixPar=c(1,1,NA,NA),
         initial.state=inits,
         err.model=err.model)

# HMM specifications
nbStates <- 2
stepDist <- "gamma"
angleDist <- "vm"
mu0 <- c(20,70)
sigma0 <- c(10,30)
kappa0 <- c(1,1)
stepPar0 <- c(mu0,sigma0)
```

```
anglePar0 <- c(-pi/2,pi/2,kappa0)
formula <- ~cov1+cos(cov2)
nbCovs <- 2
beta0 <- matrix(c(rep(-1.5,nbStates*(nbStates-1)),rep(0,nbStates*(nbStates-1)*nbCovs)),
                nrow=nbCovs+1,byrow=TRUE)

# first fit HMM to best predicted position process
bestData<-prepData(crwOut,covNames=c("cov1","cov2"))
bestFit<-fitHMM(bestData,
                nbStates=nbStates,dist=list(step=stepDist,angle=angleDist),
                Par0=list(step=stepPar0,angle=anglePar0),beta0=beta0,
                formula=formula,estAngleMean=list(angle=TRUE))

print(bestFit)

# extract estimates from 'bestFit'
bPar0 <- getPar(bestFit)

# Fit nSims=5 imputations of the position process
miFits<-MIfitHMM(miData=crwOut,nSims=5,
                  nbStates=nbStates,dist=list(step=stepDist,angle=angleDist),
                  Par0=bPar0$Par,beta0=bPar0$beta,delta0=bPar0$delta,
                  formula=formula,estAngleMean=list(angle=TRUE),
                  covNames=c("cov1","cov2"))

# print pooled estimates
print(miFits)

## End(Not run)
```

---

miHMM *Constructor of* miHMM *objects*

Description

Constructor of miHMM objects

Usage

```
miHMM(m)
```

Arguments

m	A list with attributes miSum (a miSum object) and HMMfits (a list of momentuHMM objects). miHMM objects are returned by MIfitHMM when arguments fit=TRUE, nSims>1, and poolEstimates=TRUE.

Value

An object miHMM.

MIpool *Calculate pooled parameter estimates and states across multiple imputations*

Description

Calculate pooled parameter estimates and states across multiple imputations

Usage

```
MIpool(HMMfits, alpha = 0.95, ncores = 1, covs = NULL)
```

Arguments

HMMfits	List comprised of momentuHMM objects
alpha	Significance level for calculating confidence intervals of pooled estimates (including location error ellipses). Default: 0.95.
ncores	Number of cores to use for parallel processing. Default: 1 (no parallel processing).
covs	Data frame consisting of a single row indicating the covariate values to be used in the calculation of pooled natural parameters. For any covariates that are not specified using covs, the means of the covariate(s) across the imputations are used (unless the covariate is a factor, in which case the first factor in the data is used). By default, no covariates are specified.

Details

Pooled estimates, standard errors, and confidence intervals are calculated using standard multiple imputation formulas. Working scale parameters are pooled using MIcombine and t-distributed confidence intervals. Natural scale parameters and normally-distributed confidence intervals are calculated by transforming the pooled working scale parameters and, if applicable, are based on covariate means across all imputations (and/or values specified in covs).

Note that pooled estimates for timeInStates and stateProbs do not include within-model uncertainty and are based entirely on across-model variability.

Value

A miSum object, i.e., a list comprised of model and pooled parameter summaries, including data (averaged across imputations), conditions, Par, and MIcombine (as returned by MIcombine for working parameters).

miSum$Par is a list comprised of:

beta	Pooled estimates for the working parameters

`real`	Estimates for the natural parameters based on pooled working parameters and covariate means (or `covs`) across imputations (if applicable)
`timeInStates`	The proportion of time steps assigned to each state
`states`	The most freqent state assignment for each time step based on the `viterbi` algorithm for each model fit
`stateProbs`	Pooled state probability estimates for each time step

Examples

```
## Not run:
# Extract data and crawl inputs from miExample
obsData <- miExample$obsData
inits <- miExample$inits
err.model <- miExample$err.model

# Fit crawl to obsData
crwOut <- crawlWrap(obsData,theta=c(4,0),fixPar=c(1,1,NA,NA),
                    initial.state=inits,err.model=err.model)

# Fit four imputations
bPar <- miExample$bPar
HMMfits <- MIfitHMM(crwOut,nSims=4,poolEstimates=FALSE,
                   nbStates=2,dist=list(step="gamma",angle="vm"),
                   Par0=bPar$Par,beta0=bPar$beta,delta0=bPar$delta,
                   formula=~cov1+cos(cov2),
                   estAngleMean=list(angle=TRUE),
                   covNames=c("cov1","cov2"))

# Pool estimates
miSum <- MIpool(HMMfits)
print(miSum)

## End(Not run)
```

`miSum` *Constructor of* `miSum` *objects*

Description

Constructor of `miSum` objects

Usage

```
miSum(m)
```

Arguments

m A list of attributes required for multiple imputation summaries: data (averaged across imputations), Par (the pooled estimates of the parameters of the model), conditions (conditions used to fit the model), and MIcombine (as returned by MIcombine for the working parameters).

Value

An object miSum.

---

momentuHMM *Constructor of* momentuHMM *objects*

Description

Constructor of momentuHMM objects

Usage

```
momentuHMM(m)
```

Arguments

m A list of attributes of the fitted model: mle (the maximum likelihood estimates of the parameters of the model), data (the fitHMM data), mod (the object returned by the fitHMM numerical optimizer nlm), conditions (conditions used to fit the model: dist, zeroInflation, estAngleMean, circularAngleMean stationary, formula, cons, userBounds, bounds, workcons, DM, etc.), stateNames, and rawCovs (optional – only if there are transition probability matrix covariates in the data).

Value

An object momentuHMM.

---

momentuHMMData *Constructor of* momentuHMMData *objects*

Description

Constructor of momentuHMMData objects

Usage

```
momentuHMMData(data)
```

Arguments

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

Value

An object `momentuHMMData`.

`n2w` *Scaling function: natural to working parameters.*

Description

Scales each data stream probability distribution parameter from its natural interval to the set of real numbers, to allow for unconstrained optimization. Used during the optimization of the log-likelihood. Parameters of any data streams for which a design matrix is specified are ignored.

Usage

```
n2w(par, bounds, beta, delta = NULL, nbStates, estAngleMean, DM, cons,
  workcons, Bndind)
```

Arguments

`par`	Named list of vectors containing the initial parameter values for each data stream.
`bounds`	Named list of 2-column matrices specifying bounds on the natural (i.e, real) scale of the probability distribution parameters for each data stream.
`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`	Named list indicating whether or not to estimate the angle mean for data streams with angular distributions ('vm' and 'wrpcauchy').
`DM`	An optional named list indicating the design matrices to be used for the probability distribution parameters of each data stream. Each element of `DM` can either be a named list of linear regression formulas or a matrix.
`cons`	Named list of vectors specifying a power to raise parameters corresponding to each column of the design matrix for each data stream.
`workcons`	Named list of vectors specifying constants to add to the regression coefficients on the working scale for each data stream.
`Bndind`	Named list indicating whether `DM` is NULL with default parameter bounds for each data stream.

Value

A vector of unconstrained parameters.

Examples

```
## Not run:
m<-example$m
nbStates <- 2
nbCovs <- 2
parSize <- list(step=2,angle=2)
par <- list(step=c(t(m$mle$step)),angle=c(t(m$mle$angle)))
bounds <- m$conditions$bounds
beta <- matrix(rnorm(6),ncol=2,nrow=3)
delta <- c(0.6,0.4)

#working parameters
wpar <- momentuHMM:::n2w(par,bounds,beta,log(delta[-1]/delta[1]),nbStates,
m$conditions$estAngleMean,NULL,m$conditions$cons,m$conditions$workcons,m$conditions$Bndind)

#natural parameter
p <-   momentuHMM:::w2n(wpar,bounds,parSize,nbStates,nbCovs,m$conditions$estAngleMean,
m$conditions$circularAngleMean,lapply(m$conditions$dist,function(x) x=="vmConsensus"),
m$conditions$stationary,m$conditions$cons,m$conditions$fullDM,
m$conditions$DMind,m$conditions$workcons,1,m$conditions$dist,m$conditions$Bndind,
matrix(1,nrow=length(unique(m$data$ID)),ncol=1),covsDelta=m$covsDelta,
workBounds=m$conditions$workBounds)

## End(Not run)
```

---

nLogLike *Negative log-likelihood function*

Description

Negative log-likelihood function

Usage

```
nLogLike(wpar, nbStates, formula, bounds, parSize, data, dist, covs,
  estAngleMean, circularAngleMean, consensus, zeroInflation, oneInflation,
  stationary = FALSE, cons, fullDM, DMind, workcons, Bndind, knownStates,
  fixPar, wparIndex, nc, meanind, covsDelta, workBounds, prior = NULL)
```

Arguments

wpar	Vector of working parameters.
nbStates	Number of states of the HMM.

`formula`	Regression formula for the transition probability covariates.
`bounds`	Named list of 2-column matrices specifying bounds on the natural (i.e, real) scale of the probability distribution parameters for each data stream.
`parSize`	Named list indicating the number of natural parameters of the data stream probability distributions
`data`	An object `momentuHMMData`.
`dist`	Named list indicating the probability distributions of the data streams.
`covs`	data frame containing the beta model covariates (if any)
`estAngleMean`	Named list indicating whether or not to estimate the angle mean for data streams with angular distributions ('vm' and 'wrpcauchy').
`circularAngleMean`	Named list indicating whether to use circular-linear (FALSE) or circular-circular (TRUE) regression on the mean of circular distributions ('vm' and 'wrpcauchy') for turning angles.
`consensus`	Named list indicating whether to use the circular-circular regression consensus model
`zeroInflation`	Named list of logicals indicating whether the probability distributions of the data streams are zero-inflated.
`oneInflation`	Named list of logicals indicating whether the probability distributions of the data streams are one-inflated.
`stationary`	`FALSE` if there are covariates. If `TRUE`, the initial distribution is considered equal to the stationary distribution. Default: `FALSE`.
`cons`	Named list of vectors specifying a power to raise parameters corresponding to each column of the design matrix for each data stream.
`fullDM`	Named list containing the full (i.e. not shorthand) design matrix for each data stream.
`DMind`	Named list indicating whether `fullDM` includes individual- and/or temporal-covariates for each data stream specifies (-1,1) bounds for the concentration parameters instead of the default [0,1) bounds.
`workcons`	Named list of vectors specifying constants to add to the regression coefficients on the working scale for each data stream.
`Bndind`	Named list indicating whether `DM` is NULL with default parameter bounds for each data stream.
`knownStates`	Vector of values of the state process which are known prior to fitting the model (if any).
`fixPar`	Vector of working parameters which are assumed known prior to fitting the model (NA indicates parameters is to be estimated).
`wparIndex`	Vector of indices for the elements of `fixPar` that are not NA.
`nc`	indicator for zeros in fullDM
`meanind`	index for circular-circular regression mean angles with at least one non-zero entry in fullDM
`covsDelta`	data frame containing the delta model covariates (if any)

workBounds named list of 2-column matrices specifying bounds on the working scale of the probability distribution, transition probability, and initial distribution parameters

prior A function that returns the log-density of the working scale parameter prior distribution(s)

Value

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

Examples

```
## Not run:
# data is a momentuHMMData object (as returned by prepData), automatically loaded with the package
data <- example$m$data
m<-example$m
Par <- getPar(m)
nbStates <- length(m$stateNames)

inputs <- momentuHMM:::checkInputs(nbStates,m$conditions$dist,Par$Par,m$conditions$estAngleMean,
        m$conditions$circularAngleMean,m$conditions$zeroInflation,m$conditions$oneInflation,
        m$conditions$DM,m$conditions$userBounds,m$conditions$cons,m$conditions$workcons,
          m$stateNames)

wpar <- momentuHMM:::n2w(Par$Par,m$conditions$bounds,Par$beta,log(Par$delta[-1]/Par$delta[1]),
      nbStates,m$conditions$estAngleMean,m$conditions$DM,m$conditions$cons,m$conditions$workcons,
        m$conditions$Bndind)

l <- momentuHMM:::nLogLike(wpar,nbStates,m$conditions$formula,m$conditions$bounds,
     inputs$p$parSize,data,inputs$dist,model.matrix(m$conditions$formula,data),
     m$conditions$estAngleMean,m$conditions$circularAngleMean,inputs$consensus,
     m$conditions$zeroInflation,m$conditions$oneInflation,m$conditions$stationary,
     m$conditions$cons,m$conditions$fullDM,m$conditions$DMind,m$conditions$workcons,
     m$conditions$Bndind,m$knownStates,unlist(m$conditions$fixPar),
     m$conditions$wparIndex,covsDelta=m$covsDelta,workBounds=m$conditions$workBounds)

## End(Not run)
```

---

nLogLike_rcpp *Negative log-likelihood*

Description

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

Usage

```
nLogLike_rcpp(nbStates, covs, data, dataNames, dist, Par, aInd, zeroInflation,
  oneInflation, stationary, knownStates)
```

Arguments

`nbStates`	Number of states,
`covs`	Covariates,
`data`	A `momentuHMMData` object of the observations,
`dataNames`	Character vector containing the names of the data streams,
`dist`	Named list indicating the probability distributions of the data streams.
`Par`	Named list containing the state-dependent parameters of the data streams, matrix of regression coefficients for the transition probabilities ('beta'), and initial distribution ('delta').
`aInd`	Vector of indices of the rows at which the data switches to another animal
`zeroInflation`	Named list of logicals indicating whether the probability distributions of the data streams are zero-inflated.
`oneInflation`	Named list of logicals indicating whether the probability distributions of the data streams are one-inflated.
`stationary`	`false` if there are covariates. If `true`, the initial distribution is considered equal to the stationary distribution. Default: `false`.
`knownStates`	Vector of values of the state process which are known prior to fitting the model (if any). Default: NULL (states are not known). This should be a vector with length the number of rows of 'data'; each element should either be an integer (the value of the known states) or NA if the state is not known.

Value

Negative log-likelihood

`parDef` *Parameters definition*

Description

Parameters definition

Usage

```
parDef(dist, nbStates, estAngleMean, zeroInflation, oneInflation, DM,
  userBounds = NULL)
```

Arguments

dist	Named list indicating the probability distributions of the data streams.
nbStates	Number of states of the HMM.
estAngleMean	Named list indicating whether or not to estimate the angle mean for data streams with angular distributions ('vm' and 'wrpcauchy').
zeroInflation	Named list of logicals indicating whether the probability distributions of the data streams should be zero-inflated.
oneInflation	Named list of logicals indicating whether the probability distributions of the data streams are one-inflated.
DM	An optional named list indicating the design matrices to be used for the probability distribution parameters of each data stream. Each element of `DM` can either be a named list of linear regression formulas or a matrix.
userBounds	An optional named list of 2-column matrices specifying bounds on the natural (i.e, real) scale of the probability distribution parameters for each data stream. For example, for a 2-state model using the wrapped Cauchy ('wrpcauchy') distribution for a data stream named 'angle' with `estAngleMean$angle=TRUE`), `userBounds=list(angle=matrix(c(-pi,-pi,-1,-1,pi,pi,1,1),4,2))` specifies (-1,1) bounds for the concentration parameters instead of the default [0,1) bounds.

Value

A list of:

parSize	Named list indicating the number of natural parameters of the data stream probability distributions.
bounds	Named list of 2-column matrices specifying bounds on the natural (i.e, real) scale of the probability distribution parameters for each data stream.
parNames	Names of parameters of the probability distribution for each data stream.
Bndind	Named list indicating whether `DM` is NULL with default parameter bounds for each data stream.

Examples

```
## Not run:
pD<-momentuHMM:::parDef(list(step="gamma",angle="wrpcauchy"),
    nbStates=2,list(step=FALSE,angle=FALSE),list(step=FALSE,angle=FALSE),
    list(step=FALSE,angle=FALSE),NULL,NULL)

## End(Not run)
```

plot.crwData *Plot* crwData

Description

Plot observed locations, error ellipses (if applicable), predicted locations, and prediction intervals from crwData object.

Usage

```
## S3 method for class 'crwData'
plot(x, animals = NULL, compact = FALSE, ask = TRUE,
  plotEllipse = TRUE, crawlPlot = FALSE, ...)
```

Arguments

x	An object crwData (as returned by crawlWrap).
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). Ignored unless crwPredictPlot=FALSE.
ask	If TRUE, the execution pauses between each plot.
plotEllipse	If TRUE (the default) then error ellipses are plotted (if applicable). Ignored unless crwPredictPlot=FALSE.
crawlPlot	Logical indicating whether or not to create individual plots using crwPredictPlot. See crwPredictPlot for details.
...	Further arguments for passing to crwPredictPlot

Details

In order for error ellipses to be plotted, the names for the semi-major axis, semi-minor axis, and orientation in x$crwPredict must respectively be error_semimajor_axis, error_semiminor_axis, and error_ellipse_orientation.

If the crwData object was created using data generated by simData or simObsData, then the true locations (mux,muy) are also plotted.

See Also

crwPredictPlot

Examples

```
## Not run:
# extract simulated obsData from example data
obsData <- miExample$obsData

# extract crwMLE inputs from example data
inits <- miExample$inits # initial state
err.model <- miExample$err.model # error ellipse model

# create crwData object
crwOut <- crawlWrap(obsData=obsData,
         theta=c(4,0),fixPar=c(1,1,NA,NA),
         initial.state=inits,
         err.model=err.model)

plot(crwOut,compact=TRUE,ask=FALSE,plotEllipse=FALSE)

## End(Not run)
```

`plot.miHMM` *Plot* `miHMM`

Description

For multiple imputation analyses, plot the pooled data stream densities over histograms of the data, probability distribution parameters and transition probabilities as functions of the covariates, and maps of the animals' tracks colored by the decoded states.

Usage

```
## S3 method for class 'miHMM'
plot(x, animals = NULL, covs = NULL, ask = TRUE,
  breaks = "Sturges", hist.ylim = NULL, sepAnimals = FALSE,
  sepStates = FALSE, col = NULL, cumul = TRUE, plotTracks = TRUE,
  plotCI = FALSE, alpha = 0.95, plotStationary = FALSE,
  plotEllipse = TRUE, ...)
```

Arguments

`x`	Object `miHMM` (as returned by `MIfitHMM`)
`animals`	Vector of indices or IDs of animals for which information will be plotted. Default: `NULL` ; all animals are plotted.
`covs`	Data frame consisting of a single row indicating the covariate values to be used in plots. If none are specified, the means of any covariates appearing in the model are used (unless covariate is a factor, in which case the first factor appearing in the data is used).

`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).
`cumul`	If TRUE, the sum of weighted densities is plotted (default).
`plotTracks`	If TRUE, the Viterbi-decoded tracks are plotted (default).
`plotCI`	Logical indicating whether to include confidence intervals in natural parameter plots (default: FALSE)
`alpha`	Significance level of the confidence intervals (if `plotCI=TRUE`). Default: 0.95 (i.e. 95% CIs).
`plotStationary`	Logical indicating whether to plot the stationary state probabilities as a function of any covariates (default: FALSE)
`plotEllipse`	Logical indicating whether to plot error ellipses around imputed location means. Default: TRUE.
`...`	Additional arguments passed to `plot` and `hist` functions. These can currently include `asp`, `cex`, `cex.axis`, `cex.lab`, `cex.legend`, `cex.main`, `legend.pos`, and `lwd`. See `par`. `legend.pos` can be a single keyword from the list "bottomright", "bottom", "bottomleft", "left", "topleft", "top", "topright", "right", and "center". Note that `asp` and `cex` only apply to plots of animal tracks.

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 each imputation). 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

```
## Not run:
# Extract data and crawl inputs from miExample
obsData <- miExample$obsData
inits <- miExample$inits
err.model <- miExample$err.model

# Fit crawl to obsData
crwOut <- crawlWrap(obsData,theta=c(4,0),fixPar=c(1,1,NA,NA),
                    initial.state=inits,err.model=err.model)

# Fit four imputations
bPar <- miExample$bPar
HMMfits <- MIfitHMM(crwOut,nSims=4,poolEstimates=FALSE,
```

```
                    nbStates=2,dist=list(step="gamma",angle="vm"),
                    Par0=bPar$Par,beta0=bPar$beta,delta0=bPar$delta,
                    formula=~cov1+cos(cov2),
                    estAngleMean=list(angle=TRUE),
                    covNames=c("cov1","cov2"))

miHMM <- momentuHMM:::miHMM(list(miSum=MIpool(HMMfits),HMMfits=HMMfits))
plot(miHMM)

## End(Not run)
```

---

plot.miSum *Plot* miSum

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 'miSum'
plot(x, animals = NULL, covs = NULL, ask = TRUE,
  breaks = "Sturges", hist.ylim = NULL, sepAnimals = FALSE,
  sepStates = FALSE, col = NULL, cumul = TRUE, plotTracks = TRUE,
  plotCI = FALSE, alpha = 0.95, plotStationary = FALSE,
  plotEllipse = TRUE, ...)
```

Arguments

x	Object miSum (as return by MIpool)
animals	Vector of indices or IDs of animals for which information will be plotted. Default: NULL ; all animals are plotted.
covs	Data frame consisting of a single row indicating the covariate values to be used in plots. If none are specified, the means of any covariates appearing in the model are used (unless covariate is a factor, in which case the first factor appearing in the data is used).
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).
cumul	If TRUE, the sum of weighted densities is plotted (default).

plotTracks	If TRUE, the Viterbi-decoded tracks are plotted (default).
plotCI	Logical indicating whether to include confidence intervals in natural parameter plots (default: FALSE)
alpha	Significance level of the confidence intervals (if plotCI=TRUE). Default: 0.95 (i.e. 95% CIs).
plotStationary	Logical indicating whether to plot the stationary state probabilities as a function of any covariates (default: FALSE)
plotEllipse	Logical indicating whether to plot error ellipses around imputed location means. Default: TRUE.
...	Additional arguments passed to plot and hist functions. These can currently include asp, cex, cex.axis, cex.lab, cex.legend, cex.main, legend.pos, and lwd. See par. legend.pos can be a single keyword from the list "bottomright", "bottom", "bottomleft", "left", "topleft", "top", "topright", "right", and "center". Note that asp and cex only apply to plots of animal tracks.

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 each imputation). 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

```
## Not run:
# Extract data and crawl inputs from miExample
obsData <- miExample$obsData
inits <- miExample$inits
err.model <- miExample$err.model

# Fit crawl to obsData
crwOut <- crawlWrap(obsData,theta=c(4,0),fixPar=c(1,1,NA,NA),
                    initial.state=inits,err.model=err.model)

# Fit four imputations
bPar <- miExample$bPar
HMMfits <- MIfitHMM(crwOut,nSims=4,poolEstimates=FALSE,
                   nbStates=2,dist=list(step="gamma",angle="vm"),
                   Par0=bPar$Par,beta0=bPar$beta,delta0=bPar$delta,
                   formula=~cov1+cos(cov2),
                   estAngleMean=list(angle=TRUE),
                   covNames=c("cov1","cov2"))

# Pool estimates
miSum <- MIpool(HMMfits)
plot(miSum)

## End(Not run)
```

plot.momentuHMM *Plot* momentuHMM

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 'momentuHMM'
plot(x, animals = NULL, covs = NULL, ask = TRUE,
  breaks = "Sturges", hist.ylim = NULL, sepAnimals = FALSE,
  sepStates = FALSE, col = NULL, cumul = TRUE, plotTracks = TRUE,
  plotCI = FALSE, alpha = 0.95, plotStationary = FALSE, ...)
```

Arguments

x	Object momentuHMM
animals	Vector of indices or IDs of animals for which information will be plotted. Default: NULL ; all animals are plotted.
covs	Data frame consisting of a single row indicating the covariate values to be used in plots. If none are specified, the means of any covariates appearing in the model are used (unless covariate is a factor, in which case the first factor in the data is used).
ask	If TRUE, the execution pauses between each plot.
breaks	Histogram parameter. See hist documentation.
hist.ylim	An optional named list of vectors specifying ylim=c(ymin,ymax) for the data stream histograms. See hist documentation. Default: NULL ; the function sets default values for all data streams.
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).
cumul	If TRUE, the sum of weighted densities is plotted (default).
plotTracks	If TRUE, the Viterbi-decoded tracks are plotted (default).
plotCI	Logical indicating whether to include confidence intervals in natural parameter plots (default: FALSE)
alpha	Significance level of the confidence intervals (if plotCI=TRUE). Default: 0.95 (i.e. 95% CIs).
plotStationary	Logical indicating whether to plot the stationary state probabilities as a function of any covariates (default: FALSE). Ignored unless covariate are included in formula.

... Additional arguments passed to plot and hist functions. These can currently include asp, cex, cex.axis, cex.lab, cex.legend, cex.main, legend.pos, and lwd. See par. legend.pos can be a single keyword from the list “bottomright”, “bottom”, “bottomleft”, “left”, “topleft”, “top”, “topright”, “right”, and “center”. Note that asp and cex only apply to plots of animal tracks.

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.

Confidence intervals for natural parameters are calculated from the working parameter point and covariance estimates using finite-difference approximations of the first derivative for the transformation (see grad). For example, if dN is the numerical approximation of the first derivative of the transformation `N = exp(x_1 * B_1 + x_2 * B_2)` for covariates (x_1, x_2) and working parameters (B_1, B_2), then `var(N)=dN %*% Sigma %*% dN`, where `Sigma=cov(B_1,B_2)`, and normal confidence intervals can be constructed as `N +/- qnorm(1-(1-alpha)/2) * se(N)`.

Examples

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

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

---

plot.momentuHMMData *Plot* momentuHMMData

Description

Plot momentuHMMData

Usage

```
## S3 method for class 'momentuHMMData'
plot(x, dataNames = c("step", "angle"),
  animals = NULL, compact = FALSE, ask = TRUE, breaks = "Sturges", ...)
```

Arguments

x	An object momentuHMMData
dataNames	Names of the variables to plot. Default is dataNames=c("step","angle").
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 momentuHMMData object (as returned by prepData), automatically loaded with the package
data <- example$m$data

plot(data,dataNames=c("step","angle","cov1","cov2"),
     compact=TRUE,breaks=20,ask=FALSE)
```

---

plotPR *Plot pseudo-residuals*

Description

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

Usage

```
plotPR(m, lag.max = NULL, ncores = 1)
```

Arguments

m	A momentuHMM, miHMM, HMMfits, or miSum object.
lag.max	maximum lag at which to calculate the acf. See acf.
ncores	number of cores to use for parallel processing

Details

- If some turning angles in the data are equal to pi, the corresponding pseudo-residuals will not be included. Indeed, given that the turning angles are defined on (-pi,pi], an angle of pi results in a pseudo-residual of +Inf (check Section 6.2 of reference for more information on the computation of pseudo-residuals).
- If some data streams are zero-inflated and/or one-inflated, 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).
- For multiple imputation analyses, if m is a miHMM object or a list of momentuHMM objects, then the pseudo-residuals are individually calculated and plotted for each model fit. Note that pseudo-residuals for miSum objects (as returned by MIpool) are based on pooled parameter estimates and the means of the data values across all imputations (and therefore may not be particularly meaningful).

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 momentuHMM object (as returned by fitHMM), automatically loaded with the package
m <- example$m

plotPR(m)
```

---

plotSat *Plot observations on satellite image*

Description

Plot tracking data on a satellite map. This function only works with longitude and latitude values (not with UTM coordinates), and uses the package ggmap to fetch a satellite image from Google. An Internet connection is required to use this function.

Usage

```
plotSat(data, zoom = NULL, location = NULL, segments = TRUE,
  compact = TRUE, col = NULL, alpha = 1, size = 1, states = NULL,
  animals = NULL, ask = TRUE, return = FALSE, stateNames = NULL)
```

Arguments

`data`	Data frame of the data, with necessary fields 'x' (longitude values) and 'y' (latitude values).
`zoom`	The zoom level, as defined for `get_map`. Integer value between 3 (continent) and 21 (building).
`location`	Location of the center of the map to be plotted.
`segments`	`TRUE` if segments should be plotted between the observations (default), `FALSE` otherwise.
`compact`	`FALSE` if tracks should be plotted separately, `TRUE` otherwise (default).
`col`	Palette of colours to use for the dots and segments. If not specified, uses default palette.
`alpha`	Transparency argument for `geom_point`.
`size`	Size argument for `geom_point`.
`states`	A sequence of integers, corresponding to the decoded states for these data (such that the observations are colored by states).
`animals`	Vector of indices or IDs of animals/tracks to be plotted. Default: `NULL`; all animals are plotted.

ask	If TRUE, the execution pauses between each plot.
return	If TRUE, the function returns a ggplot object (which can be edited and plotted manually). If FALSE, the function automatically plots the map (default).
stateNames	Optional character vector of length unique(states) indicating state names. Ignored unless states is provided.

Details

If the plot displays the message "Sorry, we have no imagery here", try a lower level of zoom.

References

D. Kahle and H. Wickham. ggmap: Spatial Visualization with ggplot2. The R Journal, 5(1), 144-161. URL: http://journal.r-project.org/archive/2013-1/kahle-wickham.pdf

---

plotSpatialCov *Plot observations on raster image*

Description

Plot tracking data over a raster layer.

Usage

```
plotSpatialCov(data, spatialCov, segments = TRUE, compact = TRUE,
  col = NULL, alpha = 1, size = 1, states = NULL, animals = NULL,
  ask = TRUE, return = FALSE)
```

Arguments

data	Data frame of the location data, with necessary fields 'x' (longitudinal direction) and 'y' (latitudinal direction).
spatialCov	RasterLayer-class object on which to plot the location data
segments	TRUE if segments should be plotted between the observations (default), FALSE otherwise.
compact	FALSE if tracks should be plotted separately, TRUE otherwise (default).
col	Palette of colours to use for the dots and segments. If not specified, uses default palette.
alpha	Transparency argument for geom_point.
size	Size argument for geom_point.
states	A sequence of integers, corresponding to the decoded states for these data. If specified, the observations are colored by states.
animals	Vector of indices or IDs of animals/tracks to be plotted. Default: NULL; all animals are plotted.
ask	If TRUE, the execution pauses between each plot.
return	If TRUE, the function returns a ggplot object (which can be edited and plotted manually). If FALSE, the function automatically plots the map (default).

Examples

```
stepDist <- "gamma"
angleDist <- "vm"

# plot simulated data over forest raster automatically loaded with the packge
spatialCov<-list(forest=forest)
data <- simData(nbAnimals=2,nbStates=2,dist=list(step=stepDist,angle=angleDist),
                Par=list(step=c(100,1000,50,100),angle=c(0,0,0.1,5)),
                beta=matrix(c(5,-10,-25,50),nrow=2,ncol=2,byrow=TRUE),
                formula=~forest,spatialCovs=spatialCov,
                obsPerAnimal=225,states=TRUE)

plotSpatialCov(data,forest,states=data$states)
```

---

plotStates *Plot states*

Description

Plot the states and states probabilities.

Usage

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

Arguments

m	A momentuHMM, miHMM, or miSum 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 momentuHMM 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))
```

plotStationary *Plot stationary state probabilities*

Description

Plot stationary state probabilities

Usage

```
plotStationary(model, covs = NULL, col = NULL, plotCI = FALSE,
  alpha = 0.95, ...)
```

Arguments

model	momentuHMM, miHMM, or miSum object
covs	Optional data frame consisting of a single row indicating the covariate values to be used in plots. If none are specified, the means of any covariates appearing in the model are used (unless covariate is a factor, in which case the first factor in the data is used).
col	Vector or colors for the states (one color per state).
plotCI	Logical indicating whether to include confidence intervals in plots (default: FALSE)
alpha	Significance level of the confidence intervals (if plotCI=TRUE). Default: 0.95 (i.e. 95% CIs).
...	Additional arguments passed to plot. These can currently include cex.axis, cex.lab, cex.legend, cex.main, legend.pos, and lwd. See par. legend.pos can be a single keyword from the list "bottomright", "bottom", "bottomleft", "left", "topleft", "top", "topright", "right", and "center".

Examples

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

plotStationary(m)
```

prepData *Preprocessing of the data streams and covariates*

Description

Preprocessing of the data streams, including calculation of step length, turning angle, and covariates from location data to be suitable for analysis using fitHMM

Usage

```
prepData(data, type = c("UTM", "LL"), coordNames = c("x", "y"),
  covNames = NULL, spatialCovs = NULL, centers = NULL, centroids = NULL,
  angleCovs = NULL)
```

Arguments

data	Either a data frame of data streams or a crwData object (as returned by crawlWrap). If data is a data frame, it can optionally include a field ID (identifiers for the observed individuals), coordinates from which step length ('step') and turning angle ('angle') are calculated, and any covariates (with names matching covNames and/or angleCovs). If step length and turning angle are to be calculated from coordinates, the coordNames argument must identify the names for the x- (longitunal) and y- (latitudinal) coordinates. With the exception of ID and coordNames, all variables in data are treated as data streams unless identified as covariates in covNames and/or angleCovs.
type	'UTM' if easting/northing provided (the default), 'LL' if longitude/latitude. If type='LL' then step lengths are calculated in kilometers and turning angles are based on initial bearings (see turnAngle). Ignored if data is a crwData object.
coordNames	Names of the columns of coordinates in the data data frame. Default: c("x","y"). If coordNames=NULL then step lengths, turning angles, and location covariates (i.e., those specified by spatialCovs, centers, and angleCovs) are not calculated. Ignored if data is a crwData object.
covNames	Character vector indicating the names of any covariates in data dataframe. Any variables in data (other than ID) that are not identified in covNames and/or angleCovs are assumed to be data streams (i.e., missing values will not be accounted for).
spatialCovs	List of Raster-class objects for spatio-temporally referenced covariates. Covariates specified by spatialCovs are extracted from the raster layer(s) based on the location data (and the z values for a raster stack or brick) for each time step. If an element of spatialCovs is a raster stack or brick, then z values must be set using setZ and data must include column(s) of the corresponding z value(s) for each observation (e.g., 'time').
centers	2-column matrix providing the x-coordinates (column 1) and y-coordinates (column 2) for any activity centers (e.g., potential centers of attraction or repulsion) from which distance and angle covariates will be calculated based on the location data. If no row names are provided, then generic names are generated for the

distance and angle covariates (e.g., 'center1.dist', 'center1.angle', 'center2.dist', 'center2.angle'); otherwise the covariate names are derived from the row names of `centers` as `paste0(rep(rownames(centers),each=2),c(".dist",".angle"))`. As with covariates identified in `angleCovs`, note that the angle covariates for each activity center are calculated relative to the previous movement direction (instead of standard direction relative to the x-axis); this is to allow the mean turning angle to be modelled as a function of these covariates using circular-circular regression in `fitHMM` or `MIfitHMM`.

`centroids` List where each element is a data frame containing the x-coordinates ('x'), y-coordinates ('y'), and times (with user-specified name, e.g., 'time') for centroids (i.e., dynamic activity centers where the coordinates can change over time) from which distance and angle covariates will be calculated based on the location data. If any centroids are specified, then `data` must include a column indicating the time of each observation, and this column name must match the corresponding user-specified name of the time column in `centroids` (e.g. 'time'). Times can be numeric or POSIXt. If no list names are provided, then generic names are generated for the distance and angle covariates (e.g., 'centroid1.dist', 'centroid1.angle', 'centroid2.dist', 'centroid2.angle'); otherwise the covariate names are derived from the list names of `centroids` as `paste0(rep(names(centroids),each=2),c(".dist",` As with covariates identified in `angleCovs`, note that the angle covariates for each centroid are calculated relative to the previous movement direction (instead of standard direction relative to the x-axis); this is to allow the mean turning angle to be modelled as a function of these covariates using circular-circular regression in `fitHMM` or `MIfitHMM`.

`angleCovs` Character vector indicating the names of any circular-circular regression angular covariates in `data` or `spatialCovs` that need conversion from standard direction (in radians relative to the x-axis) to turning angle (relative to previous movement direction) using `circAngles`.

Value

An object `momentuHMMData`, i.e., a dataframe of:

`ID` The ID(s) of the observed animal(s)

`...` Data streams (e.g., 'step', 'angle', etc.)

`x` Either easting or longitude (if `coordNames` is specified or `data` is a `crwData` object)

`y` Either norting or latitude (if `coordNames` is specified or `data` is a `crwData` object)

`...` Covariates (if any)

If `data` is a `crwData` object, the `momentuHMMData` object created by `prepData` includes step lengths and turning angles calculated from the best predicted locations (`crwData$crwPredict$mu.x` and `crwData$crwPredict$mu.y`). Prior to using `prepData`, additional data streams or covariates unrelated to location (including z-values associated with `spatialCovs` raster stacks or bricks) can be merged with the `crwData` object using `crawlMerge`.

See Also

crawlMerge, crawlWrap, crwData

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)
cov1 <- rnorm(10)

data <- data.frame(coord1=coord1,coord2=coord2,cov1=cov1)
d <- prepData(data,coordNames=c("coord1","coord2"),covNames="cov1")

# include additional data stream named 'omega'
omega <- rbeta(10,1,1)
data <- data.frame(coord1=coord1,coord2=coord2,omega=omega,cov1=cov1)
d <- prepData(data,coordNames=c("coord1","coord2"),covNames="cov1")

# include 'forest' example raster layer as covariate
data <- data.frame(coord1=coord1*1000,coord2=coord2*1000)
spatialCov <- list(forest=forest)
d <- prepData(data,coordNames=c("coord1","coord2"),spatialCovs=spatialCov)

# include 2 activity centers
data <- data.frame(coord1=coord1,coord2=coord2,cov1=cov1)
d <- prepData(data,coordNames=c("coord1","coord2"),covNames="cov1",
              centers=matrix(c(0,10,0,10),2,2,dimnames=list(c("c1","c2"),NULL)))

# include centroid
data <- data.frame(coord1=coord1,coord2=coord2,cov1=cov1,time=1:10)
d <- prepData(data,coordNames=c("coord1","coord2"),covNames="cov1",
              centroid=list(centroid=data.frame(x=coord1+rnorm(10),
                                                y=coord2+rnorm(10),
                                                time=1:10)))

# Include angle covariate that needs conversion to
# turning angle relative to previous movement direction
u <- rnorm(10) # horizontal component
v <- rnorm(10) # vertical component
cov2 <- atan2(v,u)
data <- data.frame(coord1=coord1,coord2=coord2,cov1=cov1,cov2=cov2)
d <- prepData(data,coordNames=c("coord1","coord2"),covNames="cov1",
              angleCovs="cov2")
```

---

print.miHMM *Print* miHMM

Description

Print miHMM

Usage

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

Arguments

x	A miHMM object.
...	Currently unused. For compatibility with generic method.

Examples

```
## Not run:
# Extract data and crawl inputs from miExample
obsData <- miExample$obsData
inits <- miExample$inits
err.model <- miExample$err.model

# Fit crawl to obsData
crwOut <- crawlWrap(obsData,theta=c(4,0),fixPar=c(1,1,NA,NA),
                    initial.state=inits,err.model=err.model)

# Fit four imputations
bPar <- miExample$bPar
HMMfits <- MIfitHMM(crwOut,nSims=4,poolEstimates=FALSE,
                   nbStates=2,dist=list(step="gamma",angle="vm"),
                   Par0=bPar$Par,beta0=bPar$beta,delta0=bPar$delta,
                   formula=~cov1+cos(cov2),
                   estAngleMean=list(angle=TRUE),
                   covNames=c("cov1","cov2"))

miHMM <- momentuHMM:::miHMM(list(miSum=MIpool(HMMfits),HMMfits=HMMfits))
print(miHMM)

## End(Not run)
```

---

print.miSum *Print* miSum

Description

Print miSum

Usage

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

Arguments

x	A miSum object.
...	Currently unused. For compatibility with generic method.

Examples

```
## Not run:
# Extract data and crawl inputs from miExample
obsData <- miExample$obsData
inits <- miExample$inits
err.model <- miExample$err.model

# Fit crawl to obsData
crwOut <- crawlWrap(obsData,theta=c(4,0),fixPar=c(1,1,NA,NA),
                    initial.state=inits,err.model=err.model)

# Fit four imputations
bPar <- miExample$bPar
HMMfits <- MIfitHMM(crwOut,nSims=4,poolEstimates=FALSE,
                   nbStates=2,dist=list(step="gamma",angle="vm"),
                   Par0=bPar$Par,beta0=bPar$beta,delta0=bPar$delta,
                   formula=~cov1+cos(cov2),
                   estAngleMean=list(angle=TRUE),
                   covNames=c("cov1","cov2"))

# Pool estimates
miSum <- MIpool(HMMfits)
print(miSum)

## End(Not run)
```

---

print.momentuHMM *Print* momentuHMM

Description

Print momentuHMM

Usage

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

Arguments

x	A momentuHMM object.
...	Currently unused. For compatibility with generic method.

Examples

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

print(m)
```

---

pseudoRes *Pseudo-residuals*

Description

The pseudo-residuals of momentuHMM models, as described in Zucchini and McDonad (2009).

Usage

```
pseudoRes(m, ncores = 1)
```

Arguments

m	A momentuHMM, miHMM, HMMfits, or miSum object.
ncores	number of cores to use for parallel processing

Details

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

A continuity adjustment (adapted from Harte 2017) is made for discrete probability distributions. When the data are near the boundary (e.g. 0 for "pois"; 0 and 1 for "bern"), then the pseudo residuals can be a poor indicator of lack of fit.

For multiple imputation analyses, if m is a miHMM object or a list of momentuHMM objects, then the pseudo-residuals are individually calculated for each model fit. Note that pseudo-residuals for miSum objects (as returned by MIpool) are based on pooled parameter estimates and the means of the data values across all imputations (and therefore may not be particularly meaningful).

Value

If m is a momentuHMM, miHMM, or miSum object, a list of pseudo-residuals for each data stream (e.g., 'stepRes', 'angleRes') is returned. If m is a list of momentuHMM objects, then a list of length length(m) is returned where each element is a list of pseudo-residuals for each data stream.

References

Harte, D. 2017. HiddenMarkov: Hidden Markov Models. R package version 1.8-8.

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

Examples

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

---

setModelName   *Set* `modelName` *for a* `momentuHMM`, `miHMM`, `HMMfits`, *or* `miSum` *object*

Description

Set `modelName` for a `momentuHMM`, `miHMM`, `HMMfits`, or `miSum` object

Usage

```
setModelName(model, modelName)
```

Arguments

`model`	`momentuHMM`, `miHMM`, `HMMfits`, or `miSum` object
`modelName`	Character string providing a name for the model. See `fitHMM` and `MIfitHMM`.

Value

`model` object with new `modelName` field

Examples

```
m <- example$m
mName <- setModelName(m, modelName="example")
```

---

setStateNames   *Set* `stateNames` *for a* `momentuHMM`, `miHMM`, `HMMfits`, *or* `miSum` *object*

Description

Set `stateNames` for a `momentuHMM`, `miHMM`, `HMMfits`, or `miSum` object

Usage

```
setStateNames(model, stateNames)
```

Arguments

`model`	momentuHMM, miHMM, HMMfits, or miSum object
`stateNames`	Character string providing state names for the model. See fitHMM and MIfitHMM.

Value

`model` object with new `stateNames` field

Examples

```
m <- example$m
mName <- setStateNames(m, stateNames=c("encamped","exploratory"))
```

---

simData *Simulation tool*

Description

Simulates data from a (multivariate) hidden Markov model. Movement data can be generated with or without observation error attributable to temporal irregularity or location measurement error.

Usage

```
simData(nbAnimals = 1, nbStates = 2, dist, Par, beta = NULL,
  delta = NULL, formula = ~1, formulaDelta = ~1, covs = NULL,
  nbCovs = 0, spatialCovs = NULL, zeroInflation = NULL,
  oneInflation = NULL, circularAngleMean = NULL, centers = NULL,
  centroids = NULL, obsPerAnimal = c(500, 1500), initialPosition = c(0,
  0), DM = NULL, cons = NULL, userBounds = NULL, workBounds = NULL,
  workcons = NULL, stateNames = NULL, model = NULL, states = FALSE,
  retrySims = 0, lambda = NULL, errorEllipse = NULL)
```

Arguments

`nbAnimals`	Number of observed individuals to simulate.
`nbStates`	Number of behavioural states to simulate.
`dist`	A named list indicating the probability distributions of the data streams. Currently supported distributions are 'bern', 'beta', 'exp', 'gamma', 'lnorm', 'norm', 'pois', 'vm', 'vmConsensus', 'weibull', and 'wrpcauchy'. For example, `dist=list(step='gamma', ang` indicates 3 data streams ('step', 'angle', and 'dives') and their respective probability distributions ('gamma', 'vm', and 'pois').
`Par`	A named list containing vectors of initial state-dependent probability distribution parameters for each data stream specified in `dist`. The parameters should be in the order expected by the pdfs of `dist`, and any zero-mass and/or one-mass

parameters should be the last (if both are present, then zero-mass parameters must preceed one-mass parameters).

If `DM` is not specified for a given data stream, then `Par` is on the natural (i.e., real) scale of the parameters. However, if `DM` is specified for a given data stream, then `Par` must be on the working (i.e., beta) scale of the parameters, and the length of `Par` must match the number of columns in the design matrix. See details below.

`beta` Matrix of regression parameters for the transition probabilities (more information in "Details").

`delta` Initial value for the initial distribution of the HMM. Default: `rep(1/nbStates,nbStates)`. If `formulaDelta` includes covariates, then `delta` must be specified as a k x (`nbStates`-1) matrix, where k is the number of covariates and the columns correspond to states 2:`nbStates`. See details below.

`formula` Regression formula for the transition probability covariates. Default: `~1` (no covariate effect). In addition to allowing standard functions in R formulas (e.g., `cos(cov)`, `cov1*cov2`, `I(cov^2)`), special functions include `cosinor(cov,period)` for modeling cyclical patterns, spline functions (`bs`, `ns`, `bSpline`, `cSpline`, `iSpline`, and `mSpline`), and state- or parameter-specific formulas (see details). Any formula terms that are not state- or parameter-specific are included on all of the transition probabilities.

`formulaDelta` Regression formula for the initial distribution. Default: `~1` (no covariate effect). Standard functions in R formulas are allowed (e.g., `cos(cov)`, `cov1*cov2`, `I(cov^2)`).

`covs` Covariate values to include in the simulated data, as a dataframe. The names of any covariates specified by `covs` can be included in `formula` and/or `DM`. Covariates can also be simulated according to a standard normal distribution, by setting `covs` to `NULL` (the default), and specifying `nbCovs>0`.

`nbCovs` Number of covariates to simulate (0 by default). Does not need to be specified if `covs` is specified. Simulated covariates are provided generic names (e.g., 'cov1' and 'cov2' for `nbCovs=2`) and can be included in `formula` and/or `DM`.

`spatialCovs` List of `RasterLayer-class` objects for spatially-referenced covariates. Covariates specified by `spatialCovs` are extracted from the raster layer(s) based on the simulated location data for each time step (if applicable). The names of the raster layer(s) can be included in `formula` and/or `DM`. Note that `simData` usually takes longer to generate simulated data when `spatialCovs` is specified.

`zeroInflation` A named list of logicals indicating whether the probability distributions of the data streams should be zero-inflated. If `zeroInflation` is `TRUE` for a given data stream, then values for the zero-mass parameters should be included in the corresponding element of `Par`.

`oneInflation` A named list of logicals indicating whether the probability distributions of the data streams should be one-inflated. If `oneInflation` is `TRUE` for a given data stream, then values for the one-mass parameters should be included in the corresponding element of `Par`.

`circularAngleMean`
An optional named list indicating whether to use circular-linear (FALSE) or circular-circular (TRUE) regression on the mean of circular distributions ('vm'

and 'wrpcauchy') for turning angles. For example, `circularAngleMean=list(angle=TRUE)` indicates the angle mean is be estimated for 'angle' using circular-circular regression. Whenever circular-circular regression is used for an angular data stream, a corresponding design matrix (`DM`) must be specified for the data stream, and the previous movement direction (i.e., a turning angle of zero) is automatically used as the reference angle (i.e., the intercept). Default is `NULL`, which assumes circular-linear regression is used for any angular distributions. Any `circularAngleMean` elements corresponding to data streams that do not have angular distributions are ignored. `circularAngleMean` is also ignored for any 'vmConsensus' data streams (because the consensus model is a circular-circular regression model).

`centers` 2-column matrix providing the x-coordinates (column 1) and y-coordinates (column 2) for any activity centers (e.g., potential centers of attraction or repulsion) from which distance and angle covariates will be calculated based on the simulated location data. These distance and angle covariates can be included in `formula` and `DM` using the row names of `centers`. If no row names are provided, then generic names are generated for the distance and angle covariates (e.g., 'center1.dist', 'center1.angle', 'center2.dist', 'center2.angle'); otherwise the covariate names are derived from the row names of `centers` as `paste0(rep(rownames(centers),each=2),c(".dist",".angle"))`. Note that the angle covariates for each activity center are calculated relative to the previous movement direction instead of standard directions relative to the x-axis; this is to allow turning angles to be simulated as a function of these covariates using circular-circular regression.

`centroids` List where each element is a data frame consisting of at least `max(unlist(obsPerAnimal))` rows that provides the x-coordinates ('x') and y-coordinates ('y) for centroids (i.e., dynamic activity centers where the coordinates can change for each time step) from which distance and angle covariates will be calculated based on the simulated location data. These distance and angle covariates can be included in `formula` and `DM` using the names of `centroids`. If no list names are provided, then generic names are generated for the distance and angle covariates (e.g., 'centroid1.dist', 'centroid1.angle', 'centroid2.dist', 'centroid2.angle'); otherwise the covariate names are derived from the list names of `centroids` as `paste0(rep(names(centroids),ea` Note that the angle covariates for each centroid are calculated relative to the previous movement direction instead of standard directions relative to the x-axis; this is to allow turning angles to be simulated as a function of these covariates using circular-circular regression.

`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 obervations generated for each animal are uniformously picked from this interval. Alternatively, `obsPerAnimal` can be specified as a list of length `nbAnimals` with each element providing the number of observations (if single value) or the bounds (if vector of two values) for each individual. Default: `c(500,1500)`.

`initialPosition`

2-vector providing the x- and y-coordinates of the initial position for all animals. Alternatively, `initialPosition` can be specified as a list of length `nbAnimals` with each element a 2-vector providing the x- and y-coordinates of the initial position for each individual. Default: `c(0,0)`.

`DM` An optional named list indicating the design matrices to be used for the probability distribution parameters of each data stream. Each element of `DM` can either be a named list of regression formulas or a "pseudo" design matrix. For example, for a 2-state model using the gamma distribution for a data stream named 'step', `DM=list(step=list(mean=~cov1, sd=~1))` specifies the mean parameters as a function of the covariate 'cov1' for each state. This model could equivalently be specified as a 4x6 "pseudo" design matrix using character strings for the covariate: `DM=list(step=matrix(c(1,0,0,0,'cov1',0,0,0,0,1,0,0,0,'cov1',0,0,0,0,1,0,0,0,0` where the 4 rows correspond to the state-dependent paramaters (mean_1,mean_2,sd_1,sd_2) and the 6 columns correspond to the regression coefficients.

Design matrices specified using formulas allow standard functions in R formulas (e.g., `cos(cov)`, `cov1*cov2`, `I(cov^2)`). Special formula functions include `cosinor(cov,period)` for modeling cyclical patterns, spline functions (`bs`, `ns`, `bSpline`, `cSpline`, `iSpline`, and `mSpline`), `angleFormula(cov,strength)` for the angle mean of circular-circular regression models, and state-specific formulas (see details). Any formula terms that are not state-specific are included on the parameters for all `nbStates` states.

`cons` Deprecated. An optional named list of vectors specifying a power to raise parameters corresponding to each column of the design matrix for each data stream. While there could be other uses, primarily intended to constrain specific parameters to be positive. For example, `cons=list(step=c(1,2,1,1))` raises the second parameter to the second power. Default=NULL, which simply raises all parameters to the power of 1. `cons` is ignored for any given data stream unless `DM` is specified.

`userBounds` An optional named list of 2-column matrices specifying bounds on the natural (i.e, real) scale of the probability distribution parameters for each data stream. For example, for a 2-state model using the wrapped Cauchy ('wrpcauchy') distribution for a data stream named 'angle' with `estAngleMean$angle=TRUE)`, `userBounds=list(angle=matrix(c(-pi,-pi,-1,-1,pi,pi,1,1),4,2,dimnames=list(c("mean_1"` specifies (-1,1) bounds for the concentration parameters instead of the default [0,1) bounds.

`workBounds` An optional named list of 2-column matrices specifying bounds on the working scale of the probability distribution, transition probability, and initial distribution parameters. For each matrix, the first column pertains to the lower bound and the second column the upper bound. For data streams, each element of `workBounds` should be a k x 2 matrix with the same name of the corresponding element of `Par0`, where k is the number of parameters. For transition probability parameters, the corresponding element of `workBounds` must be a k x 2 matrix named "beta", where k=`length(beta0)`. For initial distribution parameters, the corresponding element of `workBounds` must be a k x 2 matrix named "delta", where k=`length(delta0)`. `workBounds` is ignored for any given data stream unless `DM` is also specified.

`workcons` Deprecated. An optional named list of vectors specifying constants to add to the regression coefficients on the working scale for each data stream. Warning: use of `workcons` is recommended only for advanced users implementing unusual parameter constraints through a combination of DM, cons, and workcons. workcons is ignored for any given data stream unless DM is specified.

stateNames
Optional character vector of length nbStates indicating state names.

model
A momentuHMM, miHMM, or miSum 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, states, initialPosition, lambda, errorEllipse, and, if covariate values different from those in the data should be specified, covs, spatialCovs, centers, and centroids.

states
TRUE if the simulated states should be returned, FALSE otherwise (default).

retrySims
Number of times to attempt to simulate data within the spatial extent of spatialCovs. If retrySims=0 (the default), an error is returned if the simulated tracks(s) move beyond the extent(s) of the raster layer(s). Instead of relying on retrySims, in many cases it might be better to simply expand the extent of the raster layer(s) and/or adjust the step length and turning angle probability distributions. Ignored if spatialCovs=NULL.

lambda
Observation rate for location data. If NULL (the default), location data are obtained at regular intervals. Otherwise lambda is the rate parameter of the exponential distribution for the waiting times between successive location observations, i.e., 1/lambda is the expected time between successive location observations. Only the 'step' and 'angle' data streams are subject to temporal irregularity; any other data streams are observed at temporally-regular intervals. Ignored unless a valid distribution for the 'step' data stream is specified.

errorEllipse
List providing the upper bound for the semi-major axis (M; on scale of x- and y-coordinates), semi-minor axis (m; on scale of x- and y-coordinates), and orientation (r; in degrees) of location error ellipses. If NULL (the default), no location measurement error is simulated. If errorEllipse is specified, then each observed location is subject to bivariate normal errors as described in McClintock et al. (2015), where the components of the error ellipse for each location are randomly drawn from runif(1,min(errorEllipse$M),max(errorEllipse$M)), runif(1,min(errorEllipse$m),max(errorEllipse$m)), and runif(1,min(errorEllipse$r),max(
If only a single value is provided for any of the error ellipse elements, then the corresponding component is fixed to this value for each location. Only the 'step' and 'angle' data streams are subject to location measurement error; any other data streams are observed without error. Ignored unless a valid distribution for the 'step' data stream is specified.

Details

- x- and y-coordinate location data are generated only if valid 'step' and 'angle' data streams are specified. Vaild distributions for 'step' include 'gamma', 'weibull', 'exp', and 'lnorm'. Valid distributions for 'angle' include 'vm' and 'wrpcauchy'. If only a valid 'step' data stream is specified, then only x-coordinates are generated.
- If DM is specified for a particular data stream, then the initial values are specified on the working (i.e., beta) scale of the parameters. The working scale of each parameter is determined by the link function used. The function getParDM is intended to help with obtaining initial values on the working scale when specifying a design matrix and other parameter constraints.

- Simulated data that are temporally regular (i.e., `lambda=NULL`) and without location measurement error (i.e., `errorEllipse=NULL`) are returned as a `momentuHMMData` object suitable for analysis using `fitHMM`.
- Simulated location data that are temporally-irregular (i.e., `lambda>0`) and/or with location measurement error (i.e., `errorEllipse!=NULL`) are returned as a data frame suitable for analysis using `crawlWrap`.
- 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 `formula` 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.
- When covariates are not included in `formulaDelta` (i.e. `formulaDelta=~1`), then `delta` is specified as a vector of length `nbStates` that sums to 1. When covariates are included in `formulaDelta`, then `delta` must be specified as a k x (`nbStates`-1) matrix of working parameters, where k is the number of regression coefficients and the columns correspond to states 2:`nbStates`. For example, in a 3-state HMM with `formulaDelta=~cov1+cov2`, the matrix `delta` has three rows (intercept + two covariates) and 2 columns (corresponding to states 2 and 3). The initial distribution working parameters are transformed to the real scale as `exp(covsDelta*Delta)/rowSums(exp(covsDelta*Delta))`, where `covsDelta` is the N x k design matrix, `Delta=cbind(rep(0,k),delta)` is a k x `nbStates` matrix of working parameters, and `N=length(unique(data$ID))`.
- State-specific formulas can be specified in `DM` using special formula functions. These special functions can take the names `paste0("state",1:nbStates)` (where the integer indicates the state-specific formula). For example, `DM=list(step=list(mean=~cov1+state1(cov2),sd=~cov2+state2(cov1)))` includes `cov1` on the mean parameter for all states, `cov2` on the mean parameter for state 1, `cov2` on the sd parameter for all states, and `cov1` on the sd parameter for state 2.
- State- and parameter-specific formulas can be specified for transition probabilities in `formula` using special formula functions. These special functions can take the names `paste0("state",1:nbStates)` (where the integer indicates the current state from which transitions occur), `paste0("toState",1:nbStates)` (where the integer indicates the state to which transitions occur), or `paste0("betaCol",nbStates*(nbStates-1))` (where the integer indicates the column of the `beta` matrix). For example with `nbStates=3`, `formula=~cov1+betaCol1(cov2)+state3(cov3)+toState1(cov4)` includes `cov1` on all transition probability parameters, `cov2` on the `beta` column corresponding to the transition from state 1->2, `cov3` on transition probabilities from state 3 (i.e., `beta` columns corresponding to state transitions 3->1 and 3->2), and `cov4` on transition probabilities to state 1 (i.e., `beta` columns corresponding to state transitions 2->1 and 3->1).
- Cyclical relationships (e.g., hourly, monthly) may be simulated using the `consinor(x,period)` special formula function for covariate `x` and sine curve period of time length `period`. For example, if the data are hourly, a 24-hour cycle can be simulated using `~cosinor(cov1,24)`, where the covariate `cov1` is a repeating series of integers `0,1,...,23,0,1,...,23,0,1,...` (note that `simData` will not do this for you, the appropriate covariate must be specified using the `covs` argument; see example below). The `cosinor(x,period)` function converts `x` to 2 covariates `cosinorCos(x)=cos(2*pi*x/period)` and `consinorSin(x)=sin(2*pi*x/period` for inclusion in the model (i.e., 2 additional parameters per state). The amplitude of the sine wave is thus `sqrt(B_cos^2 + B_sin^2)`, where `B_cos` and `B_sin` are the working parameters correponding to `cosinorCos(x)` and `cosinorSin(x)`, respectively (e.g., see Cornelissen

2014).

When the circular-circular regression model is used, the special function `angleStrength(cov,strength,by)` can be used in `DM` for the mean of angular distributions (i.e. 'vm', 'vmConsensus', and 'wrpcauchy'), where `cov` is an angle covariate (e.g. wind direction), `strength` is a positive real covariate (e.g. wind speed), and `by` is an optional factor variable for individual- or group-level effects (e.g. ID, sex). This allows angle covariates to be weighted based on their strength or importance at time step t as in Rivest et al. (2016).

- 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

If the simulated data are temporally regular (i.e., `lambda=NULL`) with no measurement error (i.e., `errorEllipse=NULL`), an object `momentuHMMData`, i.e., a dataframe of:

`ID` The ID(s) of the observed animal(s)

`...` Data streams as specified by `dist`

`x` Either easting or longitude (if data streams include valid non-negative distribution for 'step')

`y` Either norting or latitude (if data streams include valid non-negative distribution for 'step')

`...` Covariates (if any)

If simulated location data are temporally irregular (i.e., `lambda>0`) and/or include measurement error (i.e., `errorEllipse!=NULL`), a dataframe of:

`time` Numeric time of each observed (and missing) observation

`ID` The ID(s) of the observed animal(s)

`x` Either easting or longitude observed location

`y` Either norting or latitude observed location

`...` Data streams that are not derived from location (if applicable)

`...` Covariates at temporally-regular true (`mux`,`muy`) locations (if any)

`mux` Either easting or longitude true location

`muy` Either norting or latitude true location

`error_semimajor_axis` error ellipse semi-major axis (if applicable)

`error_semiminor_axis` error ellipse semi-minor axis (if applicable)

`error_ellipse_orientation` error ellipse orientation (if applicable)

`ln.sd.x` log of the square root of the x-variance of bivariate normal error (if applicable; required for error ellipse models in `crawlWrap`) ln.sd.y   log of the square root of the y-variance of bivariate normal error (if applicable; required for error ellipse models in crawlWrap)

error.corr   correlation term of bivariate normal error (if applicable; required for error ellipse models in crawlWrap)

References

Cornelissen, G. 2014. Cosinor-based rhythmometry. Theoretical Biology and Medical Modelling 11:16.

McClintock BT, London JM, Cameron MF, Boveng PL. 2015. Modelling animal movement using the Argos satellite telemetry location error ellipse. Methods in Ecology and Evolution 6(3):266-277.

Rivest, LP, Duchesne, T, Nicosia, A, Fortin, D, 2016. A general angular regression model for the analysis of data on animal movement in ecology. Journal of the Royal Statistical Society: Series C (Applied Statistics), 65(3):445-463.

See Also

prepData, simObsData

Examples

```
# 1. Pass a fitted model to simulate from
# (m is a momentuHMM 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) # mean_1, mean_2, sd_1, sd_2, zeromass_1, zeromass_2
anglePar <- c(pi,0,0.5,2) # mean_1, mean_2, concentration_1, concentration_2
omegaPar <- c(1,10,10,1) # shape1_1, shape1_2, shape2_1, shape2_2
stepDist <- "gamma"
angleDist <- "vm"
omegaDist <- "beta"
data <- simData(nbAnimals=4,nbStates=2,dist=list(step=stepDist,angle=angleDist,omega=omegaDist),
                Par=list(step=stepPar,angle=anglePar,omega=omegaPar),nbCovs=2,
                zeroInflation=list(step=TRUE),
                obsPerAnimal=obsPerAnimal)

# 3. Include covariates
# (note that it is useless to specify "nbCovs", which are overruled
# by the number of columns of "cov")
cov <- data.frame(temp=log(rnorm(500,20,5)))
stepPar <- c(log(10),0.1,log(100),-0.1,log(5),log(25)) # working scale parameters for step DM
anglePar <- c(pi,0,0.5,2) # mean_1, mean_2, concentration_1, concentration_2
stepDist <- "gamma"
angleDist <- "vm"
data <- simData(nbAnimals=2,nbStates=2,dist=list(step=stepDist,angle=angleDist),
                Par=list(step=stepPar,angle=anglePar),
                DM=list(step=list(mean=~temp,sd=~1)),
```

```
                covs=cov,
                obsPerAnimal=obsPerAnimal)

# 4. Include example 'forest' spatial covariate raster layer
# nbAnimals and obsPerAnimal kept small to reduce example run time
spatialCov<-list(forest=forest)
data <- simData(nbAnimals=1,nbStates=2,dist=list(step=stepDist,angle=angleDist),
                Par=list(step=c(100,1000,50,100),angle=c(0,0,0.1,5)),
                beta=matrix(c(5,-10,-25,50),nrow=2,ncol=2,byrow=TRUE),
                formula=~forest,spatialCovs=spatialCov,
                obsPerAnimal=250,states=TRUE,
                retrySims=100)

# 5. Specify design matrix for 'omega' data stream
# natural scale parameters for step and angle
stepPar <- c(1,10,1,5) # shape_1, shape_2, scale_1, scale_2
anglePar <- c(pi,0,0.5,0.7) # mean_1, mean_2, concentration_1, concentration_2

# working scale parameters for omega DM
omegaPar <- c(log(1),0.1,log(10),-0.1,log(10),-0.1,log(1),0.1)

stepDist <- "weibull"
angleDist <- "wrpcauchy"
omegaDist <- "beta"

data <- simData(nbStates=2,dist=list(step=stepDist,angle=angleDist,omega=omegaDist),
                Par=list(step=stepPar,angle=anglePar,omega=omegaPar),nbCovs=2,
                DM=list(omega=list(shape1=~cov1,shape2=~cov2)),
                obsPerAnimal=obsPerAnimal,states=TRUE)

# 6. Include temporal irregularity and location measurement error
lambda <- 2 # expect 2 observations per time step
errorEllipse <- list(M=50,m=25,r=180)
obsData <- simData(model=m,obsPerAnimal=obsPerAnimal,
                   lambda=lambda, errorEllipse=errorEllipse)

# 7. Cosinor and state-dependent formulas
nbStates<-2
dist<-list(step="gamma")
Par<-list(step=c(100,1000,50,100))

# include 24-hour cycle on all transition probabilities
# include 12-hour cycle on transitions from state 2
formula=~cosinor(hour24,24)+state2(cosinor(hour12,12))

# specify appropriate covariates
covs<-data.frame(hour24=0:23,hour12=0:11)

beta<-matrix(c(-1.5,1,1,NA,NA,-1.5,-1,-1,1,1),5,2)
# row names for beta not required but can be helpful
rownames(beta)<-c("(Intercept)",
                  "cosinorCos(hour24, 24)",
                  "cosinorSin(hour24, 24)",
```

```
                  "cosinorCos(hour12, 12)",
                  "cosinorSin(hour12, 12)")
data.cos<-simData(nbStates=nbStates,dist=dist,Par=Par,
                  beta=beta,formula=formula,covs=covs)

# 8. Piecewise constant B-spline on step length mean and angle concentration
library(splines2)
nObs <- 1000 # length of simulated track
cov <- data.frame(time=1:nObs) # time covariate for splines
dist <- list(step="gamma",angle="vm")
stepDM <- list(mean=~bSpline(time,df=3,degree=0),sd=~1)
angleDM <- list(mean=~1,concentration=~bSpline(time,df=3,degree=0))
DM <- list(step=stepDM,angle=angleDM)
Par <- list(step=c(log(1000),1,-1,log(100)),angle=c(0,log(10),2,-5))

data.spline<-simData(obsPerAnimal=nObs,nbStates=1,dist=dist,Par=Par,DM=DM,covs=cov)

# 9. Initial state (delta) based on covariate
nObs <- 100
dist <- list(step="gamma",angle="vm")
Par <- list(step=c(100,1000,50,100),angle=c(0,0,0.01,0.75))

# create sex covariate
cov <- data.frame(sex=factor(rep(c("F","M"),each=nObs))) # sex covariate
formulaDelta <- ~ sex + 0

# Female begins in state 1, male begins in state 2
delta <- matrix(c(-100,100),2,1,dimnames=list(c("sexF","sexM"),"state 2"))

data.delta<-simData(nbAnimals=2,obsPerAnimal=nObs,nbStates=2,dist=dist,Par=Par,
                    delta=delta,formulaDelta=formulaDelta,covs=cov)
```

---

simObsData *Observation error simulation tool*

Description

Simulates observed location data subject to temporal irregularity and/or location measurement error

Usage

```
simObsData(data, lambda, errorEllipse)
```

Arguments

data A momentuHMMData object with necessary field 'x' (easting/longitudinal coordinates) and 'y' (northing/latitudinal coordinates) `lambda` Observation rate for location data. If `NULL`, location data are kept at temporally-regular intervals. Otherwise `lambda` is the rate parameter of the exponential distribution for the waiting times between successive location observations, i.e., `1/lambda` is the expected time between successive location observations. Only the 'step' and 'angle' data streams are subject to temporal irregularity; any other data streams are kept at temporally-regular intervals. Ignored unless a valid distribution for the 'step' data stream is specified.

`errorEllipse` List providing the bounds for the semi-major axis (`M`; on scale of x- and y-coordinates), semi-minor axis (`m`; on scale of x- and y-coordinates), and orientation (`r`; in degrees) of location error ellipses. If `NULL`, no location measurement error is simulated. If `errorEllipse` is specified, then each observed location is subject to bivariate normal errors as described in McClintock et al. (2015), where the components of the error ellipse for each location are randomly drawn from `runif(1,min(errorEllipse$M),max(errorEllipse$M))`, `runif(1,min(errorEllipse$m),max` and `runif(1,min(errorEllipse$r),max(errorEllipse$r))`. If only a single value is provided for any of the error ellipse elements, then the corresponding component is fixed to this value for each location. Only the 'step' and 'angle' data streams are subject to location measurement error; any other data streams are observed without error. Ignored unless a valid distribution for the 'step' data stream is specified.

Details

Simulated location data that are temporally-irregular (i.e., `lambda>0`) and/or with location measurement error (i.e., `errorEllipse!=NULL`) are returned as a data frame suitable for analysis using `crawlWrap`.

Value

A dataframe of:

`time` Numeric time of each observed (and missing) observation

`ID` The ID(s) of the observed animal(s)

`x` Either easting or longitude observed location

`y` Either norting or latitude observed location

`...` Data streams that are not derived from location (if applicable)

`...` Covariates at temporally-regular true (`mux`,`muy`) locations (if any)

`mux` Either easting or longitude true location

`muy` Either norting or latitude true location

`error_semimajor_axis`
error ellipse semi-major axis (if applicable)

`error_semiminor_axis`
error ellipse semi-minor axis (if applicable)

`error_ellipse_orientation`
error ellipse orientation (if applicable)

`ln.sd.x`	log of the square root of the x-variance of bivariate normal error (if applicable; required for error ellipse models in `crawlWrap`)
`ln.sd.y`	log of the square root of the y-variance of bivariate normal error (if applicable; required for error ellipse models in `crawlWrap`)
`error.corr`	correlation term of bivariate normal error (if applicable; required for error ellipse models in `crawlWrap`)

References

McClintock BT, London JM, Cameron MF, Boveng PL. 2015. Modelling animal movement using the Argos satellite telemetry location error ellipse. Methods in Ecology and Evolution 6(3):266-277.

See Also

`crawlWrap`, `prepData`, `simData`

Examples

```
# extract momentuHMMData example
data <- example$m$data
lambda <- 2 # expect 2 observations per time step
errorEllipse <- list(M=c(0,50),m=c(0,50),r=c(0,180))
obsData1 <- simObsData(data,lambda=lambda,errorEllipse=errorEllipse)

errorEllipse <- list(M=50,m=50,r=180)
obsData2 <- simObsData(data,lambda=lambda,errorEllipse=errorEllipse)
```

`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 `momentuHMM` 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 momentuHMM object (as returned by fitHMM), automatically loaded with the package
m <- example$m

sp <- stateProbs(m)
```

---

stationary *Stationary state probabilities*

Description

Calculates the stationary probabilities of each state based on covariate values.

Usage

```
stationary(model, covs)
```

Arguments

model	momentuHMM, miHMM, or miSum object
covs	Either a data frame or a design matrix of covariates. If covs is not provided, then the stationary probabilties are calculated based on the covariate data for each time step.

Value

Matrix of stationary state probabilities. Each row corresponds to a row of covs, and each column corresponds to a state.

Examples

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

# data frame of covariates
stationary(m, covs = data.frame(cov1 = 0, cov2 = 0))

# design matrix (each column corresponds to row of m$mle$beta)
stationary(m, covs = matrix(c(1,0,cos(0)),1,3))
```

`summary.momentuHMMData` *Summary* `momentuHMMData`

Description

Summary `momentuHMMData`

Usage

```
## S3 method for class 'momentuHMMData'
summary(object, dataNames = c("step", "angle"),
  animals = NULL, ...)
```

Arguments

`object`	A `momentuHMMData` object.
`dataNames`	Names of the variables to summarize. Default is `dataNames=c("step","angle")`.
`animals`	Vector of indices or IDs of animals for which data will be summarized. Default: `NULL` ; data for all animals are summarized.
`...`	Currently unused. For compatibility with generic method.

Examples

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

summary(data,dataNames=c("step","angle","cov1","cov2"))
```

`timeInStates` *Calculate proportion of time steps assigned to each state (i.e. "activity budgets")*

Description

Calculate proportion of time steps assigned to each state (i.e. "activity budgets")

Usage

```
timeInStates(m, by = NULL, alpha = 0.95, ncores = 1)

## S3 method for class 'momentuHMM'
timeInStates(m, by = NULL, alpha = 0.95, ncores = 1)

## S3 method for class 'HMMfits'
timeInStates(m, by = NULL, alpha = 0.95, ncores = 1)

## S3 method for class 'miHMM'
timeInStates(m, by = NULL, alpha = 0.95, ncores = 1)
```

Arguments

m	A momentuHMM, miHMM, or HMMfits object.
by	A character vector indicating any groupings by which to calculate the proportions, such as individual ("ID") or group-level (e.g. sex or age class) covariates. Default is NULL (no groupings are used).
alpha	Significance level for calculating confidence intervals of pooled estimates. Default: 0.95. Ignored unless m is a miHMM or HMMfits object.
ncores	Number of cores to use for parallel processing. Default: 1 (no parallel processing). Ignored unless m is a miHMM or HMMfits object.

Value

If m is a momentuHMM object, a data frame containing the estimated activity budgets for each state (grouped according to by). If m is a miHMM or HMMfits object, a list containing the activity budget estimates, standard errors, lower bounds, and upper bounds across all imputations.

Examples

```
# m is a momentuHMM object (as returned by fitHMM), automatically loaded with the package
m <- example$m
timeInStates(m)
timeInStates(m, by = "ID")
```

---

trMatrix_rcpp *Transition probability matrix*

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` *Turning angle*

Description

Used in `prepData` and `simData`.

Usage

```
turnAngle(x, y, z, type = "UTM", angleCov = FALSE)
```

Arguments

`x`	First point
`y`	Second point
`z`	Third point
`type`	`'UTM'` if easting/northing provided (the default), `'LL'` if longitude/latitude.
`angleCov`	logical indicating to not return NA when x=y or y=z. Default: FALSE (i.e. NA is returned if x=y or y=z).

Value

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

If `type='LL'` then turning angle is calculated based on initial bearings using `bearing`.

Examples

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

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 momentuHMM 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, circularAngleMean,
  consensus, stationary, cons, fullDM, DMind, workcons, nbObs, dist, Bndind, nc,
  meanind, covsDelta, workBounds)
```

Arguments

`wpar` Vector of working parameters.

`bounds` Named list of 2-column matrices specifying bounds on the natural (i.e, real) scale of the probability distribution parameters for each data stream.

`parSize` Named list indicating the number of natural parameters of the data stream probability distributions

`nbStates` The number of states of the HMM.

`nbCovs` The number of beta covariates.

`estAngleMean` Named list indicating whether or not to estimate the angle mean for data streams with angular distributions ('vm' and 'wrpcauchy').

`circularAngleMean` Named list indicating whether to use circular-linear (FALSE) or circular-circular (TRUE) regression on the mean of circular distributions ('vm' and 'wrpcauchy') for turning angles.

`consensus` Named list indicating whether to use the circular-circular regression consensus model

`stationary` `FALSE` if there are covariates. If TRUE, the initial distribution is considered equal to the stationary distribution. Default: `FALSE`.

`cons` Named list of vectors specifying a power to raise parameters corresponding to each column of the design matrix for each data stream.

`fullDM` Named list containing the full (i.e. not shorthand) design matrix for each data stream.

`DMind` Named list indicating whether `fullDM` includes individual- and/or temporal-covariates for each data stream specifies (-1,1) bounds for the concentration parameters instead of the default [0,1) bounds.

`workcons` Named list of vectors specifying constants to add to the regression coefficients on the working scale for each data stream.

`nbObs` Number of observations in the data.

`dist` Named list indicating the probability distributions of the data streams.

`Bndind` Named list indicating whether `DM` is NULL with default parameter bounds for each data stream.

`nc` indicator for zeros in fullDM

`meanind` index for circular-circular regression mean angles with at least one non-zero entry in fullDM

`covsDelta` data frame containing the delta model covariates (if any)

`workBounds` named list of 2-column matrices specifying bounds on the working scale of the probability distribution, transition probability, and initial distribution parameters

Value

A list of:

...	Matrices containing the natural parameters for each data stream (e.g., 'step', 'angle', etc.)
beta	Matrix of regression coefficients of the transition probabilities
delta	Initial distribution

Examples

```
## Not run:
m<-example$m
nbStates <- 2
nbCovs <- 2
parSize <- list(step=2,angle=2)
par <- list(step=c(t(m$mle$step)),angle=c(t(m$mle$angle)))
bounds <- m$conditions$bounds
beta <- matrix(rnorm(6),ncol=2,nrow=3)
delta <- c(0.6,0.4)

#working parameters
wpar <- momentuHMM:::n2w(par,bounds,beta,log(delta[-1]/delta[1]),nbStates,
m$conditions$estAngleMean,NULL,m$conditions$cons,m$conditions$workcons,m$conditions$Bndind)

#natural parameter
p <-   momentuHMM:::w2n(wpar,bounds,parSize,nbStates,nbCovs,m$conditions$estAngleMean,
m$conditions$circularAngleMean,lapply(m$conditions$dist,function(x) x=="vmConsensus"),
m$conditions$stationary,m$conditions$cons,m$conditions$fullDM,
m$conditions$DMind,m$conditions$workcons,1,m$conditions$dist,m$conditions$Bndind,
matrix(1,nrow=length(unique(m$data$ID)),ncol=1),covsDelta=m$covsDelta,
workBounds=m$conditions$workBounds)

## End(Not run)
```

XBloop_rcpp *Get XB*

Description

Loop for computation of design matrix (X) times the working scale parameters (B). Written in C++. Used in w2n.

Usage

```
XBloop_rcpp(DM, Xvec, nbObs, nr, nc, circularAngleMean, consensus, rindex,
  cindex, nbStates)
```

Arguments

DM	design matrix
Xvec	working parameters
nbObs	number of observations
nr	number of rows in design matrix
nc	number of column in design matrix
circularAngleMean	indicator for whether or not circular-circular regression model
consensus	indicator for whether or not circular-circular regression consensus model
rindex	row index for design matrix
cindex	column index for design matrix
nbStates	number of states

Value

XB matrix

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